11th Indo-Pacific Fish Conference
Australian Society for Fish Biology Conference
AUCKLAND 2023

11th Indo-Pacific Fish Conference (IPFC) and Annual Conference of the Australian Society for Fish Biology

Conference Handbook

UNIVERSITY OF AUCKLAND
Waipapa Taumata Rau
NEW ZEALAND

AUSTRALIAN SOCIETY for FISH BIOLOGY

Contents

Welcome

Nau mai, Haere mai, Welcome

It is a pleasure and honour to welcome you all to the joint conference of the 11th Indo-Pacific Fishes Conference and the Annual Meeting of the Australian Society for Fish Biology. We have been looking forward to hosting this conference for quite some time – indeed it was first planned for 2021. It has been a long wait, but the opportunity to meet again has arrived.

We are very excited by the attendance and the diversity of the conference programme. Over 500 people have registered for the conference, with attendees coming from all around the world. The conference programme will run over five full days across five concurrent sessions, and includes around 400 oral presentations and 100 posters. Major social events will include our Welcome Ceremony at the Auckland Museum on the first evening of the conference, a catered Poster Session on Tuesday, and the Conference Dinner at the Pullman Hotel on Friday. The Owen Glenn Conference Centre, here at the University of Auckland, offers outstanding space for the conference, and to meet old and new friends during the morning and afternoon teas and lunches.

Have a wonderful time in Auckland. We hope you can find some time to explore the vibrant city, and adjacent destinations on our doorstep such as Waiheke Island, Tiritiri Matangi Island, etc. There is a diversity of restaurants, bars and delightful places to explore within a short distance of the conference venue. We are confident that you will find the joint conference of the 11th IPFC – ASFB Annual Meeting to be an enriching and inspirational event.

Ngā mihi nui

2023 Joint IPFC – ASFB Conference Organising Committee

Gold Sponsors

Auckland Museum

**SEE THE HISTORY.
HEAR THE STORIES.
FEEL THE PASSION.**

SPECIAL OFFERS AT AUCKLAND MUSEUM FOR DELEGATES OF THE INDO-PACIFIC FISH CONFERENCE:

- General Museum admission $20 – save 30%.
- Gallery Highlights Tour $14 – save 30%
- Maori cultural performance $27 – save 10%
- 10% discount at the Museum Store

Present your conference lanyard or show this advertisement at the Museum ticket desks/Museum store.

Terms and conditions: Offers valid 20-30 November 2023. Cannot be combined with any other offer. Discounts are single-use only. Valid for presenting delegate only (no guests).

Fisheries Research and Development Corporation

Proudly supporting the Australian Society for Fish Biology

2023 Indo-Pacific Fish Conference

Student Function event sponsor

We invest in research, development and extension activities to increase economic, social and environmental benefits for Australian fishing and aquaculture and the wider community.

Find out more about our work at **frdc.com.au**

NIWA

Silver Sponsor

Tourism New Zealand

Bronze Sponsor

echoview
SOUND KNOWLEDGE

evident
analytical testing systems & supplies

NEOGEN®

ViewPoint
Behavior Technology

WILDERLAB
Discovery through DNA

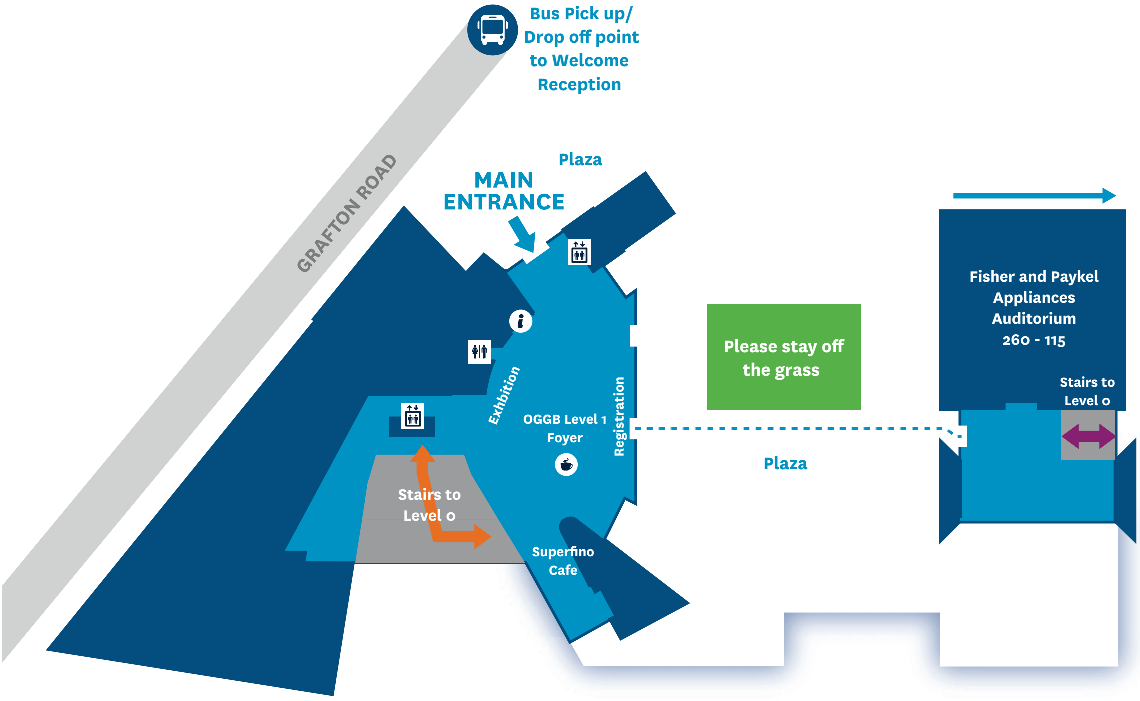
WILDLIFE
COMPUTERS

Poster Function Sponsor

Oceania Chondrichthyan Society

Conference Venue

Sir Owen G Glenn Building
12 Grafton Road, Auckland CBD, Auckland 1010



Conference WIFI

Please select the UoA-Guest-WiFi network:

Username: *ipfc11-asfb@wifi.co.nz*
Password: *JQ4f3UWq*
Or
Username: *ipfc23-asfb@wifi.co.nz*
Password: *EdDHrlrD*

Social Functions

20 November 2023 Welcome Reception (**prior RSVP required)
Auckland Museum
Parnell, Auckland 1010
Return Transport will be provided or 18 mins by walk

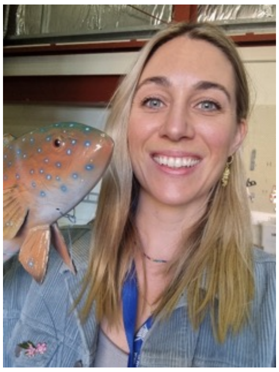
21 November 2023 Poster Function
(Sponsored by Oceania Chondrichthyan Society)
OGGB Level 0 Foyer

22 November 2023 Student Function
(Sponsored by Fisheries Research and Development Corporation)
OGGB Level 1 Foyer + Superfino Café

24 November 2023 Conference Dinner (**prior RSVP required)
Pullman Hotel
Corner Waterloo Quadrant &, Princes Street, Auckland 1010, New Zealand
10 mins by walk

Keynote Speaker

Dr. Emily Lester



Dr Emily Lester is a Fulbright Postdoctoral Scholar at the University of Hawai'i. She received her B.Sc. in Biology from the University of York and her M.Sc. and PhD from the University of Western Australia. Dr Lester's research seeks to understand how humans are inadvertently changing marine animal behaviour and fundamentally re-structuring marine systems. To do this, much of her work uses small-scale field-based experimental approaches to manipulate and explore ecological mechanisms, which are otherwise difficult to observe in the wild. She then tests predictions that emerge from this work over larger spatial scales (100s - 1000s km) in complex systems using natural experiments. Recently, her work has focused on how we can leverage the ecological insights from this work to develop conservation tools that can assess coral reef ecosystem function after disturbances events and subsequent recovery. She has been a member of the Australian Society for Fish Biology for ~5 years and is the recipient of the Australian Society for Fish Biology Early Career Travel Award.

Title:

Investigating predator-prey interactions in coral reefs: how do insights from small scale experiments manifest over reef-wide scales?

Abstract

"Relative influence of predators, competitors and seascape heterogeneity on behaviour and abundance of coral reef mesopredators"
Predators are a key determinant of ecosystem structure, impacting energy flows and nutrient cycling through both consuming prey and by inducing trait responses in prey species that mitigate predation risk. Determining the influence of predators on community dynamics is particularly challenging in coral reefs, as the dynamic landscape provides a complex backdrop against which interactions between many predator and prey species play out. Within these complex seascapes, reef sharks are the most conspicuous predators, but assessing their impact on lower trophic levels is a difficult

task. This is primarily due to their large size and mobility, which renders them unsuitable for controlled experiments. One solution to this problem involves using life-size models of reef sharks and other predatory taxa in small-scale experiments. Through this approach, we demonstrated that the behavioral responses of reef fishes to an approaching model reef shark were similar to that of an approaching human, both of which are large-bodied predators in coral reef ecosystems. Subsequently, we expanded upon these experiments to examine whether sharks could alter the behaviour of species that occupy lower trophic levels over larger, reef-wide spatial scales. To do this, we used baited remote underwater video systems (BRUVs) and determined that short term (minutes) behavioural modifications in response to sharks did not persist over longer timeframes (hours). Instead, the number of similar-sized teleost competitors and surrounding habitat features were the strongest drivers of behavioural metrics measured during BRUVs deployments. We suggest that for most fishes, the predatory threat posed by highly mobile species, such as sharks, is likely to be sporadic and transitory, whereas competition is ubiquitous and ever present. Finally, we used remote sensing techniques to measure fluctuations in reef halos – bare sand rings surrounding coral patch reefs where resident herbivores have denuded the seafloor as they shelter from predators in the nearby reef. These halo patterns have the potential to serve as rapid snapshots of the strength of species interactions that take place on coral reefs. Although these patterns form in places with higher abundance of predators and persist over many years, their size fluctuates on a seasonal basis. This is an important consideration when drawing conclusions regarding fish community composition from halo size, as the ecological signals provided by halos may fluctuate over seasonal scales. Integrating small-scale experiments and large-scale approaches demonstrates the nuanced, context-dependent nature of interactions between predatory and prey species in diverse and complex coral reef ecosystems. Ultimately, this combination of approaches provides a more holistic understanding of predator-prey interactions in coral reefs.

Dr. Jennifer Caselle

Dr. Jenn Caselle is a Research Professor with the Marine Science Institute at University of California Santa Barbara. She received her B.S. in Zoology from U.C. Berkeley and her PhD in Marine Ecology from U.C. Santa Barbara. Dr. Caselle’s research is broadly focused on the ecology of coastal marine organisms, their role in nearshore ecosystems, and the response of these ecosystems to environmental change and human impacts.. She currently splits her time in both coral reef and kelp forest ecosystems studying community dynamics, recruitment and larval dispersal and movement patterns of fishes, including top predators. Through these research themes, she has been closely involved in design and monitoring of Marine Protected Areas, in California and globally. Dr. Caselle designed and implemented a large-scale, field-based monitoring program of kelp forests in the California current ecosystem with goals of assessing long-term changes due to climate and anthropogenic impacts. This program has become the basis of Marine Protected Area monitoring throughout California and the US West coast.

Title:
Moving beyond movement – how insights from fish movements can inform effective conservation planning and fisheries management

Abstract

Understanding the movement ecology of fishes can provide insights well beyond organismal-level physiology and behavior. Several frameworks have recently been developed to unify movement ecology and the field is rapidly expanding with the development of new technologies for tracking aquatic organisms. Along with this, there is a parallel and growing need for better conservation and management of many species. In this talk I will discuss how movement studies across spatial scales, can inform conservation and management efforts. I will draw examples primarily from decades of study at the remote Palmyra atoll, in the Central Pacific using integrative methods including telemetry, biologging, surveys, molecular tools, and simulation modelling. I will touch on incorporating movement ecology to improve stock assessments, understand predator-prey and competitive interactions, the consequences of protecting predators, and informing development of MPAs, including the recent push to implement large 'blue-water' spatial protections. This talk will highlight the pivotal role of fish telemetry and movement ecology in advancing science, promoting sustainable fisheries management, and conserving aquatic ecosystems.

Tony Smith

Tony completed a PhD in fisheries science at the University of British Columbia, Canada, in 1979. He had a long career in CSIRO Fisheries in Hobart, Tasmania. His research focus included population dynamics of exploited species, harvest strategies, ecological risk assessment, ecosystem-based fisheries management, and management strategy evaluation. He has provided advice on fisheries management, not only in Australia but also internationally, including through the FAO, the Marine Stewardship Council, and to governments in the US, Canada, the EU, New Zealand, South Africa, Namibia, Ecuador and Chile. Career highlights include a Centenary of Federation Medal in 2003, appointment as a Member of the Order of Australia in 2011, winner of the Swedish Seafood Award in 2012, and recipient of the K Radway Allen Award in 2022. He was an Affiliate Professor at the University of Washington from 2013-2017 and an Adjunct Professor at the University of Tasmania from 2016-2021. He has published well over

100 papers in peer reviewed scientific journals, including in Nature and Science. He has over 17,000 lifetime citations and a current h-index of 64. Tony retired from CSIRO in 2016 but continues to provide advice on fisheries science and management within Australia.

Title:
Fishery harvest strategies in a dynamic and complex world

Abstract

Fishery harvest strategies, involving formal and pre-agreed approaches to monitoring, assessment and decision rules, are widely regarded as the gold standard for sustainable stock management. This approach was first developed several decades ago and was mainly applied to the management of commercial fisheries targeting single species whose status was determined by robust and data-rich stock assessments. Success of the approach led to calls to apply harvest strategies to a wide range of fisheries. In Australia, a formal harvest strategy policy was adopted by the Federal Government in 2006, with most of the States now having adopted similar policies. Challenges have emerged over time, however, in applying this approach to a wider range of fishery types. Some of the complexities include how to deal with multi-species fisheries, multi-sector fisheries (that are targeted not just by commercial fishers, but also by recreational and indigenous fishers), and how to coordinate and harmonize harvest strategies for stocks that span multiple management jurisdictions. Additional complexities arise from trying to manage data-limited fisheries, where model-based stock assessments are not available to determine stock status. With the recent focus on, and increasing evidence of, the impacts of global warming on marine ecosystems, the issue of shifting baselines has also come to the fore in considering how to manage individual species.

This presentation will review recent approaches to dealing with these issues of increased complexity, shifting dynamics, and generally increased uncertainty, in designing and implementing fishery harvest strategies.

IPFC Bleeker Award- Systematics

(To be revealed)

IPFC Bleeker Award- Ecology

(To be revealed)

Special Sessions

Special Session 1 Moving beyond home-ranges: how can we harness fish movement ecology to study, understand and manage ecosystem functioning?

Convenor: Julian Lilkendey (julian.lilkendey@icloud.com); Renato Morais (renato.morais@ephe.psl.eu); Robert Streit (robert.streit1@jcu.edu.au)

Recent advancements in fish tracking methods enable the study of fish movements beyond their home ranges. They unveil novel foraging behaviours, concealed habitat utilization, spawning aggregations, and larval dispersal pathways. These findings provide crucial insights into ecosystem functioning by simultaneously tracking the transfer of energy and nutrients through aquatic systems. With dynamic global changes, trophodynamics may collapse, leading to severe ecological and socio-economic consequences. To prevent this collapse, a comprehensive interdisciplinary framework is needed. This special session welcomes submissions from all fields studying fish movement, aiming to integrate fish movement ecology with research on ecosystem functioning to aid conservation and restoration efforts.

Special Session 2 Facing environmental changes: what are the genetic and epigenetic mechanisms providing resilience in fishes?".

Convenor: Lucrezia Bonzi. (lucrezia.bonzi@gmail.com)

The ability to cope with environmental changes is essential for fish resilience, and one of the key mechanisms allowing fishes to face such variations is acclimation through phenotypic plasticity. Whether acute, developmental or transgenerational, plasticity is usually associated with dynamic changes in transcription regulation and/or epigenetic modifications. This session will showcase the latest findings on the genetic and epigenetic mechanisms involved in fish responses to changing environments, and highlight the links between molecular and physiological approaches. Among others, we will discuss topics such as: the role of gene expression and transcriptional regulation in environmental acclimation, the impact of the environment on the epigenome, and the potential of genetic adaptations and/or epigenetic modifications to enhance fish resilience in a changing planet".

Special Session 3 Building a better future for fish: a symposium on fish-friendly infrastructure

Convenor: Tom Rayner (tom.rayner@dpi.nsw.gov.au); Craig Boys (craig.boys@dpi.nsw.gov.au); Rod Price (rodney.price@dpi.nsw.gov.au)

This symposium will promote collaboration and innovation in designing and implementing water infrastructure that protects and preserves biodiversity. It will unite international experts from science, engineering, policy, and social research to explore four themes: safe waterways, engineering for diversity, policy to action, and building stakeholder support. Leading experts will deliver talks summarizing current research, manufacturing and implementation, followed by a Q&A panel discussion. Attendees will gain a deeper understanding of the challenges and opportunities in this field, by exploring solutions from around the world.

Special Session 4 The evolution and ecology of fishes: assessing traits and functions in a changing world

Convenors: Dr. Jennifer Donelson (jennifer.donelson@my.jcu.edu.au) & Dr. Christopher R. Hemingson (christopher.hemingson@austin.utexas.edu)

Fishes possess an incredible diversity of morphologies, behaviors, and life histories. While exciting to study, it can be difficult to make comparisons and generalities across such a broad swathe of life. The study of organisms through the lens of traits allows for comparisons to be made between disparate taxa and ecosystems. However, which traits matter from ecological vs evolutionary perspectives are often a point of contention. In a rapidly changing world, how does evolutionary history affect the current and future evolutionary trajectories of organisms and their ecological interactions? Our goal is to showcase the knowledge gained by studying fish traits and functions, from evolutionary origins, through morphology and genetics, species co-evolution, and ecosystem functions.

Special Session 5 Larval fishes - solving phylogenetic, life-cycle and ecological questions

Convenor Jeff Leis (jeffrey.leis@utas.edu.au)

Most marine bony fishes have a two-phase life history including pelagic larvae that differ in morphology, ecology and habitat from adults. These phases operate in separate evolutionary theatres, and ecologically, effectively function as separate species. Larval morphological features provide characters for phylogenetic analysis and aspects of life history are determined during the larval phase, including recruitment and scale of genetic and demographic connectivity. Although larval survival is necessary for persistence of species, larvae are often neglected by researchers and managers focused on adults. This session will address many of the unanswered questions about the pelagic larval phase of Indo-Pacific fishes.

Special Session 7 Fish and fishery data to inform marine sanctuary design and planning

Convenor: Jordan Goetze (jordan.goetze@dbca.wa.gov.au)

The processes and data that inform marine conservation planning often vary on a case-by-case basis. With parallel processes occurring globally there is opportunity to contrast and compare approaches across a broad range of countries. This session aims to facilitate knowledge sharing on transdisciplinary data used to inform conservation planning, ranging from First Nations cultural information, to socio-economic analysis, to population models of fished species. We will ask each presenter to summarise how their research has informed the planning process and what they think are the most pressing research gaps on a final slide.

Special Session 8 Fish sensory ecology: new techniques and approaches

Convenor: Lucille Chapuis (lucille.chapuis@bristol.ac.uk)

Fishes rely on sensory systems to detect, interpret, and respond to information available in their environment: vision, audition, chemoreception, electroreception and mechanoreception. An understanding of the processes underlying each of these sensory modalities can be incredibly powerful, as it allows the interpretation of behavioural responses of fish to their (changing) environment. This special session aims both at uniting experts in different sensory modalities to collectively realise the power of innovative methodological capabilities and attract the attention of other members of the IPFC & ASFB to sensory ecology and its capacity to help some critical questions regarding fish ecology, evolution and behaviour.

Special Session 9 Fisheries and the Potential of Artificial Intelligence and Machine Learning for Improving Sustainability Outcomes

Convenor: Rich Little (Rich.Little@csiro.au); Geoff Tuck (Geoff.Tuck@csiro.au); Gretchen Grammar (Gretchen.Grammer@sa.gov.au)

Fisheries are facing significant challenges in the 21st century due to overfishing, climate change, and a rapidly growing global population, but new technologies in Electronic Monitoring (EM), Artificial Intelligence (AI) and Machine Learning (ML) offer new solutions for addressing these challenges and achieving more sustainable outcomes. This session will explore the potential of AI and ML in the fisheries industry and its role in improving sustainability outcomes, reducing costs, and sampling more rapidly. Overall, this session will provide valuable insights and information for anyone interested in the future of the fisheries industry and its potential for achieving more sustainable outcomes through the use of AI and ML.

Conference Program

Day 1, Monday 20 November 2023

8.00am - 9.30am	*Registration* *OGGB Level 0 foyer*				
9.30am - 10.45am	**Opening: Mihi (Hone Thorpe) & Welcome (IPFC & ASFB)** **Lecture Theatre 260-098** **Plenary ASFB Travel Award Presentation-Emily Lester** **Investigating predator-prey interactions in coral reefs: how do insights from small scale experiments manifest over reef-wide scales?** **Lecture Theatre 260-098**				
10.45am - 11.15am	*Morning Tea* *OGGB Level 0+1 foyer*				
11.15am - 1.00pm	**1.1A** **Themed Session A** Evolution, Taxonomy and Biogeography of Indo-Pacific Fishes	**1.2A** **Special Session 4** The evolution and ecology of fishes: assessing traits and functions in a changing world	**1.3A** **Themed Session J** Fisheries Management	**1.4A** **Themed Session K** General Session	**1.5A** **Special Session 3** Building a better future for fish: a symposium on fish-friendly infrastructure
	Lecture Theatre 260-098	**Lecture Theatre OGGB4 260-073**	**Fisher & Paykel Appliances Auditorium 260-115**	**Case Room 2 260-057**	**Case Room 3 260-055**
	Session Chair: Tom Trnski	Session Chair: Christopher Hemingson	Session Chair: Jonah Yick	Session Chair: Armagan Sabetian	Session Chair: Craig Boys & Rod Price
11.15am	3 Getting to the bottom of Indian gobioids **Helen Larson**	150 Fish on reefs: A new perspective **David Bellwood**	48 Global drivers of tropical marine herbivorous fish catches. **Lucas Lutzenkirchen****	68 The effects of climate change on seafood nutritional quality **Tanika Shalders****	44 New Learnings in Tidal Interface Fish Passage: Insights from a Cone Fishway at Manns Weir, Boyne River, Queensland **Timothy Marsden**
11.30am	25 Taxonomic revision of the genus *Stenogobius* (Teleostei: Gobioidei) from Indo-Pacific rivers **Romain Causse**	234 Assessing functional, morphological and phylogenetic composition in reef fishes to explore similarities in assembly rules among biogeographic systems **Italo Fernández-Cisternas***	53 How much fisheries benefit can there be from blue carbon restoration projects? **Vincent Raoult**	74 Novel use of environmental DNA metabarcoding to assess impacts from a large-scale seismic survey on tropical fish communities **Conrad Speed**	66 Improving downstream fish passage at flood infrastructure with New Zealand's first Encased Archimedes Screw Pump, north Waikato, New Zealand **Alicia Williams**
11.45am	70 Updates on *Encheloclarias* (Siluriformes: Clariidae), an uncommon acid-water catfish **Heok Hui Tan**	528 Functional and Taxonomic Beta-Diversity of Freshwater Fishes across Northern Australia River Basins **Osmar Luiz**	59 Molecular Monitoring in Fisheries Management – Does it work? **Madeline Green**	77 The influence of oil and gas infrastructure on marine community structure, connectivity, and fish productivity: Bass Strait, south-east Australia **Dianne McLean**	79 Broad scale prioritisation of fish barriers across Aotearoa New Zealand **Shad Mahlum**
12.00pm	26 A DNA reference library for New Caledonian freshwater fish: challenges and prospects **Marion Mennesson**	132 The rise of dietary diversity in coral reef fishes **Isabelle Ng****	72 The eradication of common carp from Tasmania **Jonah Yick**	118 Color patterning in anemonefishes **Marleen Klann**	287 A fish barrier remediation case study - Mona Vale rock riffle **Mark Groves**
12.15pm	90 A taxonomic review of central Indo-west Pacific lantern sharks (Etmopteridae: Etmopterus) **Shing-Lai Ng****	344 Scavenger richness and functional diversity modify carrion consumption in the surf zone of ocean beaches **Jesse Mosman***	73 Influence of distribution mapping sources on SAFE Ecological Risk Assessment vulnerability scores for deepwater chondrichthyans in the Southern Indian Ocean **Krystle Keller**	129 Elusive and Vulnerable: Evaluating the distribution of the Reef Manta (*Mobula alfredi*) around Oahu using Environmental DNA **Grace Tuthill-Christensen***	396 Onwards and upwards – studies of climbing in *Galaxias brevipinnis* **Eleanor Gee**
12.30pm	148 New Australian and global maximum depth records for bony fish. **Todd Bond**	57 Identifying traits for inferring potential ecosystem functions of cryptobenthic reef fishes **Lucia Pombo-Ayora***	224 Density effects on growth rates and fecundity of *Galaxias maculatus* in whitebait refuges **Andrew Watson**	135 Are parrotfishes the primary drivers of dead coral colony erosion? **Juliano Morais****	448 Accounting for interspecies and intraspecies variation in swimming performance for fish passage solutions **Rachel Crawford***
12.45pm	20 Taxonomic revision of the seahorse genus Hippocampus (Syngnathidae): hidden diversity in the pygmy seahorses **Graham Short**	Discussion	294 Environmental drivers of non-commercial reef fisheries in Guam **Leilani Sablan**	157 Life history traits of the honeycomb leatherjacket *Cantherhines pardalis* and the broom leatherjacket *Amanses scopas* (Monacanthidae) from the Solomon Islands **Valerio Visconti**	Fish Passage Discussion
1.00pm - 2.00pm	*Lunch* *OGGB Level 0+1 foyer*				

2.00pm - 4.15pm	**1.1B** **Themed Session A** Evolution, Taxonomy and Biogeography of Indo-Pacific Fishes	**1.2B** **Special Session 4** The evolution and ecology of fishes: assessing traits and functions in a changing world	**1.3B** **Themed Session J** Fisheries Management	**1.4B** **Themed Session K** General Session	**1.5B** **Special Session 3** Building a better future for fish: a symposium on fish-friendly infrastructure
	Lecture Theatre **260-098**	**Lecture Theatre OGGB4** **260-073**	**Fisher & Paykel Appliances Auditorium** **260-115**	**Case Room 2** **260-057**	**Case Room 3** **260-055**
	Session Chair: Nicholas Dunn	Session Chair: Christopher Hemingson	Session Chair: Nicholas Ling	Session Chair: Shaun Wilson	Session Chair: Craig Boys & Rod Price
2.00pm	154 Diversity and Molecular Phylogeny of Congrid eels (Anguilliformes: Congridae) of Indian Waters **Paramasivam Kodeeswaran***	437 Biological traits and their effect on individual-level processes and ecosystem-level functions **Nina Schiettekatte**	328 Digging Deeper: uncovering the social structure, population genetics and behaviour of a cryptic fisheries species, *Trypaea australiensis* **Renae Kirby****	158 Ocean Genomes – A comprehensive high-quality reference genome library for marine vertebrates **Lara Parata**	42 Towards Australia's first design guidelines for fish protection screens: Insights from a flume-based study on native species **Craig Boys**
2.15pm	181 Describing the recognised: toward description of further *Galaxias* from New Zealand **Nicholas Dunn**	143 Functional traits to predict fish futures – Pandora's Box or Rosetta Stone? **Robert Streit**	358 Otolith morphological analysis: A method to validate observer species identification and fisheries bycatch management **William Connor****	194 Regional patterns in demersal fish assemblages among subsea pipelines and natural habitats across north-west Australia **Ronen Galaiduk**	250 Laboratory-based comparison of screening materials for excluding New Zealand juvenile freshwater fishes **Mike Hickford**
2.30pm	211 Spine locking apparatus in vertical and paired fins of fishes from Japan **Gento Shinohara**	94 Evolutionary traits and ecological roles in herbivorous fishes on coral reefs **Kendall Clements**	362 Improving regional and temporal comparisons in fish life history **Eva Schemmel**	223 Understanding the void within: endocasts provide a new axis of morphological diversity for teleosts **Rodrigo Figueroa***	128 Swimming performance of juvenile green sturgeon (*Acipenser medirostris*) in relation to water diversions **Kelly Hannan**
2.45pm	251 A novel phylogeny of Syngnathidae based on morphology (Teleostei: Syngnathiformes) **Caio Dallevo-Gomes***	557 Food availability influences life history traits of a widespread herbivorous reef fish **Andrew Hoey**	367 Global shortfall in the management of major shark and ray fisheries **Samantha Sherman**	226 How well does recruitment predict abundance of adult lethrinids? **Shaun Wilson**	545 Initiatives to improve national guidance for water intake management to ensure safe passage for freshwater fish in New Zealand **Adrian Meredith**
3.00pm	568 Phylogenomics of lampreys and the evolution of diverse life history strategies **Devin Bloom**	50 Quantifying patterns versus processes in herbivorous fishes on Anthropocene coral reefs **Sterling Tebbett**	370 How low can we go? Targeted removal of exotic fish at lake Tomorata **Nicholas Ling**	296 Investigating methods to mitigate shark depredation in line-based fisheries in Queensland, Australia **Jaeden Vardon***	43 The Design of Fish Screen Facilities at River Intakes – Lessons Learnt **Paul Morgan**
3.15pm	256 Systematics of the scorpionfish genus *Neomerinthe* Fowler, 1935 **Tatsuya Matsumoto***	493 Plasticity in foraging behaviour of *Ctenochaetus striatus* linked to sedimentation, with implications for cryptic functional vulnerability **Ryan McAndrews**	389 The Ripple Effect of Predator Removal: Results from a five-year trout removal trial in a mountain stream **Jason Lieschke**	310 Stable Isotope Analysis Reveals Differential Niche Plasticity In Co-occurring Temperate Estuarine Fishes **James Wong****	109 Fish screen performance at water diversions and irrigation pumps in the Murray Darling Basin and consequences for implementing screens **Joachim Bretzel****
3.30pm	258 Multiple gene phylogeny challenges the current classification of the Indo-West Pacific sinistral flounders (Pleuronectiformes: Bothidae) **Pakorn Tongboonkua***	110 Effects of ocean warming on fish community composition and species-specific dietary shifts **Robert Lamb**	403 Challenges of managing a charter fishery to an explicit catch limit **Taylor Grosse**	324 Glow in the dark party: new records and evolutionary implications of biofluorescence in deep-sea fishes **Marcelo Melo**	45 Lessons learnt from exclusion barrier use in protecting non-migratory galaxiid strongholds in New Zealand **Sjaan Bowie**
3.45pm	261 Systematics of the Indo-West Pacific anthiadids, with emphasis on the genus Plectranthias Bleeker, 1873 and their relatives (Perciformes: Anthiadidae) **Chi Ngai Tang***	Discussion		342 The ecological importance of ray bioturbation in a temperate estuary **Molly Grew***	406 Enhancing adoption of modern fish-protection screens: insights from stakeholder engagement **Rodney Price**
4.00pm		Discussion		488 Introducing the Pacific Islands Region Acoustic Telemetry (PIRAT) Network **Thomas Tin Han**	Fish Screening and Barrier Discussion
4.15pm - 5.15pm	*Afternoon Tea* *OGGB Level 0+1 foyer*				
5.15pm - 6.30pm	Transport to Auckland Museum will be provided				
6.30pm - 8.00pm	***Welcome Reception*** ***Auckland Museum*** ***Address: Parnell, Auckland 1010***				
8.00pm	***Day 1 concludes***				

Day 2, Tuesay 21 November 2023

8.00am - 9.00am	*Arrival Tea +Coffee* *OGGB Level 0+1 foyer*				
9.00am - 10.00am	Housekeeping **Keynote - Jenn Caselle** **Moving beyond movement - how insights from fish movements can inform effective conservation planning and fisheries management** **Lecture Theatre 260-098**				
10.00am - 10.30am	*Morning Tea* *OGGB Level 0+1 foyer*				
10.30am - 12.30pm	**2.1A** **Themed Session A** Evolution, Taxonomy and Biogeography of Indo-Pacific Fishes	**2.2A** **Special Session 4** The evolution and ecology of fishes: assessing traits and functions in a changing world	**2.3A** **Themed Session B** Ecology of Indo-Pacific Fishes	**2.4A** **Themed Session F** Conservation of Indo-Pacific fishes	**2.5A** **Themed Session E** Biology and Conservation of Sharks and Top-predators
	Lecture Theatre 260-098	**Lecture Theatre OGGB4 260-073**	**Fisher & Paykel Appliances Auditorium 260-115**	**Lecture Theatre OGGB3 260-092**	**Lecture Theatre OGGB5 260-051**
	Session Chair: Michael Hammer	Session Chair: Jennifer Donelson	Session Chair: Gretchen Grammer	Session Chair: Mark Lintermans	Session Chair: Britt Finucci
10.30am	275 Taxonomic revision of the perciform genus *Acanthistius* (Günther 1859) with resolution of the identity of Acanthistius paxtoni **Younis Menkara****	140 Over a century of global decline in the growth performance of marine fishes **Helen Yan****	7 The effects of marine heatwaves on the physiology of a coral reef snapper **Shannon McMahon**	92 The implications of plastic pollution on seafood species **Nina Wootton**	2 Decomposing global trade in shark and ray meat **Aaron MacNeil**
10.45am	286 Sampling the undersampled: improving understanding of estuarine biodiversity in northern Australia **Michael Hammer**	19 Biological responses to climate change will reduce yields in tropical fisheries **Brett Taylor**	33 Growth aspects of *Mugil cephalus* Linnaeus, 1758 from Kilifi creek, Kenya **Dorcus Sigana**	141 Characteristics of a newly-discovered population of the critically endangered stocky galaxias **Mark Lintermans**	229 Estimating the Species Composition of Global Shark and Ray Fisheries **Christopher Mull**
11.00am	311 Goby spotting: Three new species descriptions and a revised guide to Info-Pacific Gobiodon genus **Courtney Hildebrandt****	269 Do all fish species have similar body size distributions and why does it matter? **Freddie Heather**	37 Transposable elements landscape of transgenerational plasticity to ocean acidification in reef fish **Taewoo Ryu**	178 Making a super seahorse: Optimising the husbandry of Endangered White's Seahorses, *Hippocampus whitei* , for the purpose of conservation stocking **Mitchell Brennan****	304 From undervalued or ignored to luxury products – shark and ray skins in an expanding global market **Rima Jabado**
11.15am	322 Taxonomic review of the pipefish genus *Corythoichthys* Kaup, 1853 (Syngnathiformes: Syngnathidae) in the Pacific Ocean **Daijiro Yuki***	549 Exploring patterns in the phenotypic diversity of individual growth across a fish species' range **John Morrongiello**	49 Contrasting habitat use and growth of two anguillid eels, *Anguilla marmorata* and *A. japonica* in sympatric subtropical rivers **Yusuke Kumai***	192 Translating environmental DNA, validated citizen science data, and local knowledge of fishes into meaningful conservation action **Joseph DiBattista**	22 Global Correlates of Shark and Ray Meat Consumption **Ana Barbosa Martins**
11.30am	353 Environmental DNA primer selection for reef-associated and pelagic Indo-Pacific and Hawaiian fish species **Van Wishingrad**	279 Using colouration as a trait to study ecosystems and communities: a case study on coral reef fishes **Christopher Hemingson**	52 The influence of macroalgal biomass and thallus density on the recruitment of coral reef fishes **Kelsey Webber***	197 Understanding effects of zoning on abundance and composition of fish assemblages across the southern Great Barrier Reef **Virginia Gilliland***	363 The next generation of shark Red Listing **Brittany Finucci**
11.45am	423 Decoding morphological diversity in deep-sea spikefishes (Triacanthodidae: Tetraodontiformes): phylogenetics, genomics, and habitat associations **Zach Heiple***	340 Ecology and evolution of a color polymorphism in two Paracirrhites hawkfishes **Samuel Greaves***	54 Examination of the function and evolutionary process of cleaner fish mimicry **Hajime Sato***	215 Dissemination of knowledge on freshwater fish in remote tropical islands. The example of research in the Solomon Islands **Clara Lord**	412 Whistle-stop tour of shark and ray biology, fisheries, policy and conservation in the Western Indian Ocean **Rhett Bennett**
12.00pm	595 Phylogenetic relationships of the New Zealand endemic clingfish Genus Modicus Hardy, 1893 (Teleostei, Gobiesocidae) **Kevin Conway**	Discussion	104 Contrasting spatial distributions from baited and non-baited stereo video methods and their implications for ocean accounts and biodiversity reporting **Gabrielle Cummins****	11 Ecological Assessment of the Siganid Fishery in Calapan City, Oriental Mindoro, Philippines **Marius Panahon**	416 Resharking leopards in Raja Ampat: a behind-the-scenes look at the StAR (*Stegostoma tigrinum* Augmentation and Recovery) project **Nesha Ichida**
12.15pm		Discussion	75 Suspended sediments and the physiology of a coral reef fish, *Amphiprion ocellaris* **Johanna Johansson***		419 A century of shark fisheries and trade in India **Zoya Tyabji***
12.30pm - 1.30pm	*Lunch* *OGGB Level 0+1 foyer*		ASFB Threatened Fishes Committee 260-040	ASFB FMC Committee Meeting 260-040B	ASFB Welfare Committee Meeting 260-057

1.30pm - 3.00pm	**2.1B** **Themed Session A** Evolution, Taxonomy and Biogeography of Indo-Pacific Fishes	**2.2B** **Themed Session J** Fisheries Management	**2.3B** **Themed Session B** Ecology of Indo-Pacific Fishes	**2.4B** **Themed Session F** Conservation of Indo-Pacific fishes	**2.5B** **Themed Session E** Biology and Conservation of Sharks and Top-predators
	Lecture Theatre 260-098	**Lecture Theatre OGGB4 260-073**	**Fisher & Paykel Appliances Auditorium 260-115**	**Lecture Theatre OGGB3 260-092**	**Lecture Theatre OGGB5 260-051**
	Session Chair: Terry Donaldson	Session Chair: Brendan Hicks	Session Chair: Kendall Clements	Session Chair: Melita Samoilys	Session Chair: Aaron MacNeil
1.30pm	498 An undescribed population of *Glyptothorax* from the Mekong River **David Boyd**	446 Whitebait: multiple species, fishing methods, values, measurements, and challenges **Dave West**	85 The escaping ability of juvenile eels via the predator's gill: developmental change and behavioral patterns of eels inside the predator **Yuha Hasegawa***	295 Clean and oil-weathered microplastics impact in-situ behaviours and survival of juvenile coral reef fish (*Pomacentrus amboinensis*) **Aneesa Delpachitra****	262 Developing Solutions to Mitigate Impacts of Fishing Trawlers on Elasmobranch, Sabah, Malaysia **Kooi Chee Ho***
1.45pm	502 A decade of ichthyological research from Australia's Research Vessel Investigator **John Pogonoski**	453 Role of herbivorous reef fishes in resilience-based management **Mary Donovan**	96 Does nest-building glue secreted by the kidney of male stickleback attract females? **Miki Nagaya***	314 Ngā Ika e Heke - Conserving migratory fish species in Aotearoa **Marine Richarson**	492 Shark activity is impacted by changing environmental conditions **Adrienne Gooden****
2.00pm	537 New records of fishes from Rangitāhua/Kermadec Region **Carl Struthers**	472 Utilising natural tags to identify seafood provenance **Rhiannon Van Eck****	55 A role for encrusting, endolithic sponges in the feeding of Indo-Pacific parrotfishes (Labridae, Scarini) **Kendall Clements**	336 Predatory and Large-bodied Fishes Depleted on Western Indian Ocean Coral Reefs **Melita Samoilys**	115 Assessing mechanisms of vulnerability in sharks occupying different marine environments **Sushmita Mukherji****
2.15pm	573 New and recent records of fishes from the Mariana Islands **Terry Donaldson**	491 Linking environmental knowledge and values on conservation actions **Alexander Vaishampayan****	107 Beyond the shell: dissecting the underwhelming habitat function of giant clam for reef fishes **Colin Wen**	343 Conserving for complementarity: A functional approach to conservation **Christopher Henderson**	288 Putting sharks on the map: identifying Important Shark and Ray Areas worldwide to inform marine spatial planning **Emiliano García-Rodríguez**
2.30pm	582 Nine species in one: evidence of hidden species diversity in the Zambezi grunter (Siluriformes, Auchenoglanididae) in southern and south-central Africa **Yonela Sithole**	496 Engaging with First Nation people through Fisheries Management 101 **Eliza Kimlin**	111 Seabirds provide diverse benefits to coral reef fishes through cross-ecosystem nutrient subsidies **Casey Benkwitt**	380 Remote sensing in remote locations: A new approach to find and prioritise barriers to fish passage for conservation **Hugh Allan****	270 Importance of the Mitchell River (Queensland, Australia) as habitat for freshwater sawfish *Pristis pristis* **Barbara Wueringer**
2.45pm	16 New insights on marine angelfish evolution from genome-scale data **Lauriane Baraf****	497 Conservation of eels in New Zealand: response to reduction of invasive fish biomass **Brendan Hicks**	119 Migration and distribution patterns of freshwater gobies of the genus *Rhinogobius* in continental rivers and tropical island's streams **Ken Maeda**	402 Prohibiting spearfishing boosts conservation outcomes for partially protected areas **April Hall**	390 Isolated seamount reefs provide potential thermal refuges for reef sharks **Ben Cresswell****
3.00pm - 3.30pm	*Afternoon Tea* *OGGB Level 0+1 foyer*				
3.30pm - 4.15pm	**2.1C** **Themed Session A** Evolution, Taxonomy and Biogeography of Indo-Pacific Fishes	**2.2C** **Themed Session J** Fisheries Management	**2.3C** **Themed Session B** Ecology of Indo-Pacific Fishes	**2.4C** **Themed Session F** Conservation of Indo-Pacific fishes	**2.5C** **Themed Session E** Biology and Conservation of Sharks and Top-predators
	Lecture Theatre 260-098	**Lecture Theatre OGGB4 260-073**	**Fisher & Paykel Appliances Auditorium 260-115**	**Lecture Theatre OGGB3 260-092**	**Lecture Theatre OGGB5 260-051**
	Session Chair: Yi-Kai Tea	Session Chair: Jane Williamson	Session Chair: Michael Kingsford	Session Chair: Dave West	Session Chair: Rima Jabado
3.30pm	29 Why several when one can unite them all? Integrative taxonomic revision of Indo-Pacific freshwater pipefish (Nerophinae) **Vincent Haÿ***	503 Determining species diversity and spatio-temporal distributions of larval fishes in Cockburn Sound, Western Australia **Jake Nilsen**	123 Molecular Pathways Underlying Cleaning Behaviour: a Study in the Wild **Daniele Romeo***	421 Environmental DNA based insights of fish diversity associated to oil platforms in the Arabian Gulf **Johan Mølgård Sørensen**	318 Survival strategies reveal rarity of Naru eagle ray, *Aetobatus narutobiei* : Exploring new ecosystem conservation measures through top-down control of elasmobranchs **Atsuko Yamaguchi**
3.45pm	31 The genome of the spotted parrotfish provides evolutionary insight into the ecological adaptation of a keystone dietary specialist **Yi-Kai Tea**	523 Modernising large-scale surveys of sea cucumbers and other benthic species using towed Remote Operated Vehicles (ROVs) and Aerial Drones **Jane Williamson**	137 The effects of habitat connectivity and complexity on the distribution of inshore reef fish communities **Alexander Jarrett****	456 Integrating thermal tolerance with population genetics to reveal the thermal landscape of a coral reef fish (*Acanthochromis polyacanthus*) **Elliott Schmidt****	289 Internal organs and body tissues of free-swimming whale sharks (*Rhincodon typus*) imaged using underwater ultrasound **Mark Meekan**
4.00pm	32 Discovery of cryptic species complex within sand diver (*Limnichthys fasciatus*), and its evolutionary implication **Yu-Jin Lee***		139 Soft corals contribute to a mosaic of habitats for fishes on coral reefs **Michael Kingsford**	506 Shortjaw kōkopu distribution, population status and threats in the Northern South Island, New Zealand **Anna Henderson**	526 Denticle Hygiene: Examining the Viral Communities of Elasmobranch Skin **Ryan Hesse****
4.15pm - 6.15pm	***Poster Function*** ***(Sponsored by Oceania Chondrichthyan Society)*** ***OGGB Level 0 foyer***				
6.15pm	***Day 2 Concludes***				

Day 3, Wednesday 22 November 2023

8.00am - 9.00am	*Arrival Tea +Coffee* *OGGB Level 0+1 foyer*				
9.00am - 10.00am	Housekeeping				
	IPFC Bleeker Award - Systematics **Lecture Theatre 260-098**				
10.00am - 10.30am	*Morning Tea* *OGGB Level 0+1 foyer*				
10.30am - 12.30pm	**3.1A** **Themed Session A** Evolution, Taxonomy and Biogeography of Indo-Pacific Fishes	**3.2A** **Themed Session C** Fisheries and Aquaculture in the Indo-Pacific	**3.3A** **Themed Session B** Ecology of Indo-Pacific Fishes	**3.4A** **Themed Session H** Management of Barriers to Fish Movement	**3.5A** **Themed Session E** Biology and Conservation of Sharks and Top-predators
	Lecture Theatre **260-098**	**Lecture Theatre OGGB4** **260-073**	**Fisher & Paykel Appliances Auditorium** **260-115**	**Lecture Theatre OGGB3** **260-092**	**Lecture Theatre OGGB5** **260-051**
	Session Chair: Travis Ingram	Session Chair: Leonardo Magnoni	Session Chair: Ivan Nagelkerken	Session Chair: Cindy Baker	Session Chair: Mark Meekan
10.30am	39 Fish using tools: Uncovering factors driving tool use evolution **Juliette Tariel-Adam**	114 Morphology and metabolic traits related to swimming in tāmure/ Australasian snapper (*Chrysophrys auratus*) selected for fast growth **Leonardo Magnoni**	145 Pacific-wide distribution of reef fish contamination **Noreen Wejieme***	196 Innovative approaches to fish passage: Harnessing the potential of Tube Fishways **Jasmin Martino**	35 The evolution of contemporary population structure in white sharks. A story of sea level change, food availability, movement and sex **Gavin Naylor**
10.45am	63 Look who's walking too: genomics and kinematics of balitorid loaches can inform our understanding of the vertebrate transition to land **Prosanta Chakrabarty**	201 El Niño–Southern Oscillation causes shifts in the vertical distribution of Pacific pelagic fishes **Juan Wang****	147 Ecological drivers and pigmentation changes underlying adult colour pattern formation in the anemonefish, *Amphiprion frenatus* **Laurie Mitchell**	413 The NZ Fish Passage Guidelines: Enabling evidence-based policy implementation **Cindy Baker**	193 Crossed saws: Evidence of hybridisation between Australian sawsharks **Ryan Nevatte**
11.00am	78 Mapping of global mitochondrial data brings new insights into taxonomy and species distribution of genus *Pampus* (Pelagiaria: Stromateidae) **Jiehong Wei***	313 Evaluating the feasibility of sustainable seafood labelling programmes in Small Island Developing States: a pilot study in Seychelles **Jessica Glass**	168 How global and local stressors interact to impact coral reef mutualisms **Theresa Rueger**	509 The Impact of Green Tape on Barrier Remediation Projects: Lessons from Queensland, Australia **Melinda Scanlon**	408 Genetic stock structure of the silky shark *Carcharhinus falciformis* in the Indo-Pacific Ocean **Chia Yun Li***
11.15am	105 How does environmental change affect the brain and behaviour in coral reef fishes? **Celia Schunter**	326 Effects of manipulating Kingfish (Seriola lalandi) routine oxygen demand and supply on ventricular and skeletal muscle mitochondrial function **Alice Harford****	175 Predicting productivity in tropical seaweed-associated fish populations **Chris Fulton**	521 Larval competency and seascape context determines the influence offshore structure have on marine metapopulation dynamics **Eric Treml**	253 The spatiotemporal patterns of young blacktip reef shark encounter-rates with predators inside 'nursery' areas **Jake Edwards-ingle****
11.30am	125 Assembly rules of coral reef fish communities along the depth gradient **Chancey MacDonald**	341 Kiribati coral reef ecological indicators, small-scale fisheries, and climate resilience **Jacob Eurich**	185 Social hierarchy formation in the sex-changing New Zealand spotty wrasse (*Notolabrus celidotus*) **Haylee Quertermous****	576 Isolation management to protect threatened native galaxiid fish species: lessons from Aotearoa New Zealand **Martha Jolly***	247 Insights into the residency of oceanic manta rays at cleaning stations on coral reefs in the Bird's Head Seascape, Indonesia **Edy Setyawan***
11.45am	131 The evolution of fast-growing coral reef fishes **Alexandre Siqueira**	395 Depleted striped trumpeter (*Latris lineata*) stocks and fisheries management in Tasmania **Alyssa Marshell**	186 Cleaner fish presence provides a 'safe-haven' from predation **Jose Ricardo Paula**	579 Modelling impacts of artificial barriers on riverine fish communities **Lukian Adams****	151 Revealing the pattern of mangrove use by juvenile sharks and stingrays **Shiori Kanno***
12.00pm	138 Dispersal and evolution in Chatham Island freshwater fish **Travis Ingram**	462 Swimming at increasing speed in steady and unsteady flows of Atlantic salmon: behaviour, oxygen consumption and overall dynamic body acceleration **Wisdom Enyam Kodzo Agbeti****	190 Overlooked mortality in the longface emperor *Lethrinus longirostris* by the didymozoid parasite infection **Tamaki Shimose**	130 Fish passage monitoring and remediation in a highly modified New Zealand ecosystem **Ryan Easton****	144 What's on the menu?: analysing stingray vomit shows species-specific resource partitioning within an intertidal nursery **Jaelen Myers****
12.15pm			199 Fish assemblages reshuffle in response to resource alteration due to the indirect effects of climate change **Ivan Nagelkerken**		184 Impact of cattle disposal on tiger shark behaviour at Norfolk Island, Australia **Jordan Matley**
12.30pm - 2.30pm	*Lunch* *OGGB Level 0+1 foyer*			ASFB AGM Lecture Theatre OGGB3 260-092	IPFC Meeting 260-057

2.30pm - 3.30pm	**3.1B** **Themed Session A** Evolution, Taxonomy and Biogeography of Indo-Pacific Fishes	**3.2B** **Themed Session C** Fisheries and Aquaculture in the Indo-Pacific	**3.3B** **Themed Session B** Ecology of Indo-Pacific Fishes	**3.4B** **Special Session 7** Fish and fishery data to inform marine sanctuary design and planning	**3.5B** **Themed Session E** Biology and Conservation of Sharks and Top-predators
	Lecture Theatre **260-098**	**Lecture Theatre OGGB4** **260-073**	**Fisher & Paykel Appliances Auditorium** **260-115**	**Lecture Theatre OGGB3** **260-092**	**Lecture Theatre OGGB5** **260-051**
	Session Chair: Alexandre Siqueira	Session Chair: Katherine Cure	Session Chair: Gerry Closs	Session Chair: Jordan Goetze	Session Chair: Asia Armstrong
2.30pm	166 Fossil marine gobies **Werner Schwarzhans**	468 Using recreational squid jigging techniques to determine the distribution and abundance of southern calamari *Sepioteuthis australis* **Daniel Yeoh**	212 Nesting and reproductive behaviour of the sand-dwelling goby, *Hazeus ammophilus* (Gobiidae), which constructs a radially aligned ditches surrounded nest **Hiroshi Kawase**	369 Broad scale synthesis of fish, shark and ray data informs fully protected area design globally **Jordan Goetze**	373 What's on the menu? Elucidating the diet and habitat use of immature white sharks in eastern Australia using biochemical tracers **Rebecca Lipscombe****
2.45pm	170 Evolutionary history of extant and fossil acanthuriforms and the genomic bases of trophic transitions **Aintzane Santaquiteria***	487 Multiple lines of evidence suggest population structure in two small-bodied northern Australian sharks **Amy Kirke***	217 Cleaner gobies' cognitive performance is linked with their ecology **Maddalena Ranucci***	397 Identifying and conserving seascape nurseries on the Great Barrier Reef **Andrew Olds**	485 Multi-disciplinary approach reveals the role of sympatric benthic sharks linking pelagic and benthic food webs **Patrick Burke***
3.00pm	172 Structural variation in clownfishes' adaptive radiation **Anna Marcionetti**	580 Parenteral hormone administration induces spawning in redclaw, *Cherax quadricarinatus* **Nur Un Nesa****	236 Diet variation of common smelt across a salinity gradient in coastal lakes on Rēkohu (Wharekauri, Chatham Island) **Grace Fortune-Kelly***	134 A tool to evaluate the impact of sanctuary zone arrangements on recreational fishers in Western Australia **Nicole Hamre***	349 Long-term incubation and successful delivery of lantern shark embryos using an artificial uterus **Keiichi Sato**
3.15pm	176 A novel phylogenomic hypothesis of Eupercaria, the new bush at the top **Elizabeth Miller**	285 Mangrove seascapes provide habitat connectivity in support of culturally important fisheries **Katherine Cure**	242 Big fish have big mouths: is snapper predation on urchins determined by mouth size? **Jessica Marinovich***	239 Systematic Marine Protected Area Planning using MARXAN in New Zealand **Naif Rushdi**	102 Spot the difference: Using artificial intelligence on individual markings of manta rays to delineate global populations **Asia Armstrong**
3.30pm - 4.00pm	*Afternoon Tea* *OGGB Level 0+1 foyer*				
4.00pm - 6.00pm	**3.1C** **Themed Session A** Evolution, Taxonomy and Biogeography of Indo-Pacific Fishes	**3.2C** **Themed Session K** General Session	**3.3C** **Themed Session B** Ecology of Indo-Pacific Fishes	**3.4C** **Special Session 7** Fish and fishery data to inform marine sanctuary design and planning	**3.5C** **Themed Session E** Biology and Conservation of Sharks and Top-predators
	Lecture Theatre **260-098**	**Lecture Theatre OGGB4** **260-073**	**Fisher & Paykel Appliances Auditorium** **260-115**	**Lecture Theatre OGGB3** **260-092**	**Lecture Theatre OGGB5** **260-051**
	Session Chair: William Ludt	Session Chair: Jodie Rummer	Session Chair: Darren Parsons	Session Chair: Tim Langlois	Session Chair: Chris Mull
4.00pm	183 Unravelling the physiological, ecological, and genomic origins of endothermy in fishes **Fernando Melendez Vazquez***	348 Remotely Operated Vehicle surveys reveal new mesophotic biodiversity in the Coral Sea Marine Park, Australia **Gemma Galbraith**	248 E Hānai 'Ai Ma Ka Muliwai: assessing the diets of forage fish in estuaries of Hawaiʻi using DNA metabarcoding **Nakoa Goo***	273 Ecological variability increases the conservation impact of marine protected areas **Nils Krueck**	165 Reproductive biology of the Melbourne skate to inform fisheries management and conservation **Bailee Woolley****
4.15pm	225 Habitat persistence? Phylogeography of mesophotic holocentrids reveals younger than expected populations **Mykle Hoban**	383 Spatiophylogenetic modelling of freshwater fish invasion potential **Amy Tims**	259 Phenotypic plasticity in Clark's Anemonefish *Amphiprion clarkii* pigmentation in response to host anemones **Jann Zwahlen***	560 Transparency in Sanctuary Zone planning: attribute analysis informed by continental scale meta-analysis **Tim Langlois**	393 Coming of Age: The Life-history of School Sharks **Alex Burton***
4.30pm	233 Diversity, distribution and evolution of colour patterns in three reef fish families **Laurent Mittelheiser****	401 Towards adaptive management for the reintroduction of a wetland specialist fish **Henry Wootton**	263 Life history traits of the migratory river sculpin in small streams on Sado Island, northern Japan **Midori Lida**	543 The contribution of fish data to the last decade of conservation planning in South Africa **Kaylee Smit***	159 The role of life cycles in temperature resilience and global billfish distributions **Matthew Hammond****
4.45pm	244 Host use drives convergent evolution in clownfish and disentangles the mystery of an iconic adaptive radiation **Nicolas Salamin**	411 How can we motivate citizen scientists to help uncover the secrets of billfish? **Laura Smith****	272 Movement and habitat use of Guam reef manta rays (Mobula alfredi) as revealed by satellite telemetry **Julie Hartup**	297 Exploring the potential benefits of partially protecting the ocean in Australia **Genevieve Phillips**	
5.00pm	257 Macroevolutionary patterns of diversity imbalance and persistence of depauperate lineages across fishes **Isaac Trindade-Santos**	445 Earliest of athletes: How changes in physiological performance over early ontogeny in coral reef fishes facilitates dispersal and connectivity **Jodie Rummer**	276 Spatial ecology and foraging behaviour of oceanic manta rays (*Mobula birostris*) in the Hauraki Gulf, Aotearoa New Zealand **Tamsin Cooper***	540 Mainstreaming marine connectivity conservation to support Sustainable Development Goal 14 "Life Below Water" **Luisa Fontoura**	
5.15pm	260 Exploring the phylogeny and depth evolution of the Indo-West Pacific cusk eels and their relatives (Ophidiiformes: Ophidioidei) **Man Kwan Wong***	459 New coral habitat expands trait options for expatriating coral-reef fishes in temperate SE Australia **David Booth**	508 Drivers of parrotfish feeding and bioerosion along an offshore reef slope on the Great Barrier Reef **Hannah Allan****	442 Social and economic dimensions of Australia's no-take marine sanctuaries **Matthew Navarro**	
5.30pm	300 Resolving the evolutionary relationships of the order Centrarchiformes using genomic data and dense taxonomic sampling **William Ludt**	460 How long before an estuary benefits from habitat repair? **Vincent Raoult**	525 Ecology of tropical reef based clupeiforms affects genomic population structure **Kynan Hartog-Burnett****	Discussion	
5.45pm			577 Herbivores in the Hot-Seat: Resilience of *Acanthurus triostegus* functions to ocean warming **Taylor Souza***	Discussion	
6.00pm - 7.00pm					
7.00pm - 8.30pm	**Student Networking Event** ***(Sponsored by Fisheries Research and Development Corporation)*** **OGGB Level 1 Foyer + Superfino Café**				
8.30pm	***Day 3 Concludes***				

Day 4, Thursday 23 November 2023

8.00am - 9.00am	*Arrival Tea +Coffee* *OGGB Level 0+1 foyer*				
9.00am - 10.00am	Housekeeping				
	IPFC Bleeker Award - Ecology **Lecture Theatre 260-098**				
10.00am- 10.30am	*Morning Tea* *OGGB Level 0+1 foyer*				
10.30am - 12.30pm	**4.1A** **Themed Session A** Evolution, Taxonomy and Biogeography of Indo-Pacific Fishes	**4.2A** **Special Session 2** Facing environmental changes: what are the genetic and epigenetic mechanisms providing resilience in fishes?	**4.3A** **Themed Session B** Ecology of Indo-Pacific Fishes	**4.4A** **Themed Session I** Novel Methods and Techniques Advancing our Understanding of Fish Biology	**4.5A** **Special Session 5** Larval fishes - solving phylogenetic, life-cycle and ecological questions
	Lecture Theatre **260-098**	**Lecture Theatre OGGB4** **260-073**	**Fisher & Paykel Appliances Auditorium** **260-115**	**Lecture Theatre OGGB3** **260-092**	**Lecture Theatre OGGB5** **260-051**
	Session Chair: Gerry Closs	Session Chair: Lucrezia Bonzi	Session Chair: Joel Williams	Session Chair: Aimee van der Reis	Session Chair: Jeff Leis
10.30am	305 Don’t Wanna Be Your Bony Wrench: phylogenetic inferences from skeletal morphology of dwarfgobies, genus Eviota (Gobiidae), and other coral-reef gobies **Diego Francisco Biston Vaz**	177 Responses of tropical damselfishes to ocean warming and habitat degradation **Moises Bernal**	282 Drivers of fish assemblage structure across a 100-meter depth gradient in the tropical western Pacific **Logen Flem***	67 The contribution of mitochondria to thermal resilience in the endemic triplefins of New Zealand **Breana Riordan****	180 Spawning phenology and offspring sex: Do protogynous hermaphrodites spawn on new moons to make males? **Jeff Shima**
10.45am	350 Introgression landscape from a ghost extinct lineage in the genome of the coastal intertidal goby in Japan **Shuya Kato***	87 Epigenomic responses to temperature in snapper (*Chrysophrys auratus*) **Maren Wellenreuther**	292 Fine-scale bathymetry data explains variability fish assemblage structure of temperate mesophotic reefs in the Hunter Marine Park **Joel Williams**	86 Asynchrony of intra-specific growth responses to climate and environmental variables along a latitudinal gradient in a coral-reef fish **Erin Reed**	368 Can DNA-metabarcoding of multi-species samples from routine egg surveys be used to monitor the ichthyoplankton assemblage? **Gretchen Grammer**
11.00am	356 Geographical barriers and secondary contact shape the phylogeography of a widespread Indo-West Pacific reef fish, the banded sergeant *Abudefduf septemfasciatus* **Ling-Lan Hsu***	268 Short-term plasticity of an anemonefish (*Amphiprion ocellaris*) visual system in response to anthropogenic changes to the light environment. **Abigail Shaughnessy***	299 Submarine groundwater discharge drives changes in reef fish community structure and function **Maya Zeff***	559 The benefits of multiple methods to survey deep reef fish assemblages: comparison of stereo panoramic drop-camera systems with baited video **Charlotte Aston***	103 Larvae of three species of the Genus *Plectranthias* (Serranidae: Anthiadinae) with characteristic pigment patterns **Yoshinobu Konishi**
11.15am	361 Morphological diversity of the oral lures of Stargazers (Uranoscopidae: Uranoscopus) **Leo MacLeod***	61 Physiological and Transcriptomic Response of Early-Life Stage Clownfish to Future Ocean Warming **Billy Moore***	306 How water flow and reef structure shape the world of fishes **Casey Bowden****	99 Can we improve reef fish surveys for reliable diversity assessments? **Cher Chow***	46 The identification of flathead larvae (F. Platycephalidae) and their seasonal and spatial distribution off south-eastern Australia **Tony Miskiewicz**
11.30am	365 Three-dimensional morphometric data reveals patterns of integration and disparity in fossil and extant tetraodontiform fishes **Emily Troyer***	24 Gut microbiome and host molecular response of Malabar grouper (*Epinephelus malabaricus*) exposed to marine heatwaves **Roger Huerlimann**	309 Predators and habitat association of post-settlement snapper (*Chrysophrys auratus*) **Darren Parsons**	136 Use of eye lens stable isotopes to recreate resource-use chronologies in three New Zealand reef fishes **Joseph Curtis****	62 Oceanic larval fish assemblages in the south-east Indian Ocean **Lynnath Beckley**
11.45am	376 Functional beta diversity of New Zealand fishes: Characterising morphological turnover along depth and latitude gradients, with derivation of functional bioregions **Elisabeth Myers**	515 Heavy metal and antimicrobial resistance in benthic shark microbiomes **Emma Kerr***	319 Understanding thermal preferences and movement patterns of trawl whiting (Sillago sp) using otolith oxygen isotopes **Melissa Tan****	203 Methodological concerns with the use of DNA metabarcoding to investigate parrotfish diets **Aimee van der Reis**	517 Ichthyoplankton diversity and distribution in the Straits of Singapore **Zeehan Jaafar**
12.00pm	381 New hadal snailfish species represents an independent radiation of vertebrates into the hadal zone **Thom Linley**	544 Epigenetic sequencing to explore environmentally-driven plastic and adaptative responses across fish populations **Floriaan Devloo-Delva**	320 Exploring the drivers of growth synchrony within and among coral reef fishes across the Pacific **Emily Fobert**	127 Comparison of two methods for determining the temperature preference of tāmure/Australasian (*Chrysophrys auratus*) **Selwyn Collins***	106 The food sources of Anguilliformes leptocephali in the Kuroshio Current and adjacent waters **Gen Kume**
12.15pm	382 Chasing the Unknown: Cavefishes **Yahui Zhao**	65 Shrinking fishes on the world’s hottest coral reefs **Jacob Johansen**	330 The effect of group size on mating system and sexual pattern of red-belted anthias, *Pseudanthias rubrizonatus* , Kagoshima Bay, Japan **Emma Moritoshi***	142 Coral reef fish, hormones and metamorphosis: a tale of adaptation **Vincent Laudet**	476 Life in the fast lane: revisiting the fast growth – high survival paradigm during the early life stages of fishes **Dominique Robert**
12.30pm - 1.30pm	*Lunch* *OGGB Level 0+1 foyer*				

1.30pm - 3.00pm	**4.1B** **Themed Session A** Evolution, Taxonomy and Biogeography of Indo-Pacific Fishes	**4.2B** **Special Session 2** Facing environmental changes: what are the genetic and epigenetic mechanisms providing resilience in fishes?	**4.3B** **Themed Session B** Ecology of Indo-Pacific Fishes	**4.4B** **Themed Session I** Novel Methods and Techniques Advancing our Understanding of Fish Biology	**4.5B** **Special Session 5** Larval fishes - solving phylogenetic, life-cycle and ecological questions
	Lecture Theatre **260-098**	**Lecture Theatre OGGB4** **260-073**	**Fisher & Paykel Appliances Auditorium** **260-115**	**Lecture Theatre OGGB3** **260-092**	**Lecture Theatre OGGB5** **260-051**
	Session Chair: Luiz Rocha	Session Chair: Moises Bernal	Session Chair: Wei-Chuan Chiang	Session Chair: Tiffany Sih	Session Chair: Lynnath Beckley
1.30pm	384 The genomics of the *Dascyllus trimaculatus* species complex **Giacomo Bernardi**	191 The epigenetic landscape of coral reef fish acclimation and adaptation to climate change **Timothy Ravasi**	337 The feeding kinematics of a surgeonfish (*Acanthurus leucosternon*) and the associated functional implications **Michalis Mihalitsis**	204 Interspecific and intraspecific difference in egg size of two mackerel species *Scomber* spp. in the western North Pacific **Mikio Watai**	14 Marine reserves supply half of the larvae to a coral reef fishery **Jeffrey Leis**
1.45pm	398 Multiple hybrid zones of coastal marine gobies around the Japanese archipelago: natural laboratories for marine hybridization **Shotaro Hirase**	210 MicroRNAs and thermal transgenerational plasticity in a coral reef fish **Lucrezia Celeste Bonzi**	339 Thermal environment mediates density-dependent effects on the growth of a commercially harvested fish **Joshua Barrow**	245 FishBase 33 years after: status and current development on life-traits **Nicolas Bailly**	36 How do larval reef fishes find reefs and the right settlement sites on them? **Peter Sale**
2.00pm	414 Widespread genetic population structure in sea chubs (Kyphosidae) **Steen Knudsen**	76 Utilizing natural analogs of future oceans to study the adaptive potential of fish communities to climate change **Michael Izumiyama***	346 The mystery of shortjaw kōkopu (*Galaxias postvectis*) spawning ecology on the West Coast **Suze Harris**	281 Otolith morphometry and FT-NIR spectroscopy as tools to discriminate archived otoliths of cryptic species, Etelis carbunculus and Etelis boweni **Kristen Dahl**	153 A transcriptome insight during larval settlement of a coral-reef fish **Marcela Herrera Sarrias**
2.15pm	415 Global biogeography of ecological specialization in coral reef fishes **Zoe Delecambre***	84 Fish in natural CO2 seeps imply core transcriptional regulations for ocean acidification acclimation **Jingliang Kang**	355 How do temperature impacts on growth and mortality shape fish size distributions and why does it matter? **Sarah Willington****	284 Reducing taxonomic lag via convolutional neural nets **Tiffany Sih**	Discussion
2.30pm	424 Comparative genomics and transcriptomic analysis of a bioluminescent cardinalfish sheds light on the evolution of microbial symbiosis **Alison Gould**	483 The molecular mechanisms underlying environmental resilience **Sheri Johnson**	374 How do cryptic goby species fare in a changing environment? **Selma Klanten**	298 Anatomy of adaptation: exploring the internal structure of locomotor fins in the terrestrial mudskipper, Periophthalmus argentilineatus, using contrast-enhanced µCT **Fabienne Ziadi-Künzli**	Discussion
2.45pm	427 Taxonomy, phylogenetic affinities, and conservation of recently discovered mesophotic fishes **Luiz Rocha**	Facing Environmental Change: Discussion	377 Goby social mixers: mixed-species group formation in a model marine system (genus *Gobiodon*) and the potential impacts of habitat degradation **Marian Wong**		Discussion
3.00pm - 3.30pm	*Afternoon Tea* *OGGB Level 0+1 foyer*				
3.30pm - 5.15pm	**4.1C** **Themed Session A** Evolution, Taxonomy and Biogeography of Indo-Pacific Fishes	**4.2C** **Special Session 8** Fish sensory ecology: new techniques and approaches	**4.3C** **Themed Session B** Ecology of Indo-Pacific Fishes	**4.4C** **Themed Session I** Novel Methods and Techniques Advancing our Understanding of Fish Biology	**4.5C** **Themed Session K** General Session
	Lecture Theatre **260-098**	**Lecture Theatre OGGB4** **260-073**	**Fisher & Paykel Appliances Auditorium** **260-115**	**Lecture Theatre OGGB3** **260-092**	**Lecture Theatre OGGB5** **260-051**
	Session Chair: Richard Coleman	Session Chair: Lucille Chapuis	Session Chair: Simon Brandl	Session Chair: Tony Hickey	Session Chair: Krystle Keller
3.30pm	429 Fish species radiations in the sea: what the flock? **Brian Bowen**	83 How active is the brain in elevated temperature? Brain imaging of larval fishes responding to olfactory cues **Jade Sourisse***	378 Local habitat composition and complexity outweigh seascape effects on fish distributions across a tropical seascape **Molly Moustaka****	335 Metabolomics and lipidomics: 'the last piece of the omic puzzle' **Sara Heim***	484 Seeing through mud – Using mobile hydroacoustic sonar to monitor environmental watering outcomes **Sam Lewis**
3.45pm	431 Phylogeography of the sabertooth blenny genus *Plagiotremus* with special consideration of Hawaiian endemics **Cameron Walsh***	40 Using the latest technology to understand fish inner ear diversity **Lucille Chapuis**	410 Identifying impacts and drivers of fish assemblages over multiple scales in coastal ecosystems **Lucy Goodridge-Gaines****	364 Mitochondrial thermo-tolerance in two Indo-Pacific anoxia-tolerant sharks **Jules Devaux**	495 A preliminary assessment of the distribution of small pelagic fish within Cockburn Sound using acoustic methods **Peter Mitchell**
4.00pm	435 Genomic assessment of an endemic Hawaiian surgeonfish, *Acanthurus triostegus sandvicensis* , reveals high levels of connectivity and fine-scale population structure **Richard Coleman**	584 What inner ear anatomy can tell us about hearing in elasmobranchs **Craig Radford**	422 Investigating shortfin mako migratory patterns through an integrative data approach **Colby Kresge***	391 Reef Song: an ecosystem-based approach to enhancing reef resilience and restoration. **Rohan Brooker**	512 The enduring legacy of the Australian Museum Ichthyology Collection: scientific progress, international influence, and pub trivia **Amanda Hay**
4.15pm	449 Genome-wide SNP discovery and phylogeography of Pacific sand lance (*Ammodytes heian* and *Ammodytes japonicus*) using MIG-seq: Implications for evolution **Jin-Koo Kim**	15 Comparison of hearing abilities in three species of sharks **Carolin Nieder***	426 The role of small fishes for coral reef energy and nutrient fluxes: a tale of two theories **Simon Brandl**	394 Otolith chemistry improves age estimation and reveals movement history of catadromous barramundi (*Lates calcarifer*) **Nut Munpholsri****	556 Pelagic marine fish eggs from Korean waters revealed by morhpology and metabarcoding analysis **Haeyoung Choi**
4.30pm	471 The evolution of stripe patterning in clownfishes **Lucy Fitzgerald***	535 Seeing the world through the eyes of coral reef fishes **Fabio Cortesi**	436 Local and regional environmental drivers of growth in *Lutjanus erythropterus* in Western Australia **Muhammad Faiq Saleh**	327 Measuring thermal limits of fish heart mitochondria in a shoestring-lockdown project **Tony Hickey**	571 The success of spiny-rayed fishes in the deep-pelagic ocean discovered using a large midwater trawl **April Cook**
4.45pm	481 The Cenozoic collapse of the West Tethyan biodiversity hotspot: a test using the fish otolith fossil record **Hadeel Saad***	404 Novel molecular methods to investigate vision in coral reef fishes **Valerio Tettamanti****	555 Chronic oxygen loss but not warming increase dishonesty in cleaner wrasses **Beatriz P Pereira***	490 eDNA and compound specific stable isotopes reveal diet specialization and overlap in co-occurring parrotfishes of the Gulf of California **Dave Carlon**	
5.00pm	486 Evolution of substrate use across global assemblages of the goatfishes (Family Mullidae) **Chloe Nash**	Discussion	522 Reconstructing long-term growth of deep-water snappers throughout the Indo-Pacific using otolith chronologies **Joseph Widdrington****		
5.15pm	***Day 4 Concludes***				

Day 5, Friday 24 November 2023

8.00am - 9.00am	*Arrival Tea +Coffee* *OGGB Level 0+1 foyer*				
9.00am - 10.00am	Housekeeping **K. Radway Allen Award Plenary - Tony Smith** **Fishery harvest strategies in a dynamic and complex world** **Lecture Theatre 260-098**				
10.00am - 10.30am	*Morning Tea* *OGGB Level 0+1 foyer*				
10.30am - 12.30pm	**5.1A** **Themed Session A** Evolution, Taxonomy and Biogeography of Indo-Pacific Fishes	**5.2A** **Special Session 1** Moving beyond home-ranges: how can we harness fish movement ecology to study, understand and manage ecosystem functioning?	**5.3A** **Themed Session B** Ecology of Indo-Pacific Fishes	**5.4A** **Themed Session G** Long Term Monitoring of Indo-Pacific Fishes	**5.5A** **Special Session 9** Fisheries and the Potential of Artificial Intelligence and Machine Learning for Improving Sustainability Outcomes
	Lecture Theatre 260-098	**Lecture Theatre OGGB4 260-073**	**Fisher & Paykel Appliances Auditorium 260-115**	**Lecture Theatre OGGB3 260-092**	**Lecture Theatre OGGB5 260-051**
	Session Chair: Chris Goatley	Session Chair: Renato Morais & Robert Streit	Session Chair: Jenni Donalson	Session Chair: Lenore Litherland	Session Chair: Geoff Tuck
10.30am	516 Inconsistent patterns of phenotypic evolution among canonical ‘living fossil’ lineages **Rafael A. Rivero-Vega***	587 Assessing ecosystem functioning through 3D AI-enhanced fish tracking: A Red Sea case study **Julian Likendey**	455 Host sharing and territorial aggression in anemonefishes: investigating the formation of mixed-species groups around Lizard Island, GBR **Carl Santiago***	113 Interviewing anglers to understand changing catch composition in the 100-year-old east coast marlin fishery **Tristan Guillemin***	329 Technical and operational development of MLAI technology for application to electronic monitoring in marine fisheries **Richard Little**
10.45am	548 A new species of eight-gilled hagfish (Agnatha, Myxinidae) based on imported fish specimens **Young-Sun Song**	100 Deriving energy landscapes from stereo-video: Investigating the 3D trajectories of butterflyfishes on a coral reef with a turbidity gradient **Emily Jupp***	458 Phenotypic change to varying thermal experience within and across generations **Jenni Donelson**	116 Informing management with bioregional maps of benthic and fish assemblages from standardised stereo-video data **Claude Spencer**	267 Using AI to monitor recreational fish catch **Culum Brown**
11.00am	558 The marine origins of freshwater osteoglossid bonytongues (arowanas and arapaimas) **Alessio Capobianco**	464 Integrating movement data and behavioural observations to assess the functional role of reef fishes **Pauline Narvaez**	475 Herbivore communities through the lens of ecological processes across Pacific coral reefs **Tye Kindinger**	206 CheckEM: an open-source tool for quality control and visualisation of stereo-video fish and benthic annotations **Brooke Gibbons**	420 Attention-guided counting of seabirds in the wild for compliance of conservation **Muhammad Saqid**
11.15am	565 The diversity, evolution and ecological importance of dwarfgobies (*Eviota*) **Christopher Goatley**	198 Aquatic parasites in a changing world: emerging threats to fisheries resources **Shokoofeh Shamsi**	477 Varying importance of environmental variables on tropical snapper growth from the equatorial Indo-Pacific region **Zhong Wang Clement Ng****	352 Meta-analysis reveals weak associations between reef fishes and corals **Pooventhran Muruga****	21 Application of an electronic monitoring system and artificial intelligence data analysis in a small-scale tuna fishery **Ahmad Catur Widyatmoko***
11.30am	567 Century-old museum and modern fish specimens reveal temporal loss of adaptive potential and connectivity changes in the marine biodiversity epicenter **Eric Garcia**	117 Small coral reef fishes with large ecological footprints **William Collins****	482 High vulnerability of coral reef food web and energy fluxes to global change **Emma Paul Costesec***	443 Megafauna models: fine-tuning established morphometric equations through citizen science data **Veronika Biskis****	Discussion
11.45am	254 Deep-sea explorations **Wei-Jen Chen**	541 Nearshore habitat utilization and movement of Hawaiian bonefish (*Albula glossodonta*) on the reef flats of Moloka’i. **Brad Smith**	489 Long-term trends in coastal catch of pelagic rays along eastern Australia **Alysha Chan****	321 Challenges and opportunities in evaluating fish community composition for reefs under restoration at unprecedented scales **Pedro Pereira**	69 Exploring the capabilities and limitations of AI in developmental stage categorization and length extraction from images of tropical fishes **Alexandru Mihai**
12.00pm	569 Integrating molecular phylogenies and fossils without a morphological matrix to investigate patterns of trait evolution: A case study using Carangaria **Lindsey DeHaan***	302 Reef fish community shifts in the Kuroshio Current region over 10-15 years under ocean warming **Masaaki Sato**	499 Spatiotemporal drivers of parrotfish distribution around Moorea, French Polynesia indicate algal resources influence ontogenetic habitat shifts of parrotfishes **Noe Castaneda***	334 Safeguarding the threatened: the status of shallow reef species from temperate to tropical Australia **Olivia Johnson****	504 Integrating computer vision into the collection of fish measurement data for stock assessment **David Middleton**
12.15pm	290 Resurrection and redescription of nominal species previously regarded as synonyms of *Setipinna tenuifilis* (Valenciennes, 1848) **Harutaka Hata**	6 Long-term biodiversity monitoring reveals few polewards shifts in Australian shallow water reef species **Yann Herrera Fuchs***		338 The influence of MPAs, reef habitat, and human population on changes in fish diversity in the center of marine diversity **John Whalen***	Discussion
12.30pm - 1.30pm	*Lunch* *OGGB Level 0+1 foyer*				

1.30pm - 3.00pm	**5.1B** **Themed Session K** General Session	**5.2B** **Special Session 1** Moving beyond home-ranges: how can we harness fish movement ecology to study, understand and manage ecosystem functioning?	**5.3B** **Themed Session B** Ecology of Indo-Pacific Fishes	**5.4B** **Themed Session G** Long Term Monitoring of Indo-Pacific Fishes	**5.5B** **Special Session 9** Fisheries and the Potential of Artificial Intelligence and Machine Learning for Improving Sustainability Outcomes
	Lecture Theatre 260-098	**Lecture Theatre OGGB4 260-073**	**Fisher & Paykel Appliances Auditorium 260-115**	**Lecture Theatre OGGB3 260-092**	**Lecture Theatre OGGB5 260-051**
	Session Chair: Gerry Closs	Session Chair: Renato Morais & Robert Streit	Session Chair: Eva McClure	Session Chair: Maya Srinivasan	Session Chair: Richard Little
1.30pm	41 Reservoirs facilitate colonization of river catchments by invasive fish through provision of pelagic larval rearing habitat **Gerard Closs**	325 Exploring movement patterns of coastal reef fishes: insights for management and conservation **Alejandro Perez Matus**	529 Animal biomass on Earth's ecosystems: are coral reefs any special? **Renato Morais**	347 Optimising and sustaining an integrated biological monitoring program for fisheries in Queensland waters: Focus on Fish and Sharks **Lenore Litherland**	572 Biology guided neural networks and applications of machine learning techniques on specimen images gathered from fish collections **Yasin Bakış**
1.45pm	524 Engaging with recreational fishers to improve aquatic habitat restoration **Geoff Collins**	60 Unveiling movement patterns across habitats and time: insights from continuous otolith microchemistry data **Armagan Sabetian**	542 Does habitat and continental shelf position influence reef fish assemblage response to major disturbance? **Eva McClure**	266 Environmental DNA in practice: calibrating methods across labs and marine parks **Maarten De Brauwer**	400 Using deep learning to automate the detection of seabird bycatch and bird scaring lines on fishing vessels **Geoff Tuck**
2.00pm	531 Using empirical data to validate and update population models: a case study using a model for Golden Perch **Henry Wootton**	539 Movements of tiger sharks at a remote Northwestern Hawaiian Island are strongly influenced by prey availability **Bradley Wetherbee**	463 The dark side of the reef: the missing contribution of nocturnal species and biomass to shallow reef communities **Tyson Jones****	366 Integrated Reef Fish Monitoring of the Great Barrier Reef **Mike Emslie**	Discussion
2.15pm	538 The successive evolution of giant marine filter-feeders over macroevolutionary time **Lauren Sallan**	552 Movement behaviour of swordfish provisions connectivity between the temperate and tropical southwest Pacific Ocean **Barrett Wolfe**		278 Optimising coastal fish monitoring and reporting through predicted versus observed abundance models **Ben Gilby**	Discussion
2.30pm	570 Why have Mesopelagic Boundary Communities only been documented off Hawaii? Likely cosmopolitanism of mesopelagic associations with landmasses and their importance **Tracey Sutton**	56 Spawning migration and habitat use of adult Pacific bluefin tuna (Thunnus orientalis) in the northwestern Pacific Ocean **Wei Chuan Chiang**		451 Long term monitoring of fish and benthic communities on inshore island fringing reefs in the Great Barrier Reef Marine Park **Maya Srinivasan**	Discussion
2.45pm		249 Wandering the ocean: movements of an oceanic manta ray satellite tracked for 10 months in the Southwest Pacific **Mark Erdmann**			Discussion
3.00pm - 3.30pm	*Afternoon Tea* *OGGB Level 0+1 foyer*				
3.30pm - 4.30pm	**Conference Closing** **Lecture Theatre 260-098**				
4.30pm - 6.00pm					
6.00pm - 11.00pm	**Conference Dinner** **Pullman Hotel** **Address: Corner Waterloo Quadrant &, Princes Street, Auckland 1010, New Zealand**				
11.00pm	***Conference Concludes***				

* Student
**ASFB student member

Automated anomaly detection in fisheries from Electronic Monitoring: Modelling human activities using Artificial Intelligence

Debaditya Acharya[1]; Dadong Wang[3]; Geoffrey N. Tuck[2]; Lorne Richard Little[2]; Saqib Muhammad[3]

[1] *Geospatial Science, RMIT University, Melbourne, Australia*

[2] *Environment, CSIRO, Hobart, Tasmania, Australia*

[3] *Data61, CSIRO, Marsfield, New South Wales, Australia*

The availability of Electronic Monitoring (EM) has enabled the remote monitoring of fishing vessels and is increasingly being used to supplement or replace on-board observers. Many complex fishing operations are periodically monitored manually to assist the fisheries operations, such as stock assessment or ensuring compliance with fishing regulations. In addition, more subtle, anomalous behaviours of interest may be captured in the videos. However, reviewing several thousand hours of EM video footage is laborious. Recently Artificial Intelligence and Machine Learning is being employed to review the footage automatically. In this work, we present a framework to detect anomalous activities automatically by modelling the human activities visible in the EM cameras utilising the recent deep learning approaches.

First, we propose to model the most common activities performed by the fishers on deck, such as walking, sitting, running, jumping, swinging, etc. This can be performed by training a deep learning-based human activity detector in a supervised manner using some training examples. Subsequently, a distribution of the activities over time can be created from the observed activities by the fishers. Analysis of the distribution of the activities can provide a correlation with normal fishing activities and can help to identify anomalous events that can require further investigation. One of the strengths of the proposed approach is that anomalous activities can be inferred if not directly observable. Additionally, the proposed approach can be integrated into a multi-camera EM system for better reliability. The proposed framework can identify anomalies automatically for real-time mitigation

Modelling impacts of artificial barriers on riverine fish communities

Adams, Lukian[1]; Schilling, Hayden[2]; Suthers, Iain[1]

[1]*University of New South Wales*

[2]*NSW Department of Primary Industries*

Artificial barriers such as dams and weirs block the movement of biota in rivers, contributing to global declines in biodiversity of freshwater fish. In this study, fish community data collected over 28 years will be used to model impacts of artificial barriers on fish communities in the Murray-Darling Basin, a major Australian river catchment. The aim of this research is to explore how artificial barriers differentially affect fish communities across space and time, and how the movement ecology of fish, physical characteristics of structures, and temporal fluctuations in river flows drive impacts. This information can be used to guide research into fish passage restoration, and prioritise locations for restoration projects.

Swimming at increasing speeds in steady and unsteady flows of Atlantic salmon *Salmo salar*: behaviour, oxygen consumption and overall dynamic body acceleration

Agbeti, Wisdom E.K.[1]; Black, Suzy[2]; Komen, Hans[1]; Lankheet, Martin[3]; Magnoni, Leonardo[2]; Palstra, Arjan P.[1]

[1] *Animal Breeding and Genomics, Wageningen University & Research, Wageningen, The Netherlands.*

[2] *Plant & Food Research, Nelson, New Zealand.*

[3] *Experimental Zoology Group, Wageningen University & Research, Wageningen, The Netherlands*

When finfish farms are moved off-shore from sheltered to exposed areas of the sea, to what extent will unsteady flow conditions affect the swimming performance of the cultured fish species? Using a Loligo swim-flume, we investigated and compared the effects of steady and unsteady flow when swimming at increasing flow speeds, on oxygen consumption (MO_2), swimming behavior, and overall dynamic body acceleration (ODBA), as determined with implanted acoustic sensor tags, of post-smolt Atlantic salmon.

Sensor tags in the abdominal cavity had no significant effects on MO_2 and locomotory parameters. MO_2 of fish swimming in unsteady flows ($R^2= 0.92$) was significantly higher (24-35%) than in steady flows ($R^2= 0.85$). Although a similar optimum swimming speed was observed, the minimum cost of transport was about 27% higher in unsteady flows than steady flow. Among the locomotory parameters evaluated, only tail beat amplitude (TBA) was significantly different between unsteady and steady flow. Significant interaction effects of flow type and flow speed with ODBA were found. ODBA was strongly and positively correlated with flow speed and MO_2 in unsteady flow ($R^2= 0.94$ and $R^2= 0.99$, respectively), than in steady flow ($R^2= 0.63$ and $R^2= 0.85$, respectively).

From these results we can conclude that 1) swimming in unsteady flow is energetically more costly for post-smolt Atlantic salmon than swimming in steady flow as indicated by higher MO_2 and TBA, 2) ODBA can be used to estimate energy metabolism of post-smolt Atlantic salmon in unsteady and steady flow conditions.

2.4B Themed Session F: Conservation of Indo Pacific fishes, 260-092, November 21, 2023, 1:30 PM - 3:00 PM

Remote sensing in remote locations: A new approach to find and prioritise barriers to fish passage for conservation

Allan, Hugh[1]; Duncan, Richard[1]; Lintermans, Mark[1]; Unmack, Peter[1]; White, Duanne[1]

[1]*Centre for Applied Water Science, University of Canberra*

Many threatened fishes have suffered significant range reductions since the introduction of alien fishes, and remain only in isolated headwater refugia. In-stream barriers like waterfalls prevent upstream invasion by alien fish, however suitable waterfalls are scarce and often on streams in remote locations. Their remoteness means current methods for finding these barriers are inefficient, and surveying and characterising them is expensive. As such, locating remnant populations of many threatened species is hard to prioritise and urgently requires knowledge of potential barriers and refuge locations to improve distributional knowledge and find suitable translocation sites for conservation.

Lidar-derived elevation models were used to find and characterise potential waterfall barriers in headwater streams, and fish community either side of waterfalls was determined using backpack electrofishing. Waterfall height and gradient was examined to investigate patterns in streams where invasion by alien species has and has not occurred. These characteristics clearly partitioned barrier and non-barrier sites, with alien fish rarely found upstream of waterfalls greater than ~1 m high. Several previously unknown barriers and populations of native fish were discovered using this new method.

Lidar-derived elevation modelling provides a new and efficient desktop-based approach to locate and prioritise barriers to fish passage in remote locations, and provide insight into distribution of native and alien species.

Preliminary site evaluation using this approach means research and management funding may be spent more efficiently on targeted surveys at more likely sites, and conservation actions can focus on understanding threatened species distribution and developing translocation plans.

Drivers of parrotfish feeding and bioerosion along an offshore reef slope on the Great Barrier Reef

Allan, Hannah L.[1]; Hoey, Andrew[2]; Mumby, Peter J. [1]

[1]*Marine Spatial Ecology Lab, School of Biological Sciences, The University of Queensland, Queensland 4072, Australia*

[2]*College of Science and Engineering, James Cook University, Queensland 4810, Australia*

Carbonate budgets describe the balance between the production and erosion of reef calcium carbonate on coral reefs, and underpin crucial ecological functions and ecosystem services. Carbonate budget models can provide holistic reef monitoring tools, which are necessary to support effective reef management decisions in response to the threat of climate change. On the Great Barrier Reef (GBR), carbonate bioerosion is primarily driven by parrotfish grazing, but our understanding of this process is mostly limited to reef crests. In order to understand how bioerosion and carbonate budgets change with depth and across a reef, we observed the feeding behaviour of parrotfish along a reef slope at Heron Island (Southern GBR). We used visual observations to explore how parrotfish feeding varies according to reef slope depth as well as characteristics of the benthos, including substrate density and microhabitat. Preliminary results suggest that parrotfish feeding rates increase with depth, while the density of substratum grazed decreases with depth. Given that substratum density can strongly influence bioerosion modelling, surveys of natural behaviour were complemented with a manipulative experiment to further investigate if parrotfish demonstrate feeding selectivity driven by substratum density, as well as other benthos traits including microhabitat availability and algal colonisation. Our data reveal the complexities in disentangling parrotfish feeding patterns across species, body size, depth and other environmental variables, often with nuanced outcomes for bioerosion. Improving our mechanistic understanding of reef functioning will aid in the development of ecologically realistic monitoring tools and carbonate budget models.

Poster Function, OGGB Level 0 Foyer, November 21, 2023, 4:15 PM - 6:30 PM

Important Shark and Ray Areas: A process for delineating critical habitats for sharks, rays, and chimaeras around the globe

Asia O. Armstrong[1,2], Amanda Batlle Morera[1], Jenny Bortoluzzi[1], Ryan Charles[1], Emiliano García Rodríguez[1], Adriana Gonzalez Pestana[1], Peter M. Kyne[1,3], Theophile Mouton[1], Giuseppe Notarbartolo di Sciara[1,4], Christoph A. Rohner[1,5], Rima W. Jabado[1,6]

[1]*International Union for Conservation of Nature Species Survival Commission Shark Specialist Group, Dubai, United Arab Emirates*
[2]*School of Science, Technology and Engineering, University of the Sunshine Coast, Hervey Bay, Qld 4655, Australia*
[3]*Research Institute for the Environment and Livelihoods, Charles Darwin University, Darwin, NT 0909, Australia*
[4]*Tethys Research Institute, 20121 Milano, Italy*
[5]*Marine Megafauna Foundation, West Palm Beach, USA*
[6] *College of Science and Engineering, James Cook University, Townsville, Qld 4811, Australia*

Spatial planning is a priority for biodiversity conservation, and area-based measures have become an essential tool to safeguard declining biodiversity. Numerous approaches have been developed for protection of specific taxa (e.g., birds, marine mammals), and these are now widely accepted and used to inform planning. However, until recently, sharks, rays, and chimaeras (hereafter 'sharks') have been largely overlooked in marine spatial planning, despite being one of the most threatened faunal lineages (37% of species are considered threatened with extinction on the IUCN Red List of Threatened Species™). The Important Shark and Ray Areas (ISRA) approach was developed to put sharks on the map. A set of four science-based criteria, incorporating seven sub-criteria was developed. Criteria are applied to delineate areas based on shark vulnerability, range restriction, life history (reproduction, feeding, resting, movement, undefined aggregations), and special attributes (distinctiveness, diversity). The ISRA Criteria can be applied to all environments where sharks occur (marine, estuarine, and freshwater), with resulting areas delineated as discrete, three-dimensional portions of habitat that are important for one or more shark species with the potential to be managed for conservation. The process involves the identification of candidate ISRAs via 13 regional expert-based workshops. Resulting candidate areas undergo independent review to ensure they meet the science-based criteria. Approved ISRAs are officially mapped and added to a publicly available eAtlas of ISRAs (www.sharkrayareas.org). Delineating important areas for sharks globally will transform shark conservation, contribute to reduced mortality, and aid species recovery in this highly threatened group.

3.5B Themed Session E: Biology and Conservation of Sharks and Top-predators, 260-051, November 22, 2023, 2:30 PM - 3:30 PM

Spot the difference: Using artificial intelligence on individual markings of manta rays to delineate global populations

Armstrong, A[1], Stevens, G[2], Armstrong, A[3], Beale, C[2], Bennett, M[3], Berthe, C[2], Couturier, L[3], Cullain, N[4], Deakos, M[2], Dudgeon, C[1], Enders, I[2], Erdmann, M[2], Etpison, M[2], Fernando, D[2], Flam, A[4], Froman, N[2], Fuentes, K[2], Germanov, E[4], Gordon, L[2], Green, L[5], Harris, J[2], Hartup, J[2], Hilbourne, S[2], Kumli, K[2], Lassauce, H[2], Marshall, A[4], McGregor, F[6], Moskvyak, O[1], Murray, A[2], Peel, L[2], Pate, J[4], Ponzo, A[2], Rubin, R[2], Sawers, T[2], Setyawan, E[7], Sobral, A[2], Toanchina, C[2], Townsend, K[1], Travers, S[2], van den Berg, C[1], van der Poll, E[2], and Richardson, A[8]

[1]*Project Manta, University of the Sunshine Coast, Hervey Bay, Qld 4655, Australia*

[2]*The Manta Trust, Catemwood House, Norwood Lane, Corscombe, Dorset, DT2 0NT, UK*

[3]*School of Biomedical Sciences, The University of Queensland, St Lucia, Qld 4072, Australia*

[4]*Marine Megafauna Foundation, West Palm Beach, Florida 33411, USA*

[5]*Manta Watch New Zealand Charitable Trust, Auckland 0984, New Zealand*

[6]*Murdoch University Research Station, Coral Bay, WA 6701, Australia*

[7]*Institute of Marine Science, The University of Auckland, Auckland 1010, New Zealand*

[8]*CSIRO Oceans and Atmosphere, Queensland Biosciences Precinct, St Lucia, Qld 4067, Australia*

Unique individual markings are common in many species and have been used to understand aspects of their movement ecology and population dynamics. Numerous elasmobranch species display persistent individual markings through time, including manta rays *Mobula alfredi* and *M. birostris*. Here we apply convolutional neural networks (CNNs) to test whether unique markings of manta rays can be used to infer relatedness among individuals, and whether these markings can provide insights into connectivity or isolation among populations. We collated 55 photographic identification (photo-ID) databases from around the globe, representing separate populations of manta rays (28 for *M. alfredi* and 27 for *M. birostris*), totaling 21,115 individual rays. We applied CNNs to these photo-IDs to analyse pattern expression of individuals. We found pattern expression was different between the two species of manta rays; and both species showed significantly more variation in pattern expression among than within populations. We found differences in pattern expression were significantly associated with geographical distances between populations for *M. alfredi*, but not for *M. birostris,* likely a consequence of their different ecology. Findings from our analyses were comparable to findings from genetic studies in the literature, providing support for this novel approach. This study highlights that pattern expression in manta rays is likely to be a heritable trait and that CNNs for pattern recognition may prove to be useful for addressing ecological questions.

The UBC Fish Collection under the Beaty Biodiversity Museum: Status, challenges, and perspectives

Bailly, Nicolas[1], Howard, Ally[1], Isfeld, Leah[1], Mukohyama, Yuli[1], Taylor, Eric B.[1,2]

[1] *University of British Columbia (UBC), Beaty Biodiversity Museum (BBM), UBC-BBM Fish Collection*

[2.] *University of British Columbia, Department of Zoology*

The UBC Fish Collection was started in the early 20th century, catalogued after 1945, and completely computerized in 1977. Managed successively under different UBC units, it is now hosted by the UBC Beaty Biodiversity Museum created in 2010. Over one year, a complete inventory was performed in preparation for storage capacity extension, and the database conversion into Specify7.

The database lists about 35,000 lots, 350,000 specimens, 3,500 species, including 11 holotypes and some 200 paratypes for 40 species. The main country origins are Canada, mainly British Columbia, 45% of lots; USA, mainly Alaska, 27%; Mexico, 11%; and Panama, 3%. Fifty-five more countries account for less than 2% each. Marine species are more represented (63%) and dominated by common and important diadromous species from British Columbia (e.g., Salmonidae, Cottidae).

Inventories remain challenging when specimens of the same species, even lots, are spread across various sub-units (types, teaching, museum displays, skeletons, etc.). Also, reporting precise statistics should be standardized for global aggregators (e.g., GBIF, OBIS, FishNet). For example: counts may include all specimens once in the collection or only current holdings; some lots are split across several jars; counts in jars with dozens of small specimens are only estimated.

Since the 1980s, the collection was enriched from projects, rather than from regular surveys, and from a few expeditions. What should be the strategy of acquisition in the future? Focusing on British Columbia and Northeast Pacific? Launching or participating in overseas expeditions? This poster will give the opportunity to gather advice from colleagues.

Fish global information infrastructure: Linking existing fish biodiversity information systems

Bailly, Nicolas[1,2]

[1.] *Quantitative Aquatics, FishBase*

Several major global biodiversity information systems have been created over the past 50 years partly or only about fishes: IUCN, FAO, Eschmeyer's Catalog of Fishes (ECoF), FishBase, Catalogue of Life (COL), FishNet, Global Biodiversity Information Facility (GBIF), Ocean Biodiversity Information System (OBIS), Fishwisepro, Sea Around us, ZooBank, World Register of Marine Species (WoRMS), Welt der Fische, iNaturalist, Fishipedia to name the main ones (Wikipedia might be added). And many more regional and national ones, or dedicated to a taxonomic group. All these systems have their own purposes and specificities that may have evolved along the years. But are there synchronization mechanisms to prevent user's confusion?

This poster will present the current situation of relationships between the major information systems. They may share data, unique identifiers, perform independent updates, but in general, all these systems have some relationships, that will be documented as a global network graph. This graph will help colleagues and newcomers to understand differences and apparent contradictions between systems. And also, to realize that all this work is not given, but requires much working time, resources, discussions and collaboration / cooperation.

This is a dream to have all these information systems connected and updated in real-time. The technology is now developed enough to implement a global infrastructure, even if there are still theoretical (assigning Global Unique IDentifiers to names and taxa) and implementation complexities (using several to many software components), but they are not limiting. Establishing full cooperation between actors in the domain remains the biggest challenge.

FishBase 33 years after: status and current development on life-traits

Bailly, Nicolas[1,2]

[1] *University of British Columbia (UBC), Institute of Oceans and Fisheries, Sea Around Us*

[2.] *Quantitative Aquatics, FishBase*

After 33 years, the biodiversity information system FishBase (www.fishbase.org) continues to gather biological, ecological, and human uses information on all fishes of the world, as well as analytical tools and estimates for global analyses. Disseminated mainly through a website, data are also available in other formats/ways for research purposes: R package, APIs, customized data extraction. However, efforts are ongoing to better serve the community to adapt new IT technologies, and to avoid discrepancies between various sources, e.g., using containers for the website, improvement of the speed of updates.

As of June 2023, the database contained information for 35,293 valid species (over the 36,532 recorded by Eschmeyer's Catalog of Fishes - ECoF), about 95,000 synonyms, 8,000 misapplied and misidentifications, 1,700 identification keys, 330,000 common names as triplets [name, language, country] for 350 languages, 200,000 country occurrences, 63,000 FAO areas occurrences, 13,100 growth parameters, 23,400 length-weight relationships, 58,000 food items, 6,700 predator-prey relationships, 6,000 species reproduction information, 4,000 on fecundity, etc. extracted from 60,000 references. And more information on, ecosystems occurrences, brains, gill area, oxygen consumption, speed, etc.

FishBase is primarily a database aggregating life-traits data at species-level. However, not all information is available for all species. There is still literature to be exploited, but one can not expect that all species will ever be studied in details for all life-history aspects. FishBase proposes several models to compute estimations of missing parameters, e.g., using Bayesian statistics or neural networks. And now, a global framework to analyse them.

The NZ Fish Passage Guidelines: Enabling evidence-based policy implementation.

Baker, Cindy[1*]; Bowie, Sjaan[3]; Egan, Eimear[1]; Franklin, Paul[1]; Gee, Eleanor[1,2]; Melchior, Michele[1]; Vodjansky, Eugene[4], Aghazadegan, Liam[4]

[1]*National Institute of Water & Atmospheric Research, Hamilton, New Zealand*
[2]*Current address: Waikato Regional Council, Hamilton, New Zealand*
[3]*Department of Conservation, Christchurch, New Zealand*
[4]*Bloxam, Burnett & Oliver, Hamilton, New Zealand*

Many of New Zealand's iconic native fishes migrate between marine and freshwater habitats during their life cycle. This makes them highly susceptible to the impacts of river fragmentation. The National Policy Statement for Freshwater Management 2020 (NPS-FM 2020) sets out objectives to restore river connectivity by remediating instream structures to improve fish passage in New Zealand. There is a long history of fish passage interventions underperforming and failing to achieve desired environmental outcomes. This arises from inappropriate transfer and application of technologies that have not been designed or tested to ensure they are fit-for-purpose.

The NZ Fish Passage Guidelines were updated in 2023 to reflect new national policies and provide current best available information on techniques to protect and restore river connectivity in New Zealand. The Guidelines collate and summarise the current evidence on appropriate solutions for designing new and remediating both low (<4m) and high (>4m) existing instream structures to provide for more effective fish passage. This enables practitioners to easily adopt evidence-based practices and follow transparent and defensible processes for implementing national policy. We expect the new policies to drive a step-change in actions to restore fish passage in New Zealand and the 2023 NZ Fish Passage Guidelines to support both improved remediation and effectiveness monitoring of evidence-based solutions.

Biology guided neural networks and applications of machine learning techniques on specimen images gathered from fish collections

Bakış, Yasin[1]; Altıntaş, Bahadır[1,2]; Bart, Henry[1]; Wang, Xiaojun[1]

[1]*Tulane University Biodiversity Research Institute*

[2]*Bolu Abant Izzet Baysal University*

A new science discipline has emerged within the last decade at the intersection of informatics, computer science and biology which uses most recent technologies to analyse biological data but from the images. Machine learning is one of the most applied data analysis methods for image datasets. Biology Guided Neural Networks, a project that we have started in 2019, proposed extraction of biological features of fish from images of preserved collection specimens, and application of machine learning techniques for variety of analysis with the guidance of biological knowledge. We have built a data management system for the purpose of harvesting and filtering the data, capturing metadata and finally serving the data to machine learning scientists. Here, we will present our work on object detection, automated species identification, trait extraction, landmarking, applicability and accuracy of these methods with the improvements that we have performed. We have created workflows for different these applications that usually starts with raw images and end with products such as landmarked fish specimen images or an object detection model. We will describe fine tunings on some of the currently available methods for species identification, as well as on the models that we have generated for object detection, species identification, and automated landmark extraction. Finally, we will describe the pitfalls that has caused the most difficulty during the image processing and the neural network analysis part of our workflows.

The basal Eocene (ca. 55.5 Ma) Tethian marine fish fauna from southwestern Russia

Bannikov, Alexander F. [1]

[1] *Borissiak Paleontological Institute, Russian Academy of Sciences, Profsoyuznaya 123 – 117647 Moscow, Russia*

Excavations in the Paleogene deposits outcropping along the Kheu River in Gerpegezh, Republic of Kabardino-Balkaria, northern Caucasus (SW Russia) led to the discovery of a new basal Eocene fish assemblage from a sapropelitic layer deposited in response to the greenhouse conditions associated to the Paleocene-Eocene Thermal Maximum (PETM, ca. 55.5 Ma). At least three more fossil fish localities characterized by exceptional preservation originated during the anoxic event associated to the PETM, one in Denmark, the other in Egypt, and the third in Turkmenistan. The ichthyofauna of the Gerpegezh locality still has not been investigated in detail. However, a cursory survey of the material collected from the Kheu River sapropelitic layer revealed the presence of anguilliforms, clupeiforms and several percomorphs, many of which represented by larval or juvenile individuals. Unfortunately, most of the fish specimens are badly damaged by the pirite which usually replaces the original bony substance in the sapropelitic layer. Preliminary list of the basal Eocene Gerpegezh teleost fish fauna is as follows: Anguilliformes cf. Georgidentidae indet.; “*Opsithrissops*”-like lower teleosts; Clupeidae indet.; Cyclosquamata indet.; Ophidiiformes indet.; Lampridiformes cf. Lophotidae indet.; Aulostomoidei indet.; Syngnathidae indet.; *Gerpegezhus paviai* Bannikov et Carnevale, 2012; Scorpaenoidei indet.; Percoidei indet.; Priacanthidae juv.; *Mene* sp.; “*Avitoluvarus*” sp.; *Kushlukia* cf. *permira* Dan.; Gempylidae indet.; Scombridae gen. et sp. indet.; *Auxides* sp.; *Eospinus* sp.; Diodontidae gen. et sp. indet.; *Balkaria histiopterygia* Bannikov, Tyler, Arcila et Carnevale, 2016. The fauna’s composition differs greatly from those of Denmark, Egypt and Turkmenistan, although it reveals certain similarity to the latter.

New insights on marine angelfish evolution from genome-scale data.

Baraf, Lauriane[1]

[1] *College of Science and Engineering, James Cook University, Townsville, QLD, 4811, Australia*

The degree of systematic resolution across the teleost tree of life has increased exponentially since the introduction of phylogenetic methods in the 1970s as a mean to resolve evolutionary histories. With advances in sequencing technologies, the leap from genetics to genomics has been equally rapid. However, despite numerous well-supported phylogenetic reconstructions, many nodes in the fish tree of life have remained a challenge to resolve. Factors underlaying the astonishing diversity of teleosts, particularly across taxonomically broad assemblages such as fishes associated with tropical reefs, have intrigued evolutionary biologists for decades. Identifying and understanding the implications of those factors require comprehensive genetic material and robust phylogenetic frameworks. Here, we investigate the sources of systematic and biological discordance in the phylogenomics of the family of marine angelfish (*F:* Pomacanthidae). The phylogenetic reconstruction for 45 pomacanthid species across all nine genera, inferred from target capture of ultra-conserved elements of the genome, was largely congruent with prior analyses and helped to resolved previously contentious nodes. Combined concordance factor analyses on unphased and phased datasets, branch length and introgression tests, allowed an in-depth examination of the factors underlying the remaining topological discordance. Preliminary results suggest that longstanding phylogenetic conflict in the family Pomacanthidae arose from rapid diversification and ancient introgression events. Overall, this project helped identify key evolutionary processes that shaped the complex evolution of marine angelfishes and improve our understanding on how to diagnose discordance in genome-scale phylogenies.

2.5A Themed Session E: Biology and Conservation of Sharks and Top-predators, 260-051, November 21, 2023, 10:30 AM - 12:30 PM

Global Correlates of Shark and Ray Meat Consumption

Barbosa Martins, Ana[1]; Babckock, Elizabeth[2]; Jabado, Rima[3]; Judah, Aaron[1]; Kasana, Devanshi[4]; MacNeil, Aaron[1]; Mull, Christopher[1]; Renshaw, Samantha[1]; Schlawinsky, Merle[5]; Tyabji, Zoya[1].

[1] *Dalhousie University*

[2] *University of Miami*

[3] *Elasmo Project*

[4] *Florida International University*

[5] *James Cook University*

The commercialization of sharks and rays, and their products generate jobs and income for a range of stakeholders, with shark and ray meat playing an important role in food and nutritional security in many coastal communities. The consumption of shark and ray meat is directly influenced by ecological (e.g., species diversity, and availability) and economic (e.g., product value and catch effort) factors. However, the influence of social and cultural characteristics, aspects that strongly influence eating habits and dietary preferences of communities, are poorly understood. Here, we identify the main correlates of shark and ray meat consumption through a systematic literature review, focusing on socioeconomic and cultural dimensions, and evaluate regional variation in shark and ray meat consumption on a global scale. Across the studied regions, several correlates were reported in the literature as drivers or barriers of shark and ray meat consumption, such as price and sensory perception (taste, texture, smell), health benefits or risks, eating habits, convenience of preparation, cultural and religious traditions, and livelihood and food security. With the decline of some shark and ray populations worldwide and lack of data to inform management, we emphasize the incorporation of correlates of consumption to help identify key aspects of shark and ray meat production and trade, as well as guide managers to ensure both shark and ray conservation and livelihoods.

Thermal environment mediates density-dependent effects on the growth of a commercially harvested fish

Barrow, Joshua[1], Garland, Anna[2], Morrongiello, John[1]
[1]*School of Biosciences, University of Melbourne, Parkville, Vic, 3010, Australia*
[2]*Department of Agriculture and Fisheries, Qld, 4000, Australia*

Spatiotemporal variation in temperature, abundance, and fishery harvest are important drivers of somatic growth in fish. Temperature effects can manifest via different pathways: Directly, through temperature-sensitive physiological pathways and the regulation of metabolic activity; and indirectly, through stimulation of the food web. Both pathways are important in determining fish growth, but understanding their relative importance is challenging in the field and thus seldom compared. Density-dependent processes influence competition and food availability, while fisheries harvest can reduce densities as well as truncating population size-structure. Here, we provide a critical evaluation of relationships between total fishery catch, standardised catch-per-unit-effort (CPUE, a proxy for abundance), and two contrasting temperature variables: 1) annual mean temperature from important months for growth (direct); and 2) a regressed temperature variable representing temperature-mediated changes in the food web (indirect) on life stage-dependent fish growth. We used otoliths from pearl perch (*Glaucosoma scapulare*) captured across over five degrees of latitude in Queensland, Australia. Overall, indirect temperature better explained growth variation than direct temperature. There was a strong relationship between growth and relative abundance, but this was mediated by indirect temperature such that growth was positively associated with warming at low densities and negatively associated with warming at high densities. Furthermore, this effect varied across latitude and maturity. We suggest that competition for resources and environmentally mediated food availability play crucial roles in driving pearl perch growth. Our results provide valuable insights into how temperature and fishing affect growth, with implications for growth modelling techniques and subsequent management of fisheries.

Updating FishNet2 to serve the needs of the ichthyological research community

Bart, Henry[1]; Bakiş, Yasin[1]; Wang, Xiaojun[1]; Cruz, Shannon[1]

[1]*Tulane University Biodiversity Research Institute*

The original FishNet and its successor, FishNet2, have served the needs of researchers for quality metadata on specimens in ichthyological research collections since 1999. Originally a distributed-query based network, the platform changed to a cached-based query system when Tulane University took over management of the system in 2009. FishNet2 currently comprises data from 75 institutions globally and provides researchers access to 4.8 million records, representing nearly 50 million fish specimens. It is the most trusted biodiversity portal for scholarly research on fishes. However, the proprietary software on which the platform was built is past end of service life and needs to be updated. This poster will describe revisions that are being made to most of FishNet2's operating system, codebase and other system components thanks to generous support we've received from the US National Science Foundation. The updates are being made using the latest technology and Open-Source products. The relational database design will have built-in flexibility to add data fields not currently reported to FishNet2 users. New search and results-reporting features are also being implemented. We are also implementing new data cleaning services and for reporting data enhancements to data providers. We are offering a variety of support services for FishNet2 data providers and users, including a FishNet2-specific R package, a web forum for communicating with users and data providers, a FishNet2 hosted Integrated Publishing Toolkit service, and a new and improved FishNet2 API. The FishNet2 user base is being expanded to include educators and the general public.

Oceanic larval fish assemblages in the south-east Indian Ocean

Beckley, Lynnath[1]; Olivar, Maria-Pilar[2]

[1]*Murdoch University, Perth, Australia*

[2] *Institut de Ciències del Mar, Barcelona, Spain*

Day and night depth-stratified sampling of oceanic fishes using a 1m^2 multi-net (500-micron mesh) was undertaken in May and June 2019 along 110°E across about 30° of latitude in the SE Indian Ocean. In total, 166 species of fishes were recorded, of which >90% were mesopelagics that were mostly larval and transforming stages although some juveniles and adults were also caught. The families Myctophidae (lanternfishes; 60 species), Phosichthyidae (lightfishes; 2 species) and Gonostomatidae (bristlemouths; 5 species) were numerically dominant. Abundance, species richness and diversity increased from the cooler waters south of the Sub-tropical Front to the more northern tropical waters influenced by the Indonesian Through Flow. Clustering of integrated abundance data (0-500 m depth) showed five major fish assemblages along the transect. When linked to oceanographic variables, surface temperature, surface salinity and dissolved oxygen at 400 m depth provided the best fitting model explaining horizontal distribution patterns. Separate vertical distribution analyses of larvae showed them to be concentrated in the epipelagic zone during both day and night. Cluster analysis of larval samples from the upper 200m of the water column revealed several groupings. The relationships between mean values of oceanographic variables per depth stratum and larval fishes were examined with distance-based linear models and temperature and dissolved oxygen were found to be the most significant variables. Overall, this comprehensive study has highlighted the influence of different oceanographic conditions on horizontal and vertical distributions of larvae in the SE Indian Ocean.

Fish on reefs: A new perspective

Bellwood, David R[1]

[1]*James Cook University*

Fishes are the quintessential conduits for human interest and activity in the aquatic realm. We look, catch, admire, and eat them. As coral reefs change in the Anthropocene fishes are our guides to help us understand and come to terms with this change; but how do we read the messages that fishes are conveying? Arguably one of the most revealing approaches is to view fishes through the lens of ecosystem functions. Fishes are involved in almost every key function on coral reefs. I will therefore provide an overview of recent fish research in the Reef Function Hub at JCU, outlining the transformational insights gained from four years of dedicated research on reef ecosystem functions. The results emphasise the strong links between fishes and the physical environment, while offering some hope for the future of coral reefs, the fish that live on them, and the people who can’t resist studying them.

2.3B Themed Session B: Ecology of Indo-Pacific Fishes, 260-115, November 21, 2023, 1:30 PM - 3:00 PM

Seabirds provide diverse benefits to coral reef fishes through cross-ecosystem nutrient subsidies

Benkwitt, Casey[1]; Graham, Nick[1]

[1]*Lancaster University, UK*

Tropical coral reefs thrive in part by relying on natural nutrient inputs from other ecosystems, with mobile animals providing one such link. However, humans have disrupted many of these nutrient pathways, the implications of which are poorly understood. Here, we integrate our recent and forthcoming results from three archipelagos across the Indian and Pacific Oceans to illustrate how natural nutrient subsidies provided by seabirds move through coral-reef food webs, consequently influencing the behaviour, demography, and functional role of reef fishes. Around islands with healthy seabird populations, seabirds transport nutrients from pelagic feeding grounds to nearshore coral reefs, where the nutrients are assimilated by benthic organisms and can enhance benthic primary productivity. In turn, seabird-derived nutrients are transferred through multiple trophic levels of coral-reef food webs, including herbivorous, omnivorous, and piscivorous fishes. Herbivores in particular exhibit altered behavior and grazing rates, as well as faster growth rates, with increasing seabird-derived nutrients. However, there are some demographic trade-offs between increased growth and decreased fecundity in a functionally-important parrotfish. Scaling up to entire assemblages, fish biomass and productivity are often greater around seabird-rich islands. Collectively, these data demonstrate that the benefits of seabird-derived nutrients for coral-reef fishes are evident across large spatial scales and disparate locations. Such wide-reaching effects further suggest that restoring lost nutrient pathways provided by mobile animals should be considered as part of coral reef conservation plans.

Whistle-stop tour of shark and ray biology, fisheries, policy and conservation in the Western Indian Ocean

Bennett, Rhett[1,2]; van Beuningen, Dave[1]; Ebert, Dave[3,2]; Bernard, Anthony[2,4]; Davids, Aseeqah[2]; Juby, Roxy[2]; Sitoe, Jorge[1]; Sidat, Naseeba[1]; Fernando, Stela[5]; Oddenyo, Remy[1]; Razafindrakoto, Christelle[1]; Abdulla, Abdalla[1]; Mensa, Jean[1]

[1]*Wildlife Conservation Society*

[2]*South African Institute for Aquatic Biodiversity*

[3]*Pacific Shark Research Center, Moss Landing Marine Laboratories*

[4]*Department of Zoology and Entomology, Rhodes University*

[5]*Instituto Oceanográfico de Moçambique*

The Western Indian Ocean (WIO), encompassing South Africa to Somalia, Seychelles, Madagascar and the Mascarene Islands, is home to at least 224 chondrichthyan (shark, ray and chimaera) species. Taxonomy and biogeography have been advanced through updated species checklists for the WIO, with recent surveys revealing at least 25 new country records and range extensions. Chondrichthyan research priorities, highlighted though ecological and biological data gap analyses, include reproductive periodicity, gestation period, breeding season, parturition season, movement behaviour, genetic connectivity, and identification of aggregation, nursery, parturition and breeding areas, particularly for threatened species.

Long-term monitoring of artisanal catches revealed >60 (mostly threatened) shark and ray species being landed. FAO Fishing Area 51 reported the 3rd largest chondrichthyan catch globally over the past three decades. WIO states reportedly landed >163,000 t and exported >10,000 t of chondrichthyan products, including 950 t of fins, from 2012–2019, although reported catch and export volumes are gross underestimates. Owing to overexploitation, 40% of WIO chondrichthyan species are threatened. Baited video surveys revealed several hotspots for chondrichthyan abundance and diversity but confirmed generally low abundances of coastal sharks and rays in most areas.

Conservation and management of chondrichthyans in the WIO require dramatic improvement, through improved ecological and biological knowledge, improved fishery and trade monitoring and reporting, and strengthened fisheries policy, management measures and enforcement. To increase protection for threatened chondrichthyans and improve implementation of binding measures under conservation agreements, a proposal was submitted to have 29 shark and 21 ray species legally protected throughout the WIO.

Responses of tropical damselfishes to ocean warming and habitat degradation

Bernal, Moisés A. [1]

[1] *Department of Biological Sciences, College of Science and Mathematics, Auburn University, Auburn, Alabama, USA*

Anthropogenic activities are leading to unprecedented changes in the world's climate, which can be detrimental to marine species. Most marine organisms are ectotherms that are heavily influenced by the temperature of the surrounding environments. Increasing temperatures usually leads to higher energetic requirements, and if these demands are not met, there can be cascading negative effects on key processes such as reproduction, locomotion and development. Recent studies have shown how adaptation and acclimation can lead to mechanisms for compensation to ocean warming. Still, questions remain on the molecular mechanisms associated with compensation to thermal stress, the role of developmental and transgenerational exposure in the context of warming, as well how warming and habitat degradation can influence marine fishes. With this in mind, this seminar will focus on the molecular, behavioural and physiological responses to temperature fluctuations in tropical damselfishes.

The genomics of the *Dascyllus trimaculatus* species complex

Bernardi, Giacomo[1]; Roberts, May[1]; Salas, Eva[1]

[1]*Department of Ecology and Evolutionary Biology, University of California Santa Cruz, California, USA*

The three spot dascyllus, *Dascyllus trimaculatus*, is part of a species complex that comprises four recognized species, *D. albisella, D. strasburgi, D. auripinnis,* which are restricted to the Hawaiian, Marquesas, and Line Islands, respectively, as well as *D. trimaculatus*, which has a broad distribution from the Red Sea to French Polynesia and north to Japan. We have used genomic approaches (RAD sequencing and whole-genome resequencing) to evaluate the potential for species boundaries in this complex. We found that genomic data are consistent with *D. albisella* and *D. strasburgi* as being isolated and well-defined species. In contrast, we have found that *D. trimaculatus* shows a major genetic divergence between Indian and Pacific Oceans, with a hybrid zone in Cocos-Keeling and Christmas Island, thus defining two genetic entities. In addition, a population in French Polynesia displays another major genetic divergence from the main Pacific clade. Finally, we found that while *D. auripinnis* may be identified genetically, it also introgresses clinally with a Japanese population in the north, and likely a Fijian population in the south. As a whole, the *D. trimaculatus* species complex displays a panel of speciation modes, from ancient allopatric divergence to recent peripatric speciation, and some examples of continuing gene flow among populations.

“Ghosts in the machine” of diversification analysis

Berv, Jacob S.[1,2,3]

[1]Department of Ecology and Evolutionary Biology, 1105 North University Avenue, Biological Sciences Building, University of Michigan, Ann Arbor, Michigan, 48109-1085, USA

[2]University of Michigan Museum of Paleontology, 1105 North University Avenue, Biological Sciences Building, University of Michigan, Ann Arbor, Michigan, 48109-1085, USA

[3]University of Michigan Museum of Zoology, 1105 North University Avenue, Biological Sciences Building, University of Michigan, Ann Arbor, Michigan, 48109-1085, USA

The application of statistical models to the study of speciation and extinction has revolutionized our understanding of macroevolutionary history. Recently, several studies have reported inverse latitudinal gradients in speciation rates, contrary to predictions from ecological theory, which posits that the latitudinal diversity gradient derives from increased speciation toward the tropics. In research currently in preparation, I investigated these global patterns using simulations to study whether and when the models commonly used to study patterns of diversification may provide misleading results. I focused on scenarios where a lack of biological realism concerning heterogeneous patterns of molecular evolution can drive pre-determined outcomes in statistical analyses of lineage diversification. I find that a very weak correlation between a phenotypic trait of interest, such as body mass, and the underlying rate of molecular evolution can induce a strong spurious correlation between the phenotypic trait and the estimated speciation rate. Incorporating increased biological realism into these models, I show that global patterns reported in the literature across many taxonomic groups may be statistical artifacts.

Genomic signatures associated with ecological transitions in freshwater catfish clades of marine origin, with emphasis on an adaptive radiation

Betancur-R, Ricardo[1]; Rincon-Sandoval, Melissa[1]; De-Kayne, Rishi[2]

[1] Scripps Institution of Oceanography, University of California San Diego, 8622 Kennel Way, La Jolla, CA 92037

[2] Department of Ecology and Evolutionary Biology, University of California Santa Cruz, Santa Cruz, CA 95064

Colonization of vacant habitats has played a crucial role in shaping the evolutionary trajectory of various taxa, sometimes resulting in adaptive radiations (ARs). In Australia and New Guinea (AU-NG), freshwater fish communities predominantly consist of lineages that have evolved from marine ancestors, encompassing numerous instances of ARs. One such group are the ariids (sea catfishes), which include an AR in AU-NG and multiple geographically independent, non-radiating freshwater lineages worldwide. We investigated the influence of three major habitat transitions (marine-to-freshwater, stenohaline-to-euryhaline, and water column) on episodic diversifying selection in candidate genes and changes in transposable element (TE) content. We assembled a chromosome-level reference genome from one species in the AR and generated whole-genome resequencing data for 66 additional species. After combining this dataset with additional pre-existing data, we produced a robust phylogenomic framework for 119 species, across which we observed 10-12 marine-to-freshwater transitions (1 in AU-NG), 9-11 stenohaline-to-euryhaline transitions (5-7 in AU-NG), and 5-6 transitions (3-4 in AU-NG) to pelagic planktivory. Across these transitions, we identified signatures of positive selection associated with various functional categories, including osmoregulation (aquaporins), gill rakers (FGF proteins), and body shape and size. The AU-NG AR exhibited fewer positively-selected genes compared to other freshwater clades, and had reduced genomic TE content. This aligns with previous work showing that species occupying novel habitat regimes may undergo adaptive changes in TE coverage. Our findings underscore the significance of adaptive selection in molding organismal traits in response to environment characteristics, especially when these traits play a pivotal role in AR.

The mechanisms of habitat change in the cavefish *Astyanax mexicanus*

Bilandžija, Helena[1]; Čupić, Mateo[1]; Horvatiček, Marina[1]; Klein, Valentina[2]; Lukić, Marko[1]

[1]*Rudjer Boskovic Institute, Department of Molecular Biology, Bijenicka 54, 10000 Zagreb, Croatia*

[2]*University of Zagreb, Department of Biology, Rooseveltov trg 6, 10000 Zagreb, Croatia*

The Mexican tetra, *Astyanax mexicanus*, is a teleost fish which consists of cave-dwelling and river-dwelling populations. Cavefish diverged from surface fish as recently as 30,000 years ago but show fascinating morphological, physiological and neurological adaptations, including the loss of eyes and pigmentation, increased mechano- and chemosensory capabilities, altered metabolism, and different levels of neurotransmitters. This raises the question what mechanisms enabled such rapid evolution of adaptive traits. We have previously shown that surface fish has extensive phenotypic plasticity when exposed to darkness, the most important environmental characteristic distinguishing cave from surface habitats. On the other hand, cavefish show reduced plasticity, and their adaptative traits have a genetic basis. This suggests that canalization and genetic assimilation were involved in cavefish evolution, but the molecular mechanisms remain unknown. We are currently investigating the molecular basis of plasticity in surface fish and the possible role of epigenetics, including DNA methylation, in the evolution of cavefish traits.

5.4A Themed Session G: Long Term Monitoring of Indo-Pacific Fishes, 260-092, November 24, 2023, 10:30 AM - 12:30 PM

Megafauna models: fine-tuning established morphometric equations through citizen science data

Biskis, Veronika N.[1,2]; Holmes, Bonnie E.[3]; Lear, Karissa M.[4]; Morgan, David L.[4]; Townsend, Kathy A.[2], Wueringer, Barbara E.[1, 5]

[1] *Sharks And Rays Australia, Bungalow, Queensland 4870, Australia*

[2] *School of Science, Technology and Engineering, University of the Sunshine Coast, Hervey Bay QLD 4655, Australia*

[3] *School of Science, Technology and Engineering, University of the Sunshine Coast, Sippy Downs QLD 4655, Australia*

[4] *Freshwater Fish Group & Fish Health Unit, Centre for Sustainable Aquatic Ecosystems, Harry Butler Institute, Murdoch University, Murdoch, Western Australia 6150, Australia*

[5] *School of Natural Sciences, Macquarie University, New South Wales 2109, Australia*

Patchy data for globally threatened species poses challenges in both establishing historic baselines and assessing current distributions. In the case of sawfishes, previous research has relied on trophy rostra to fill data gaps, pairing size, location, and date information for a more complete indicator of decline. However, the established morphometric models that allow estimation of total length from rostra are restricted by the data available to generate them, with many constructed purely via juveniles. This is of concern due to changing rostrum morphology with size, creating a potential overestimation of total length and unfounded assumptions of maturity. This study seeks to identify a single model to be used for each sawfish species, accurate across all life stages. Published models are assessed for accuracy through an independent dataset from the Sharks And Rays Australia (SARA) citizen science database, and ontogenetic shifts in rostrum morphology are explored. Rostrum-to-length morphometric models (RLMs) were confirmed for each of *Pristis spp.*, while error was exposed through application to adult *Anoxypristis cuspidata*, due to changing rostrum morphology with body size. This study highlights the problems associated with extrapolating total lengths of animals beyond the size bounds used to produce the original model. For historically exploited species like sawfishes, represented in collections by trophies alone, these methods outline a critical step prior to use in further ecological study.

Don’t Wanna Be Your Bony Wrench: phylogenetic inferences from skeletal morphology of dwarfgobies, genus *Eviota* (Gobiidae), and other coral-reef gobies

Vaz, Diego[**1**]; Goatley,Christopher[2]; Tornabene, Luke[3]

[1] *Marine Laboratory, University of Guam. 303 University Dr, Mangilao, Guam, USA 96923.*

[2] *University of Southampton. National Oceanography Centre, Waterfront Campus European Way, SO14 3ZH Southampton, UK.*

[3] *Burke Museum and University of Washington Fish Collection. School of Aquatic and Fishery Sciences. 1122 NE Boat Street FTR Building, Seattle, WA, USA 98105.*

Dwarfgobies (genus *Eviota*) are a speciose group of cryptobenthic fishes distributed across Indo-Pacific coral reefs. Species of this genus are characterized by their diminutive size (< 30 mm) and for having a very short life span of less than 100 days. Integrative taxonomy in conjunction with underwater photography employed in the last thirty years led to an explosion in descriptions of new species, currently with 128 species. Despite the recent advances on the taxonomy, skeletal anatomy of *Eviota* is poorly known. This study presents accounts of the skeleton of more than 30 species of *Eviota* in addition to comparisons with *Gobiodon*, *Paragobiodon*, *Pleurosicya*, and *Brianinops*. The interopercle of all examined species of *Eviota* extends anteriorly, contacting the lower jaw and lacking the retroarticular-interopercle ligament. In other gobies the interopercle does not contact and is connected to the lower jaw through the retroarticular-interopercle ligament. Species in a clade of *Eviota* united by branched pectoral-fin rays have the posterior tip of the interopercle shaped like a wrench, which articulates directly with the posterior ceratohyal. This condition is different than the observed in any other Gobiidae (and Teleostei) to date. *E. prasites*, *E. bifasciata*, *E. atriventris*, *E. lachdeberei*, *E. nigriventris*, *E. infulata*, and *E. seebrei* lack the posterior portion of the mesethmoid. Other species of *Eviota* and other gobiid genera have a trapezoidal posterior portion of the mesethmoid that extend posteriorly to the posterior region of the ethmoid cartilage. The phylogenetic significance and implications resulting from these skeletal variations are discussed.

1.1B Themed Session: A. Evolution, Taxonomy and Biogeography of Indo-Pacific Fishes, 260-098, November 20, 2023, 2:00 PM - 4:15 PM

Phylogenomics of lampreys and the evolution of diverse life history strategies

Bloom, Devin D.[1]; Hughes, Lily[2], Lang, Nick[3], Mayden, Rick[3], Piller, Kyle[4]

[1]*Western Michigan University*

[2]*North Carolina Museum of Natural History*

[3]*Saint Louis University*

[4]*Southeastern Louisiana University*

Lampreys are a group of >40 jawless fishes revered for their ecological and cultural value, maligned as invasive species, and iconic for holding a key phylogenetic position in early vertebrates. They also exhibit unique life history combinations, exhibiting parasitic and non-feeding adults, and anadromous (migratory) and freshwater resident species. Theory model predicts anadromy should evolve from marine ancestors in temperate regions. However, empirical and conceptual hypotheses based on lamprey biology propose freshwater species are derived from anadromous ancestors. Non-parasitic life histories are hypothesized descend from parasitic lineages, yielding parasitic/non-parasitic “species pairs”. In this study we present a phylogenomic analysis of lampreys and explore the evolution of diadromy and parasitic life histories in this clade. Contrary to previous phylogenetic work we found *Geotria* and *Mordacia* are sister taxa, supporting a monophyletic southern hemisphere lineage. Petromyzontidae is well support as monophyletic, and we propose a revised classification of genera within this family. We found the ancestral state for crown lampreys is ambiguous, but anadromy evolved early in crown lampreys. Anadromy evolved at least seven, and as many as ten times in lampreys. Most anadromous lampreys are nested within freshwater clades, suggesting this life history strategy is not the ancestral state for lampreys. Less than half non-parasitic species have clear parasitic sister lineage, and there are diverse clades of non-parasitic species, indicating non-parasitic life history strategies are advantageous in many ecological contexts.

New Australian and global maximum depth records for bony fish.

Jamieson, Alan[1]; Maroni, Paige[1]; **Bond, Todd[1]**

[1]*Minderoo-UWA Deep-Sea Research Centre, The University of Western Australia, Crawley, Australia.*

A new maximum depth record for bony fish (Teleostei) has been set at 8336 m deep in the Izu-Ogasawara Trench (NW Pacific Ocean) and an Australian depth record has been set at 6177 m deep at the eastern margin of the Diamantina Fracture Zone (SE Indian Ocean). Sampling was undertaken using baited landers which provided video footage of both records. The Australian record was accompanied with two trapped specimens which also represent the deepest fish caught in Australia. Molecular analyses of these Australian fish have identified them as *Paraliparis selti*; snailfish, only previously recorded from Atacama Trench (SE Pacific Ocean). No samples were collected where the deepest fish was filmed in Japan however, two specimens were collected from 8022 m and represent the deepest fish ever caught. Using molecular analyses, these individuals were identified as *Pseupodoliapris belyaevi*. Both depth records and accompanying specimens enable us to contextualize our findings on a global scale and demonstrate the progress in hadal fish research in the last decade. The increasing availability of data reveals clearer distribution patterns and facilitates more accurate predictions. These records (and the many zeros surrounding them) begin to resolve trends in hadal biogeography, bathymetry and ecology.

4.2B Special Session 2 Facing environmental changes: what are the genetic and epigenetic mechanisms providing resilience in fishes?, 260-073, November 23, 2023, 1:30 PM - 3:00 PM

MicroRNAs and thermal transgenerational plasticity in a coral reef fish

Bonzi, Lucrezia C.[1]; Donelson, Jennifer M.[2]; Spinks, Rachel K.[2]; Munday, Philip L.[2]; Ravasi, Timothy[2,3]; Schunter, Celia[1]

[1] The Swire Institute of Marine Science, School of Biological Sciences, The University of Hong Kong, Hong Kong SAR

[2] ARC Centre of Excellence for Coral Reef Studies, James Cook University, Australia

[3] Marine Climate Change Unit, Okinawa Institute of Science and Technology Graduate University, Japan

The ability to respond and acclimate to environmental perturbations is the basis of the persistence of organisms in rapidly changing environments. Crucial for species resilience over climate change time scales are acclimation strategies that are passed on from parents to the next generations, so called parental effects. The epigenetic mechanisms responsible for such molecular and, ultimately, phenotypic plasticity are often still unknown. In this study we benefited from the ability of a coral reef fish to acclimate over a generation to elevated water temperature to investigate the possible involvement of microRNAs (miRNAs) in such thermal transgenerational plasticity. We exposed mothers, fathers and offspring of the spiny damselfish *Acanthochromis polyacanthus* to increased water temperature simulating future climate change conditions. Offspring livers were then analyzed for miRNA expression changes due to the offspring's own thermal exposure experience, as well as the ones of their two parents. Our findings characterize not only the miRNA repertoire involved in thermal acclimation, but also investigate the shared and unique signatures of each generation and each parent in shaping this epigenetic response. Overall, with this study we provide insights into an unexplored epigenetic mechanism putatively involved in a fish's thermal acclimation potential, providing a new piece to the puzzle of mechanisms underlying transgenerational phenotypic plasticity.

Can small habitat enhancements benefit fish assemblages adjacent to the Sydney Opera House?

Beretta, Giglia A[1]; Bombonato, Emma[2]; Goad, Alex[3]; Booth, David J[1]

[1]*Fish Ecology Lab, University of Technology Sydney*

[2]*Environmental Sustainability, Sydney Opera House,*

[3]*Reef Design Lab, Melbourne*

Natural edge habitats around urban harbours are mostly replaced by featureless walls and docks, to the detriment of suitable habitat for estuarine fishes. We surveyed nearshore fish assemblages along the southern shoreline of Sydney Harbour for 2 years prior to the establishment of eight small artificial habitats ("reef pods") along the eastern edge of the Sydney Opera House (in 2019), where hard rocky reef structure is sparse. Reef pods and harbour reference sites were surveyed (visual *in-situ* surveys and from stationary GoPro cameras) at 6-8 week intervals. We found 25 species of fishes utilising these nearshore habitats, with species richness differing seasonally. The reef pods attracted 9 fish species not observed at that or other sites previously, including 4 endangered Whites seahorses in 2022. Overall, we showed that small artificial habitat enhancements can benefit the nearshore fish communities in urbanised estuaries.

New coral habitat expands trait options for expatriating coral-reef fishes in temperate SE Australia

Booth, David[1]; Beretta, Giglia[1]

[1]*Fish Ecology Lab, University of Technology Sydney*

Two decades of monitoring have revealed over 100 species of coral-reef fish expatriating into SE Australian waters to rocky reef habitats (“vagrants”). Feary et al. (2014) reviewed the taxa of coral-reef fish that did (and did not) make the poleward journey into temperate waters, and developed a list of key characteristics that relate to this. These traits of those that appeared poleward included larger larvae, benthic nesters, broader diet (e.g., lower reliance on corals for food or shelter). Recently, we have observed and commenced monitoring new beds of *Pocillopoa aliciae*, a subtropical hard coral that has rapidly expanded over temperate reef “urchin barrens” in the last few years. We show that an additional 8 species of vagrant fish have now been recorded in Sydney, only on these coral beds, which also support a much greater overall density of vagrant species (and some temperate species) than surrounding rocky reefs. Tropicalisation of temperate waters can therefore be enhanced by expanding habitats (in this case, subtopia corals) which can facilitate establishment of coral-reef species otherwise unsuited to local temperate habitats.

How water flow and reef structure shape the world of fishes

Bowden, Casey[1]; Bellwood, David[1]; Streit, Robert[1]

[1]*Research Hub for Coral Reef Ecosystem Functions, and College of Science and Engineering, James Cook University, Townsville, Queensland 4814, Australia*

The environment reef fishes live in is an important part of their ecology. Fishes use all three dimensions of their environment for many purposes such as sheltering and feeding. The importance of three-dimensional structure for fishes is increasingly recognised. However, this increased focus is usually limited to one part of the world that fishes live in: the structure of the substratum. The other critical, yet often overlooked component is water itself. Water is the very medium in which fishes live and is regularly considered a key factor in broader coral reef ecology. Despite its importance, our knowledge of how water flow impacts fish at small scales, directly relevant to their behaviour, is still limited. To understand the full extent of reef fish ecology, we must further our knowledge of the nature of hydrodynamics at small scales; at the scale of fishes and the 3-dimensional structures that fishes utilise. Here I present novel approaches to measure how fish movement interacts with benthic structure and water flow. The key is to scale down our measurements to the world of coral reef fishes – centimetres to meters. In doing so we gain a more comprehensive understanding of the reef environment and how it shapes fish behaviour.

Ngā Ika e Heke- The Department of Conservation’s freshwater migratory species programme

Bowen, Jane[1]; Goodman, Jane[1]; Richarson, Marine[1]

[1]*Department of Conservation, New Zealand*

Ngā Ika e Heke, the Department of Conservation’s national freshwater migratory species programme, was established in 2018 to improve the security of four species, addressing the need for landscape-level, catchment management. Target species of the programme are shortjaw kōkopu (*Galaxias postvectis*) Threatened – Nationally Vulnerable, īnanga (*Galaxias maculatus*) At Risk – Declining, tuna / longfin eel (*Anguilla dieffenbachii*) At Risk – Declining, and lamprey / kanakana / piharau (*Geotria australis*) Threatened – Nationally Vulnerable. This work programme first sought to update our understanding of the population status of the four species and the threats to them; and then to work collaboratively with our Treaty partners and others throughout Aotearoa New Zealand to identify sites to restore habitat and reduce these identified threats. Some species had not had comprehensive surveys of their population status for over 20 years, and with others new techniques have and are being developed to understand where they spawn. Barriers to migration and changes to instream and riparian habitat are some of the key threats and pressures that we aim to remove or reduce over time. At the Department of Conservation this work is supported by a network of 12 rangers, 2 work programme co-ordinators, and national science and technical support staff. This poster compliments several presentations at this conference that introduce the species and the programme, the work that has been done to date, and what we hope to achieve in the future.

Fish species radiations in the sea: what the flock?

Bowen, Brian W.[1]; Canfield, Sean J.[2]; Coleman, Richard R.[3]; Copus, Joshua M.[1]; Hoban, Mykle[1]; Whitney, Jonathan L.[4]

[1]*Hawaiʻi Institute of Marine Biology, University of Hawaiʻi, 46-007 Lilipuna Road, Kāneʻohe, HI 96744*

[2]*Department of Animal Science, University of California at Davis, 2403 Meyer Hall, Davis, CA 95618*

[3]*Rosenstiel School of Marine, Atmospheric, and Earth Sciences, University of Miami, 4600 Rickenbacker Causeway, Miami, FL 33149-1031*

[4]*NOAA Pacific Islands Fisheries Science Center 1845 Wasp Boulevard, Building 176, Honolulu HI 96818*

Species flocks are proliferations of closely-related species, often with sympatric distributions, sometimes in depauperate habitat. Such radiations are abundant in ancient freshwater lakes, but less common in marine habitats. Examples from the Indo-Pacific fish fauna include the triplefins (family Tripterygiidae), diminutive reef dwellers in the shallow waters of New Zealand, including at least 24 endemic species with many sympatric distributions. This group appears to have evolved via a local radiation that includes both ecological and geographic divergences. The rockfishes (genus *Sebastes*) consist of approximately 110 species, with 62 in the northeastern Pacific and 28 in the northwest Pacific Ocean. Many rockfish sister-species are indistinguishable with morphometrics but differ in coloration and habitat use. Surfperches (family Embiotocidae) are endemic to the temperate North Pacific with 13 genera and about 25 species occupying a variety of habitats including sand bottom, seagrass, kelp forests, and estuaries. A key trait of the rockfishes and surfperches is viviparity (bearing live young), bypassing the dispersive pelagic stage. The triplefins occupy a depauperate habitat with abundant ecological opportunity. Hence these species flocks can arise due to the intrinsic feature of restricted dispersal, or they can be geographically clustered, promoted by extrinsic ecological circumstances.

Lessons learnt from exclusion barrier use in protecting non-migratory galaxiid strongholds in New Zealand

Bowie, Sjaan[1]; Nelson, Dean[2]

[1]Department of Conservation, Freshwater Species Team

[2]Department of Conservation, Twizel District Office

Some of our highly threatened non-migratory galaxiids cannot cope and/or compete with some undesirable species, such as brown trout (*Salmo trutta*), that continue to expand into new areas under changing climates. In these situations, exclusion barriers, which impede or prevent the upstream and/or downstream movement of undesirable fish species, can help protect key locations by keeping undesirable species out and providing a safe refuge area. Exclusion barriers have increasingly been used as a key conservation tool to protect remaining non-migratory galaxiid strongholds. We have found ongoing monitoring and maintenance are crucial to success. Active management of macrophytes and backwater habitat upstream may improve the security of these populations. Where drops of >1m were not possible, other features such as overhangs, shallow aprons and non-physical barrier features (e.g. shallow, high water velocity) can be successful to prevent undesirable species access. We will present lessons learnt from barrier designs installed, management and monitoring results over the last 20 years.

An undescribed population of *Glyptothorax* from the Mekong River

Boyd, David[1]

[1]*Louisiana State University Museum of Natural Science, Baton Rouge, Louisiana, USA*

An undescribed population of catfish in the genus *Glyptothorax* is identified in the Mekong River in Thailand and Cambodia. The population is most closely related to *G. platypogonides* genetically and phenotypically but is difficult to discern based on external morphological characters alone, with differences in general color hue (and not pattern) being the primary diagnostic character. *G. platypogonides* is wide-ranging but restricted to drainages including and west of the Chao Phraya River in Thailand while the undescribed population is endemic to the Mekong. Although separated from *G. platypogonides* by greater average genetic distance than is observed between many recognized sister-species pairs of *Glyptothorax*, the undescribed population is not readily identifiable without locality data. The advantages and disadvantages of describing the Mekong population as a new species vs. subspecies are discussed, particularly regarding their bearing on the interpretation of biodiversity in freshwater obligate organisms in branches of biology “downstream” of taxonomy.

1.5B Special Session 3: Building a better future for fish: a symposium on fish-friendly infrastructure, 260-055, November 20, 2023, 2:00 PM - 4:15 PM

Towards Australia's first design guidelines for fish protection screens: Insights from a flume-based study on native species.

Boys, Craig[1]; Baumgartner, Lee[2]; Doyle, Katherine[2]; Robinson, Wayne[2]

[1]*NSW Department of Primary Industries, Port Stephens Fisheries Institute, Taylors Beach, NSW Australia*

[2]*Charles Sturt University, Gulbali Research Institute, Thurgoona, NSW Australia*

Fish protection screens play a vital role in safeguarding fish populations from entrapment and mortality in irrigation systems. However, the design of these screens often lacks sufficient empirical data. In Australia, limited research has been conducted on the swimming behaviour of native fish species in front of screens, posing significant challenges in developing effective fish protection measures. In this presentation, we will present the results of a study investigating the swimming behaviour of two prominent Australian native fish species, the Golden perch and Murray cod, in the presence of a simulated fish-protection screen. The study was conducted in a large outdoor flume, and its findings have provided the groundwork for the development of Australia's first screen design guidelines tailored specifically to these species. These guidelines address the specific requirements of Australian species and therefore contribute to the overall environmental sustainability of the irrigation industry. The outcomes of our research underscore the significance of employing empirical data to inform fisheries management and highlight the potential of experimental flumes as a valuable tool for evidence-based guidelines in aquatic resource management, particularly in regions where research is limited.

4.3C Themed Session B: Ecology of Indo-Pacific Fishes, 260-115, November 23, 2023, 3:30 PM - 5:15 PM

The role of small fishes for coral reef energy and nutrient fluxes: a tale of two theories

Brandl, Simon J.[1]; Casey, Jordan M.[1]; Schiettekatte, Nina M.D.[2]; Yan, Helen F.[3]; Renzi, Julianna J.[4]; Mercière, Alexandre[5]; Côté, Isabelle M.[6]; Parravicini, Valeriano[5]

[1]*Department of Marine Science, The University of Texas at Austin, Marine Science Institute, Port Aransas, TX 78373, USA*

[2]*Hawai'i Institute of Marine Biology, University of Hawai'i at Mānoa, Kāne'ohe, HI, USA*

[3]*College of Science and Engineering, James Cook University, Townsville, Queensland, Australia*

[4]*Department of Ecology, Evolution, and Marine Biology, University of California, Santa Barbara, Santa Barbara, CA, USA*

[5]*PSL Université Paris: EPHE-UPVD-CNRS, USR 3278 CRIOBE, Université de Perpignan, Perpignan, France*

[6]*Earth to Ocean Group, Department of Biological Sciences, Simon Fraser University, Burnaby, British Columbia, Canada*

Energy fluxes through coral reef food webs are difficult to trace, as countless organisms can contribute to the sequestration and transfer of carbon to higher trophic levels. However, a dichotomy is often drawn between energy harnessed from pelagic pathways and carbon obtained from benthic productivity. Small, site-attached (‘cryptobenthic’) reef fishes have been highlighted as a crucial conduit of energy to larger fishes, but when, where, and why these communities emerge as important contributors to reef energy fluxes, and the sources of their productivity, is unknown. Here, we use evidence from the South Pacific to reveal determinants of cryptobenthic fish communities, their trophic structure, and their role for coral reef elemental cycling. Despite being separated only by a narrow reef crest, forereef and backreef habitats exhibit vastly different benthic composition and harbor fundamentally different cryptobenthic fish communities: on the forereef, few cryptobenthic fishes exist and size-spectrum analyses suggest that small fish communities are largely fueled by external subsidies. In contrast, the backreef supports vibrant cryptobenthic fish assemblages with traditional, bottom-up trophic structures. These results suggest differences in the trophic functioning of small fish communities, which are corroborated by elemental analyses. Indeed, the majority of carbon in backreef communities is obtained from benthic algae, while forereef communities exhibit a strong pelagic carbon signature. Importantly, these stark divergences in trophic structure and energy sources also correlate with community-level differences in demographic dynamics, resulting in fundamentally different rates of carbon production, transfer, and turnover from benthic or pelagic sources in the two habitats.

Systematic Marine Protected Area Planning using MARXAN in New Zealand.

Rushdi, Naif [1]; Breen, Dan[1]; Murdoch-Tighe; Levi[1], O'Campo, Jeffrey[1]; Scott, Oliver[1]

[1]*Auckland University of Technology*

Marine Protected Areas (MPAs) often aim to meet multiple objectives including conserving a representative range of biodiversity, including fishes, and can also support sustainable use in customary, recreational and commercial fisheries. There is a significant history of analysing options for MPA networks in New Zealand using modelling of fisheries and habitat data. We present geospatial analyses of marine habitat and other data using the site prioritisation tool MARXAN at national, regional and local scales. These identify gaps in existing and proposed networks of MPAs at all scales, identify priority areas for conservation and explore alternate management options. Implementation of the recommendations from similar studies in New Zealand has been slow. We discuss the potential reasons for this and how working directly with coastal communities in a participatory approach is essential for change to occur.

Making a super seahorse: Optimising the husbandry of Endangered White's Seahorses, *Hippocampus whitei,* for the purpose of conservation stocking

Brennan, Mitchell[1,2]; Aponte Arevalo, Diego[1]; Booth, David[1]; Ede, Courtney[1]; Harasti, David[3]

[1] *Fish Ecology Lab, School of Life Sciences, University of Technology, Sydney*

[2] *Sydney Institute of Marine Science*

[3] *Fisheries Research, New South Wales Department of Primary Industries*

The White's Seahorse (*Hippocampus whitei*) is endemic to eastern Australia and in 2020 was listed as Endangered in New South Wales due to significant population declines primarily attributed to the loss and degradation of natural habitats. Since 2020, a conservation stocking program using captive-bred seahorses has been implemented to recover wild populations, with some success. To improve the survival of captive-bred seahorses translocated into the wild, we investigated the aquarium conditions for juvenile seahorses from birth until attaining a suitable release size, aimed at increasing growth rate and performance, reducing time spent in captivity and improving fitness. Growth rate was measured under different temperatures (19°C, 22°C and 25°C), food treatments (enriched and non-enriched *Artemia* nauplii), and stocking densities (approx. 1^{-L}, 0.5^{-L} and 0.2^{-L}). We show that by utilising optimal rearing conditions, *H. whitei* can attain a suitable release size (TL > 5cm) within three months and survival rate from birth to release can be >90%. The husbandry methods described here can reduce the time juvenile seahorses spend in captivity prior to translocation and improve fitness, potentially leading to increased wild-survival post-release whilst reducing the costs of rearing. The results demonstrate best practice for *H. whitei* rearing for the purpose of conservation stocking.

Fish screen performance at water diversions and irrigation pumps in the Murray Darling Basin and consequences for implementing screens

Bretzel, Joachim[1,2]; Boys, Craig[2]; Doyle, Katherine[1]; Watts, Robyn[1]; Vu Vi, An[1]; Baumgartner, Lee[1];

[1]Gulbali Institute, Charles Sturt University, Australia
[2]NSW Department of Primary Industries, Port Stephens Fisheries Institute, Australia

Modern fish protection screens at water diversions in Australia are designed to protect native fish species by minimising entrainment. We conducted field-based investigations of fish entrainment at different types of water diversions in the Murray Darling Basin, both with and without fish screens. In all cases fish screens reduced the number of fish entrained. This was observed at a large gravity-fed channel outlet, as well as both small and large pumps. Without screens, threatened species across all size classes, as well as fingerling Murray cod (*Maccullochella peelli*) released as part of an official stocking program, were entrained. At all sites, screens significantly reduced entrainment, also evidenced by mark and release trials. The results demonstrate that programs to install modern fish protection screens in the Murray-Darling Basin should lead to improved survival and enhance the conservation of native fish. Additionally, these efforts can increase the success of stocking both recreationally-targeted and threatened fish species, while protecting other aquatic animals. We also found that screens significantly decreased the volume of debris entering irrigation systems, which in turn will have the added benefit of less blockages, less maintenance and improved efficiency of water delivery for farmers.

Reef Song: an ecosystem-based approach to enhancing reef resilience and restoration

Brooker, Rohan[1, 2]; Barneche, Diego[1, 2]; Gilmour, James[1, 2]; Meekan, Mark[2]; Parsons, Miles[1, 2]; Pygas, Daniel[1, 2]; Thomas, Luke[1, 2]; Wilson, Shaun[1, 2]

[1] *Australian Institute of Marine Science, Perth, Australia*

[2] *UWA Oceans Institute, Perth, Australia*

Coral reefs are exposed to increasingly frequent and severe disturbance, limiting their time and opportunity for recovery. There is a clear need to explore new ways of enhancing coral health and resilience, to amplify recovery potential where possible. Ecosystem-based methods that take advantage of natural patterns and processes may prove particularly valuable, reducing the inputs required to establish recovery and promote resilience.

Coral reefs support complex communities of fishes, many of which have a close relationship with corals. A growing body of evidence suggests reef fishes can support coral health; however, additional work is required to determine if and how these relationships can be harnessed to improve reef resilience and recovery.

The Reef Song project, part the Australian Coral Reef Resilience Initiative (ACRRI), aims to address this issue. In a multi-year approach, Reef Song brings together novel research from Australia's east and west coasts to identify (a) how fishes influence coral growth and resilience, (b) how we can support coral-associated fish communities to enhance positive effects, and (c) how this knowledge can inform practical, scalable solutions to improve coral recovery and restoration efforts.

In this talk, I will outline the justification and goals of the Reef Song project, present an overview of key experiments and collaborative work, provide an update on our current progress and initial findings, and discuss the next steps.

Using AI to monitor recreational fish catch

Brown, Culum[1]; Aubin, Sam[2]; Gorkin, Rob[2]; Hughes, Julian[3]; Knott, Nathan[3]; Pini-Fitzsimmons, Joni[3]

[1]*Macquarie University*

[2]*In2iti0n*

[3]*NSW Department of Primary Industries*

Recreational fishing is an extremely popular past time and there has been growing investment in associated infrastructure such as boat ramps and fish cleaning tables to promote the activity. Despite the large number of people involved in the activity we have surprisingly little quantitative knowledge about what fish are caught, where they are caught, in what numbers and at what size. Here we present the early outcomes of an Artificial Intelligence system we are developing to gather this sort of information at fish cleaning tables. The system relies on a camera mounted over the table that streams live footage to the cloud where it is analysed using object recognition system trained to recognise common recreational fishes. Not only will this system provided detailed information about recreational fish catch but it also provides details on the use of recreational fishing facilities which facilitates appropriate management of and investment in this infrastructure. Moreover, our system will be able to quantify the waste that is produced at cleaning tables which has implications for the management of adjacent marine ecosystems. The project is funded by the NSW Recreational Fishers Trust.

Accounting for interspecies and intraspecies variation in swimming performance for fish passage solutions

Crawford, Rachel[1,2]; Dupont, Deborah[2]; Franklin, Paul[2]; Gee, Eleanor[3]; Hick, Brendan[4]; Nolte, Dana[2]

[1]*School of Science, Environmental Research Institute, The University of Waikato, Hamilton, New Zealand*

[2]*National Institute of Water and Atmospheric Research, Hamilton, New Zealand*

[3]*Waikato Region Council, Hamilton New Zealand*

[4]*Morphum Environmental Ltd, Hamilton, New Zealand*

Instream structures worldwide fragment river networks, posing barriers to fish movement. To design effective solutions for accommodating fish communities, comprehensive knowledge of swimming abilities, behaviours, and niches across species is crucial. Our study tested the critical swimming speed of nine migratory New Zealand species. We determined maximum allowable speeds for fishways based on the endurance swimming of the lowest performing species (*Galaxias maculatus*) and modelled the effect of individual variation in endurance on passage success.

Results revealed significant interspecies and intraspecies variation in critical swimming speed. *Galaxias brevipinnis*, *Galaxias postvectis*, *Galaxias argenteus,* and *Retropinnna retropinna* demonstrated the strongest swimming abilities, while *Galaxias maculatus* and *Anguilla dieffenbachii* exhibited weaker performance. Additionally, body length was positively correlated with swimming speed (U_{crit}), supporting the notion that fish passage barriers are selectively disadvantageous for weaker species and smaller individuals within a species.

Previous designs based on average swimming ability only benefit fish that exceed the species' average. Our model demonstrates the deleterious effect this has on passage success of weaker individuals. This study emphasizes the need for designs that consider variation within and between species, encompassing habitat preferences, morphologies, physiologies, and life history strategies.

Multi-disciplinary approach reveals the role of sympatric benthic sharks linking pelagic and benthic food webs

Burke, Patrick J.[1]; Meyer, Lauren[2]; Raoult, Vincent[1,3]; Huveneers, Charlie[2]; Williamson, Jane E.[1,4]

[1]*School of Natural Sciences, Macquarie University, North Ryde, NSW, Australia*

[2]*College of Science and Engineering, Flinders University, Bedford, SA, Australia*

[3]*School of Environmental and Life Sciences, University of Newcastle, Ourimbah, NSW, Australia*

[4]*Sydney Institute of Marine Science, 19 Chowder Bay Road, Mosman, NSW, Australia*

Quantifying the trophic role of a species is key to understanding its ecology and ecological role. Predator-prey relationships and prey consumption influence community composition, ecosystem stability, nutrient transport, and nutrient cycling between habitats through ingestion, egestion, and excretion. Despite the regular occurrence of sawsharks in Australian temperate fisheries, there remains limited information on their trophic ecology or habitat use, but both species are assumed to be benthic consumers. We used fatty acid and stable isotope profiles along with stomach content analysis to investigate the trophic ecology of two sympatric species of sawsharks, the common sawshark (*Pristiophorus cirratus*) and southern sawshark (*Pristiophorus nudipinnis*) in south-eastern Australia. Stable isotope analysis of δ13C, δ15N, and δ34S in sawshark muscle revealed that *P. nudipinnis* fed at a higher trophic level than *P. cirratus*, and mixing models and stomach contents indicated *P. nudipinnis* was surprisingly reliant on pelagic and benthopelagic prey sources. In contrast, *P. cirratus* preyed on more benthic invertebrate species, not found in *P. nudipinnis*. This bentho-pelagic partitioning between species was supported by *P. nudipinnis* fatty acid profiles having higher levels of tracers associated with dinoflagellate basal sources (16:1/16:0, 22:6ω3) than *P. cirratus*, indicating a reliance on pelagic food webs. Our study demonstrates that sawsharks are mesopredators that play a substantial role linking pelagic and benthic food webs and highlights the value of incorporating multiple biochemical tracers to provide a comprehensive representation of an animal's trophic ecology and role within and between ecosystems.

Coming of age: the life-history of school sharks

Burton, Alex[1,2]; Smith, Adam[1]

[1]*School of Mathematical and Computational Sciences, Massey University, New Zealand*

[2]*School of Natural Sciences, Massey University, New Zealand*

Fundamental gaps in our knowledge of the biology of many elasmobranch species around the world remain, including the critically endangered school shark (*Galeorhinus galeus*), of which New Zealand has the last remaining stable population and fishery. In the first study of its kind, we compiled allometric and life-history data on school sharks from almost every population of school sharks around the globe. We used hierarchical Bayesian models to examine the transition of school sharks through various life-history stages, including birth and maturation, across the world's geographically dispersed populations. The lengths at which life-history stage transitions occur did not appear to vary substantially across these populations. We show that the rate of clasper growth relative to total length can be used to quantify the degree of maturation in males. We relate this new metric to qualitative reproductive characteristics. Development of testes happens at various stages of maturation, and semen was only detected in fully mature males. Our study adds to our understanding of school sharks, and our methods may be used to similar effect for other species, to better inform conservation and management of elasmobranchs.

The marine origins of freshwater osteoglossid bonytongues (arowanas and arapaimas)

Capobianco, Alessio[1,2,3,4]; Andrews, James V.[3,4]; Friedman, Matt[3,4]

[1]*GeoBio-Center LMU, Ludwig-Maximilians-Universität München, Munich, Germany*

[2]*Department of Earth and Environmental Sciences, Paleontology & Geobiology, Ludwig-Maximilians-Universität München, Munich, Germany*

[3]*Museum of Paleontology, University of Michigan, Ann Arbor, Michigan, United States of America*

[4]*Department of Earth and Environmental Sciences, University of Michigan, Ann Arbor, Michigan, United States of America*

Osteoglossid bonytongues (arowanas and arapaimas) are today limited to four genera living in tropical freshwaters of South America, Africa, Southeast Asia and Australia. However, the fossil record for this group reveals a much more diverse past, including not only freshwater forms found in places as distant as Wyoming and Queensland, but strikingly also marine forms in fossil deposits worldwide dating from 66 to 40 million years ago. Some of these marine bonytongues, such as †*Magnigena* from the Paleocene of Saudi Arabia, are particularly relevant for their age—within a poorly understood yet crucial timespan recently termed Patterson's Gap—and for their location at the intersection between the Tethyan and Indo-Pacific ocean basins. Novel micro-computed tomography of three-dimensionally preserved fossils reveals key morphological characters to place this early Cenozoic radiation of marine bonytongues into a phylogenetic context. We show that, rather than representing an evolutionary offshoot distantly related to modern arowanas and arapaimas, marine bonytongues form—together with some extinct freshwater taxa—a diverse 'cloud' of several lineages from which the few surviving freshwater forms originated. Biogeographic analyses support a marine ancestry of crown osteoglossids, followed by marine long-distance dispersal and several independent invasions of freshwaters in separate landmasses, some leading to extant arowanas and arapaimas. Our study highlights how inclusion of fossil data into phylogenetic and biogeographic analyses can radically change our understanding of the evolutionary history of living organisms, and prompts for further re-examination of the anatomy and physiology of extant osteoglossids in light of their marine ancestry.

eDNA and compound specific stable isotopes reveal diet specialization and overlap in co-occurring parrotfishes of the Gulf of California

Carlon, David B.[1]; Ely, Taylor[2]

[1]*Bowdoin College, Brunswick, Maine, USA*

[2]*University of Hawaii, Manoa, Honolulu, Hawaii, USA*

The feeding ecology of tropical parrotfishes is crucial to the processes that maintain diverse and productive reef ecosystems, yet remains unresolved in many ecological contexts because diet analysis is limited by observational or biochemical methods. We jointly applied eDNA metabarcoding and compound specific stable isotope analysis (CSIA) to the diets of three common and co-occurring species (*Scarus ghobban*, *S. rubroviolaceus*, and *S. perrico*) and their hybrids (*S. compressus*) from rocky reefs in the Gulf of California. We used six barcoding primers including a 23S rRNA plastid gene that could distinguish the relative importance of eukaryotic vs. prokaryotic food items. A principal components approach (PCA) using relative read counts (RRC) found that the three species diverged in ingested food items along axes that contained complex mixtures of branching red, coralline, and epiphytic green algae; as well as diatoms, dinoflagellates, and cyanobacteria. The 23S plastid gene could resolve subtleties in diet, with *S. perrico* ingesting predominantly branching red algae, coralline algae, and epiphytic green algae. Both *S. rubroviolaceus* and *S. ghobban* ingested branching and coralline red algae, but also consumed large quantities of cyanobacteria. CSIA analysis of the essential amino acids clearly separated *S. perrico* from the other two species, but a fingerprinting approach could not resolve assimilated foods with respect to several eukaryotic macroalgal groups and the cyanobacteria. On these rocky reefs, our combined eDNA + CSIA approach indicates that highly productive macroalgae and cyanobacteria are consumed by all three species, but the proportions of different functional shifts depending on species.

5.3A Themed Session B: Ecology of Indo-Pacific Fishes, 260-115, November 24, 2023, 10:30 AM - 12:30 PM

Spatiotemporal drivers of parrotfish distribution around Moorea, French Polynesia indicate algal resources influence ontogenetic habitat shifts of parrotfishes

Castañeda, Noe[1]; Adam, Thomas[2]; Burkepile, Deron[1,2]; Caselle, Jennifer [2]

[1] *Department of Ecology, Evolution, & Marine Biology, University of California, Santa Barbara*

[2] *Marine Science Institute, University of California, Santa Barbara*

Parrotfishes play an important role in benthic dynamics on coral reefs by impacting the prevalence of algae and facilitating corals. Adult parrotfishes are often positively correlated with algal productivity suggesting food availability strongly influences their distribution. However, the temporal and spatial responses of parrotfishes to available resources can be dynamic. We examined the spatiotemporal patterns of parrotfish abundance around the island of Moorea, French Polynesia to understand the drivers of ontogenetic habitat shifts of scarids. First, we used surveys of fish communities across ~200 reef sites around Moorea to identify the current spatial correlates of parrotfish stage structure in lagoon habitats. Then, we used time series of fish communities spanning a seventeen year time period (2005 – 2022) across 18 sites to explore the relationship between abundances of parrotfishes of different life stages and benthic communities over time. The current spatial distribution of parrotfish is highly variable across the reefs of Moorea, with the abundance of juveniles positively associated with habitat availability and the abundance of adults/subadults positively associated with algal resources. Using our time series, we found a significant increase in the average size of parrotfish found in the lagoons over time, which corresponded to increased algal resources, suggesting there is retention of adult parrotfish in lagoons/nursery habitats as algal availability increases. Using both long-term and fine-scale data of parrotfish distribution, we can make inferences about how shifts toward algal-dominated reefs may alter ontogenetic habitat shifts and redirect movement of parrotfishes across reef habitats.

Taxonomic revision of the genus *Stenogobius* (Teleostei: Gobioidei) from Indo-Pacific rivers

Causse, Romain[1]; Lord, Clara[1]; Mennesson, Marion Isabelle[1]; Keith, Philippe[1]; Hubert, Nicolas[2]

[1]*Muséum national d'Histoire naturelle, UMR BOREA 8067 (MNHN-CNRS-Sorbonne Université-IRD-UCBN-UA), 43 rue Cuvier, 75231 Paris Cedex 05, France.*

[2]*UMR 5554 ISEM (IRD, UM, CNRS), Université de Montpellier, Place Eugène Bataillon, 34095 Montpellier cedex 05, France*

Indo-Pacific freshwater habitats are colonised by amphidromous species, adapted to these distinctive habitats, which are fragmented and isolated from one another. Amphidromous species count molluscs, decapod crustaceans and fish and among fish species, Gobiiformes represent most of the stream biodiversity. Taxonomic revisions have been recently undertaken on various goby taxa such as Sicydiinae and Eleotridae but many groups remain unattended. In this study, we focused on the widespread *Stenogobius* genus (Oxudercidae) composed of 28 presumably valid species and distributed from the Indian Ocean to French Polynesia. *Stenogobius* are found on sandy bottom in lower to middle course of rivers; they are psammivorous and play an important role in the degradation of organic matter. The last - very complex - review on *Stenogobius* species was written by Watson in 1991 and only based on morphological characters and some doubts about the number of valid species were highlighted. Our revision was undertaken using integrative taxonomy on 395 specimens (including 175 types specimens) by combining 35 morphomeristic characters and molecular data (113 sequences of partial *COI* gene - 516 bp). The results we found are particularly surprising as instead of many *Stenogobius* species with each a restricted distribution area there is in fact one main widespread species, *S. genivittatus* (Valenciennes, 1837) distributed from the South African East Coast to East Pacific locations (Hawaii, French Polynesia). This first taxonomic revision led us to synonymise 12 species names with *S. genivittatus*. This type of work has important implications in terms of conservation and species protection.

Look Who's Walking Too: Genomics and kinematics of balitorid loaches can inform our understanding of the vertebrate transition to land

Chakrabarty, Prosanta [1]; Boyd, David[1,2], Crawford, Callie[3]; Faircloth, Brant[1] ; Flammang, Brooke[4]; Hart, Pamela[5] ; Page, Lawrence[2] ; Randall, Zachary[2] ; Suvarnaraksha, Apinun[6;] Webber-Schultz, Amani[4],
[1] *Museum of Natural Sciences, Department of Biological Sciences, Louisiana State University, Baton Rouge, LA, USA*
[2] *Florida Museum of Natural History, University of Florida, Gainesville, FL, USA*
[3] *Coastal Carolina University, Department of Biology, Conway, SC, USA*
[4] *New Jersey Institute of Technology, Rutgers University, Newark, NJ, USA*
[5]*The University of Alabama, Department of Biological Sciences, Tuscaloosa, AL, USA*
[6] *Maejo University, Faculty of Fisheries Technology and Aquatic Resources, Chiangmai, Thailand*

Convergence is the occurrence of similar but independently evolved genotypic or phenotypic innovations. The recently discovered blind cave loach, *Cryptotora thamicola*, walks and climbs waterfalls with a salamander-like gait and has a robust pelvic girdle that connects to the vertebral column (a.k.a., a "hip") which is unlike most fishes outside of the Balitoridae and Tetrapodomorpha. Having a hip permitted the vertebrate invasion of land. Devonian fishes like *Tiktaalik* had the first weight-bearing morphology of their pelvic girdle that would eventually lead to the evolution of a hip and allow walking on land. Because that transition happened over 400 million years ago in the Devonian, insights from an extant walking fish with a hip can help us better understand the origin of quadrupedal walking. Evolutionary research on the morphology, kinematics, and genomics of balitorids will shed light on the origins and evolution of tetrapods.

Long-term trends in coastal catch of pelagic rays along eastern Australia

Chan, Alysha[1]; Jaine, Fabrice[1,2]; Niella, Yuri[1]; Peddemors, Victor[2,3]; Williamson, Jane[1,2]

[1]*School of Natural Sciences, Wallumattagal Campus, Macquarie University, North Ryde, NSW, Australia*

[2]*Sydney Institute of Marine Science, Mosman, NSW, Australia*

[3]*New South Wales Department of Primary Industries, Fisheries Research, Sydney Institute of Marine Science, Mosman, NSW, Australia*

Targeted and unintentional harvesting of pelagic sharks and rays is responsible for unprecedented pressure on their populations at a global scale. Along the east coast of Australia, pelagic rays (cownose, eagle and mobulid) aggregate and travel in large fevers, and are often caught in government-sanctioned bather protection gillnets. This study describes temporal and spatial trends in distribution and occurrence of pelagic rays along the east coast of Australia using historical catch data (2010-2022) of these rays in the Queensland Shark Control Program (QSCP) and the New South Wales Shark Meshing (Bather Protection) Program (NSW SMP). In total, 2,192 pelagic rays were caught in the QSCP and SMP over the 12-year period, with 68.4% of rays released alive. Spatial and temporal analyses of catch per unit effort highlighted 2015-2016 and areas around Newcastle (NSW) as the period and region with highest catch of pelagic rays, respectively. Whilst there were distinct spatial ranges for each family/species, all three families were found to co-occur primarily on the Sunshine and Gold coasts in Queensland. Exploration into the demography of catches, the use of generalised additive models, and mapping of species presences in areas of interest over time are used to further elucidate the drivers of pelagic ray occurrences and interactions between these rays. This research provides novel insights into the distributions and interactions of pelagic rays along the east coast of Australia and may inform effective management and conservation of species, which is currently hindered by a paucity of baseline information.

The role of fish in coral recruitment on complex artificial reef structures

Chapeau, Marion[1]; Esquivel-Muelbert, Juan[2]; Madin, Joshua[1]; Schiettekatte, Nina[1]

[1]*Hawai'i Institute of Marine Biology, University of Hawai'i at Mānoa, Kaneohe, Hawaii, USA*

[2]*Department of Biological Sciences, Macquarie University, Sydney, NSW, Australia*

Coral reefs are declining worldwide due to threats like overfishing and climate change. After disturbances, coral recruitment on bare surfaces is the first step towards recovery of the coral community. Herbivorous fish can have a positive influence on coral recruitment by decreasing the competition with algae. Meanwhile, the 3D structure of the reef impacts the settlement and survival of coral recruits. We know little about how herbivory and structure of the reef interact to facilitate coral settlement. In this study, we deployed caged (to exclude herbivorous fish) and uncaged concrete substrates (n = 170) with different levels of surface complexity (17 surface designs) in Kāne'ohe Bay in Hawai'i, USA. We recorded coral settlement, coral survival, and algal cover on the substrates. We also quantify herbivory by counting fish bites on uncaged substrates. On substrates open to fish (uncaged treatment), we anticipate that algal biomass will remain low and coral recruitment will be high, specifically in deeper parts of complex designs that are protected from incidental mortality by herbivore bites. Conversely, on blocks where fish were excluded (caged treatment), we anticipate high algal biomass and low coral recruitment and survival overall. This study will provide a better understanding of the role herbivorous fish play in coral recruitment on complex surfaces and therefore provide insights for conservation and restoration efforts.

4.2C Special Session 8 Fish sensory ecology: new techniques and approaches, 260-073, November 23, 2023, 3:30 PM - 5:15 PM

Using the latest technology to understand fish inner ear diversity

Chapuis, Lucille[1,2]; Collin, Shaun P.[3], Yopak, Kara E.[4], Simpson, D. Stephen[1], Radford, Craig A.[2]

[1]*University of Bristol, School of Biological Sciences, Bristol, UK*

[2]*University of Auckland, Leigh Marine Laboratory, Institute of Marine Science, Auckland, New Zealand*

[3] *La Trobe University, School of Agriculture, Biomedicine and Environment, Melbourne, Australia*

[4]*University of North Carolina Wilmington, Department of Biology and Marine Biology, Center for Marine Science, Wilmington, NC, USA*

Compared to other animal taxa, there is an astonishing diversity in fish inner ear size and shape. This high variability relates to distinct morphological elements: area/volume of the ears, macular organs, semi-circular canals, and sensory epithelia (relative to the size of the fish and its brain); presence, mass and shape of otoliths; and orientation patterns of the hair cells. The evolutionary and functional implications of this high variability are unknown and represent one of the biggest mysteries of sensory biology. Here, we use a novel toolkit to investigate the structure-to-function links in the inner ears of several cartilaginous fish species (sharks, rays, and chimaeras). Combining three-dimensional bioimaging, geometric morphometry, and finite element analysis, we show how reconstructions of this complex sensory organ and modelling of its function can help us to understand the role it plays in the acoustic ecology of these species. Questions that can be explored with this toolkit are identified, the different methods are justified, and the remaining challenges are highlighted as avenues for future work.

Deep-sea explorations

Chen, Wei-Jen[1]; Samadi, Sarah[2]

[1]*Institute of Oceanography, National Taiwan University, Taipei, Taiwan*

[2]*Institut de Systématique, Évolution, Biodiversité, Muséum National d'Histoire Naturelle, Paris, France*

The deep sea is by far the largest habitat on earth, occupying more than 90% of the total volume of the world’s oceans, and a number of new species and unexpected diversity still await discovery. However, the deep sea has long been thought to be infertile and such kind of “knowledge” was only challenged by the great historical expeditions at the end of the 19th century, notably the circumnavigations of the HMS Challenger (Challenger Expedition of 1872–76). The results of this expedition not only discovered the Challenger Deep, which is the deepest known point in the Earth's seabed, but also demonstrated that life is present and diverse at every depth in the oceans. In today’s presentation, I will first introduce the deep-sea explorations carried out through our Tropical Deep Sea Benthos program (TDSB). The expeditions under the TDSB were launched in the early 1980s explored the deep-sea benthos of the tropical Indo-Pacific with the focus on the golden triangle of marine biodiversity in the South-Eastern Asia that extends to Taiwan in the North and to New Caledonia in the South. These expeditions have allowed the establishment of an impressive collection of tropical deep-sea animals including fishes. Thus, in second half of my presentation, I will show some advanced results from the research based on this collection and demonstrate how the obtained data may allow the renewal of the biodiversity, ecology and evolutionary studies of deep-sea fishes, especially those living on seamounts that were rather poorly studied before.

Spawning migration and habitat use of adult Pacific bluefin tuna (*Thunnus orientalis*) in the northwestern Pacific Ocean

Chiang Wei-Chuan[1, 2], Shia-Jhong Lin[1], Kai-Chieh Yang[3], Andre M. Boustany[4], Qi-Xuan Chang[1], Theodore E.J. Reimer[2], Michael Castleton[2], Sen Jan[3], Yuan-Shing Ho[1], Barbara A. Block[2]

1. *Eastern Marine Biology Research Center, Fisheries Research Institute, Taiwan*
2. *Hopkins Marine Station, Stanford University, USA*
3. *Institute of Oceanography, National Taiwan University, Taiwan*
4. *Monterey Bay Aquarium, USA*

Pacific bluefin tuna (*Thunnus orientalis*) is a highly migratory species that mainly inhabit the temperate regions of the North Pacific Ocean. To reveal the population dynamics of this commercially and ecologically important species, it is essential to understand its spawning migration. A total of three Pacific bluefin tuna were tagged pop-up satellite archival tags (PSATs) on May 2021, and tags remain affixed were a total of 128 days-at-liberty. The total linear displacements were from 797 to 2,743 km from deployment to pop-up locations. The deepest descent recorded was 1,458 m, and the coldest temperature visited 2.6°C. The time spent at depth was significantly different between daytime and nighttime, where fish displayed a regular crepuscular pattern of ascending into the surface layer at dusk and remaining there until the following dawn, where the fish descended past the mixed-layer depth. The Pacific bluefin tuna exhibited shallow oscillatory diving and frequently visited the surface at both daytime and nighttime when staying at spawning ground and showed longitudinal movement patterns correlated with Sea Surface Height anomaly and mesoscale eddies. This study tracked adult Pacific bluefin tuna in the spawning ground and obtained insight into spawning migration, seasonal movement, and habitat use of this species in the northwestern Pacific Ocean. The large-scale international cooperative tagging operations and more data from spawning grounds may provide insights into Pacific bluefin tuna spawning migration behavior and address important scientific questions for proper fisheries management.

Pelagic marine fish eggs from Korean waters revealed by morphology and metabarcoding analysis

Choi, Hae-Young[1]; Choi, Heechan[2]; Yoon, Seokhyun[2]; Kim, Sung[3]

[1]*South Sea Fisheries Research Institute*

[2]*National Institute of Fisheries Science*

[3]*Korea Institute of Ocean Science & Technology*

Pelagic eggs can be used to investigate the spawning of various fishes because most marine teleosts release large quantities of separate pelagic eggs as a spawning strategy. In this study, we collected pelagic eggs from Korean waters for each season from 2019 to 2021 and identified them based on morphological traits and COI barcoding and metabarcoding. A total of 122 taxa were found, of which 98 were identified to species level, 14 to genus level, and 10 were unidentified. There were not only commercial species (*Scomberomorus niphonius*, *Scomber japonicus*, etc.), but also unrecorded species (*Alepes djedaba*, *Trachipterus jacksonensis*, etc.). The information on appearance of fish eggs can be applied to the monitoring of spawning on the various species.

Can we improve reef fish surveys for reliable diversity assessments?

Cher Chow[1], Viviana Brambilla[1,2], Maria Dornelas[1,2], Garrett Fundakowski[1], Andrew Hoey[4], Joshua Madin[3], Tiago Marques[5,6], Nina Schiettekatte[3]

[1]*Centre for Biological Diversity, School of Biology, University of St Andrews, St Andrews, UK*

[2]*MARE, Guia Marine Laboratory, Faculty of Sciences, University of Lisbon, Lisbon, Portugal*

[3]*Hawai'i Institute of Marine Biology, University of Hawai'i at Mānoa, Kāne'ohe, Hawai'i, USA*

[4]*College of Science and Engineering, James Cook University, Townsville, Queensland, Australia*

[5]*Centre for Research into Ecological and Environmental Modelling, University of St Andrews, St Andrews, UK*

[6]*Departamento de Biologia Animal, Centro de Estatística e Aplicações, Faculdade de Ciências da Universidade de Lisboa, Portugal*

Evaluating assemblage diversity requires methods that can adequately detect presence and estimate abundance of species with minimal bias. Widely implemented methods in coral reef ecology for mobile fish assemblages have different drawbacks. Specifically, rare species are difficult to detect with diver surveys, and traditional counts of maximum individuals in a single frame (MaxN) from video surveys are likely conservative for non-shoaling fish species. This study compares existing survey methods with an emerging modelling method from terrestrial ecology, Random Encounter Staying Time (REST) modelling. REST models estimate densities of fish species in video arrays without the need for individual recognition, using species detections and time observed in the video frame instead. We surveyed reef fish assemblages at three sites at Moku o Lo'e, Hawai'i using three different methods: diver point counts, video surveys with MaxN, and video surveys with REST. MaxN video surveys resulted in the highest species richness (33-37 species), almost half of which were absent from other methods. We found that abundance estimates from REST models were consistently lower than those from diver point counts and MaxN, often exceeding one order of magnitude. Our comparison questions whether REST models are robust to assumption violations regarding randomness of movement and clustering of individuals, with effects particularly evident for site-attached species. However, we reiterate the advantages of video surveys in detecting rare species. Our results demonstrate that considering diversity in the spatial scale of active ranges, foraging movement, and sociality is critical for improving methods to estimate reef fish diversity.

Evolutionary traits and ecological roles in herbivorous fishes on coral reefs

Clements, Kendall D.

School of Biological Sciences, University of Auckland, Auckland, New Zealand

Understanding the relationship between evolutionary traits and ecological roles of coral reef fish taxa requires distinguishing evolutionary cause and ecological effect. This distinction has been blurred in recent literature on herbivory in these systems, partly because of a failure to (a) identify dietary targets and how these underpin trophic evolutionary diversification in various fish clades, and (b) relate this diversification to successional processes and spatial variation of benthic biota. Trophic diversification involves adaptive divergence of the functional traits that underpin feeding, including food selection. The effects of feeding can be interpreted in the functional sense of ecological roles, but these ecological effects of feeding don’t necessarily have anything to do with adaptive diversification. I will discuss these issues with reference to grazing fishes, especially scarine parrotfishes. These fishes are widely understood as playing critical roles in bioerosion and sediment transport on reefs, but these are effects, not causes, of feeding, and so are not directly related to an understanding of evolutionary diversification in parrotfishes. Understanding the selection pressures associated with trophic trait diversification in this speciose clade requires a more detailed appraisal of the food resources that drive feeding. An integrated approach involving high power microscopy and molecular metabarcoding of feeding substrata, diet metabarcoding and trophic biomarkers reveal complex relationships between parrotfish trophodynamics and successional dynamics in epilithic and endolithic photoautotroph assemblages. Such integrated approaches will be necessary to predict how ecological roles of particular herbivorous fish taxa will shift in response to disturbances such as climate change and sedimentation.

Reservoirs facilitate colonization of river catchments by invasive fish through provision of pelagic larval rearing habitat

Closs, Gerry[1], Bylak, Aneta[2], Easton, Ryan[1], Kukuła, Krzysztof[2], Reid, Malcolm[1]

[1]*University of Otago, New Zealand*

[2]*University of Rzeszów, Poland*

Dams on rivers are known to facilitate the colonisation and spread of aquatic alien and native invasive species, but the actual mechanisms involved are poorly understood. Since the construction of the Solina Dam on the upper San River system in Poland, European perch (*Perca fluviatilis*) have expanded their distribution into the headwaters of this river system, becoming a native invader. In this study, we assessed the spread of perch in detail over time upstream of the Solina Reservoir, and used otolith trace element microchemistry to determine the spawning and larval rearing locations of perch in the catchment upstream of the dam. Extensive sampling over several years across the catchment upstream of the Solina Reservoir confirmed the widespread occurrence of perch into the headwaters of the tributary river systems, with smaller size classes dominating locations closer to the Solina Reservoir. Despite perch being widely distributed upstream of the Solina Reservoir, otolith microchemical analysis indicated the populations from various reservoir tributaries shared a common spawning and larval rearing habitat, most likely the Solina Reservoir. Our results suggest that reservoirs can facilitate the colonisation of river systems by providing a critical habitat element that would be otherwise missing from riverine landscapes, i.e., an extensive and productive pelagic larval rearing environment. This research shows that the impacts of large dams can extend many kilometers upstream from the river reaches directly affected by the resulting impoundment.

4.1C Themed Session A Evolution, Taxonomy and Biogeography of Indo-Pacific Fishes, 260-098, November 23, 2023, 3:30 PM - 5:15 PM

Genomic assessment of an endemic Hawaiian surgeonfish, *Acanthurus triostegus sandvicensis*, reveals high levels of connectivity and fine-scale population structure

Coleman, Richard R.[1]; Bowen, Brian W.[2].

[1]*Rosenstiel School of Marine, Atmospheric, and Earth Sciences, University of Miami, 4600 Rickenbacker Causeway, Miami, FL 33149-1031*

[2]*Hawaiʻi Institute of Marine Biology, University of Hawaiʻi, 46-007 Lilipuna Road, Kāneʻohe, HI 96744*

The Hawaiian Archipelago has served as a natural laboratory to assess genetic connectivity patterns across a broad spectrum of taxonomic and ecological diversity. Almost all these studies were based on a few targeted loci, but technologies now allow us to assess population structure with genomic coverage and greater resolution. Here, we provide a SNP-based analysis for an endemic surgeonfish, *Acanthurus triostegus sandvicensis* (manini) across the Hawaiian Archipelago and adjacent Johnston Atoll ($N = 461$). Based on 3,649 SNPs, manini showed population structure in the main Hawaiian Islands, but genetic homogeneity across most of the northwestern extent of the archipelago (overall $FST = 0.033$, $P < 0.001$). Net migration occurred from Johnston Atoll into Hawaiʻi, providing further support for Johnston Atoll being a pathway for dispersal (or colonization) into Hawaiʻi. These results highlight the higher efficacy of genomic sequencing to characterize fine-scale patterns of connectivity relative to a targeted loci approach and, moving forward, may invoke a reassessment of past connectivity studies in a genomics framework.

Fish passage in the Australian tropics – lessons from four seasons of fishway monitoring

Collins, Geoff[1,2]

[1]*OzFish Unlimited, Townsville, QLD, Australia, 4810*

[2]*Centre for Tropical Water and Aquatic Ecosystem Research (TropWATER), James Cook University, Townsville, QLD, Australia, 4810*

Rivers and wetlands of Australia’s eastern tropics have been heavily impacted by decades of land-use change. The capacity for fish to migrate throughout impacted catchments has been diminished through habitat modification, declining water quality and physical barriers to fish passage. There are thousands of constructed barriers to fish passage in Australia’s north-eastern tropics and these include pipes and culverts, urban drains, earthen bunds, causeways, weirs and irrigation infrastructure. The cumulative effect of habitat fragmentation on this scale is an overall decline in ecosystem services and the fish stocks they support that is difficult to quantify, but likely to be substantial.

Fishways (or fish ladders) are increasingly being constructed in the Australian tropics to improve the connection between habitats, yet there is limited data on their efficacy in tropical river systems. Here, we present results from four seasons of fish monitoring work in the wet and dry tropics of north-east Queensland. We discuss our findings in the context of contemporary habitat quality and condition, and factors contributing to differences observed within and between catchments. We also present examples of community involvement in monitoring work, and the increasing role of environmental stewardship in fish passage science.

Comparison of two methods for determining the temperature preference of tāmure/Australasian snapper (*Chrysophrys auratus*)

Collins, Selwyn[12]; Black, Suzy[2]; Cook, Denham [3]; Herbert, Neill [1]; Magnoni, Leonardo [2]; Rapson, Jimmy [1]

[1]*Leigh Marine Laboratory, Institute of Marine Science, University of Auckland*

[2]*Seafood Production Group, The New Zealand Institute for Plant and Food Research Limited*

[3]*University of Waikato Coastal Marine Field Station, 58 Cross Road, Sulphur Point, Tauranga, 3114, New Zealand*

Water temperature influences the physiological function and performance of fish, providing incentive for behavioural thermoregulation in heterogeneous thermal environments to maintain ideal body temperatures. Seacage aquaculture environments are generally thermally homogenous and consequently should be located in water of preferential or at least tolerable temperatures. The preferred temperature (T_{pref}) that fish select when presented a choice of temperatures has been measured with several methods, but direct comparison of methods is rarely investigated. Understanding T_{pref} and tolerances is important for resolving the context of animal function in different environments (e.g. seacage aquaculture) and to understand how they correlate with ecophysiological performance metrics (e.g. growth, aerobic scope). Therefore, our work measured T_{pref} of tāmure/Australasian snapper (*Chrysophrys auratus*) across a range of body sizes (50-200g) using two methods: the thermal shuttlebox and thermal gradient tank. The shuttlebox provided a dynamic thermal environment where fish can behaviourally adapt to systematic changes of temperature through time. Conversely, the gradient tank presents a spatially differentiated, and static, range of temperatures enabling fish to respond to a simpler spatial thermal pattern. The differing experimental temperature regimes appear to elicit different thermoregulation behaviours. Both methods showed similar, although unexpectedly low T_{pref}; however, the shuttlebox indicated a wider range of preference between individuals than the gradient tank. Results of this comparison highlight that snapper are eurythermal, and provide insight into their behavioural suitability for aquaculture in offshore environments.

5.2A Special Session 1 Moving beyond home-ranges: how can we harness fish movement ecology to study, understand and manage ecosystem functioning?, 260-073, November 24, 2023, 10:30 AM - 12:30 PM

Small coral reef fishes with large ecological footprints

Collins, William[1]; Bellwood, David[1]; Morais, Renato[1]

[1] *Research Hub for Coral Reef Ecosystem Functions, College of Science and Engineering and ARC Centre of Excellence for Coral Reef Studies, James Cook University, Townsville, QLD, 4811, Australia*

Seascape connectivity can facilitate key ecosystem functions in complex ecosystems like coral reefs. Many reef fishes move across the seascape, bridging different ecosystems. However, their role in shaping important functions, such as biomass production and nutrient cycling, is still poorly understood. This study, therefore, assesses the extent of natural movements of cardinalfishes (Apogonidae), one of the major contributors to nocturnal fish biomass production with the potential for a major role in transferring energy and nutrients between sandy ecosystems and adjacent coral reefs. Consistent with previous work, showing their ability to move distances of 100 s to 1000 s of metres when displaced, we reveal that these small fishes undergo major voluntary nocturnal foraging forays extending up to at least 145 m from reef structures. Their estimated daily movement distances are at least 430 times greater than expected based solely on body size-home range expectations. Given their large travel distances and strong homing abilities, apogonids may provide a major conduit for material transfer between lagoonal soft sediment habitats and adjacent coral reefs. These results highlight the potential importance of apogonids in the cross-system or cross-habitat transport of energy and nutrients on coral reefs.

Engaging with recreational fishers to improve aquatic habitat restoration

Collins, Geoff[1,3]; Copeland, C.[2,3]

[1]*OzFish Unlimited, Townsville, QLD, Australia, 4810*

[2]*OzFish Unlimited, Ballina, NSW, Australia, 2478*

[3]*Centre for Tropical Water and Aquatic Ecosystem Research (TropWATER), James Cook University, Townsville, QLD, Australia, 4810*

Habitat restoration and monitoring techniques are increasingly being applied to improve aquatic ecosystems. Citizen science and volunteer initiatives are expanding the scope of environmental rehabilitation and data collection programs, as well as contributing to improved environmental stewardship in communities. A high proportion of the Australian population are directly or indirectly involved in recreational fishing—an activity that relies on healthy aquatic ecosystems to support fisheries productivity—yet there is historical a disconnect between fishers' perceptions of the ecosystem services that support their activities, and their engagement in restoration work to improve these ecosystems. For the past five years we've been working with recreational fishers and the broader community in north Queensland (Australia) to conduct seasonal waterway monitoring, and to implement habitat improvement programs in the Australian tropics. More broadly across Australia, OzFish Unlimited is engaging with thousands of recreational fishers every year to improve the condition of aquatic habitats, including oyster reefs, seagrass meadows and stream-banks. Here we present case studies of our work to improve fish habitat, including successful project delivery and partnerships, as well as challenges for implementation and engagement.

Otolith morphological analysis: A method to validate observer species identification and fisheries bycatch management

Connor, William[1]; Coulson, Peter[1]; Marshell, Alyssa[1] Masere, Cara[2]
[1] *Institute for Marine and Antarctic Studies, University of Tasmania, Hobart, TAS, Australia*
[2] *Australian Antarctic Division, Kingston, TAS, Australia*

Four species of grenadiers (*Macrourus* spp.) are the primary bycatch within the Patagonian toothfish longline fishery at the Heard and McDonald Islands (HIMI). The Australian Fisheries Management Authority (AFMA) have managed this fishery since 2003 by setting limits on the amount of grenadier bycatch. Over time, the bycatch limits for all four grenadier species, which are identified by fishery observers using external morphological characteristics, have been adjusted based on improved understanding of species composition. Currently, the *Macrourus caml* and *M. whitsoni* bycatch limit differs to *M. holotrachys* and *M. carinatus*. However, there is a lack of specific bycatch limits for each individual species, highlighting the importance of accurate grenadier identification. We measured and compared the shape and size of 800 otoliths among all four *Macrourus* species collected from HIMI's longline fishery between 2015 and 2021. The otolith shape data were analysed using random forest models to assess observer accuracy and identify important otolith shape parameters contributing to species identification. Our investigation will describe new findings highlighting species differences in otolith shape, providing baseline otolith shape knowledge valuable for current and future fishery observers. This provides a tool that highlights the level of accuracy of species identification by observers under challenging conditions and determines if additional observer training is needed to improve the accuracy of onboard grenadier species identification. Furthermore, our study will help shape management measures which support AFMA's goal of shifting the management of *Macrourus* species from a pooled group to individual grenadier species.

Phylogenetic relationships of the New Zealand endemic clingfish Genus *Modicus* Hardy, 1983 (Teleostei, Gobiesocidae)

Conway, Kevin W.[1]; Fujiwara, Kyoji[2]; Keith, Katrina, D.[1]; Stewart, Andrew L.[3]; Summers, Adam P.[4]; Trnski, Thomas[5]

[1]*Department of Ecology and Conservation Biology, Texas A&M University, College Station, TX 77843, USA*

[2]*National Museum of Nature and Science, 4-1-1 Amakubo, Tsukuba, Ibaraki, 305-0005, Japan*

[3]*Museum of New Zealand Te Papa Tongarewa, 169 Tory Street, Wellington, New Zealand*

[4]*Friday Harbor Laboratories, University of Washington, Friday Harbor, WA 98250, USA*

[5]*Auckland War Memorial Museum Tāmaki Paenga Hira, Auckland, New Zealand*

The genus *Modicus* was established in 1983 for two species, *Modicus minimus* and *Modicus tangaroa* and represents one of the eight gobiesocid genera that are endemic to New Zealand. In the original description, *Modicus* was tentatively placed within the subfamily Aspasminae together with genera found in the western tropical Atlantic (*Aspasma*, *Aspasmichthys*, *Liobranchia*) and western Indian Ocean (*Aspasmodes*, *Lissonanchus*). A recent molecular phylogenetic study of the Gobiesocidae investigated the relationships of 82 species of clingfishes (representative of 42 genera) and proposed several revisions to the classification scheme. This study did not include the material of *Modicus,* which was considered *incertae sedis* within Gobiesocidae and in need of "further investigation". We report on the results of a collaborative investigation to assess the phylogenetic relationships of *Modicus*. Our results, based on a combination of DNA sequences (obtained from *M. minimus*) and morphological characters, points to a close relationship between *Modicus* and two other genera of New Zealand endemic clingfishes (*Dellichthys* and *Trachelochismus*).

The golden opportunity – biomonitoring sandy beach marine fishes using environmental DNA.

Cook, Heath[1]; Therkildsen, Nina[2]; Bemis, William[1]

[1] *Department of Ecology and Evolutionary Biology, Cornell University*

[2] *Department of Natural Resources and the Environment, Cornell University*

Sandy beaches make up over 70% of the world's open-ocean coastlines and provide important ecological, economic, recreational, and cultural services. Threats to these ecosystems continue to accelerate including climate change, sea level rise, global population growth, and coastal development. However, seine nets, the traditional near-shore marine biomonitoring method, are not effective in heavy waves, miss highly mobile large predators, and are challenging to deploy on a crowded beach. Emerging technologies may provide a solution and this study uses environmental DNA (eDNA) metabarcoding to survey the biodiversity of surf zone icthyofauna on the western Indian Ocean coast of South Africa. eDNA metabarcoding is successful at detecting surf zone fishes with some surprising detections of taxa, although it remains challenging to distinguish species utilising different habitats within the surf zone. Finally, this study aims to inform beach managers of another potential tool for aiding the conservation of these important but difficult to sample ecosystems.

The success of spiny-rayed fishes in the deep-pelagic ocean discovered using a large midwater trawl

Cook, April[1]; Moore, Jon[2], Sutton, Tracey[1]

[1]*Nova Southeastern University, Dania Beach, FL USA*

[2]*Florida Atlantic University, Fort Pierce, FL USA*

The standard dogma regarding fish assemblages in the deep-pelagic ocean (water column below 200 m depth) is that they are comprised largely of basal, soft-rayed fishes such as Myctophiformes, Stomiiformes, and Aulopiformes. While the diversity of soft-rayed fishes in the deep sea is certainly much greater than the derived, spiny-rayed fishes, it is the abundance and biomass of the latter that has been historically underestimated. Our view of the deep sea has been framed by what we can catch with relatively small, research-sized, rectangular midwater trawls (RMTs) towed from single-warp oceanographic vessels. Large, dual-warp midwater trawls (LMTs) have only been used repeatedly for research in the last two decades. In 2011, the most extensive large-trawl sampling of meso- and bathypelagic fish assemblages occurred in the Gulf of Mexico as part of the *Deepwater Horizon* disaster damage assessment. During this sampling we found that spiny-rayed fishes were collected in much higher ratios than those of RMTs, and that this fauna represented a large proportion of fish biomass below 200 m. This program used both RMTs and LMTs to collect deep-pelagic fauna in the northern Gulf of Mexico between 0-1500 m depth. Data will be presented comparing the catches of basal, soft-rayed fishes to the more derived, spiny-rayed fishes using these two gear types. The resulting synthesis suggests that while soft-rayed fishes do indeed numerically dominate the deep-pelagic domain, the notion that spiny-rayed fishes are not successful in this habitat is likely a function of historical gear bias rather than evolutionary processes.

Spatial ecology and foraging behaviour of oceanic manta rays (*Mobula birostris*) in the Hauraki Gulf, Aotearoa New Zealand

Cooper, Tamsin[1]; Constantine, Rochelle[1]; Della Penna, Alice[1]; Erdmann, Mark[2]; Green, Lydia[3]; Setyawan, Edy[1]

[1]*University of Auckland - Waipapa Taumata Rau*

[2]*Conservation International Aotearoa*

[3]*Manta Watch New Zealand Charitable Trust*

The movement ecology and associated behaviours of large marine animals are often dictated by dynamic environment features influencing resource availability. Understanding these drivers of movement is critical for predicting how species will respond to stressors and changes in environmental conditions, and for informing future management and conservation efforts. Oceanic manta rays (*Mobula birostris*) are a globally endangered species which are frequently sighted along the northeastern coast of Aotearoa/ New Zealand during the warm-water season of the austral summer to early autumn. Despite this, little is currently known about their movements in these waters. Since 2019, 20 satellite tags have been deployed as part of a collaborative research effort. Here we focus on the results of six SPLASH10 tags deployed between 2021 and 2023 which demonstrate fine-scale data for the movements and foraging behaviors of manta rays within the Hauraki Gulf/ Te Moananui-ō-Toi. Tagged mantas ranged from ~3.6 to 4.8m disc width and included four males and two females, one of which was pregnant at the time of tagging. The combined tracks provide 295 GPS locations (accurate to 20m) collected from transmission periods ranging between 20 to 89 days, and reveal high use of the outer Gulf waters around the outer islands and to the southern Gulf area of Coromandel. Comparison of movements to environmental variables provide insight into the fine-scale environmental drivers of horizontal movements and diving behaviors within these productive Gulf waters where the mantas primarily feed on zooplankton.

Poster Function, OGGB Level 0 Foyer, November 21, 2023, 4:15 PM - 6:30 PM

OceanOmics: Bolstering marine research and conservation with genomic technologies

Corrigan, Shannon [1,2]; Ayad, Marcelle [1,2]; Bayer, Philipp [1,2]; Bennett, Adam[1,2]; De Jong, Emma [2]; Depiazzi, Anna [2]; Doran, Adrianne[2]; Edwards, Richard[2]; Goncalves, Priscilla [1,2]; Fraser, Matthew[1,2]; Hogan, Hayley[2]; Huet, Lauren[2]; Missen, Laura[2]; Parata, Lara[2]; Peirce, Tyler[2]; Pearce, Jessica[1,2]; Raes, Eric [1,2]; Rauschert, Sebastian[1,2]; Burnell, Steve[1,2]

[1] *Minderoo Foundation, Perth, Australia*
[2] *Minderoo OceanOmics Centre at UWA, Oceans Institute, University of Western Australia, Perth, Australia*

The ocean covers around 71% of Earth's surface and supports 90% of its biosphere. Despite being the largest and most exploited realm on our planet, more than 80% of the ocean is unmapped, unexplored, and unobserved. The OceanOmics program at the Minderoo Foundation set out to revolutionise how we observe, measure, and understand life in our ocean. We are working with globally renowned scientists and industry partners to innovate eDNA-based marine genomics technologies to transform how we collect biodiversity data across dynamic space and time. This involves optimisation and scaling of eDNA collection, processing, and characterisation, including the development of novel approaches for species detection and quantification. To enable ocean-scale eDNA-based biodiversity surveys, OceanOmics is committed to generating and openly publishing reference genomic resources for thousands of species of marine vertebrates, as well as developing the most comprehensive analytical tools for marine sequencing data based on standardised, reproducible processes and artificial intelligence. We have demonstrated the scalability of eDNA technologies by deployment from our shipboard sequencing laboratory in multiple research expeditions across Australia. The development and application of such comprehensive marine genomics tools, and the generation of large-scale marine vertebrate biodiversity baselines are powerful assets that will facilitate the rapid, accurate and large-scale generation of biodiversity data and ultimately accelerate ocean conservation efforts that can halt biodiversity loss.

4.2C Special Session 8 Fish sensory ecology: new techniques and approaches, 260-073, November 23, 2023, 3:30 PM - 5:15 PM

Seeing the world through the eyes of coral reef fishes

Cortesi, Fabio[1,2]; Marshall, Justin[2]; Mitchell, Laurie[3]; Musilová, Zuzana[4]; Stieb, Sara[2,5]; Tettamanti, Valerio[2]

[1]*School of The Environment, University of Queensland, Brisbane, Australia*

[2]*The Queensland Brain Institute, University of Queensland, Brisbane, Australia*

[3]*Okinawa Institute of Science and Technology, Okinawa, Japan*

[4]*Faculty of Science, Charles University, Prague, Czech Republic*

[5]*Department of Fish Biology and Evolution, EAWAG, Kastanienbaum, Switzerland*

Fishes have conquered almost every aquatic niche on the planet, ranging from clear mountain streams to the relative darkness of the deep sea. At the core of fish vision lie the opsin proteins that, together with a chromophore, form the light-sensitive photopigments. The vertebrate ancestor already possessed five such opsins (four cone- and one rod-opsin) sensitive to the ultraviolet-to-red light spectrum. Using a comparative genomic approach in over 100 fish species, we recently showed that visual opsins continued to proliferate and diversify at astonishing rates in teleosts. Here, I aim to give an insight into our latest efforts to unravel why fishes may have so many opsin genes, showcasing how recent technological advances in the sequencing and reverse genetic space can be leveraged in non-model species to increase our knowledge quickly and efficiently. First, I will provide an overview of opsin gene evolution at the macroevolutionary scale, revealing strong correlations between the number and types of opsin genes and the light environment fishes inhabit. I will then focus on coral reef fishes showing examples of how feeding ecology and intra-specific communication can drive differences in opsin gene repertoires and gene expression at the microevolutionary scale. Finally, I will give an example of how the CRISPR/Cas9 technology can be used to study visual processing in fishes.

Isolated seamount reefs provide potential thermal refuges for reef sharks

Cresswell, Ben[1]; Barnett, Adam[1]; Galbraith, Gemma[1]; Heron, Scott[1]; Hoey, Andrew[1]; Jones, Geoff[1]; McCormick, Mark[2]

[1]*James Cook University of North Queensland, Townsville, Queensland, Australia*

[2]*The University of Waikato, New Zealand*

The grey reef shark, *Carcharhinus amblyrhynchos,* is a common Indo-Pacific reef shark with high site fidelity and reef residency. For sharks occupying isolated reef systems such as those found on remote seamounts and pinnacles, moving between depths may be a mechanism to avoid unfavourable thermal conditions. Previous studies have highlighted this species' capacity for vertical movement, however our knowledge is still lacking on how such movements may vary in response to rising ocean temperature or how such movement might vary depending on life stage or sex. Here we use acoustic telemetry to understand how *C. amblyrhynchos* moved among depths and temperatures on a seamount reef in the Coral Sea, during a year that was 1.5°C warmer than long-term averages. The maximum internal temperature of sharks consistently tracked surrounding SST. However, they exhibited greater depth use during summer, regularly moving to depths of >100m, and spending a greater amount of time in cooler water. In winter, most individuals remained in the upper 35m. Throughout the year, daily minimum internal temperatures were consistent, suggesting thermal preference behaviour in these animals. Diurnal patterns in depth use varied diurnally across seasons with the greatest use of depth during summer nights. While there were no differences in overall depth use between sexes, small females stayed nearer the surface than small males, while larger individuals used more similar depths. Together our results demonstrate the potential for reef sharks to behaviourally regulate internal body temperature through the use of depth and highlight several vulnerabilities to ocean warming.

Contrasting spatial distributions from baited and non-baited stereo video methods and their implications for ocean accounts and biodiversity reporting

Cummins, Gabrielle[1]; Griffin, Kinglsey[1]; Spencer, Claude[1]; Thompson, Samuel[1]; Gibbons Brooke[1]; Navarro, Matthew[1]; Partridge, Julian[1] and Langlois, Tim[1]

[1]*Oceans Institute and School of Biological Sciences, The University of Western Australia, 35 Stirling Highway, Crawley, WA 6009, Australia*

How fish assemblages respond to fishing pressure, habitat degradation and overall environmental change, makes them useful ecosystem condition metrics for inclusion in ocean accounts and biodiversity reporting in general. An important research output, for both ocean accounts and marine park reporting, are reliable spatial distribution models of key metrics.

The application of baited underwater stereo-video systems (BRUVs) is increasing rapidly as a standardised cost-effective, non-extractive method for estimating relative abundance and size-structure of demersal fishes across multiple habitats and depths. Baited video has been shown to sample greater abundance of fished species than other methods but has some known behavioural biases that can influence the assemblage sampled.

Stereo panoramic drop-camera systems do not use bait and may provide a more representative sample of the fish assemblage. We compare spatial distribution models, and their error, for fish assemblage metrics generated from both baited and non-baited video systems inside and outside protected areas across tropical, sub-tropical and temperate locations along the Western Australian continental shelf, to illustrate the potential biases and strengths of using multiple data sources.

Mangrove seascapes provide habitat connectivity in support of culturally important fisheries

Cure, Katherine[1]; Depczynski, Martial[1,2]; Hickey, Sharyn[2]; Howard, Azton[3]; McCarthy, Phillip[3]; Pyke, Damon[3]; Radford, Ben[1,2]

[1]*Australian Institute of Marine Science, Crawley, WA*

[2]*The University of Western Australia, Crawley, WA*

[3]*Bardi Jawi Rangers, One Arm Point, Kimberley, WA*

Across northern Australia, mangroves are abundant and provide good fishing grounds because they are sheltered, easy to access, and have high abundances of sought-after food fish. In the western Kimberley, high tidal fluctuations along mangrove creeks result in fish typically moving at high tide across the spatially connected seascape of mangrove and coral reef habitats for food and shelter. Conservation planning for Indigenous Protected Areas (IPAs) and marine parks requires a better understanding of the links between fish populations across these habitat mosaics, and how these interact with recreational and cultural fishing activities. We used five years of annual fish surveys using baited stereo-video (BRUVS) in the Bardi Jawi IPA, together with high resolution Sentinel 2 satellite derived mangrove and coral reef habitat spatial models to quantify fish abundance, diversity, biomass, and community composition in adjacent coral reef and mangrove habitats. Mangroves showed a unique representation of cultural fisheries target species, which occurred in higher abundance and biomass than at adjacent coral reefs. Mangrove density and proximity to mangroves were key predictors of the abundance and biomass of cultural fisheries targets. Ensuring that spatially heterogenous habitat mosaics inclusive of mangrove habitats are adequately protected and accounted for in conservation planning is key for fish populations to remain healthy and available for local remote communities who depend on these resources.

Use of eye lens stable isotopes to recreate resource-use chronologies in three New Zealand reef fishes

Curtis, Joseph[1]; Wing, Stephen[1]

[1]*University of Otago, 362 Leith Street, Dunedin North, Dunedin 9016*

Fishes often undergo dramatic social and morphological changes throughout development that may drive ontogenetic shifts in diet and habitat association. Resulting patterns in resource use can underpin relationships between fish size and trophic role, vulnerability to environmental disturbance, and the community consequences of size-specific mortality. We quantified relationships between size and resource use in three important reef fishes in Aotearoa New Zealand: banded wrasse/tāngāngā (*Notolabrus fucicola*), butterfish/mararī (*Odax pullus*), and blue cod/rāwaru (*Parapercis colias*). Specifically, we measured stable isotopes in muscle and sequentially deposited eye lens layers, which record patterns of diet and habitat occupancy tracing back to the early life history of an individual fish. We applied these data to describe relative size-structured trophic positions of these species at the population and individual level. We observed patterns of change in eye lens isotopic records that did not always align with population-level trends, providing information about individual variation in trophic ontogenies and movement among habitats. Additionally, using an expansive collection of rāwaru/blue cod, we measured size-structured changes in resource use that varied with sampling location, indicating context-dependencies in patterns of trophic ontogeny and potential information about critical habitats. In all three species, our data allow novel insight into the life history of these important reef fishes, in particular by providing high-resolution measurements of resource use chronologies at the individual level. Our findings suggest ways in which stable isotopes of eye lenses can contribute to understanding of fish ecology, with broad potential for useful application to other species and research settings.

Otolith morphometry and Fourier transform near-infrared (FT-NIR) spectroscopy as tools to discriminate archived otoliths of newly detected cryptic species, *Etelis carbunculus* and *Etelis boweni*

Dahl, Kristen[1]; Barnett, Beverly[2]; Boiston Widdrington, Joseph[3]; Kline, Bill[2]; MacDonald, Jed[4]; O'Malley, Joseph[1]

[1]*National Marine Fisheries Service, Pacific Islands Fisheries Science Center, NOAA, 1845 Wasp Boulevard, Building 176, Honolulu, Hawaii 96818, USA*

[2]*Panama City Laboratory, National Marine Fisheries Service, Southeast Fisheries Science Center, NOAA, 3500 Delwood Beach Road, Panama City, Florida 32408, USA*

[3]*Southern Seas Ecology Laboratories, School of Biological Sciences, University of Adelaide, North Terrace, South Australia 5005, AU*

[4]*Oceanic Fisheries Programme, Pacific Community (SPC), Noumea BP D5 98848, New Caledonia*

Cryptic speciation was recently verified in *Etelis carbunculus*, an important component of federally managed bottomfish fisheries in the Pacific Territories of the United States. As a result, archived otolith collections used for fishery assessment are now contaminated with newly described *E. boweni* in areas where these species co-occur. We compared the efficacy of otolith morphometrics and Fourier transform near-infrared (FT-NIR) spectroscopy to discriminate species first using voucher (i.e., known species) otoliths (n = 93) from the SW Pacific, then applied optimal models to archived otoliths (n = 91) collected around Guam. Significant and distinguishable differences in otolith morphometrics as well as FT-NIR spectral absorbance patterns were observed between *E. carbunculus* and *E. boweni* voucher samples. Classification models applied using both morphometric measurements (quadratic discriminant analysis) and FT-NIR spectral data (partial least squares discriminant analysis) were able to predict species with a high degree of accuracy despite a relatively large spatial area of specimen collection (±10° latitude and longitude) and regardless of whether otoliths were whole (i.e., unbroken). Further, each method identified members of newly described *E. boweni* in the archived collection of *E. carbunculus* otoliths captured around Guam, confirming that the species' distributions overlap in this region. The identification of both *E. carbunculus* and *E. boweni* in the archived catch from Guam has important implications for fisheries management; therefore, it is imperative that the corresponding otolith collections are examined to ensure that the otoliths are assigned to the correct species.

A novel phylogeny of Syngnathidae based on morphology (Teleostei: Syngnathiformes)

Dallevo-Gomes, Caio I. A.[12]; Mattox, George M. T.[2]

[1]*Instituto de Biociências, Universidade de São Paulo*

[2]*Laboratório de Ictiologia de Sorocaba, Universidade Federal de São Carlos, campus Sorocaba*

Syngnathidae is an unique family of teleosts with a remarkable array of characters, such as a body armour composed of interlocking bony rings, opercular opening reduced to a pore and one of the most unique modes of reproduction in the animal kingdom, the incubation of the eggs by the male in a brood pouch. The diversity of Syngnathidae is represented by the pipefishes, seadragons and seahorses, one of the most famous and distinct group of fishes. The Syngnathidae represents one percent of all teleost diversity with more than 300 species in 57 genera, 25 of which were included in this study so far.

Phylogenetic studies on the Syngnathidae were focused on molecular data, with only a precladistic study based on morphology in the 1950s, and a tentative study based on branchial arch skeleton in the 1980s. This work aims at a phylogeny based exclusively on morphological characters, thus expanding the current knowledge of features used as diagnosis on taxonomic studies, by combining osteological and myological data from cleared and stained specimens. The 64 characters proposed so far in this study include patterns of bony armour, feeding apparatus, branchial arches and myology. A comparative anatomy approach to the Syngnathidae opens a window in the classification and evolutionary history of the group.

Dermal armour of Syngnathidae: encasing a diversity of forms

Dallevo-Gomes, Caio I. A.[12]; Mattox, George M. T.[2]

[1]*Instituto de Biociências, Universidade de São Paulo*

[2]*Laboratório de Ictiologia de Sorocaba, Universidade Federal de São Carlos, campus Sorocaba*

Syngnathids have a rare configuration of tegument among teleosts, a dermal armour composed of interlocked ossifications that gives a great degree of body protection in exchange of flexibility. The dermal armour encases the whole body, as each bony ring articulates with its horizontally adjacent rings through the main keel of each bony plate, and each bony ring is formed by the connection of the bony plates with its vertically adjacent plates by interlocking secondary keels.

The dermal plates and their configuration are one of the most important taxonomic features of the family, with characters such as number of rings, configuration of bony ridges, presence of scutella and other characters used to separate different genera and species within the Syngnathidae. This striking plethora of information sourced from taxonomic descriptions found in the literature, combined with a detailed study of cleared and stained bony rings, provided an outstanding diversity in size, shape and configuration of bony rings, plates keels and ornamentation of bony plates, each unique to a taxa, with those patterns being found also on the surface of other bones throughout the skeleton. These 13 dermal armour characters are one of the most important features of an ongoing phylogenetic work based on morphology of syngnathids.

Newly discovered populations of Clutha flathead galaxiid (*Galaxias 'species D'*) in the Cardrona Valley likely facilitate downstream dispersal of individuals.

Davies, Isaac[1]

[1]*University of Otago, Dunedin*

The discovery of two new populations of Clutha flathead galaxiid (*Galaxias 'species D'*) likely explain the recorded presence of the species in the lower Cardrona River in 2019. In 2019, the Department of Conservation recorded the presence of Clutha flathead galaxiids in the lower Cardrona River, near the Wānaka township. It was hypothesised that the fish would be dispersing from populations which were found in tributaries of the Cardrona River which were connected to the main river stem at sometime within the year and within reasonable proximity to the sighting. None of the current known populations of Clutha flathead fit those descriptions.

During an electric fishing survey carried out for the Clutha Fisheries Trust between the 16th of January to the 31st of January 2023, two new populations of Clutha flathead galaxiid were discovered in streams which fit the description of those which could supply the galaxiids to the lower Cardrona River. The survey was conducted using an electric fishing machine and a combination of hand nets and a stop net. These new populations are both on the upstream side of farm water intakes which likely protects the species from invasion by migratory fish species such as the brown trout (*Salmo trutta*) and means that the two populations have the potential to continue to serve as source populations for the lower Cardrona Valley.

Environmental DNA in practice: calibrating methods across labs and marine parks

De Brauwer, Maarten[1]; Ayad, Marcelle[2]; Berry, Olly[3]; Bessey, Cindy[3]; Deagle, Bruce[4]; Dunstan, Piers[1]; Goncalves, Priscila[2]; Herbert, Shane[5]; Noble, Luke[6]; Snape, Natale[7]; White, Nicole[5]

[1] *CSIRO, Coasts and Oceans Research program, Hobart, Australia*

[2] *Minderoo Foundation, Perth, Australia*

[3] *CSIRO, Environomics Future Science Platform, Perth, Australia*

[4] *CSIRO, National Fish Collection, Hobart, Australia*

[5] *eDNA Frontiers, Perth, Australia*

[6] *EnviroDNA, Melbourne, Australia*

[7] *TropWater, Townsville, Australia*

As human pressures on the marine environment increase, so does the need for more accurate monitoring data to support effective marine resource management. Australia’s marine park network is one of the largest in the world, which can pose considerable challenges to monitor effectively. Environmental DNA (eDNA) surveys offer a valuable additional method to resource managers’ toolboxes by providing fish community data cheaper and on larger scales than many established methods. While eDNA methods are increasingly being integrated into monitoring programs globally, large-scale uptake in marine park monitoring remains limited due to a variety of technical, logistical, and budgetary reasons. Analyses of eDNA surveys are usually outsourced to external service providers but lab-specific protocol variations can be hard to understand and assess by non-experts. To overcome this issue, we conducted a ring-test comparing eDNA surveys from tropical and temperate Australian marine parks analysed by five different laboratories. Laboratories started with the same samples and used both a standardised and lab-specific workflow. Preliminary results show clear distinctions between habitat and latitude for all laboratories and workflows. Further analyses will investigate how different laboratory protocols affect representation of fish assemblages and how these can be interpretated for future eDNA surveys. Outcomes of this study will provide insights in improving eDNA workflows for monitoring and increase integration options for eDNA methods in marine resource management.

Integrating molecular phylogenies and fossils without a morphological matrix to investigate patterns of trait evolution: A case study using Carangaria

DeHaan, Lindsey[1,2]; Friedman, Matt[1,2]

[1]*Department of Earth and Environmental Sciences, University of Michigan, Ann Arbor, Michigan*

[2]*University of Michigan Museum of Palenotology, Ann Arbor, Michigan*

Investigating the tempo and mode of trait evolution through geologic time is a central focus among evolutionary biologists and is often approached using a time-calibrated phylogeny and a matching phenotypic dataset of extant species. However, there is agrowing body of literature highlighting the importance of including paleontological data when modelling trait evolution because of the unique data captured by fossils. In particular, incorporation of paleontological evidence can change or strengthen macroevolutionary inferences. Currently, only a few exemplar clades with well-described fossils and an available morphological matrix of extinct and extant taxa can be subjected to a combined phylogenetic analysis in a total-evidence framework to provide the comparative foundation for such work. Here we test a variety of ways of inserting fossils into a molecular phylogeny without a morphological matrix using Carangaria (flatfishes, billfishes, and jacks) as a model system. We fit models of continuous trait evolution to trees of living species only and those with fossils inserted to test the impact on inferences of mode of phenotypic evolution from (1) inserting fossils into a phylogeny generally and (2) contrasting approaches to fossil insertion. A model of diffusive evolution was repeatedly favored for phylogenies with inserted fossils, regardless of how those fossils were inserted. Significantly, exclusion of fossils reduces statistical support for the model. Morphological matrices are critical when resolving the precise interrelationships among fossil and extant taxa, but other approaches using approximate phylogenetic placements of fossil taxa might still have value in macroevolutionary analysis.

4.1B Themed session A: Evolution, Taxonomy and Biogeography of Indo-Pacific Fishes, 260-098, November 23, 2023, 1:30 PM - 3:00 PM

Global biogeography of ecological specialization in coral reef fishes

Delecambre, Zoé[1] ; Casey, Jordan[2]; Dube, Caroline[1]; Floeter, Sergio[3]; Friedlander, Alan[4]; Gaboriau, Théo[5]; Leprieur, Fabien[6]; Morais, Renato[1]; Nunes, Lucas[3]; Paul Costesec, Emma[1]; Siqueira, Alexandre[7]; Parravicini, Valeriano[1]

[1]*Centre de Recherche Insulaire et Observatoire de l’Environnement, Université de Perpignan, Perpignan, France*

[2]*Department of Marine Science, University of Texas at Austin Marine Science Institute, Port Aransas, Texas, United States of America*

[3]*Departamento de Ecologia e Zoologia, Universidade Federal de Santa Catarina, Florianopolis, Santa Catarina, Brazil*

[4]*Pristine Seas, National Geographic Society, Hawai’i Institute of Marine Biology, University of Hawai’i, Hawai’i, United States of America*

[5]*Département de Biologie computationnelle, Université de Lausanne, Lausanne, Switzerland*

[6]*MARBEC, Université de Montpellier, CNRS, IFREMER, IRD, Montpellier, France*

[7]*Research Hub for Coral Reef Ecosystem Functions, James Cook University, Townsville, Australia*

The role of ecological specialization in shaping evolutionary and biogeographical patterns remains unresolved. Ecological specialization may represent an evolutionary dead-end or offer evolutionary advantages depending on specific geographical contexts. To date, few studies have examined ecological specialization at a global scale, especially for reef fishes. Here, we describe global biogeographical and evolutionary patterns of reef fish specialization, exploring both the Grinnellian and Eltonian dimensions of the ecological niche. First, we assemble the largest dataset on reef fish trophic interactions to date, including dietary information for more than 5,000 individuals across 500 reef fish species at 18 locations across the globe. Then, we match these data with reef fish global distributions, using the breadth of their realized thermal niche as a proxy for thermal specialization. We reveal that species richness is positively associated with trophic specialization, while isolated, peripheral reefs are dominated by trophic and thermal generalists. Further, we demonstrate a trade-off in specialization, with both wide and narrow ecological niches representing valuable strategies on coral reefs: while specialization may be favoured in biodiversity hotspots, generalists have a higher colonization capacity and thus represent an advantageous strategy in isolated reefs. This work sheds new lights on the origin and maintenance of fish communities in coral reef systems through time and space.

Clean and oil-weathered microplastics impact *in-situ* behaviours and survival of juvenile coral reef fish (*Pomacentrus amboinensis*)

Delpachitra, Aneesa M[1]; Burritt, David J[3]; McCormick, Mark I[4]; Allan, Bridie JM[2]

[1,2] *Department of Marine Science, University of Otago, Dunedin, New Zealand*

[3] *Department of Botany, University of Otago, Dunedin, New Zealand*

[4]*Coastal Marine Field Station, School of Science, University of Waikato, Tauranga, New Zealand*

Globally, coral reefs are highly threatened by environmental stressors, including microplastics and crude oil, both of which have been documented to exert sublethal effects on coral reef fish. Crude oil, when in contact with seawater, can form water accommodated fractions (WAFS), releasing polyaromatic hydrocarbons (PAHs) which are toxic for marine life. In addition, microplastics have a high affinity for the adsorption of chemicals such as PAHs. Here, we show that when Ambon damselfish (*Pomacentrus amboinensis*) are exposed to the dual threat of oil and microplastic pollution (either clean polystyrene (PS) microplastics or oil-weathered PS microplastics and controls), *in situ* risk taking behaviour and survival rates are both significantly impacted. Specifically, we observed that activity and movement of fish placed onto coral patch reefs was reduced in fish exposed to clean PS microplastics, and further reduced in fish exposed to oil-weathered PS microplastics. In addition, predator-induced mortality rates were heightened in both microplastic groups when compared to controls, with the highest mortality recorded in the oil-weathered PS microplastic group. This research provides evidence towards the minimally investigated synergistic impacts of oil spills and microplastic pollution on coral reef fish. Management of either stressor may therefore provide greater benefits to marine life than previously estimated, by reducing the threat of this combined impact to coral reefs.

Mitochondrial thermo-tolerance in two tropical anoxia-tolerant sharks

Devaux, Jules[1]; Harford, Alice[1]; Renshaw, Gillian[2]; Hickey, Tony[1]

[1]Applied Surgery and Metabolism Laboratory, School of Biological Sciences, University of Auckland, New Zealand

[2]School of Allied Health Sciences, Griffith University, Gold Coast, Queensland, Australia

The epaulette shark (*Hemiscyllium ocellatum*) and grey-carpet shark (*Chiloscyllium punctatum*) are two champions of anoxia-tolerance, surviving 1 and 2.5 hours, respectively, of anoxia at tropical temperatures. Both are well adapted to anoxia that frequently occurs on coral reef platforms, however, these sharks are also exposed to another deadly threat: warning waters. The epaulette shark lives on a knife's edge, with a critical upper temperature (CT_{max}) of 36.2 ºC. This is only ~1 ºC above the reef temperature in summer. Our group has been the first to show that temperate fish hearts fail due to mitochondrial uncoupling just below CT_{max}. As temperature rises, mitochondria consume more oxygen, however, are less linked to oxidative phosphorylation and fail to provide sufficient ATP for the increased demands of a heat-stressed heart. While we have linked mitochondrial plasticity to oxygen dept in the two anoxia-tolerant sharks, mitochondrial thermos-tolerance remains unresolved. To address this, we sought to determine whether mitochondrial failure dictates heart failure approaching CT_{max} in both elasmobranchs. Using respirometry, we show that mitochondrial oxygen consumption in both epaulette and grey-carpet sharks accelerates as temperature rises. However, at 35.6 ºC, the portion of respiration not attributed to ATP production increases substantially, indicating to uncoupling of the mitochondria. Substrate utilization, particularly succinate, was altered similarly with temperature in both species, whereas anoxic-exposure triggered a contrasted response between species. Overall, heart mitochondria in epaulette and grey-carpet sharks appear to be similarly sensitive to heat stress, uncoupling from oxidative phosphorylation approaching CT_{max}, and failing the hot heart.

Epigenetic sequencing to explore environmentally-driven plastic and adaptative responses across fish populations

Devloo-Delva, Floriaan[1]; Deagle, Bruce[1]; White, William[1]

[1]*CSIRO Australian National Fish Collection*

Environmental changes and phenotypic responses are directly linked through epigenetics - the cellular mechanism that switches genes on or off. In natural populations, the ability to rapidly change gene-expression determines how a species can cope with environmental extremes. Such plastic responses are crucial for populations to persist in the initial stages of adaptation. In this talk, we focus on DNA methylation of CpG dinucleotides, one of the main epigenetic modifications in vertebrates. Using reduced-representation bisulfite sequencing, we measured these methylation changes across experimental conditions and natural populations of the School Shark and the Antarctic Toothfish. We sequenced 127 School Sharks and identified 500,000 CpG sites and 45,000 single nucleotide polymorphisms (SNPs). For the 144 Antarctic Toothfish, we found 1.5 million CpG sites and 1.5 million SNPs. We then compared the epigenetic and genetic variability within and between taxa, and identified several genes associated with local environmental conditions. We also studied the stability of the methylation signals between tissue types and quantified the amount of biologically-driven variation versus population-level methylation. Overall, the methylation and nucleotide variations provide information on the adaptive potential of populations, while population-specific methylation sites can inform on the degree of ecological differentiation. These results highlight the use of epigenetic sequencing for identifying environmental association, ecological separation.

Taxonomic review of the triplefin genus *Enneapterygius* (Tripterygiidae) in Japanese waters

Dewa, Yuna[1]; Motomura, Hiroyuki[2]

[1]*Graduate School of Agriculture, Forestry and Fisheries, Kagoshima University, Kagoshima, Japan*

[2]*The Kagoshima University Museum, Kagoshima, Japan*

The genus *Enneapterygius* Rüppell, 1835 (Perciformes: Tripterygiidae), the most speciose group in the family Tripterygiidae, currently includes 63 valid species. They are widely distributed in tropical to temperate Indo-Pacific waters, and inhabiting intertidal rock pools or subtidal rocky or coral reefs, although a few species occur in the deep sea. Of the 63 valid species in the genus, 19 species are previously known from Japanese waters. During ichthyofauna surveys of the Ryukyu Islands, southern Japan, four undescribed species, *Enneapterygius* spp. 1–4, are recognized: *Enneapterygius* spp. 1 and 2 (collected from Yaku-shima island, Osumi Islands), *Enneapterygius* sp. 3 (the Amami, Okinawa and Yaeyama islands), and *Enneapterygius* sp. 4 (widely from the Ryukyu Islands). The validity of *Enneapterygius minutus* (Günther, 1877), previously regarded as a junior synonym of *Enneapterygius philippinus* (Peters, 1868) and closely related to *Enneapterygius* sp. 3, is also confirmed. The present study brings the total number of the species of *Enneapterygius* recorded from Japanese waters to 25. In addition, the taxonomic status of *Enneapterygius etheostoma* (Jordan and Snyder 1902), one of the most common triplefins in Japanese waters, occurring both of Japanese mainland and islands area, is discussed. Detailed intraspecific variations and molecular analysis of the species are provided in this study.

Translating environmental DNA, validated citizen science data, and local knowledge of fishes into meaningful conservation action

DiBattista, Joseph[1]

[1]*Australian Museum Research Institute, Australian Museum*

Small volumes of water containing environmental DNA (eDNA) are increasingly being combined with metabarcoding to generate biodiversity data for specific fractions of our planet's flora and fauna. To date, however, few studies have employed this technique in combination with validated citizen science programs aimed at recording fishes in our rivers, estuaries, and oceans. Even fewer studies have incorporated local knowledge sourced from regular users of coastal and marine sites of conservation importance as a point of reference and/or to build complimentary data sets. I will here present two cases studies in which we combined eDNA detections based on metabarcoding sequence data, validated citizen science observations, and/or local knowledge. I will also discuss the strengths and weaknesses of each these data sets, and how a combined approach can provide more robust conclusions related to the conservation of resident and migratory fishes.

New and recent records of fishes from the Mariana Islands

Donaldson, Terry J.[1]; Burdick, David R.[1]; Lindfield, Steven[2]; Mundy, Bruce C.[3]; Myers, Robert F.[4]; Tibbatts, Brent [5]

[1]*University of Guam Marine Laboratory/EPSCoR, Guam, USA*

[2]*Coral Reef Research Foundation, Koror, Palau*

[3]*Ocean Research Explorations, Honolulu, Hawaii USA*

[4]*Coral Graphics, Wellington, Florida, USA*

[5]*Division of Aquatic and Wildlife Resources, Mangilao, Guam USA*

The most recent checklist of fishes of the Mariana Islands lists 1,106 species including 1,020 that are inshore or epipelagic, the vast majority of which inhabit coral reefs Included in the list are 97 species indicated as new records without further comment other than to identify the basis of the record as an examined or collected specimen (21), photograph (57) or reliable sighting (16) and at least 16 additional species identified only to genus, 13 of which have since been described as new. In light of a growing body of research that extends the occurrences of many shorefishes to depths below 300 m as well as other species of shorefish lineages that may occur exclusively below the mesophotic zone, we expand our use of the terms reef fishes, inshore fishes or shorefishes to include the rariphotic zone, as well as even deeper-dwelling species that inhabit these zones at higher latitudes. Based on this, we include at least 116 additional species that have recently been discovered in the Mariana Islands that occur or are likely to occur at depths of approximately 500 m or less. but many have not. Here, we consolidate into a single publication, photographs and other information that represent new records of inshore and epipelagic fishes, or that validate previously documented occurrences of them within the Mariana Islands and associated banks and seamounts.

Phenotypic change to varying thermal experience within and across generations

Donelson, Jennifer[1]

[1]*College of Science and Engineering, James Cook University, Townsville QLD 4811*

While many tropical fish species and populations exhibit high sensitivity and negative impacts from acute ocean warming, with development and cross-generational exposure thermal plasticity can occur and improve performance. Whether this plasticity measured in an experimental setting can be adaptive will depend on a range of aspects. In many instances, all traits will not exhibit the same level of acclimation in response to a given thermal change. Or instead, specific timing of thermal exposure is required to elicit plasticity of a certain trait. What can we learn from multigenerational experiments that simulate future ocean warming? Here I explore a three-generation experiment with the coral reef damselfish (*Acanthochromis polyacanthus*) to discuss patterns of plasticity depending on warming in the grandparent, parent, and current generation and how this helps us understand the potential for adaptive response to ocean warming.

Role of herbivorous reef fishes in resilience-based management

Donovan, Mary[1,2]

[1]*Arizona State University*

[2]*Hawai‘i Monitoring and Reporting Collaborative*

Resilience-based management is an approach to maintain or increase the resistance and/or recovery capacity of reefs to local and global stressors. Given that both local and global stressors are increasing in intensity and frequency on reefs worldwide, this approach to local management has recently gained traction. The potential for herbivorous fishes to play an outsized role in reef resilience has led to herbivore fisheries management to arise as a key tool in resilience-based management. Yet, the evidence for managing herbivore populations for this ecosystem-based objective is largely lacking at scales relevant to management. Meanwhile, herbivore catch can be a large component of overall reef fisheries, especially for Pacific islands such as Hawai‘i. I will share how we have worked collaboratively across agencies and institutions to compile evidence related to the implementation of herbivore-based management in Hawai‘i. With 20,242 fish transects compiled from multiple sources alongside data on 27 biophysical and human drivers we have analysed how multiple drivers explain spatial gradients in herbivore populations and herbivory processes. We have also uncovered evidence that herbivores have played a role in explaining disparate trajectories across reefs following a major heatwave in 2015. I will conclude with discussing how these lines of evidence have contributed to decision making related to nearshore fisheries management as part of the Holomua Marine Initiative.

Describing the recognised: toward description of further *Galaxias* from New Zealand

Dunn, Nicholas[1]; Waters, Jonathan[2] , Wallis, Graham[2] , Crow, Shannan[3]

[1]*Biodiversity System and Aquatic Unit, Department of Conservation, Christchurch, New Zealand*

[2]*Department of Zoology, University of Otago, Dunedin, New Zealand*

[3]*National Institute of Water and Atmospheric Research, Christchurch, New Zealand*

The endemic, non-diadromous *Galaxias vulgaris* species complex (Family Galaxiidæ) comprises six described species and at least six further lineages of freshwater fishes across eastern South and Stewart islands, New Zealand. Molecular diversity within the complex is long-recognised, but habitat-influenced phenotypic convergence among lineages and divergence of body form within lineages has hindered formal descriptions. Using an integrative approach, we aim to develop taxonomic descriptions for five new *Galaxias* candidate species. From the late 1970s, isozyme, mitochondrial and nuclear DNA, and most recently genome-wide SNPs have revealed and provided support for phylogenetically separate candidate species. Molecular studies based on material from extensive field surveys have increased identification of allopatric geographic distributions of candidate species, with some limited overlap of species complex members. Candidate species also display differences in habitat preferences and putative spawning habitat characteristics of the slow-fasting flowing lotic habitats occupied. Multivariate analyses of geometric and linear morphometric measures independently revealed separation of genetically recognized candidate species from other member of the species complex. Owing in part to the conservative body plan of *Galaxias*, individual linear morphometric characters describing head form dominate in diagnoses. Formal description of these candidate species is integral to the management and protection of these important components of New Zealand's biodiversity, as well as enabling further focussed fundamental research on the ecology and biology of the species complex.

Fish passage monitoring and remediation in a highly modified New Zealand ecosystem

Ryan R. Easton[1], Eddy Dowle[1], Gert-Jan Jeunen[1], Hayley Bosley[1], Jemma Geoghegan[1], Peter Whigham[1], Tony Moore[1], Gerry Closs[1]

[1]*University of Otago, Dunedin, New Zealand*

The Murihiku [Southland] region of Te Waipounamu, Aotearoa [South Island, New Zealand] is a landscape dominated by agriculture which has led to a freshwater ecosystem fragmented by road crossing culverts, weirs and fords. Southland has a diverse range of freshwater fish species, with the majority considered taonga [treasured]. The diversity of these species and differences in life-history, swimming ability and climbing ability means that each species, and each life-history stage within these species, has different challenges when presented with a migration barrier. Therefore, in order to maximize river connectivity, different species/life-stages will need to be considered, requiring different remediation methods. Multiple remediation methods have been encouraged for use in New Zealand, however the effectiveness of these remediation methods have yet to be tested at a large scale in-situ. One method to test the efficacy is to compare the community assemblage upstream and downstream, before and after barrier remediation, and even similarity of viral/parasite communities. The methods to achieve these assessments all have limitations, with traditional monitoring efforts like electrofishing being time and cost intensive, causing some waterways to be overrepresented, and some species underrepresented. However, newer methods such as eDNA sampling have issues involving limits of detection, are currently unable to provide relative abundance metrics, and can be costly to process. Here we cover our efforts to develop a prioritisation and monitoring plan to assess barrier remediation effectiveness, including eDNA collection method testing and fish virome investigation, and present some preliminary data on species distribution upstream/downstream of identified barriers.

Reconstructing Ancestral Reproductive Modes In Sharks: How Difficult Is It to Evolve (and Re-evolve) Viviparity?

Edde, Diala[1]; Trindade-Santos, Isaac[1]; Sallan, Lauren[1]

[1]*Macroevolution Unit, Okinawa Institute of Science and Technology, Onna, Okinawa, Japan*

Oviparity is widely considered to be the ancestral mode of reproduction in vertebrates. In contrast, viviparity is assumed to result from relatively rare pathways related to greater parental care, as supported by observations of major modern groups (i.e., teleosts, mammals, birds, etc…) with one dominant strategy. However, sharks (Elasmobranchii), show a diversity of viviparous and oviparous species, as well as several modes of embryonic nutrition. It remains unclear how many times these modes evolved, or ease of reversion and switching. Here, we assembled the largest existing dataset of reproductive modes in chondrichthyans (N = 371) and phylogenetic comparative methods (AncThresh, SIMMAP) to reconstruct ancestral character states and transition rates between reproductive modes. Our results strongly suggest that the earliest ancestor of sharks was viviparous lecithotrophic. This fits with evidence from the fossil record and vertebrate phylogeny; placoderm stem-jawed fishes exhibited widespread viviparity, and "shark" egg capsules date only back to 350 Mya, long after the origin of Chondrichthyes. The best fit models show that reproductive modes originated and reappeared multiple times even within families. Switching occurred at a high rate, with a low amount of evolutionary change (threshold "liability") required to change from even egg-laying to full placentation. Given that amphibians and reptiles also exhibit high diversity in reproductive mode, our results suggest that change in reproductive mode was almost routine for vertebrates ancestrally, but has become set in mammals, birds and teleosts for other reasons. Sharks are a better model of the vertebrate default mode than more speciose groups.

The spatiotemporal patterns of young blacktip reef shark encounter-rates with predators inside ‘nursery’ areas.

Edwards-Ingle, C Jake[1]; Allan, JM Bridie[1]; Rayment, J William[1]; Rummer, L Jodie[2].

[1]*Department of Marine Science, University of Otago, Dunedin 9016, New Zealand*

[2]*Marine Biology, College of Science and Engineering, James Cook University, Townsville 4814, Australia*

The shallow-water refuge paradigm states that juvenile fishes can reduce predation pressure by utilising shallow-water areas which exclude predators. However, the blacktip reef shark (*Carcharhinus melanopterus*) distribution surrounding Moorea, French Polynesia, does not follow this paradigm, instead neonatal blacktip reef sharks utilise these shallow-waters almost exclusively despite high spatial overlap with predatory adult conspecifics. Temporal overlap and habitat characteristics, such as habitat complexity, are known to influence predator-prey encounter-rates, and thus the chances of predation. By recognising the potential influence of these factors on predation risk, we may be able to identify why neonatal blacktips utilise shallow-water areas despite spatial overlap with predators. Using a novel method involving an unmanned aerial vehicle (UAV), densities of blacktip neonates and adults in reef flats were surveyed with encounter-rates measured using a local index of colocation. Here, we demonstrate that time of day (i.e., dawn, day, and dusk) and habitat characteristics (i.e., rugosity) influenced both abundances and encounter-rates of young blacktips and their predators in terrestrial reef flats surrounding Moorea. More predator-prey encounters were observed in reef flats with greater benthic complexity and more encounters occurred during the day compared to crepuscular times, with dawn displaying the lowest encounters. Furthermore, predatory adult blacktips are found in greater relative abundance at dusk but drastically reduced relative abundance from shallow ‘nursery-grounds’ during dawn and day. By understanding the spatiotemporal patterns behind what makes a ‘safe’ nursery for young blacktips, effective conservation tools can be prioritised in protecting areas that may disproportionately contribute to blacktip recruitment.

Integrated Reef Fish Monitoring of the Great Barrier Reef

Emslie, Mike[1]; Bierwagen, Stacy[1]; Carter, Alex[2]; Ceccarelli, Dani[1]; Henderson, Chris[3]; Olds, Andrew[3]; Sinclair-Taylor, Tane[1]; Smith, Tim[2]; Srinivasan, Maya[2]; Stowar, Marcus[1]

[1]*Australian Institute of Marine Science*

[2]*TropWATER, James Cook University*

[3]*University of Sunshine Coast*

Monitoring of natural ecosystems provides fundamental knowledge to assess the status and trends in biological communities, changes in environmental conditions, and the responses of ecosystems to extrinsic and intrinsic stressors. In 2021 several knowledge gaps were identified for reef fish monitoring on the Great Barrier Reef, including lack of knowledge of deep-water inter-reef fishes, fish assemblages in coastal nursery seascape and fringing reefs around continental islands. These knowledge gaps were addressed by establishing an Integrated Reef Fish Monitoring Program across much of the GBR for fish species of recreational, commercial, biocultural, and ecological significance. A collaborative multi-institutional project team has provided new insights into important fishery species such as tropical snapper, red emperor and coral trout. The project has also worked closely with Traditional Owners to co-develop the sample design in the Nursery Seascape component, as well as provide hands on training for Traditional Owner Sea Rangers. Preliminary analyses have revealed a holistic view of spatial distributions of reef fish assemblages, but also have drawn ontogenetic linkages between coastal nursery seascapes and adult populations further offshore, as revealed by the habitat use of rarely observed juveniles of important target species and large aggregations of adults offshore in deep inter-reef waters. This project is providing the first characterisations of reef fish assemblages of previously unexplored coastal nursery and deep-water inter-reef habitats.

Resharking leopards in Raja Ampat: a behind-the-scenes look at the StAR (*Stegostoma tigrinum* Augmentation and Recovery) project

Ichida, Nesha[1]; Dudgeon, Christine[2]; Erdmann, Mark[3]; Dove, Alistair[4]; Fahmi[5]; Hadfield, Catherine[6]; Heatubun, Charlie[7]; Herwata, Iqbal[8]; Hoopes, Lisa[4]; Meyer, Erin[6]; Neal, Leah[4]; Sianipar, Abraham[8]

[1]*Thrive Conservation, Bali, Indonesia*

[2]*University of the Sunshine Coast, Brisbane, Australia*

[3]*Conservation International Aotearoa, Auckland, New Zealand*

[4]*Georgia Aquarium, Atlanta, USA*

[5]*National Research and Innovation Agency of the Republic of Indonesia, Jakarta, Indonesia*

[6]*Seattle Aquarium, Seattle, USA*

[7]*Regional Research and Innovation Agency of West Papua Province, Manokwari, West Papua, Indonesia*

[8]*Konservasi Indonesia, Sorong, Papua Barat, Indonesia*

Conservation translocations have long played an important role in threatened species recovery plans for terrestrial wildlife, but have been used much less commonly in the marine realm. Here we provide an overview of the world's first conservation translocation program for a threatened elasmobranch species: the StAR project. Since the 1990s, the Indo-Pacific leopard shark *Stegostoma tigrinum* has been hunted throughout much of its range for the shark fin trade, leading to dramatic population declines and a 2016 IUCN Red Listing as EN. In an interesting conservation asymmetry, the species is currently thriving in large aquariums, where its husbandry is now well-established and successful breeding is commonplace. The StAR project was conceived in late 2019 by a group of conservationists, scientists, government officials and aquarium professionals as an ambitious plan to re-establish a healthy, genetically diverse breeding population of leopard sharks in the Raja Ampat archipelago in Indonesia through the introduction of captive-bred juveniles sourced from genetically-appropriate broodstock in accredited Aquariums. Importantly, though leopard sharks were nearly extirpated from Raja Ampat by the early 2000s, the region is now a well-enforced sanctuary for sharks and rays, providing an excellent natural laboratory to develop and refine a robust protocol for conservation translocations of threatened elasmobranchs. Here we present a summary of three years' of comprehensive planning and implementation which led to the world's first conservation translocation of an endangered shark species in January 2023, and a brief look at how we aim to leverage this success through the ReShark initiative.

.

3.2A Themed Session C: Fisheries and Aquaculture in the Indo-Pacific, 260-073, November 22, 2023, 10:30 AM - 12:30 PM

Kiribati coral reef ecological indicators, small-scale fisheries, and climate resilience

Eurich, Jacob G.[1,2]; Friedman, Whitney R.[3]; Donovan, Mary K.[4]; Gephart, Jessica A.[5]; Golden, Christopher D. [6]; Seto, Katherine L. [3]; Tekiau, Aranteiti[7]; Zamborain-Mason, Jessica[6]; McCauley, Douglas J[2,8]

[1]*Environmental Defense Fund, Santa Barbara, CA, USA*

[2]*Marine Sciences Institute, University of California, Santa Barbara, Santa Barbara, CA, USA*

[3]*Environmental Studies Department, University of California at Santa Cruz, Santa Cruz, CA, USA*

[4]*Center for Global Discovery and Conservation Science and School of Geographical Sciences and Urban Planning, Arizona State University, Tempe, AZ, USA*

[5]*Department of Environmental Science, American University, Washington, DC, USA*

[6]*Department of Nutrition, Harvard T.H. Chan School of Public Health, Harvard University, Boston, MA, USA*

[7]*Ministry of Fisheries and Marine Resource Development, Coastal Fisheries Division, Bikenibeui, Tarawa, Republic of Kiribati*

[8]*Department of Ecology, Evolution and Marine Biology, University of California, Santa Barbara, Santa Barbara, CA, USA*

Climate change and increasing human pressure are impacting many coral reef ecosystems. However, spatial scale can confound, or in some instances obscure, the impacts of anthropogenic activities on the structure of ecological communities that have direct bearing on human well-being. Further, the scarcity of data-rich gradients of human pressure makes it difficult to isolate changes associated with anthropogenic impacts versus non-human influences over time. Here, we established a unique ecosystem-wide marine resource baseline assessment of eight independent coral reef atolls across an environmental and anthropogenic gradient in the Gilbert Island chain, Kiribati, to compare ecological indicators of coral reef condition and estimate conservation potential. We quantified the local abundance of frequently harvested and functionally important fish and invertebrate reef species, as ecological indicators, and associated habitats to empirically-derive estimates of available biomass, reef function, and stock status. We found that local human influence, assessed by underwater community surveys and a national social survey, greatly outweighs oceanographic conditions in their influence on each of the quantified ecological indicators. Islands with elevated human influence – measured by high population density, percentage of fishing households, fishing effort, derelict (lost or discarded) fishing gear, and plastic pollution – were associated with significantly lower ecosystem condition. Further, stock status of fished species was disproportionately lower on islands with high fishing effort when compared to islands with low anthropogenic influence. This type of insight is valuable for strategically shaping small-scale fisheries management and the relationships between people and coral reefs.

1.2A Special Session 4: The evolution and ecology of fishes: assessing traits and functions in a changing world, 260-073, November 20, 2023, 11:15 AM - 1:00 PM

Assessing functional, morphological and phylogenetic composition in reef fishes to explore similarities in assembly rules among biogeographic systems

Fernández-Cisternas, Ítalo[1,2]; Garmendia, Vladimir[1,2]; Landaeta, Mauricio[1,4]; Pérez, María Fernanda[3,5]; Pérez-Matus, Alejandro[1,2]; Rezende, Enrico L.[3]; Ruz, Catalina[2]

[1]*Millennium Nucleus for the Ecology and Conservation of Temperate Mesophotic Reef Ecosystem (NUTME), Las Cruces, Chile*

[2]*Subtidal Ecology Laboratory and Marine Conservation Center, Estación Costera de Investigaciones Marinas, Pontificia Universidad Católica de Chile, Santiago, Chile*

[3]*Departamento de Ecología, Center of Applied Ecology and Sustainability (CAPES), Pontificia Universidad Católica de Chile, Santiago, Chile*

[4]*Laboratorio de Ictiología e Interacciones Biofísicas (LABITI), Instituto de Biología, Facultad de Ciencias, Universidad de Valparaíso, Valparaíso, Chile*

[5]*Instituto de Ecología and Biodiversidad (IEB), Alameda 340, Santiago, Chile*

Understanding how functional traits and demographic processes determine the formation of species assemblages under different environmental conditions may help elucidating how ecosystem functions and species coexist. Reef fish are an excellent model for studying assembly rule patterns due to their remarkable taxonomic and functional diversity, which are strongly correlated with their habitat. Here we test if three isolated biogeographic reef fish assemblages with an independent evolutionary history exhibit ecological and functional convergence. We studied assemblages from three different ecoregions: Warm Temperate South East Pacific (WTSEP), Juan Fernandez archipelago and Desventuradas (JFD), and Easter Island (EI). We combined hierarchically-structured underwater visual census with four independent replicates per ecoregion, geometric morphometry and molecular data to obtain taxonomic, functional, and phylogenetic diversity indices within and across ecoregions. Cluster analysis and functional space were created to explore similarities between traits. Analyses indicate that functional diversity and taxonomic composition vary significantly across ecoregions, whereas the functional space demonstrates strong similarities in the composition of functional traits. For example, despite the diversity in form of head shape, most species in the three ecoregions tend to cluster within the central region of the morphological space. Interestingly, WTSEP displays significantly lower functional and phylogenetic diversity compared to other ecoregions, indicating a strong convergence of functional traits within the WTSEP assemblage. Our findings suggest that, despite their differences in biogeographic and historical processes that shaped the species composition of each ecoregion, reef fish assemblages apparently adapt to functionally match common environmental conditions and tend to exhibit ecological convergence.

Exploring the relationship between egg deposition in *Schroederycthys chilensis* and kelp morphological attributes in nesting sites in Chile

Fernández-Cisternas, Ítalo[1,2]; Beldade, Ricardo[1,3]; Pérez-Matus, Alejandro[1,2,3] ; Walker, Tomás[2]

[1]*Millennium Nucleus for the Ecology and Conservation of Temperate Mesophotic Reef Ecosystem (NUTME), Las Cruces, Chile*

[2]*Subtidal Ecology Laboratory and Marine Conservation Center, Estación Costera de Investigaciones Marinas, Pontificia Universidad Católica de Chile, Santiago, Chile*

[3]*Departamento de Ecología, Pontificia Universidad Católica de Chile, Santiago, Chile*

On terrestrial environments, the nest-site selection in birds and mammals is related to physical attributes of trees, which could vary in response to variation in habitat characteristics. Similarly, elasmobranch species use different habitats to lay their eggs including kelp, however the habitat characteristics that drive oviposition site selection is poorly understood. Here, we study different physical attributes of kelp at individual and patch scale to determine the characteristics that drive oviposition site selection in the red-spotted catshark *Schroederycthys chilensis.* We selected 5 sites across a latitudinal gradient (19°S-39°S), encompassing most of the range overlap between kelp *Lessonia trabeculata* and *S. chilensis* in Chile. We conducted a SCUBA monitoring, measuring physical attributes of kelp (holdfast diameter, number of stipes, stipe length and total kelp length) with and without egg presence, and measuring the density of kelp within patch. We found a positive relationship between egg number and stipe length. *S. chilensis* tend to select taller kelp individuals within a kelp forest patch. Finally, there was not a relationship between egg number per algae and density of kelp forest. Our results suggest that female *S. chilensis* prioritize vertical separation from the substrate (longer stipe lengths) when selecting kelp individuals to anchor their eggs. However, the utilization of a kelp patch is not determined by the size of the kelp within the patch. Since kelp forest size structure is changing by overharvesting (high densities of shorter algae), the unsuitable kelp substrate could be limiting breeding densities for local population of *S. chilensis*.

1.4B Themed Session: K. General Session, 260-057, November 20, 2023, 2:00 PM - 4:15 PM

Understanding the void within: endocasts provide a new axis of morphological diversity for teleosts

Figueroa, Rodrigo T.[1,2]; Friedman, Matt[1,2]

[1]*Department of Earth and Environmental Sciences, University of Michigan, USA*

[2]*InstitutionMuseum of Paleontology, University of Michigan, USA*

Ray-finned fishes represent the most diverse group of extant vertebrates, with most of this diversity within teleosts. The substantial morphological variety and long evolutionary history of actinopterygians means there are few features that can be directly compared across modern and fossil taxa. In several vertebrate groups, the endocast—internal mould of the space within the neurocranium—represents an important axis of diversity which is directly comparable among lineages with diverse external structure due to morphological conservativeness. Despite this, the study of actinopterygian endocasts has been effectively restricted to Paleozoic fossils and a handful of extant examples, but virtually no information for teleosts. Here we demonstrate that teleosts bear much more complex and morphologically diverse endocasts than previously expected, suggesting a new system for examining phenotypic evolution in this group. Teleost endocasts, as in Paleozoic fossils, can be divided into three areas loosely corresponding to brain regions (forebrain, midbrain and hindbrain) plus large inner ears. The proportions between these regions vary among taxa, although boundaries between these regions might be difficult to precisely identify. Within the sampled taxa, the forebrain and inner ear regions are the most morphologically diverse, with a handful of clades showing novel specializations (e.g. laterally elongated horizontal canal in the skeletal labyrinth of aulopiforms). Our results demonstrate that teleost endocasts can be directly compared to examples from the fossil record. Thus, providing an important new axis of morphological diversity for understanding patterns of clade-wide diversification and rates of evolution in actinopterygians including both fossil and living lineages.

The next generation of shark Red Listing

Finucci, Brittany[1]; Jabado, Rima W.1; Rigby, Cassandra L.[1]

[1]*IUCN Species Survival Commission Shark Specialist Group, Dubai, United Arab Emirates*

The International Union for Conservation of Nature (IUCN) Red List of Threatened Species is the world's most comprehensive inventory of the global conservation status of animal, fungi, and plant species. In response to the growing awareness and concern of fisheries impacts on chondrichthyans (sharks, rays, and chimaeras), the IUCN Species Survival Commission Shark Specialist Group (SSG) was established in 1991 and is now recognized as the leading authority on the status of chondrichthyan fishes. All 1200+ species of sharks, rays, and chimaeras have now undergone at least one round of the Red List assessment (RLA) process. RLAs are living documents and are updated every ten years. Some species are now being globally reassessed for the third time, shedding light on the increasing extinction risk of this group over recent decades. Over the course of this process, RLAs have been designed to provide updated and evidence-based data on the global status of each species. Continued advancements in knowledge and expertise needs to be gathered from the SSG and wider global research community to update assessments and ensure this knowledge accurately captures the status of a species throughout its entire range. This can lead to conservation action for priority threatened species groups. Despite progress in our knowledge of chondrichthyan biology, population trends, and threats, crucial species-specific knowledge gaps still exist. Without this information, data must be inferred from alternative sources. Here, the most needed and useful information often missing for RLAs will be provided to guide future research efforts.

4.1C Themed Session A Evolution, Taxonomy and Biogeography of Indo-Pacific Fishes, 260-098,
November 23, 2023, 3:30 PM - 5:15 PM

The evolution of stripe patterning in clownfishes

Fitzgerald, Lucy[1]; Salamin, Nicolas[1]

[1]*Department of Computational Biology, University of Lausanne, Lausanne, Switzerland*

Clownfishes have some of the most iconic color patterns in the marine environment. There have been many proposed functions of coloration from an evolutionary perspective such as species recognition, mimicry, or sexual selection. Clownfish have three main colors (orange, white, and black) and zero to three stripes with some species having a bar across the top of their head. Additionally, their coloration has been linked to their anemone host association. The loss of stripes occurred caudal-rostrally with the common ancestor having three stripes 12 million years ago. Yet, the evolutionary genomics behind the loss of stripes remains unknown. Using a phylogenomic approach with the full genomes of the 28 species, we analyzed the mapping of white stripe presence/absence and did stochastic mapping and ancestral reconstruction of the number of stripes. We then tested for all coloration-related genes (~200) if the number of stripes across the clownfish phylogenetic tree was associated with changes in non-synonymous vs. synonymous substitutions (dN/dS) values. Looking at the color proportion of the white stripes, we investigate the associations between the number of stripes and branch dN/dS. Our results give us insights into the genomic mechanisms driving stripe patterning.

Drivers of fish assemblage structure across a 100-meter depth gradient in the tropical western Pacific

Flem, Logen[1,2]; Asher, Jacob[3]; Taylor, Brett[1,2]

[1]*University of Guam Marine Laboratory, Mangilao, Guam*

[2]*University of Guam Sea Grant, Mangilao, Guam*

[3]*Red Sea Global, Riyadh, Saudi Arabia*

Guam, of the Mariana Archipelago, contains more than one thousand fish species, many of which contribute to the island's commercial, cultural, and subsistence fisheries. These species occupy vertical habitat gradients including shallow (<30 meters) to mesophotic depths (>30 and <150 meters). Analyzing fish assemblage structure, namely species composition and abundance, remains a challenge across this full depth range. However, the utility of stereo baited remote underwater video systems (stereo-BRUVS) provides access to the nearshore mesophotic zone. Through the deployment of 160 stereo-BRUVS, we captured an island-spanning snapshot of reef fish-assemblages across a 100-meter depth range. Factors known to influence reef fish assemblages include *depth*, *fishing pressure*, surface *wave exposure*, and *habitat characteristics* (e.g., type, percent cover, complexity). These primary factors and others (e.g., MPA status, site accessibility by boat, seafloor slope) were incorporated in complementary univariate mixed-effects models with multivariate evaluations of assemblage structure. From this we determine the hierarchy and magnitude of their influence on fish assemblage structure across reefs of Guam, and thus identify environmental drivers operating on multiple scales that influence spatial assemblages of coral reef fishes while assessing the influence of fishing pressure on targeted commercial species. The results of this study provide valuable insight for island-scale fisheries management along with greater understanding of factors influential to shallow and mesophotic reef ecology.

Exploring the drivers of growth synchrony within and among coral reef fishes across the Pacific

Fobert, Emily[1]; Barrow, Josh[1]; Halford, Andrew R[2]; Macdonald, Jed[2]; Moore, Brad[3]; Morrongiello, John[1]; Taylor, Brett[4]

[1]*School of BioSciences, University of Melbourne, Parkville, VIC 3010, Australia*

[2]*Pacific Community (SPC), Noumea, New Caledonia, 98848*

[3] *National Institute of Water and Atmospheric Research, Nelson, New Zealand*

[4] *University of Guam Marine Laboratory, Mangilao, Guam 96923*

Understanding the spatio-temporal scales of population and trait dynamics is becoming increasingly important in the face of large-scale ecological pressures, such as climate change, overharvesting, and habitat degradation. Spatial synchrony – when temporal patterns of abundance, growth, or survival show parallel fluctuation across populations – is of growing interest to ecologists, as synchronous fluctuations can increase the vulnerability of populations to stochastic events, with potential consequences for local population persistence and community structure. Understanding the scales of synchrony is also a vital aspect of coastal fisheries management in the Pacific, as it can inform the scale of management efforts. Recent research has shown that both climate and exploitation can have a synchronizing effect on marine population dynamics. Though most studies on synchrony have generally focused on geographically distinct populations of the same species, synchrony can also occur across different species. In this study, we use individual-based, annually resolved growth estimates from otoliths of six coral reef fish species spanning seven island locations across the Pacific to assess patterns in synchrony in the interannual variation of growth rates, both within and among species across their geographic range. We identify local and large-scale climatic drivers that contribute to spatial scaling in synchronous fluctuations of growth rates, and assess the impact of fishing pressure on the strength of growth synchrony. Our results provide critical information on the spatial dynamics and the scale of intra- and interspecific trait synchrony in Pacific coral reef fish assemblages, which in turn have implications for the management of coastal fisheries.

Mainstreaming marine connectivity conservation to support Sustainable Development Goal 14 “Life Below Water”

Fontoura, Luisa[1]; Maina, Joseph Mbui[1]

[1] *School of Natural Sciences, Macquarie University, Sydney, Australia*

Mounting scientific evidence supports the role of ecological connectivity in maintaining biodiversity and sustaining ecosystem services on coral reefs. Still, conservation management tools focused on protecting reefs from human and climate change pressure have often missed that reefs are not isolated systems. One of the major obstacles to implementing marine connectivity conservation policy is the vast disconnect between scientific evidence and management actions on the ground, particularly in coral reefs, which inhibits the transition from science and policy into action. With a wealth of scientific information available, the science of marine connectivity conservation is poised for a translational process involving place-based applications and experiential learning with ongoing stakeholder collaboration. Community-based marine managed areas offer an excellent setting for prototyping participatory place-based research in translational connectivity conservation science into practice. Integrating connectivity science with local knowledge to inform spatially adaptive fisheries management can potentially benefit fisheries-dependent livelihoods in the estimated 450 community-based marine-managed areas in the Pacific and Western Indian Ocean. Within this context, we propose a small-scale fisheries management decision framework underpinned by evidence-based marine connectivity conservation benefits across spatiotemporal scales. Finally, using reef fish connectivity patterns within Community-Based Managed Areas Networks located in Fiji and Kenya as examples, we discuss where existing uncertainties and gaps in marine connectivity research and complex governance structures can be synergistically addressed while engaging stakeholders in participatory place-based research.

Diet variation of common smelt across a salinity gradient in coastal lakes on Rēkohu (Wharekauri, Chatham Island)

Fortune-Kelly, Grace[1]; Ara, Motia; Ingram, Travis

[1] *Te Whare Wānanga o Ōtākou/ The University of Otago, Ōtepoti/ Dunedin, Aotearoa/ New Zealand*

Coastal freshwaters are experiencing intensifying salinity regimes and strengthened oceanic connectivity as sea level rise and more extreme weather events continue to augment. Rēkohu (Wharekauri, Chatham Island), off the east coast of Aotearoa (New Zealand) has unique low-lying lakes that are likely to be subject to such changes. These lakes provide a valuable contrast to mainland Aotearoa, as they have been being spared from the introduction of invasive fish, but lacustrine biology on the island remains understudied. *Retropinna retropinna* (common smelt) are the most widespread lake-dwelling fish on the island. As mobile generalists, understanding their diet across abiotic gradients, such as salinity, can show key characteristics of their own ecological role and give insight into community structure, present and future. We analysed stomach contents of common smelt across 10 lakes (seven freshwater and three salt-influenced) on Rēkohu. Diet between salt-influenced and freshwater lakes showed shifts in composition with smelt in freshwater consuming insect larvae (Trichoptera and Diptera) and zooplankton (Cladocera and Copepoda), while diet in salt-influenced lakes was dominated by crustacean shredders (Amphipoda and Isopoda). These shifts may reflect resource availability and have implications on the trophic role common smelt play in these systems. Lower between lake variation amongst salt-influenced lake diets was observed, suggesting homogenisation with salinity is possible. Given the increasing threat of sea level rise to the many low altitude coastal lakes on Rēkohu, further development of biotic and ecological data, and monitoring changes across salinity gradients is becoming ever more pressing.

Reappraisal of Indo-Pacific holdings of the Scripps Institution of Oceanography Marine Vertebrate Collection

Frable, Benjamin[1]; Arcila, Dahiana[1]

[1]Marine Vertebrate Collection, Scripps Institution of Oceanography, University of California San Diego, 9500 Gilman Drive, La Jolla, CA 92093-0244, USA.

The Marine Vertebrate Collection of the Scripps Institution of Oceanography (SIO) at the University of California San Diego is one of the largest ichthyological collections in the United States. Its holdings consist of over two million specimens representing over 6000 species of fish. Major collections are derived predominantly from the eastern Pacific, including significant representation from the Tropical Eastern Pacific, as well as pelagic and deep-sea species worldwide. Early collection efforts, led by Carl Hubbs and Richard Rosenblatt, focused heavily on the eastern Pacific. Nonetheless, a considerable number of historic collections were undertaken throughout the Indo-Pacific, including some of the earliest specimens collected by Randall in Hawaii, the *Naga* Expedition, and collections throughout Micronesia. In recent decades, Indo-Pacific representation within the collection has significantly expanded due to intensified collection efforts, strategic collaboration, and exchanges. However, the collection is still sometimes overlooked in research efforts. Herein, we summarize the Indo-Pacific holdings of SIO both of nearshore and pelagic and deep-sea fishes, recent growth from regions such as the South China Sea, Central Pacific, and the Hawaiian Islands, as well as our future plans for growth. We also highlight our extensive and growing molecular collection and our digitization and data accessibility efforts. We encourage global investigators to make full use of the valuable resource, visit SIO, and engage in collaborative efforts to secure and study important specimens, thereby advancing the understanding of marine biodiversity in this region.

“Coastal Fishes of New Zealand” – the 5th edition

Francis, Malcolm[1]

[1]*Retired, formerly NIWA*

“Coastal Fishes of New Zealand” is a popular and authoritative guide to the identification of commonly seen fish living within a kilometre of the New Zealand shore and in less than 50 metres water depth. It has been available since 1988, with the first edition containing 146 underwater photographs in a 126-page book. “Coastal Fishes” has been regularly reprinted and expanded, with the 4th edition published in 2012 containing 275 photos and running to 267 pages. A 5th edition, to be published in 2024, will have a wider scope including 50 further species. These will include very shallow estuary species such as stargazers, midwater species such as anchovy and pilchards, as well as species that are increasingly regularly encountered in open water such as tuna, sharks, giant manta ray and sunfish. The use of underwater photographs showing live fish in their natural setting is a hallmark of the book.

Understanding the drivers of Grey Nurse Shark movement and capture in fisheries gear along the east coast of Australia

Fuenzalida, Pablo[1]; Dwyer, Ross[1]; Kilpatrick, Carley[2, 3]; Scales, Kylie[1]; Schoeman, David[1]

[1]*School of Science, Technology and Engineering, University of the Sunshine Coast, Maroochydore DC, Queensland, 4558, Australia*

[2]*Shark and Ray Research Group & Molecular Fisheries Laboratory, School of Biomedical Sciences, The University of Queensland, St Lucia, Queensland 4072, Australia*

[3]*Queensland Parks and Wildlife Service and Partnerships, Department of Environment and Science, Manly, Queensland 4179, Australia*

Earth's oceans harbour a remarkable assemblage of marine megafauna, many of which exhibit migratory movements that can span continents and oceanic basins. Understanding when, where, and why animals move throughout their migratory range can assist managers in efforts to reduce detrimental fisheries interactions and promote population persistence. The Grey Nurse Shark (*Carcharias taurus*) has a global distribution, with their east Australian population categorised as critically endangered. Over the past decade, the Queensland Department of Agriculture and Fisheries and New South Wales Department of Primary Industries have been tracking the movements of east Australian *C. taurus* using coded acoustic tags and a nationwide array of acoustic receivers to gain insights into their movement ecology. Both states also host a shark-control program, deploying gear such as gillnets and drumlines at popular bathing beaches to reduce the risk of harmful interactions with other dangerous shark species. Our study aims to determine the intrinsic and extrinsic drivers of occurrence and capture risk in shark control equipment for *C. taurus*. We model environmental influences on occurrence and movements of tagged *C. taurus* along the east coast of Australia and test the effectiveness of these models in predicting the likelihood of capture in shark control program gear. The outcomes of this study uncover new ecological information on this charismatic marine predator and will be crucial in assisting conservation managers in creating spatially protected areas and reducing threats associated with the shark control program.

Poster Function, OGGB Level 0 Foyer, November 21, 2023, 4:15 PM - 6:30 PM

A preliminary revision of the clingfish subfamily Diademichthyinae (Gobiesocidae)

Kyoji, Fujiwara[1]; Hiroyuki, Motomura[2]

[1]*National Museum of Nature and Science, 4-1-1 Amakubo, Tsukuba, Ibaraki 305-0005, Japan*

[2]*The Kagoshima University Museum, 1-21-30 Korimoto, Kagoshima 890-0065, Japan*

The clingfish subfamily Diademichthyinae was recently redefined on the basis of molecular data and some osteological features, and mainly comprised Indo-Pacific wide spread species. Although 17 genera with 36 valid species are currently assigned to the subfamily, the numbers are not accurate due to the presence of polyphyletic genera confirmed from previous studies and poorly known species. These problems were partially resolved but a taxonomic revision of the subfamily has never been completed. A perspective on the exact members of diademichthyine clingfishes is recently becoming clearer, confirming the need for a number of taxonomic treatments. As a result of preliminary revision of Diademichthyinae in this study, 15 genera with 35 species, including three undescribed genera and species, were recognized. Species of the two undescribed genera have previously been included in *Lepadichthys* as the *L. lineatus* complex (including four valid species) and *L. trishula*, respectively. In addition to the exclusion of the five species from *Lepadichthys*, *L. bilineatus* was synonymized under *L. ctenion*, whereas *L. springeri*, previously regarded as a junior synonym of *L. misakius*, was resurrected as a valid species. The remaining undescribed genus is monotypic with an undescribed species and can be distinguished from other genera of the subfamily by the unique combination of morphological characters and colour patterns. Two undescribed species were found from *Propherallodus* and *Liobranchia*, the latter being a senior synonym of *Aspasmodes* and *Pherallodichthys*. *Unguitrema* was also synonymized under *Discotrema* which includes two valid species (*D. zonatum* and *U. nigrum* were synonymized under *D. monogrammum*).

Predicting productivity in tropical seaweed-associated fish populations

Fulton, Christopher[1,2]; Barneche, Diego[1,2]; Birt, Matthew[1]; Depczynski, Martial[1,2]; Faubel, Cal[1,2]; Ford, Brendan[1]; Holmes, Thomas[2,3]; Radford, Ben[1,2]; Tinkler, Paul[4]; Wilson, Shaun[1,2]

[1]*Australian Institute of Marine Science, Indian Ocean Marine Research Centre, Crawley, 6009, Western Australia*

[2]*Oceans Institute, Indian Ocean Marine Research Centre, The University of Western Australia, Crawley, 6009, Western Australia*

[3]*Department of Biodiversity, Conservation & Attractions, Kensington, 6151, Western Australia*

[4]*Centre for Integrative Ecology, School of Life and Environmental Sciences, Deakin University Warrnambool Campus, Warrnambool, Victoria, Australia*

Sargassum meadows are a globally significant habitat in tropical seascapes where they support a wide diversity of fishes during their juvenile and adult life history stages. These seaweed meadows are highly dynamic habitats, which has raised questions around how resident fish populations, including species that underpin small-scale fisheries across the Indo-Pacific (e.g., *Leptoscarus vaigiensis*), respond to periodic shifts in local primary production. We used a metabolic approach to scale *Sargassum* net primary production (NPP) and fish consumption rates from individuals to populations at the meadow scale. In doing so, we were able to calculate the fraction of NPP that fluxes into seaweed-associated fishes. We then tested whether (1) multiple abiotic variables predict meadow NPP and (2) whether changes in meadow NPP predict browsing fish herbivory rates. Our first model indicated a strong effect of local sea temperature on meadow NPP across our four study regions. Remarkably, strong local effects down to site level appeared to swamp any potential signal from large-scale climatic indicators (e.g., equatorial-Southern Oscillation Index) that varied strongly over the 11-year timeframe of our dataset. Our second model revealed that meadow-scale NPP is a strong predictor of consumption by herbivorous fishes across Ningaloo. Collectively, our models provide a framework for predicting shifts in fish biomass and productivity arising from spatial and sea temperature effects on *Sargassum* meadows that can directly inform conservation and fisheries management of these prominent tropical Indo-Pacific habitats and their resident fish populations.

Species diversity of the synodontid genus *Synodus* Scopoli, 1777 in the Indo-Pacific Ocean

Furuhashi, Ryusei[1]; Motomura, Hiroyuki[2]

[1] *The United Graduate School of Agricultural Sciences, Kagoshima University, Kagoshima, Japan*

[2] *The Kagoshima University Museum, Kagoshima, Japan*

The lizardfish genus *Synodus* (Aulopiformes: Synodontidae), inhabiting variable environments, including sandy bottoms and rocky and coral reefs in warm waters of the world, consists of 47 valid species, of which 34 valid species are known from the Indo-Pacific Ocean. However, a genetic tree constructed with sequences of the Indo-Pacific species of *Synodus* registered in DNA databases and sequences analyzed by the authors showed 37 distinct clades in the genus from the Indo-Pacific Ocean. Of these, 21 clades (including some undescribed species) had morphological information based on voucher specimens, and their genetic distances highly agreed with morphological differences. Then, we attempted to identify the remaining 16 clades without morphological information by referring to the positional relationship in the tree and locality information, and found that nine clades were assigned to nine described species, while the remaining seven clades were most likely not assigned to any known species. In addition, 13 of 34 valid species of *Synodus* in the Indo-Pacific Ocean are not considered to correspond to any of the 37 clades. Therefore, at least 50 species of *Synodus* are distributed in the Indo-Pacific Ocean.

Exploring the genetic structure and evolutionary history of marine fish populations in Micronesia

Gaither, Michelle[1]; Amirthalingam, Pavithiran[1]; O'Malley, Joseph[2]; Schemmel, Eva[2]; Barsis, Nadia [1]; Marciante, Victoria[1]

[1] *Department of Biology | Genomics and Bioinformatics Cluster, University of Central Florida*

[2] *The National Oceanic and Atmospheric Administration (NOAA)*

Most marine species exist in metapopulations or assemblages of subpopulations inhabiting discrete habitat patches that are often separated by large stretches of unsuitable habitat. Connectivity between subpopulations is most often achieved by dispersal via ocean currents during the larval phase. Estimating connectivity among marine populations is essential to understanding the dynamics of metapopulations and the likelihood of population persistence. Micronesia is a vast area in the north Pacific with hundreds of islands that are thought to serve as vital stepping-stones between the central and western Pacific Ocean. Yet only two phylogeographic studies have been conducted in the region and none have been conducted across the 800 km Mariana Archipelago that includes Guam and Saipan, leaving many unanswered questions about metapopulation dynamics and dispersal pathways across this vast area. To understand dispersal dynamics of marine fishes across the region, we co-sampled four species (two shallow- and two deep-water species) across the Marianas and using the double digest restriction site-associated DNA sequencing (ddRAD-seq) approach we resolved tens of thousands of SNPs for each species. We then used this dataset to explore the population structure of each species. While initial assessments indicate little population structure across the archipelago, we do find differing patterns of migration. We use these data to define populations for management and conservation, while also examining the role of historic sea level change in population dynamics.

Regional patterns in demersal fish assemblages among subsea pipelines and natural habitats across north-west Australia

Galaiduk, Ronen[1,2], Bond, Todd[2,3], Case, Mark[1], Cooper, Tim[2,4], McLean, Dianne[1,2], Radford, Ben[1,2], Smith, Luke[2,5], Taylor, Michael[2,3]

[1]*Australian Institute of Marine Science, Indian Ocean Marine Research Centre (IOMRC), Perth, WA, Australia.*

[2]*Oceans Institute, The University of Western Australia, Perth, WA, Australia.*

[3]*School of Biological Sciences, The University of Western Australia, Perth, WA, Australia.*

[4]*BHP, Perth, WA, Australia.*

[5]*Woodside Energy, Perth, WA, Australia.*

Regional patterns of fish diversity, abundance, distribution, and assemblage composition are driven by a combination of biotic conditions and interactions with abiotic geomorphic environment, but these interactions can be altered through anthropogenic infrastructure, such as those associated with oil and gas extraction. Our study utilises data on fish relative abundance and diversity obtained from 1546 baited remote underwater video (BRUV) deployments. These BRUV deployments were conducted between 2004 – 2019 in depths of 9 – 170 m across 2000 km of coastline in north-west Australia on natural habitats and subsea pipelines to understand the influence of oil and gas infrastructure on fish assemblages. A total of 450 fish taxa from 56 families were observed, with populations dominated by generalist and invertebrate carnivore taxa. At the regional scale, subsea pipelines had lower diversity than natural environments, but possessed a higher abundance of piscivorous and herbivorous fish taxa. Multivariate analyses showed clear patterns in fish assemblage composition which were explained best using proximity to oceanic shoals and banks, depth, and to a lesser extent, proximity to oil and gas infrastructure. Fish assemblages in shallow-water and close to shoals were characterised by a diversity of site-attached (e.g., wrasses, tuskfish), reef-associated taxa (e.g., emperors). Mesophotic fish assemblages were characterised by important commercial (e.g., goldband snapper), wide-ranging (e.g., sharks) and sand-affiliated (e.g., toadfish, threadfin bream) taxa. Proximity to pipelines and platforms ranked low as predictors in the multivariate analyses suggesting a negligible regional influence of these structures on fish communities in comparison to depth and shoal habitats.

Remotely Operated Vehicle surveys reveal new mesophotic biodiversity in the Coral Sea Marine Park, Australia

Galbraith, Galbraith[1]; Cresswell, Benjamin[1]; Hoey, Andrew[1]; McClure, Eva[1]

[1]*College of Science and Engineering, James Cook University, Townsville, Australia*

Australia’s mesophotic coral ecosystems remain unexplored and understudied relative to other global locations with deep-reef habitats. We present new diver-independent methods using Remotely Operated Vehicles (ROVs) developed to survey the mesophotic habitats of Australia’s Coral Sea Marine Park (CSMP). We modified consumer-grade ROVs to facilitate the cost-effective and efficient simultaneous survey of fish and benthic communities at depths below that of conventional diving. Our ROV surveys conducted over 3 years, 15 reefs and depths between 3 -110 m in the CSMP recorded 325 species of coral reef fishes, sixteen of which are not previously known from the region, and significant depth range extensions for seventy-eight fish species. Four of the new occurrence records represent significant range extensions into the Coral Sea from adjacent biogeographic regions and thirteen of these species are not known from the neighbouring Great Barrier Reef, despite its close proximity. We also recorded a wide variety of mesophotic benthic habitats including extensive areas of mesophotic coral ecosystems at depths between 70 -110m with coral cover estimates of up to 80%. These habitats support diverse and abundant fish communities and, based on these preliminary findings, we discuss the potential for greater connectivity between mesophotic habitats in the Coral Sea and surrounding biogeographic regions than previously known.

5.1A Themed Session A: Evolution, Taxonomy and Biogeography of Indo-Pacific Fishes, 260-098, November 24, 2023, 10:30 AM - 12:30 PM

Century-old museum and modern fish specimens reveal temporal loss of adaptive potential and connectivity changes in the marine biodiversity epicenter

Garcia, Eric[1]; Baldisimo, Jem[1]; Bird, Chris[2]; Bucol, Abner[3]; Carpenter, Kent[1]; Clark, Rene[4]; Lopez, Ivan[1]; Pinsky, Malin[4]; Reid, Brendan[4]; Roberts, Roy[2]; Whalen, John[1]

[1]*Old Dominion University, VA, USA*

[2]*Texas A&M University-Corpus Christi, TX,USA*

[3]*Silliman university, Dumaguete City, Negros Oriental, Philippines*

[4]*Rutgers University, New Brunswick, NJ, USA*

Recording genetic signatures of prolonged anthropogenic activity on natural populations is a central goal of evolutionary biologists who traditionally have been limited by the paucity of appropriate datasets. Historical and museum collections represent invaluable assets that can allow researchers to directly measure genetic change. Here, by enriching shotgun whole-genome libraries from museum specimens of *Spratelloides delicatulus* collected by the *USS Albatross* expedition in the early 1900's as well as cotemporary collections, we provide unprecedented documentation of temporal genetic change across the Philippines, where the blue sprat is exploited for consumption and as bait for other fisheries. Early results show higher heterozygosity across time points in populations from the Sulu archipelago (southern Philippines) compared to southern Luzon (central Philippines), but an overall temporal reduction of genetic diversity in all sampled populations. Moreover, PC and F_{ST} analyses revealed temporal divergence in every population, but differentiation was highest between spatial samples. Interestingly, we found high divergence and distinct genetic clusters within the Sulu archipelago indicating that spatial population isolation is not solely driven by geographic distance. Outlier loci analysis and additional populations are currently being processed. Overall, our spatiotemporal analysis of genetic change provides rare evidence of the loss of adaptive potential in a tropical marine species, and can inform the management of marine resources in the Philippines where marine biodiversity and anthropogenic stressors are exceptionally high.

Putting sharks on the map: identifying Important Shark and Ray Areas worldwide to inform marine spatial planning.

Emiliano García-Rodríguez[1]; Asia O. Armstrong[1,2], Amanda Batlle Morera[1], Jenny Bortoluzzi[1], Ryan Charles[1], Adriana Gonzalez Pestana[1], Peter M. Kyne[1,3], Theophile Mouton[1], Giuseppe Notarbartolo di Sciara[1,4], Christoph A. Rohner[1,5], Rima W. Jabado[1,6]

[1]*International Union for Conservation of Nature Species Survival Commission Shark Specialist Group, Dubai, United Arab Emirates*
[2]*School of Science, Technology and Engineering, University of the Sunshine Coast, Hervey Bay, Qld 4655, Australia*
[3]*Research Institute for the Environment and Livelihoods, Charles Darwin University, Darwin, NT 0909, Australia*
[4]*Tethys Research Institute, 20121 Milano, Italy*
[5]*Marine Megafauna Foundation, West Palm Beach, FL, USA*
[6] *College of Science and Engineering, James Cook University, Townsville, Qld 4811, Australia*

Sharks, rays, and chimaeras (hereafter ‘sharks’) face a high risk of extinction, with 37% of species assessed as threatened on the IUCN Red List of Threatened Species™. Immediate action is required to halt population declines and allow for species recovery. Area-based measures are key for biodiversity conservation but commonly do not focus on sharks, and existing ones often fail to provide them adequate protection. The Important Shark and Ray Areas (ISRA) approach delineates discrete, three-dimensional portions of habitat, important for one or more shark species, that have the potential to be managed for conservation. The ISRA project, launched in 2022, has begun working through 13 global regions, bringing together regional experts to contribute knowledge and identify critical shark habitats. In the Central and South American Pacific, 65 ISRA were identified based on science-driven criteria and have passed an independent review process. Areas were delineated in all countries in the region, and beyond national jurisdictions. Further, 11 Areas of Interest and five candidate ISRAs were mapped as potentially important areas for which existing evidence was not sufficient to meet the criteria. Results from the Mediterranean and Black Seas, and Western Indian Ocean regions will also be presented, with examples of how criteria to identify ISRA were applied, and knowledge gaps identified in each region. ISRA findings provide the foundation to include sharks in the decision-making processes when designing protected areas, and for marine spatial planning. This can help governments and policymakers advance shark conservation and meet global biodiversity and conservation targets.

How long before an estuary benefits from habitat repair?

Gaston, Troy[1]; Bennett, Mark[1]; Cuerel, Ben[1],; Raoult, Vincent[1,2]

[1]*University of Newcastle*

[2]*Macquarie University*

Coastal wetlands, including saltmarsh, have suffered historical degradation due to extensive human activities and development within the coastal zone. Wetlands have been drained, infilled and disconnected from the estuaries for stock grazing, agriculture, and urban development. Growing recognition of the ecological importance of saltmarsh ecosystems has seen an increase in habitat rehabilitation efforts with state and local governments funding a variety of projects (active and passive) aimed at returning ecological function and resilience for saltmarsh into the future. Apart from changes in aerial extent, the current knowledge of the ecological flow-on benefits of saltmarsh rehabilitation in Australia is limited. This project aims to identify the nutritional dependency of resident fish (Glassfish, Yellowfin Bream and Tarwhine) on the surrounding saltmarsh at Burrill Lake, NSW, pre and post rehabilitation. The targeted rehabilitation of more than 21.8 ha of saltmarsh at the northern end of Burrill Lake has provided a great opportunity to quantify the potential flow-on benefits. The results estimate that saltmarsh offers a significant contribution to all three species regardless of proximity to the rehabilitation site. For both Yellowfin Bream and Tarwhine, saltmarsh contribution to diet averaged 30% and 50% respectively, however, did not change over time. For Glassfish, the contribution of saltmarsh increased by ~10% over the study period from 20% up to 30%. This study shows that changes to estuarine foodwebs may occur within timescales as little as 16-months, providing a useful measure of the effectiveness of rehabilitation efforts in terms of enhancing estuarine ecological function.

Onwards and upwards – studies of climbing in *Galaxias brevipinnis*

Gee, Eleanor[1,2]; Baker, Cindy[1]; Franklin, Paul[1]; Tieman, Gordon[1]; Williams, Peter[1]

[1]*The National Institute of Water and Atmospheric Research, New Zealand*

[2]*Current Address: Waikato Regional Council*

In steep locations in Aotearoa New Zealand, fish passage is often provided only for climbing species, and designs often implicitly assume high rates of climbing success. We studied how juvenile *Galaxias brevipinnis* use climbing to pass instream barriers. Known as kōaro in Aotearoa New Zealand and climbing galaxias in Australia, *G. brevipinnis* is regarded as one of the strongest climbers of the freshwater fishes of Aotearoa New Zealand and populations have been observed above large waterfalls. However, climbing ability has not previously been quantified, and nor has the relationship between climbing ability and morphological factors such as length and weight of an individual.

Fish were allowed to voluntarily attempt to climb a ramp with a small flow. Ramps varied from 45° to 85° and had either a smooth or slightly roughened surface. We found that success rates were high if fish attempted to climb, but many did not. We will present comparisons of success probability between different ramp slopes and roughnesses, and across gradients of fish length, weight and depth. Quantifying climbing ability and understanding how morphological characteristics of fish that change with age influence climbing success can help improve the design of fish passage structures to facilitate upstream migration.

CheckEM: an open-source tool for quality control and visualisation of stereo-video fish and benthic annotations

Gibbons, Brooke[1]; Goetze, Jordan[2]; Langlois, Tim[1]; Navarro, Matthew[1]; Monk, Jacquomo[3]; Spencer, Claude[1]

[1]*School of Biological Sciences and the Oceans Institute, The University of Western Australia, Crawley, Western Australia, 6009*

[2]*Department of Biodiversity, Conservation and Attractions, Kensington, Western Australia, 6151*

[3]*Institute for Marine and Antarctic Studies, University of Tasmania, Hobart, Tasmania, 7001*

Effective management of the marine environment at continental and global scales relies on interoperable and reusable data from long-term monitoring. The use of forward facing stereo imagery to survey fish and benthic assemblages is becoming widespread globally due to its ability to collect abundance and body-size data in a robust, cost-effective and non-destructive manner. A recent synthesis of Australian stereo-video datasets revealed a series of common mistakes in spatial metadata, taxonomic identification and body-size annotation. We created an open-source R shiny app, CheckEM, to provide immediate feedback and checks on metadata and annotations of fish and benthic stereo-imagery to integrate into annotation workflows and improve the interoperability and reusability of data. The interactive web-based app allows users to compare annotations against accepted local and global life history traits, including expected spatial distribution, body-size and length-weight relationships. It creates interactive plots and tables in a graphical interface, provides summarised data and error reports to download, and enables users to produce synthesis datasets from multiple annotation sets. Rapid, cost-effective and robust environmental reporting at continental and global scales will rely on data being Findable, Accessible, Interoperable and Reusable. CheckEM improves the interoperability and reusability of fish and benthic assemblage stereo-video annotations and will greatly improve the efficiency of future syntheses for long-term monitoring.

Optimising coastal fish monitoring and reporting through predicted versus observed abundance models

Gilby, Ben L.[1]; Goodridge Gaines, Lucy A. [2]; Henderson, Christopher J. [2]; Borland, Hayden P.[2]; Coates-Marnane, Jack[3]; Connolly, Rod M.[4]; Maxwell, Paul S.[5]; Mosman, Jesse[2]; Olds, Andrew D.[2]; Perry, Hannah J. [2]; Saeck, Emily[3]; Tsoi, Iris[3]

[1]School of Science, Technology and Engineering, University of the Sunshine Coast, Petrie, 4502, Queensland, Australia

[2]School of Science, Technology and Engineering, University of the Sunshine Coast, Maroochydore DC, 4558, Queensland, Australia

[3]Healthy Land and Water, Level 19/160 Ann St, Brisbane City 4000, Queensland, Australia

[4]Coastal and Marine Research Centre, Australian Rivers Institute, School of Environment and Science, Griffith University, Gold Coast, QLD 4222, Australia

[5]Alluvium Consulting, Fortitude Valley 4006, Queensland, Australia

Effective ecological monitoring is predicated on establishing links between focal indicator metrics and drivers of change. While many coastal environmental monitoring programs focus strongly on the physical parameters of ecosystems, including water quality, sediment characteristics, and ecosystem extent and quality, comparatively fewer have incorporated metrics indexing the condition of animal assemblages. We surveyed fish assemblages in six ecosystems across 13 estuaries in southeast Queensland, Australia, over three years (for n>1800) to establish patterns in fish responses to key environmental variables and create models useful for environmental monitoring and reporting. Spatial and temporal patterns were established for fish species richness and the abundance of five indicator species. These metrics all varied significantly between years, ecosystems and estuaries, and then according to several spatial (e.g. seascape connectivity) and temporal (e.g. water quality) attributes of coastal seascapes. Variable relationships with median turbidity and chlorophyll A concentrations challenge the assumption that clear waters with high and consistent salinity support more fish. The resulting models were used to calculate predicted values for each replicate, and to illustrate the efficacy of four different approaches for translating predicted and observed values into estuary-wide report card grades. Overall, the percentage of sites within an estuary that scored above predicted values for each year was found the most effective for this purpose given the degree to which this value varies around means, and the consistency in scores between years within estuaries. We discuss requirements for ongoing predictions over time, and challenges in establishing effective and rapid monitoring protocols.

2.4A Themed Session F: Conservation of Indo-Pacific Fishes, 260-092, November 21, 2023, 10:30 AM - 12:30 PM

Understanding effects of zoning on abundance and composition of fish assemblages across the southern Great Barrier Reef

Gilliland, Virginia[1]; Raoult, Vincent[1]; McSpadden, Kristen[2]; Duce, Stephanie[3]; Gaston, Troy[2]; Joyce, Karen[4]; Williamson, Jane[1]

[1]*Marine Ecology Group, School of Natural Sciences, Wallumattagal Campus, Macquarie University, Sydney, NSW, Australia*

[2] *School of Environmental and Life Sciences, University of Newcastle, Ourimbah, New South Wales, Australia*

[3] *College of Science and Engineering, James Cook University, Townsville, Queensland, Australia.*

[4] *College of Science and Engineering, James Cook University, Nguma-bada Campus, Cairns, Queensland, Australia.*

Over recent years, many studies have shown the establishment of marine protected areas and zoning are key tools for fisheries management and biodiversity conservation across the Great Barrier Reef. However, these findings are not universal, and some studies report no difference between overall biodiversity in fished versus unfished areas. Advances in remote sensing technology offers the ability to continue exploring these relationships with a new perspective by capturing larger areas and reaching depths scuba divers are unable to reach. Here we use underwater remotely operated vehicles (ROV) to identify differences in reef-associated fish assemblages among fished and unfished reefs to understand the effectiveness of zoning across the Great Barrier Reef. We ask 1) How does the diversity and abundance of reef-associated fishes differ between fished Habitat Protection zones and unfished Marine National Parks? We also assess relationships between observed assemblages and physical characteristics of habitat, asking 2) How does reef-associated fish assemblage composition relate to habitat type and structural complexity? We examine these questions across multiple reefs providing the first study of this size at a fine spatial resolution. Results suggest that fish abundance and species richness are correlated with complexity and habitat type, with the most complex habitat supporting the highest numbers of fishes. When accounting for habitat type and complexity, unfished reefs also had higher abundances than fished reefs. We emphasise that managers should consider ROVs as a valued technology in this realm and future studies should continue to use them as tools to assess species and habitats.

Evaluating the feasibility of sustainable seafood labelling programmes in Small Island Developing States: a pilot study in Seychelles

Glass, Jessica R.[1,2]; Belle, Kalsey[3]; Berke Gregory[4]; Bodin, Nathalie[5,6]; Burt, April J.[7,8]; Duncan, Murray I.[9,10,11]; Morgan, Sian K.[12,13]; Pillay, Pavitray[14]; Talma, Sheena[15,16]

[1]*University of Alaska Fairbanks, College of Fisheries and Ocean Sciences, Fairbanks Alaska 99775, USA*

[2]*South African Institute for Aquatic Biodiversity, Makhanda, 6140, South Africa*

[3]*La Misere, Mahé, Seychelles*

[4]*Independent Marine Consultant, Anse La Mouche, Mahé, Seychelles*

[5]*Sustainable Ocean Seychelles, Mahé, Seychelles*

[6]*Data for Ecosystem and Ocean Health, 37540 Saint sur Loire, France*

[7]*Department of Plant Sciences, Oxford University, South Parks Road, OX1 3RB, UK*

[8]*Seychelles Islands Foundation, La Ciotat Building, Mont Fleuri. P.O. Box 853, Victoria, Mahé, Seychelles*

[9]*Department of Environment, University of Seychelles, Anse Royale, Mahe, Seychelles*

[10]*Blue Economy Research Institute, University of Seychelles, Anse Royale, Mahe, Seychelles*

[11]*Department of Ichthyology and Fisheries Science, Rhodes University, Makhanda, South Africa*

[12]*SeaBright Solutions, Point Roberts, Washington, USA 98281*

[13]*Aquatic Ecosystems Research Lab, University of British Columbia, Vancouver, BC Canada V6T 1Z4*

[14]*WWF South African Sustainable Seafood Initiative and Fisheries Programme, WWF South Africa, Newlands, Cape Town, 7725 South Africa*

[15]*Talma Consultancy, Mahé, Seychelles*

[16]*Nekton, Begbroke Science Park, Oxford, UK*

The Republic of Seychelles is one of six African Small Island Developing States (SIDS) and has a marine-based economy reliant on fisheries and international tourism. Seychelles has been flagged by the United Nations as highly vulnerable to climate change. Climatic threats are compounded with population declines of key fishery species. A progressive national stance towards ocean sustainability and an emerging economy partially driven by tourists are two of several factors that make Seychelles a good candidate for a sustainable seafood labelling and consumption programme, which would provide market-based incentives for fishery harvesters, regulators, buyers and consumers to improve sustainable practices. To address the feasibility of such a programme, we conducted a pilot study and mapped supply chain structure to examine incentives and challenges. We gathered data in the form of surveys (N = 267) from artisanal fishers, local consumers, tourists, regulators, restaurants and hotels, and fishery industry representatives. 64% of fishers would like to see a programme implemented but only 34% thought it would be successful. Stakeholders identified several barriers and benefits that primarily spanned socioeconomic and regulatory themes. Our pilot results indicate the sociocultural and economic impacts of sustainability programmes in Seychelles are as important as environmental considerations, a finding pertinent to anyone undertaking similar research efforts in other SIDS. We advocate for the necessity of thorough, location-based research and in-depth stakeholder consultation to elucidate economic, societal, behavioural and cultural factors that will affect the success of designing and implementing seafood labelling programmes in SIDS.

The diversity, evolution and ecological importance of dwarfgobies (*Eviota*)

Goatley, Chris[1]; Vaz, Diego[2]; Tournament, Luke[3]

[1]*University of Southampton, UK*

[2]*University of Guam, Guam, USA*

[3]*University of Washington, USA*

Coral reefs house exceptional biodiversity, with around 6,000 species of fishes calling reefs home. Remarkably, more than one in seven of these fishes fall into a single family, the Gobiidae. In this presentation, I will discuss the ecological role of these small fishes on coral reefs, which play critical functions in coral reef trophodynamics due to their short lifespans, rapid growth rates and extraordinary reproductive capacity. I will then introduce a standardised sampling method used to study the diversity and abundance of gobies and other cryptobenthic fishes, then move on to discuss the results of a series of surveys conducted on coral reefs in Australia, the United Arab Emirates and Oman. These results highlight the ubiquitous abundance of gobies on coral reefs and reveal that there is very likely a treasure trove of taxonomic diversity awaiting description. The presentation will include a discussion of the evolutionary history of the Gobiidae, and other small reef fish taxa, considering the pressures and benefits of life as some of the world’s smallest vertebrates.

Broad scale synthesis of fish, shark and ray data informs fully protected area design globally

Goetze, Jordan[1,2]; Langlois, Tim[3,4]; Harvey, Euan[2]; Wilson, Shaun[5,3]; Fisher, Rebecca[5,3]; Heithaus, Michael[6]; MacNeil, Aaron[7]; Heupel, Michelle[8,9]; Simpfendorfer, Colin[10,8]; Meekan, Mark[3]; Chapman, Demian[11,6]; et al.

[1]*Marine Science Program, Biodiversity and Conservation Science, Department of Biodiversity, Conservation and Attractions, Perth, Western Australia, Australia*

[2]*School of Molecular and Life Sciences, Curtin University, Perth, Western Australia, Australia, 2Marine Science Program*

[3]*The UWA Oceans Institute, University of Western Australia, Perth, Western Australia, Australia*

[4]*School of Biological Sciences, University of Western Australia, Perth, Western Australia, Australia*

[5]*Australian Institute of Marine Science, Perth, Western Australia, Australia*

[6]*Institute of Environment, Department of Biological Sciences, Florida International University, North Miami, Florida, USA*

[7]*Ocean Frontier Institute, Department of Biology, Dalhousie University, Halifax, Nova Scotia, Canada*

[8]*Institute for Marine and Antarctic Studies, University of Tasmania, Hobart, Tasmania, Australia*

[9]*Australian Institute of Marine Science, Townsville, Queensland, Australia*

[10]*College of Science and Engineering, James Cook University, Townsville, Queensland, Australia*

[11]*Sharks and Rays Conservation Program, Mote Marine Laboratory, Sarasota, Florida, USA*

Ecosystem-based fisheries and conservation management are often used to mitigate human stressors. Understanding the effectiveness of these management tools relies on the availability of robust information on the abundance and size distributions of fish assemblages, collected at appropriate spatial and temporal scales. Baited remote underwater video systems (BRUVs) are a popular tool for collecting data on fish assemblages across a range of depths and are well suited to sampling predatory species, often targeted by fishers. Data from over 18,000 BRUVs deployments around Australia and globally, were synthesised to assess the effectiveness of fully protected areas for fish, sharks, and rays. We found significant conservation benefits for fish and reef-associated sharks, but not rays or wide-ranging sharks. Importantly, we identify design factors that increase conservation benefits from fully protected areas, including connectivity between protected areas, extending boundaries from shore to deeper waters and embedding protected areas within areas of effective fisheries management. Findings on management effectiveness and design principles were communicated to marine park planners, the public, community reference and sector advisory groups to inform the design and assist in community support for marine parks in Australia.

E Hānai ʻAi Ma Ka Muliwai: Assessing the Diets of Forage Fish in Estuaries of Hawaiʻi Using DNA Metabarcoding

Goo, Nakoa[1]

[1]*University of Hawaiʻi at Mānoa*

[2]*Hawaiʻi Institute of Marine Biology*

Native forage fishes that inhabit Hawaiʻi estuaries have been harvested for centuries as a bait and food resource. These species enhance ecological productivity by supporting energy transfer between lower levels of the food web to higher trophic levels. Following nearly a century of commercial exploitation and habitat degradation, the conservation status of these species remains uncertain due to a variety of threats, including impacts associated with climate change and introduced species. Observed declines in populations of native forage fish made by local fishermen have ignited an urgent call to action in communities where these species once provided an important subsistence fishing resource for generations. This presentation will highlight ongoing research to assess the dietary composition of the Hawaiian endemic species *nehu* (*Encrasicholina purpurea*), and *ʻiao* (*Atherinomorus insularum*), along with the invasive goldspot herring (*Herklotsichthys quadrimaculatus*) using DNA metabarcoding techniques. Comparisons of diet composition among forage fish populations from the islands of Oʻahu, Molokaʻi, Maui, and Hawaiʻi will be used to determine whether native forage fishes are being impacted via competitive interactions with goldspot herring. This project aims to address threats to native biodiversity by investigating causes of decline in forage fish populations by providing an improved understanding of food web dynamics in estuaries throughout the Hawaiian archipelago. Outcomes from this research will inform the co-development of management recommendations through collaboration with communities and resource managers to support the replenishment of native forage fish populations throughout Hawaiʻi.

Shark activity is impacted by changing environmental conditions

Gooden, Adrienne[1,2]; Butcher, Paul[1,2]; Kelaher, Brendan[1]; Niella, Yuri[3]

[1] *National Marine Science Centre, Southern Cross University, Coffs Harbour, NSW, Australia*

[2] *New South Wales Department of Primary Industries, National Marine Science Centre, Coffs Harbour, NSW, Australia*

[3] *School of Natural Sciences, Faculty of Science and Engineering, Macquarie University, North Ryde, 2113, Sydney, New South Wales, Australia*

Environmental fluctuations can drive changes in animal behavior, triggering annual migrations for food, optimal weather, or reproduction, as well as short-term activity changes. Using acoustic accelerometer tags deployed on over 700 white (*Carcharodon carcharias*) and bull (*Carcharhinus leucas*) sharks from 2020 to 2023, we explored how environmental conditions (i.e., temperature, tides, moon phase and time of day) influence the activity of sharks in Eastern Australian waters. We identified that white sharks were more active between 1800 - 2400 at lower latitudes (-25 to -30 ^{o}S) and least active between 1800 - 2400 at higher latitudes (-40 ^{o}S). Bull sharks, however, were most active at lower latitudes (-20 ^{o}S) during the day (0800 – 1600) and least active in latitudes between -25 ^{o}S and -35 ^{o}S between 0600 – 1200. Exploration of how environmental conditions influence the activity of white and bull sharks are still being assessed. Overall, our study provides a comprehensive understanding for the assessment of long-term changes in shark activity for bite mitigation, as well as any impacts from ocean warming and coastal development.

Translocation of native freshwater species: balancing good intentions with science and pragmatism

Goodman, Jane[1]; Bowen, Jane[1]; Richarson, Marine[1]

[1]*Department of Conservation, New Zealand*

Most translocations proposals start with the best of intentions. However, the process is inherently risky, might not be the most appropriate conservation strategy and may ultimately do more harm than good. Addressing freshwater conservation issues through the use of translocations appeals to some conservation advocates as it is perceived as an easy fix. This poster highlights some important ecological and scientific considerations and provides information on the Department of Conservation's process in authorising translocations of native species.

Individuals or groups seeking to move freshwater fish require approval from either the Department of Conservation or Fisheries New Zealand under regulation s26ZM of the Conservation Act. Inherent risks with translocations cover a wide range of domains, from environmental and ecological risks to cultural and economic considerations. As a basis for advice and assessment of applications, technical advisors in the Department use a recently developed framework for risk analysis. Applicants must identify the conservation issue addressed by the translocation. Monitoring and ongoing management plans for the newly released fish are also required.

Adequate mitigation of the risks and impacts of translocated populations on communities and habitats at site is often difficult to achieve. In many cases the Department considers that the best approach for native species' conservation is through habitat restoration and protection in their current area of occupancy.

Identifying impacts and drivers of fish assemblages over multiple scales in coastal ecosystems

Goodridge Gaines, Lucy[1]; Borland, Hayden[1]; Gilby, Ben[2]; Henderson, Christopher[1]; Mosman, Jesse[1]; Olds, Andrew[1]; Perry, Hannah[1]

1. *School of Science, Technology and Engineering, University of the Sunshine Coast, Maroochydore DC 4558, Queensland, Australia*
2. *School of Science, Technology and Engineering, University of the Sunshine Coast, Petrie 4502, Queensland, Australia*

Coastal seascapes are increasingly impacted by human activities which occur over multiple spatial scales. These multi-scaled impacts change the extent, connectedness and condition of coastal ecosystems, and alters their value for many fish species. Disentangling the scales over which these impacts occur, and quantifying how the spatial context of natural habitats can mediate these impacts on fish assemblages, can help prioritise and optimise restoration efforts. We quantified the relative effect of catchment, estuary and habitat level impacts on fish diversity and abundance throughout southeast Queensland. At broad landscape scales (i.e. catchment), we show that catchments with higher heterogenous natural habitat extent and lower chlorophyll-a concentrations consistently support a higher abundance and diversity of fish, particularly fish of high fisheries value. At more narrow spatial scales (i.e. estuary context and habitat condition), spatial variables were more important than habitat condition in structuring fish abundance and diversity. Sites that were closer to vegetated habitats patches (especially mangrove and seagrass) and key physical attributes of estuaries (especially the estuary mouth) typically had higher fish abundance and diversity. Our results show that maintaining natural catchments that can filter contaminants, combined with heterogeneous seascapes, support more abundant and diverse fish assemblages. Management that enhances these characteristics through restoration efforts will maximise fish and fisheries value across coastal landscapes.

Comparative genomics and transcriptomic analysis of a bioluminescent cardinalfish sheds light on the evolution of microbial symbiosis

Gould, Alison[1]; Henderson, James[1]

[1]*California Academy of Sciences, San Francisco, CA*

Bioluminescence has evolved multiple times within the family of cardinalfishes (Apogonidae). While many bioluminescent cardinalfishes are able to produce their own light, species in the genus *Siphamia* rely on bacterial symbionts to help them glow. The fish cultivates a dense population of *Photobacterium mandapamensis* in an abdominal light organ attached to the gut, which it acquires during larval development. Using long-read sequencing and Hi-C methods, we assembled chromosome-level genomes of three *Siphamia* species, including the broadly distributed urchin cardinalfish, *S. tubifer*, and compared them to the genomes of several non-luminous cardinalfishes. The *Siphamia* genomes are comprised of 23 chromosomes and have high synteny with the non-luminous orbiculate cardinalfish, *Sphaeramia orbicularis*. To identify putative genes involved in the symbiosis, we compared gene expression in the host light organ in the presence and absence of its luminous symbiont, as well as to that of other tissues, including the gut, brain, and eye. We identified several immune-related genes with supressed expression in the light organ in the presence of the bioluminescent symbiont, including some related to the adaptive immune system. Similarly, genes involved in antigen processing and presentation were supressed in the symbiotic light organ compared to the intestine. Genes involved in the host's circadian rhythm and extracellular matrix receptors were upregulated in the light organ in the presence of its symbiont. By comparing these genes to the non-luminous cardinalfish species, we can investigate the genetic mechanisms involved in the evolution of bioluminescent symbiosis and beneficial host-microbe associations more broadly.

Clownfishes’ obligatory mutualism may lead to their demise

Goulet, Tamar[1]; Goulet, Denis[1]

[1]*University of Mississippi*

From their common names, clownfish or anemonefish, to their anthropomorphism in the movie ‘Finding Nemo,’ *Amphiprion* fish conjure cuteness and invoke compassion. Clownfishes’ mandatory reliance on sea anemones, however, may lead to the demise of this iconic fish. For 19 years, we censused the population of the two band anemonefish, *Amphiprion bicinctus*, in a 200 x 50 m study site (10000m^2, 0 to 15m depth), off the coast of Israel in the Gulf of Eilat (Aqaba), Red Sea. Fish were ascribed to size categories based on total length: adult (> 75mm), juvenile (45–75mm), or settler (< 45mm).

In 1996, the site contained 197 fishes: 17 adults (5 breeding pairs), 43 juveniles, and 137 settlers. By 2015, the anemonefish population declined by 73%, to 52 individuals: 21 adults (8 breeding pairs), 24 juveniles, and 7 settlers. This dramatic drop in the anemonefish population size, and the shift in the age structure, did not occur in a void. In the Gulf of Eilat, *A. bicinctus* obligatorily inhabits either *Entacmaea quadricolor* or *Heteractis crispa*. In 1996, 205 anemones (96 *E. quadricolor* and 109 *H. crispa*) were initially tagged at the study site. By 2015, the anemone population plummeted to 15 *E. quadricolor* and 12 *H. crispa*. In 1996, the sea anemone habitat was not saturated with *A. bicinctus*, but by 2015, all remaining 27 anemones were occupied. Anemonefishes’ requirement for an obligatory mutualism may be their downfall, leading to a reduction in intra and interspecific biodiversity.

Poster Function, OGGB Level 0 Foyer, November 21, 2023, 4:15 PM - 6:30 PM

Spatial distribution of an anemonefish population: effects on recruitment, survivorship, and the ramifications of a reduction in sea anemone habitat

Goulet, Denis[1]; Goulet, Tamar[1]

[1]*University of Mississippi*

In the Gulf of Eilat (Aqaba), Red Sea, the anemonefish *Amphiprion bicinctus* obligatorily inhabits either the sea anemone *Entacmaea quadricolor* or *Heteractis crispa.* We investigated the effects of inhabited and uninhabited anemones' locations, and conspecific anemonefish, on *A. bicinctus'* population dynamics in a 200x50m study site (0-15m depth). We followed the spatial distribution of the population, including newly settled individuals, in 13 censuses from October 1996 to August 1997, with additional censuses up to 2015. We recorded the number of anemonefish in each anemone, ascribing fish into size classes: adult (> 75mm total length), juvenile (45–75mm), or settler (< 45mm). Despite fewer *E. quadricolor* than *H. crispa*, more adult and juvenile anemonefish associated with *E. quadricolor*. Conversely, most settlers associated with *H. crispa*. As fish grew, increasing the number of adult anemonefish, uninhabited *E. quadricolor* distribution became significantly clustered relative to the nearest anemone that hosted an adult fish. The distribution relative to adult-hosting anemone neighbors of uninhabited *H. crispa* fluctuated between significantly dispersed and random. Adult anemonefish may prevent recruitment not only to the anemones in which they reside but also to the nearby preferred *E. quadricolor* anemones. From 1997 to 2015 the number of anemones and fish fell by 86% and 74%, resulting in significantly more fish per anemone. Also in 2015, every anemone of both species was occupied, forcing settlers to interact with their larger conspecifics, potentially resulting in higher settler mortality. Dwindling sea anemone population may lead to the demise of the anemonefish population.

Can DNA-metabarcoding of multi-species samples from routine egg surveys be used to monitor the ichthyoplankton assemblage?

Grammer, Gretchen[1]; Appleyard, Sharon[2]; Bailleul, Frederic[1]; Catalano, Sarah[1]; Ivey, Alex[1]; McGrath, Annette[3]; Miskiewicz, Anthony[4,5]; Ward, Timothy[6]

[1]*South Australian Research and Development Institute, Adelaide, South Australia, Australia*

E-mail: gretchen.grammer@sa.gov.au

[2]*CSIRO Australian National Fish Collection, Hobart, Tasmania, Australia*

[3]*Data 61, CSIRO, Brisbane, Queensland, Australia*

[4]*School of Biological, Earth & Environmental Sciences, University of New South Wales, Sydney, NSW, Australia*

[5] *Ichthyology Department, Australian Museum Research Institute, Australian Museum, Sydney, NSW, Australia*

[6]*Institute of Marine and Antarctic Studies, University of Tasmania, Hobart, Tasmania, Australia*

Broadscale ichthyoplankton surveys covering over 350,000 km^2 are routinely undertaken in shelf waters off south-eastern Australia to support management of the Commonwealth Small Pelagic Fishery and South Australian Sardine Fishery. Each survey is designed to sample eggs of target species and obtain estimates of spawning biomass using the Daily Egg Production Method. Several hundred samples are taken per survey, but only limited additional information is collected to monitor the marine environment. Our project evaluated the potential for using mtDNA-metabarcoding (mtDNA-mb) from multi-species egg and larval samples to obtain information to support management of Australia's marine estate, including the spawning habitat of data-poor species and responses of pelagic ecosystems to climate change. Two cytochrome oxidase sub-unit I (COI) mtDNA-mb assays were used to identify eggs and larvae of fish species and compared with a morphological approach. We found that morphological identifications provided overall-estimates of abundance (albeit often only to family level), and required high levels of taxonomic skill, are time consuming and expensive, and can include errors. The two mtDNA-mb assays performed similarly and identified more species and genera compared to the morphological approach. However, mtDNA-mb only provides a species list per sample with no quantitative abundance information (e.g., sequence read number ≠ abundance). Other limitations include: abundant species may swamp assays causing rarer species to go undetected, and individual species respond to assay amplification differently. The best ways forward may involve hybrid approaches that integrate abundance data from coarse morphological identifications and species lists from mtDNA-mb.

Ecology and evolution of a color polymorphism in two *Paracirrhites* hawkfishes

Greaves, Samuel[1]; Donaldson, Terry[2]; Whitney, Jonathan[3]; Gaither, Michelle R.[1]

[1]*Department of Biology, University of Central Florida, Orlando, Florida, USA*

[2]*UOG Marine Laboratory, University of Guam, Mangilao, Guam, USA*

[3]*Pacific Islands Fisheries Science Center, National Oceanic and Atmospheric Administration, Honolulu, Hawai'i, USA*

Color polymorphisms, or distinct, stable, and non-continuous variations in color patterns among individuals of a species are present in many taxa. However, coloration's involvement in survival and mate choice often creates high selective pressure on the trait, which is expected to lead to fixation or divergence, rather than maintenance. Of particular interest are polymorphisms that are not linked to sex or life stage and are found in sympatry, such as those found within the hawkfish genus *Paracirrhites*. Two species within the genus, *P. arcatus* and *P. hemistictus* have a similar Light/Melanistic dimorphism, where both morphs are sympatric. Building on previous study conducted in Hawaii on *P. arcatus*, we surveyed reefs in Guam for these two species to identify if the morphs were occupying different environmental niches, particularly focusing on gradients in depth and substrate type. We also created reference genomes and conducted whole genome resequencing of approximately 30 individuals per morph of both species from Guam and *P. arcatus* from Hawaii. Preliminary results suggest that the partial segregation of morphs across the surge zone in Hawaii is not present in Guam. When comparing morphs, genome scans reveal several regions with elevated FST values. These differences were greater in Hawaii compared to Guam, corroborating the survey results. Nevertheless, there are a small number of outlier regions that are associated with several genes. Ultimately, our results will provide insight into whether the color morphs are stable or diverging and whether morph is linked to other traits.

Molecular Monitoring in Fisheries Management – Does it work?

Green, Madeline[1,2]

[1]*CSIRO Environment, Hobart, Tasmania, Australia*

[2]*University of Tasmania, Hobart, Tasmania, Australia*

The United Nations Sustainable Develop Goal (SDG) 14 calls for management action that delivers ecosystem resilience, combats illegal fishing, and provides economic development opportunities for developing states. To successfully achieve this goal, the tools used for Monitoring, Control and Surveillance (MCS) of fisheries need to be improved. Current methods for monitoring fishing activity include logbooks, Electronic Monitoring, on-board observers, and inspections. Each of these methods, though effective tools for MCS, have weak points in the process where non-compliant behaviour can go unmonitored. Where two or more of these tools are used collectively the vessel landings and by-catch interactions are more certain. This presentation will introduce an additional tool to the MCS toolbox discussing how Molecular Monitoring (MM) may benefit fisheries monitoring systems. A novel approach, MM has the capacity to improve fishery landing estimates by providing an accurate record of catch, taxonomically resolved using DNA. This presentation will summarise the current field of MM and its application on different vessels, noting when it is appropriate to use MM and how best to interpret results. Molecular Monitoring while a potentially powerful tool may not be suitable across all fisheries sectors and the nuances of interpreting molecular data requires discussion. Nonetheless, MM is gaining interest from fisheries regulators and offers a possible solution to the challenge that is MCS in fisheries systems. Only with an improved understanding of fisheries landings can we accurately assess the impact fishing activities are having on marine ecosystems and appreciate the steps required to uphold SDG14 commitments.

The ecological importance of ray bioturbation in a temperate estuary

Grew, Molly[1]; Duce, Stephanie[2]; Gaston, Troy[2]; Griffin, Andrea[1]; Raoult, Vincent[1,3]

[1]*University of Newcastle, NSW, Australia*

[2]*James Cook University, QLD, Australia*

[3]*Macquarie University, NSW, Australia*

Within estuaries, rays provide a vital role as predators and bioturbators, modifying their habitat through foraging and predation. During foraging activities, rays provide important ecosystem services via bioturbation such as nutrient cycling, oxygen penetration and sediment structuring. The amount of sand turned over by these foraging activities can be significant and measurable through the abundance, volume and turnover of the ray feeding pits in the area. It has been estimated that complete turnover of sediment by rays in a 60m^2 area occurs in 102 days with new feeding pits forming daily. However, turnover rates and volume of sediment displaced over time can be habitat and species-specific. Further research on the rate of bioturbation by rays within estuaries is necessary to deepen our knowledge of the ecological importance rays have within an ecosystem. To understand this importance of rays to ecosystem services within an estuary requires a quantitative analysis of ray bioturbation. The current study assessed the volume of sand displaced over a seven-day period by rays during foraging activities. To achieve this, a drone was used to map a site with bioturbation activity, as evident from the presence of feeding pits, then create Digital Elevation Models to obtain volumetric measurements of the feeding pits present in the area. We expected rays to displace high volumes of sand on a daily and weekly basis, contributing to the bioturbation in the system.

Assessing the global extent of climate risk for genetically informed populations of Yellowtail Kingfish, *Seriola lalandi.*

Grier, Ben[1]; Kim, Sun[1]; Pandolfi, John[1]

[1]*School of Biological Sciences, The University of Queensland, St Lucia, Queensland, Australia*

Anthropogenic climate change pressures are increasingly impacting organisms at individual, population and species levels. Understanding the dynamics of climate risk that a species faces is key to understanding the impacts of climate change on species and possibility of biodiversity responses such as adaptation, migration or extirpation. The Yellowtail Kingfish (*Seriola lalandi*) is an ecologically and commercially important species, contributing to large fisheries and aquaculture yields globally, including in South Africa, the South Pacific, North-West Pacific and North-East Pacific regions. While poleward range expansion has previously been predicted for the species in eastern Australia, underlying climate risk and possible impacts on the species have not been studied at a global scale. Using an original variation of ecological niche modelling, this study aims to quantify the species' population-specific vulnerability and exposure to climate hazards. Coupling CMIP6 Earth System Models and occurrence data, the historical (1850-2000) climatic niches of four genetically-informed populations of *S. lalandi* are compared to projected (2001-2100) environmental conditions of the SSP1-2.6 and SSP5-8.5 trajectories. Niche differentiation among distinct populations and complex regional climate trajectories lead to distinct magnitudes of climate risk and rates of change in risk among the populations, with populations in eastern boundary upwelling systems experiencing reduced climate risk. Exposed to conditions near upper thermal thresholds, low latitude and shallow-depth populations experience greater magnitudes of climate risk. This study produced standardised risk scores that can inform fisheries management and conservation globally, providing insights into when and where possible impacts and species responses to climate change may occur.

Challenges of managing a charter fishery to an explicit catch limit

Grosse, Taylor A[1]; Sarginson, Nikki[1]; Syers, Clinton[1]

[1]*Department of Primary Industries and Regional Development, Western Australia*

The West Coast Demersal Scalefish Resource comprises over 100 species between Kalbarri and Augusta and is currently 13 years through a twenty-year recovery plan. The resource is formally allocated between commercial and recreational (including charter) sectors. A 2021 stock assessment of indicator species showed limited recovery and further management action was required to reduce fishing pressure. A stakeholder-based harvest strategy reference group reviewed the stock assessment against the harvest strategy recovery plan and made recommendations to reduce the fishing mortality limit by 50 percent to allow the resource to recover. Consequently, a 50 percent reduction in fishing mortality limits for all sectors was approved by the Minister for Fisheries in 2022.

Following an extensive consultation process, a decision was made to implement a catch quota system as the principal management arrangement to manage the charter fishing component of the recreational the sector to its allocated 20-tonne limit. Given the charter sector had been exceeding its limit in previous years, managing the sector to its revised 20-tonne limit across 97 licence holders posed significant challenges, requiring an average catch reduction of 63 percent.

To ensure the continued viability of the charter industry while managing the sector to its revised mortality limit, 6,000 tags were allocated to 21 licence holders in the west coast zone who demonstrated ongoing and recent reliance on demersal-based fishing activities. For those who were not granted tags, an alternative option was provided to engage in highly sustainable, low-take methods for "catch to cook" when undertaking aquatic tours.

A fish barrier remediation case study– Mona Vale rock riffle

Groves, Mark[1]; Margetts, Bellinda[2]; Mullaney, Mark[2]

[1]*WSP New Zealand Ltd*

[2]*Christchurch City Council*

The use of riffles as a means to remove vertical barriers on waterways is not a new practice, but it has been evolving and improving over time and is more relevant today than ever with the strengthening emphasis on fish passage in New Zealand. Case studies are an important means to share developments and learnings to facilitate on-going improvement.

This presentation will cover the design and construction process for the Mona Vale riffle in Christchurch which has been installed to remove an existing fish passage barrier (concrete weir). The presentation will cover the practical aspects of riffle design including management of flood risk, estimation of hydraulic performance, sediment control, Safety in Design, and risk management. Key learnings from the project will be summarised and shared as well as follow on monitoring work.

The project included input and review from experts in riffle design from Charles Sturt University and incorporated learnings from computational fluid dynamics (CFD) modelling to create more varied flow conditions and increased resting opportunities that represents a snapshot of current good practice.

The remediation of this weir is intended to be used as a case study for weir fish passage barriers nationwide, through resources provided by the New Zealand Fish Passage Advisory Group.

“Project Kingfish”: a collaboration with recreational anglers to research and inform the management of yellowtail kingfish (*Seriola lalandi*) off eastern Australia

Guillemin, Tristan[1,2]; Goddard, Belinda[1,2]; Harcourt, Rob[2]; Hughes, Julian;[3] Jaine, Fabrice [1,2]; Schilling, Hayden[4]; Suthers, Iain[5]; Taylor, Matt[4]

[1] *Sydney Institute of Marine Science, Mosman, NSW, Australia.*

[2] *School of Natural Sciences, Macquarie University, North Ryde, NSW, Australia.*

[3] *New South Wales Department of Primary Industries, Mosman, NSW, Australia*

[4] *New South Wales Department of Primary Industries, Port Stephens, NSW, Australia*

[5] *School of Biological, Earth & Environmental Sciences, University of New South Wales, Sydney, NSW, Australia*

Highly regarded for their great taste and awesome fighting abilities, yellowtail kingfish (*Seriola lalandi*) are one of Australia’s most iconic recreational species, and support important commercial fisheries. Despite forming a single genetic stock throughout south-eastern Australia and New Zealand, major knowledge gaps exist regarding their movements, connectivity and spawning locations. Funded by the New South Wales (NSW) Recreational Fishing Trust, “Project Kingfish” is a multi-year research program addressing these knowledge gaps. Through close work with the recreational fishing community, we have promoted scientific data collection from spawning-sized kingfish throughout eastern Australia. Using nationwide citizen science data generated via the NSW Game Fish Tagging Program, the team has analysed data from over 40,000 kingfish tagged and released by recreational anglers between 1973-2022 to identify and describe connectivity between fishery jurisdictions over the geographical extent of the stock. Tapping into their countless years of experience and knowledge, Project Kingfish has teamed up with specialist recreational anglers to deploy satellite tags on mature-sized kingfish, with 24 deployed so far, to gain insights into movements and important habitats for the spawning stock. Through a series of dedicated fishing competitions and a science communication campaign on social media, Project Kingfish has engaged with recreational anglers to promote sustainable fishing practices and highlight research results that will feed directly into informing the management of the east Australian kingfish stock.

5.4A Themed Session G: Long Term Monitoring of Indo-Pacific Fishes, 260-092, November 24, 2023, 10:30 AM - 12:30 PM

Interviewing anglers to understand changing catch composition in the 100-year-old east coast marlin fishery

Tristan A, Guillemin[1]*, Leah Gibbs[2], Julian G. Pepperell[3], Jane E. Williamson[1,4]

[1]*School of Natural Sciences, Macquarie University, 2109, Australia*

[2]*University of Wollongong, Wollongong, 2522, Australia*

[3]*Pepperell Research and Consulting Pty Ltd, Noosaville, 4566, Australia*

[4]*Sydney Institute of Marine Science, Building 19 Chowder Bay Road, Mosman, New South Wales 2088, Australia*

As our world evolves and changes, so do our fisheries, and understanding these changes is key to their management. As scientists, we often focus on environmental or biological changes as these are easily measurable and analysable. However, social aspects can also be key drivers of fishery change, but are often overlooked by scientists who routinely value quantitative over qualitative data. The east coast of Australia is home to one of the world's oldest recreational marlin fisheries. Analyses of game fishing club records (1933-2022) and data from the NSW Department of Primary Industries (DPI) recreational gamefish tagging program (1973-2022) revealed long term changes in species composition of the catch. To understand the drivers of these changes, we conducted surveys of marlin anglers at fishing tournaments and online, and interviewed a subset of anglers to record changes they had observed during their time in the fishery. Anglers identified a range of factors that had changed over time including: improvements in boats facilitating fishing effort further offshore; adoption of new technologies such as sounders, GPS and sonar; and increased knowledge of fishing techniques specific to the different marlin species. Many of the changes that anglers identified and the timing of these changes aligned with changes observed in species composition of the catch data. This research highlights the importance of considering social aspects alongside traditional biological and ecological analyses in understanding and managing fisheries.

Prohibiting spearfishing boosts conservation outcomes for partially protected areas

Hall, April[1]; Cameron, Darren[2] ; Kingsford, Michael[3]

[1]*Centre for Tropical Water and Aquatic Ecosystem Research, James Cook University, Townsville, Australia*

[2]*Great Barrier Reef Marine Park Authority, Townsville, Australia*

[3]*Marine Biology and Aquaculture, College of Science and Engineering and ARC Centre of Excellence for Coral Reef Studies, James Cook University, Townsville, Australia*

Partially Protected Areas (PPAs) are a ubiquitous management tool, prevalent in many Marine Protected Area (MPA) networks globally; yet their ecological effects are often poorly understood. PPAs aim to limit fishing effort and/ or prohibit specific fishing methods to balance conservation outcomes with use of the area for recreational and/or commercial fisheries. Here, we provide strong evidence showing how prohibition of spearfishing inside PPAs can boost conservation outcomes on coral reefs. We examined conservation outcomes for two kinds of PPAs on the southern Great Barrier Reef (GBR), where recreational spearfishing is prevalent. Both zones allow limited line fishing, however Conservation Park Zones (CPZs) also allow spearfishing, whereas Special Management Areas (SMAs) do not. Both kinds of PPAs supported a greater biomass of fisheries targets compared to less regulated Habitat Protection Zones, however, density and biomass of targeted fish was significantly greater in SMAs where spearfishing was prohibited, especially for key target species coral trout. Indeed, SMAs supported a similar density and biomass of coral trout to unfished No-Take zones, and had twice the density of CPZs, where spearfishing is allowed. This outcome contrasts with some previous studies, and we propose that the success of PPAs in our study region is likely due to a combination of strong enforcement and compliance, as well as the presence of adjacent, long established, and highly effective no-take zones. Our results emphasize the benefits of tailoring restrictions inside PPAs to locally relevant activities, and highlight the contribution of PPAs to conservation outcomes in multi-use MPAs.

Sampling the undersampled: improving understanding of estuarine biodiversity in northern Australia

Hammer, Michael[1]; Larson, Helen[1,2]; Adams, Mark[3,4]; Austin, Chris[1,5]; McGee, Matthew[6]; Moore, Glenn[7]; Unmack, Peter[4,6]

[1]*Museum and Art Gallery of the Northern Territory*

[2]*Museum of Tropical Queensland*

[3]*South Australian Museum*

[4]*University of Canberra*

[5]*Deakin University*

[6]*Monash University*

[7]*Western Australian Museum*

Mangrove environments provide critical ecosystem services and support rich and specialised estuarine biodiversity. Yet as a narrow band of typically difficult to access, inhospitable and variable habitat much remains to be documented to science about mangrove biota, which hinders a full awareness of the uniqueness of these systems and their management needs. In northern Australia, these sampling challenges are exacerbated by remoteness, extreme daily tidal variation, large seasonal and interannual variation in flow/floods and outright dangerous animals. This presentation showcases recent taxonomic advances on estuarine gobies based on three key pillars to better sample a poorly known regional mangrove fauna, namely a focus on zonation (microhabitats), adapting field techniques, and incorporating citizen science. Specific examples are included across the Snubnose Gobies (*Pseudogobius*), Mangrove Gobies (*Mugilogobius*) and Bearded Worm Gobies (*Taenioides*), with links made to the conservation and protection of their habitat being a focal point for future human industry.

The role of life cycles in temperature resilience and global billfish distributions

Hammond, Matthew[1]; Banks, Sam[1] Boyce, Daniel[4] Kopf, Keller[1] Pepperell, Julian[3] Udyawer, Vinay[2]

[1]*Charles Darwin University*

[2]*Australian Institute of Marine Science*

[3]*Pepperell Research and Consulting Pty Ltd*

[4]*Bedford Institute of Oceanography, Fisheries and Oceans Canada*

Understanding a species physical tolerance can be highly informative when predicting how organisms will respond to changing environments. Most of the research conducted on the physical tolerance of fishes focuses on adults. This is problematic because a populations resilience to a changing environment is dependent on the most sensitive life stage. An environmental constraint and group of animals where this is currently relevant is temperature and billfish. Most of the information on the temperature thresholds of this group come from commercial fisheries, bycatch data or electronic tags. Both sources focus almost exclusively on adults. In the present study ambient water temperature data is being extracted from literature sources to calculate the global mean preferred and tolerated temperatures of different life stages, for ten billfish species. Mean temperature tolerance data will then be used in conjunction with Intergovernmental Panel on Climate Change (IPCC) predictions and the known ranges of different life stages to estimate if currently populated regions will become uninhabitable for any species by the year 2050 and 2100. Preliminary results collected from 66 literature sources suggests that spawning adults are the most temperature sensitive while larvae and adults are the most resilient. They also suggest that spawning adults and larvae from species inhabiting latitudes near the equator have a wider thermal tolerance then those that typically occur in latitudes closer to the poles. This study will help to define the temperature thresholds of billfish populations and predict how billfish will respond to global increases in ocean temperature.

A tool to evaluate the impact of sanctuary zone arrangements on recreational fishers in Western Australia

Hamre, Nicole[1]; Langlois, Tim[1]; Navarro, Matt[1]

[1]*University of Western Australia*

Coastal ecosystems contribute disproportionately per unit area to the delivery of ecosystem services. Marine spatial planning (MSP), whereby areas of the ocean are allocated to different marine uses, has emerged as a key way to manage pressures on coastal ecosystems and maximise ecosystem service benefits. However, deciding which activities to allow where is a difficult challenge requiring information of how different spatial arrangements alter the benefits and costs for marine users. In this project we aim to inform the spatial planning of the Proposed South Coast Marine Park and Review and Expansion of Marmion Marine Park in Western Australia. We have developed a tool which provides managers with the ability to conduct management strategy evaluation to explore the impacts of alternative arrangements of no-take marine sanctuaries on recreational fishers. Preliminary results suggest some arrangements have greater impacts on recreational fishing experiences than others, with impacts varying depending on distance to access points, and inclusion of unique sites (e.g., those with important islands) within the sanctuary network.

Swimming performance of juvenile green sturgeon (*Acipenser medirostris)* in relation to water diversions

Hannan, Kelly[1]; Cocherell, Dennis[1]; Fangue, Nann; Steel, Anna[1]

[1]*University of California, Davis*

Fish populations are in decline worldwide. This is particularly true in areas where anthropogenic alterations have created impediments to natural fish movement, such as water diversions. Most water diversions are open and unmodified allowing fish to become entrained (i.e., pulled into); however, recent advances to prevent fish entrainment (e.g., fish protective screens) are being considered. Green sturgeon, *Acipenser medirostris,* are an anadromous fish whose juveniles out-migrate in a system with over 3,000 unscreened water diversions. Thus, the swimming performance of juvenile green sturgeon, of two different size classes (~2.5 and 5cm FL), was quantified after a 2wk exposure to two different temperatures (15 and 18°C) using fixed velocity endurance tests. The water velocities ranged from 30 to 50cm s^{-1}. Physiological metrics (cortisol, lactate, and glucose) were measured at different time points following the swimming tests (0, 15, 30, and 60min) to examine recovery following impingement (i.e., prolonged contact with the screen) to provide information about the activation of the stress axis as well as reliance on anaerobic or aerobic metabolism. Sturgeon were found to have reduced endurance swimming ability upon exposure to decreased temperature compared to fish exposed to elevated temperatures. We expect to see increases in cortisol, lactate, and glucose following impingement. The results of this study will provide information on the sublethal impacts of fish screens and recovery from impingement. Understanding the physiological ecology as well as the behaviour of fishes, particularly those with complex life history strategies, can better inform fisheries management.

Effects of manipulating Kingfish (*Seriola lalandi*) routine oxygen demand and supply on ventricular and skeletal muscle mitochondrial function

Harford, Alice[1]; Danielo, Quentin[2]; Hickey, Anthony[1]; Khan, Javed[2]; McArley, Tristan[3]; Morgenroth, Daniel[3]; and Sandblom, Erik[3].

[1]*Applied Surgery and Metabolism Laboratory, School of Biological Sciences, University of Auckland, Auckland, New Zealand*

[2]*National Institute of Water and Atmospheric Research, Northland Marine Research Centre, PO Box 147, Ruakaka 0151, New Zealand*

[3]*Department of Biological and Environmental Sciences, University of Gothenburg, PO Box 463, 405 30 Gothenburg, Sweden*

Yellowtail kingfish (*Seriola lalandi*) are a highly active marine species, with increasing value in commercial aquaculture. While practices which manipulate oxygen (O_2) dynamics through metabolic demand and environmental O_2 supply have been shown to impact juvenile growth rate in fish development, there has been no work exploring the effects of O_2 at the subcellular level. In addition, manipulations of O_2 supply or demand via changes in environmental factors such as O_2 levels or salinity, may impact whole-animal performance. Still, there has been little work exploring the physiological effects at a subcellular level. Mitochondria (mt) consume O_2 and are pivotal in central metabolism, directly impacting growth, and dictating whole animal performance. Here we explore the effects of manipulating O_2 demand and supply on mt in yellowtail kingfish ventricle and skeletal muscle by exposure to chronic hyperoxia (200 % [O_2], 35 ppt) and to hyposalinity (100 % [O_2], 17.5 ppt). Chronic exposure to hypoosmotic conditions resulted in greater overall biomass, while it lowered relative ventricular mass compared to control fish. Mitochondrial respiratory flux for most measures remained consistent with control fish, with the exception of cytochrome c oxidase (COX) respiration. Chronic hyperoxia had no impact on overall morphology, and no significant effect on ventricle mt respiration, yet increased COX activity in skeletal muscle. These data indicate that lowering routine mt O_2 demands in *S. lalandi* with hypoosmotic conditions has more impact than increasing O_2 availability, and that this may enhance biomass output while maintaining mt integrity.

Morphometric study of widely distributed species of *Bregmaceros* (Bregmacerotidae: Teleostei), with a focus on Indian Ocean forms

Harold, Antony S.[1]; Baltzegar, D. Andrew[2]

[1]*Grice Marine Laboratory, College of Charleston, Charleston, South Carolina 29412, USA*

[2]*Center for Human Health and the Environment, North Carolina State University, Raleigh, North Carolina 27695, USA*

Bregmaceros species (Codlets) are miniature gadiform fishes mainly occurring in epi- to mesopelagic habitats. The range of the genus is circumglobal in tropical to warm temperate regions with the majority of species in the Indo-Pacific. They have a moderately elongate body shape, a well-defined caudal fin, and a subdivided dorsal fin including a single occipital ray followed by a long-based second dorsal fin typically of about 40 to 65 rays. There have been two major reviews of the genus and 15 species are currently recognized. A complex of widely distributed forms that have been confused with *B. mcclellandi* (new species description in preparation) and another with *B. atlanticus* are the focus of our study. We present the results of morphometric analysis based on a set of standard morphometric characters, size-sheared principal components analysis, and regressions. Principal components analysis shows there to be regionalized morphometric variation in a broadly distributed undescribed species characterized by high anal-fin ray counts (59 to 66) and similarly within *B. atlanticus* (51 to 59). We found that both of these species complexes have a distinct form in the Indian Ocean characterized by both morphometry and pigmentation. Although we have produced a description of a new species from the eastern tropical Pacific (publication pending) resolution of the currently reported morphological variation in Indian Ocean forms awaits incorporation of molecular data and phylogenetic analysis in a future collaborative effort.

The mystery of shortjaw kōkopu (*Galaxias postvectis*) spawning ecology on the West Coast

Harris, Suze[1]

[1]*Te Papa Atawhai (Department of Conservation)*

The Te Papa Atawhai (Department of Conservation) Ngā Ika e Heke programme is dedicated to the conservation and management of four native species with migratory life cycles. This presentation will focus on the elusive shortjaw kōkopu (*Galaxias postvectis*) classified as Threatened—Nationally Vulnerable in the New Zealand Threat Classification System. Shortjaw kōkopu are secretive, nocturnal, and typically inhabit streams with native riparian vegetation. There remains a significant knowledge gap regarding their spawning ecology; with present knowledge of their spawning behaviour and locations based on a study in the early 2000s. The West Coast of the South Island of Aotearoa provides a haven of ideal shortjaw kōkopu habitat making it an model region for further research. The data and observations from two field seasons will be summarised in this talk describing the methodology used to closely monitor their body condition, habitat utilization and spawning condition within the Kaniere Catchment.

3.3C Themed Session B: Ecology of Indo-Pacific Fishes, 260-115, November 22, 2023, 4:00 PM - 6:00 PM

Ecology of tropical reef based clupeiforms affects genomic population structure

Hartog-Burnett, Kynan[1]; Kingsford, Michael[1]

[1]*College of Science and Engineering, James Cook University*

Clupeiform fishes are a globally critical group in supporting higher trophic levels and fisheries. Population scale studies of this group have focused on temperate species and found little variation. Tropical species have shorter, faster lives, and the impact of these key life history differences on observed genomic stock structure has not been investigated. We present data from sister species of tropical reef-based clupeiforms with differing spatial ecologies, *Spratelloides delicatulus* and *S. gracilis*. Sampling was performed along the Great Barrier Reef in a nested design of latitudes and reefs. We aimed to understand the spatial scale for genomic differentiation of “sprat” stocks and how spatial ecology, reef geomorphology and molecular diversity influences connectivity. The species share characteristics of demersal spawning and short lives but differ in habitat use. While both species have closer relations to coral reefs than true pelagics; *S. delicatulus* is common in shallow backreef waters, while *S. gracilis* is observed on reef slopes and surrounding waters. This contrast in environmental preference appears to have influenced the genomic structure and connectivity observed. We argue that reef fidelity, spawning behaviour and reef geomorphology play key roles in maintaining genomic diversity at small spatial scales; contrasting with results for temperate synonyms.

Movement and habitat use of Guam reef manta rays (*Mobula alfredi)* as revealed by satellite telemetry

Hartup, Julie[1,2]; Erdmann, Mark[3], Kottermair, Maria[1,4],Setyawan, Edy[5]

[1]*Micronesian Conservation Coalition, Hagåtña, Guam*

[2]*Manta Trust, Dorset, United Kingdom*

[3]*Conservation International Aotearoa, Auckland, New Zealand*

[4]*University of Queensland, Brisbane, Australia*

[5]*Institute of Marine Science, University of Auckland, Auckland, New Zealand*

Satellite telemetry has proven an effective technique for investigating the horizontal and vertical movements of the reef manta ray *Mobula alfredi.* The patterns of habitat use thus revealed are critically important to designing effective management regimes for this large, mobile, and threatened species. On Guam, using well-established photo-identification techniques, we have documented 61 individual manta rays in the local population since 2008, with a high rate of resighting of individuals. While we have confirmed several coastal cleaning and feeding aggregation sites on Guam, our understanding of the patterns and potential seasonality of habitat use of Guam's reef manta rays remains extremely limited, and we have no data on their diving behaviour and use of offshore habitats. Here we report preliminary results of the first satellite tagging to be conducted on reef manta rays in the Micronesia region, based upon ten SPLASH10F towed GPS-fastloc archival satellite tags deployed on seven juvenile/sub-adult and three adult reef manta rays. Deployment periods ranged from 4 to 120 days, with an average of 49.6 days. Preliminary results revealed several hotspots of visitation by all individuals on Guam's northwest coastline and an additional hotspot of visitation for adults on the exposed northeast coastline. Individuals made frequent (daily) dives to depths of 100-300 meters, with one juvenile recording a maximum depth dive of 592 m and one adult male recording multiple dives below 600 m. Results from this study will be used to formulate recommendations for improved management of this species in local waters.

Poor labelling of shark products in Australia’s fish and chip shops

Hasan, Md Robiul[1]; Chaplin, Jennifer[1]; Braccini, Matias[2]

[1]*Centre for Sustainable Aquatic Ecosystems, Environmental and Conservation Sciences, Murdoch University, 90 South Street, Murdoch, WA 6150, Australia*

[2]*Western Australian Fisheries and Marine Research Laboratories, Department of Primary Industries and Regional Development, North Beach, WA 6920, Australia*

Australia generally has a good reputation for promoting sustainable management of fisheries and protecting endangered and threatened shark species. In Australia, consumers mainly purchase shark products from retail outlets called fish and chip shops. Accurate and precise labelling of shark products is essential to ensure that consumers can make informed choices about the types of shark products they consume. However, little is known about the labelling practices in fish and chip shops. We conducted a review of the online menus to assess the quality of labelling of shark products in fish and chip shops across Australia. Using a google search, we identified 1132 fish and chip shops and found that most (n = 850, 75%) had online menus and most of these (n = 712, 84%) either were or could be selling shark products. The shark products in most shops were typically labelled using generic terms such as 'fish and chips' (38%), 'flake' (37%) or unspecified 'shark' (9%). The remaining shops (16%) provided species-specific labels with only 41% of these also providing information about the area of origin, which varied considerably, from specific town names to ‘local’ or ‘imported’. We argue that policymakers should focus on improving labelling practices, including species name and area of origin, as this has the potential to enable consumers to purchase products obtained from sustainable shark fishing, and would reward retailers who use informative product labels.

2.3B Themed Session B: Ecology of Indo-Pacific Fishes, 260-115, November 21, 2023, 1:30 PM - 3:00 PM

The escaping ability of juvenile eels via the predator’s gill: its developmental change and behavioral patterns of eels inside the predator

Yuha, Hasegawa[1]; Kazuki, Yokouchi[2]; Nobuto, Fukuda[2]; Katsuya, Hirasaka[1]; Kazuki, Mine[1];Yuuki, Kawabata[1]

[1] Graduate School of Fisheries and Environmental Sciences, Nagasaki University

[2] Japan Fisheries Research and Education Agency

We have clarified that juvenile Japanese eels can escape via the predator’s gill after they are captured. However, the detailed factors that enable the escape are not clear. Therefore, we conducted experiments to investigate the following elements: (1) developmental change in escaping ability via the predator’s gill, and (2) escape paths and behavioral patterns of eels inside the predator.

(1) Eels change their behavior and morphology significantly as they transition from pelagic to benthic habitats. We observed their escaping behavior via the predator’s gill using seven different developmental stages, ranging from pre-settle glass eels to yellow eels. Our findings revealed that only individuals beyond the middle stage of glass eels (i.e., after the settlement in the freshwater habitat) could escape after being captured.

(2) Predator-prey experiment was conducted in the X-ray video system. Behavioral observations showed that all captured eels ($n = 32$) had at least a portion of their bodies swallowed into the predator's stomach. Surprisingly, after being swallowed, most individuals attempted to escape by going backward through the predator's digestive tract, and nine individuals succeeded in escape. Some eels exhibited circling behavior along the stomach wall, possibly searching for escape routes from the predator’s stomach.

Our findings indicate that eels escape from the digestive tract toward the gill of predatory fish. Our study further suggests that it is necessary for eels to develop their muscle strength and locomotor performance as well as tolerance to the anaerobic and acidic environment, to facilitate a successful escape through the digestive tract.

Three distinct species included in specimens identified as *Priacanthus tayenus* (Priacanthidae) based on morphological and molecular analyses

Hashimoto, Shintaro[1]; Motomura, Hiroyuki[2]

[1] *Graduate School of Agriculture, Forestry and Fisheries, Kagoshima University, Kagoshima, Japan*

[2] *The Kagoshima University Museum, Kagoshima, Japan*

The genus *Priacanthus* Oken, 1817 is currently known from 12 valid species. The present study revealed that specimens previously identified as *Priacanthus tayenus* Richardson, 1846 includes three morphotypes, viz., Type A (endemic to the Indian Ocean), and Types B and C (distributed in the western Pacific Ocean). Type A is clearly distinguished from Types B and C by having fewer scales (e.g., fewer lateral-line scales and scale rows below lateral line). Types B and C are very similar to each other and are considered to co-occur in Southeast Asia. However, Type B can be distinguished by having a larger blotch on membrane between the last pelvic-fin ray and abdomen than that of Type C. Furthermore, each type formed a monophyletic clade on the neighbor-joining phylogenetic tree based on COI, differences being approximately 4.5–5.0% between Type A and Types B, C, and approximately 3.5% between Types B and C. *Priacanthus tayenus* was originally described from China, thus a nominal name *P. tayenus* is considered to be applied to either Types B or C. *Priacanthus holocentrum* Bleeker, 1849 and *Priacanthus schmittii* Bleeker, 1846 are known as junior synonyms of *P. tayenus*. However, because no type specimens of the former are known, *P. holocentrum* is considered here as *nomen dubium*. The nominal name *P. schmitti* is probably applicable to Type A because its holotype has fewer scales and the type locality is western Sumatra (Indian Ocean).

Resurrection and redescription of nominal species previously regarded as synonyms of *Setipinna tenuifilis* (Valenciennes, 1848)

Hata, Harutaka[1]; Lavoué, Sébastien[2] ; Pogonoski, John[3]

[1]*National Museum of Natural History, Smithsonian Institution, 10th and Constitution Ave NW, Washington, DC 20560, USA*

[2]*School of Biological Sciences, Universiti Sains Malaysia, 11800, Penang, Malaysia*

[3]*Australian National Fish Collection, National Research Collections Australia, Commonwealth Scientific and Industrial Research Organisation, GPO Box 1538, Hobart, Tasmania 7001, Australia*

Species of the genus *Setipinna* (Clupeiformes: Engraulidae) are commercially important and baseline taxonomy is critical to their identification and management. Within the genus, species with 13–17 lower gill rakers, short pectoral fin (reaching to first to 21st anal-fin ray origin), and ventral scutes less than 30, have been regarded as synonyms of *Setipinna tenuifilis* (Valenciennes, 1848), a species widely distributed in the Indo-West Pacific region. However, morphological examination and genetic data (from mitochondrial cytochrome b and COI genes) of specimens of *Setipinna tenuifilis* obtained throughout its distribution, revealed that this species comprises at least four species. Additionally, examination of available type specimens, original descriptions, as well as many non-type specimens confirm the applicable names for these four species as: true *Setipinna tenuifilis* [distributed from India to Singapore; total gill rakers (1TGR) 22–26; vertebrae (VN) 45–47; pectoral fin length (PL) ≧ 36.9% SL; melanophores scattered on body (MoB) only above level of eye], *Setipinna gilberti* Jordan & Starks, 1905 [northwestern Pacific from East China Sea to northern Vietnam; 1TGR 26–30; VN 47–50; PL ≦ 36.4% SL], *Setipinna papuensis* Munro, 1964 [Indonesia to PNG; 1TGR 26–31; MoB below level of lower margin of eye; jet black dorsum], and an undescribed species [northern Australia; 1TGR 22–26; VN 46; PL ≧ 36.3%SL; MoB below level of lower margin of eye]. Moreover, these four species are distinguished from *Setipinna paxtoni* Wongratana, 1987 by translucent pectoral fin (vs. jet black in *S. paxtoni*) and silver body (vs. yellow).

The enduring legacy of the Australian Museum Ichthyology Collection: scientific progress, international influence, and pub trivia

Hay, Amanda[1]; McGrouther, Mark[1]

[1]*Australian Museum Research Institute, Australian Museum*

The Australian Museum was established in 1827 and therefore considered one of the oldest natural history museums in the world. Since 1864, there has been an almost unbroken sequence of fish Curators/Researchers building and refining the largest collection of fishes in the Southern Hemisphere. Here I discuss the scientific progress and international influence attained by building and refining this collection of larval and adult fishes. I will also share fascinating histories and that accompany individual specimens and collections, including tales related to attempted assassinations, deep sea “aliens”, and the world’s most famous (and ugliest) fish.

2.1C Themed session A: Evolution, Taxonomy and Biogeography of Indo-Pacific Fishes, 260-098,
November 21, 2023, 3:30 PM - 4:15 PM

Why several when one can unite them all? Integrative taxonomic revision of Indo-Pacific freshwater pipefish (Nerophinae)

Haÿ, Vincent[1]; Keith, Philippe[1]; Lord, Clara[1] ; Mennesson, Marion[1]

[1]*UMR 8067, Biologie des organismes et écosystèmes aquatiques (BOREA), Sorbonne Université, Muséum national d'Histoire naturelle, Université de Caen Normandie, Université des Antilles, CNRS, IRD, CP26, 43 rue Cuvier 75005 Paris, France.*

The family Syngnathidae (seahorses, sea dragons and pipefishes) is a fascinating group and is represented by more than 300 species included in about fifty genera. Species are mostly distributed in tropical and temperate marine coastal waters, but about 30 species inhabit Indo-Pacific tropical island rivers. There are currently six freshwater genera of Nerophinae (trunk-brooders): *Belonichthys*, *Coelonotus*, *Doryichthys*, *Lophocampus*, *Microphis* and *Oostethus*. Unlike other Syngnathidae, freshwater pipefish have been little studied; the taxonomy of Nerophinae is unclear and only based on morphomeristic data. Since their description, the scientific status of each species and genus has changed many times. The purpose of our study is to undertake a revision of this group based on an integrative taxonomy approach. By combining molecular data from four mitochondrial markers (5415 bp), morphomeristic data with a character mapping study and ecological data, we now recognize a single genus as valid, *Microphis*, as opposed to the six previously accepted. Our results also reveal one new candidate species, ***Microphis nicoleae*** **sp. nov.**, and the resurrection of two others: *Microphis torrentius* and *Microphis vaillantii*. This study shows the relevance of integrative taxonomy for higher taxa delineation, using data integration by congruence.

Poster Function, OGGB Level 0 Foyer, November 21, 2023, 4:15 PM - 6:30 PM

Unmasking pipefish otoliths using synchrotron-based scanning X-ray fluorescence

Haÿ, Vincent[1]; Berland, Sophie[1]; Keith, Philippe[1]; Lord, Clara[1]; Medjoubi, Kadda[2]; Mennesson, Marion[1]; Somogyi, Andrea[2]

[1]*UMR 8067, Biologie des organismes et écosystèmes aquatiques (BOREA), Sorbonne Université, Muséum national d'Histoire naturelle, Université de Caen Normandie, Université des Antilles, CNRS, IRD, CP26, 43 rue Cuvier 75005 Paris, France.*

[2]*Synchrotron Soleil, 91192 Saint-Aubin, France.*

Scientists use otoliths to trace fish life history, especially fish migrations. Otoliths incorporate signatures of individual growth and environmental use. For many species, distinct increment patterns in the otolith are difficult to discern; thus, questions remain about crucial life history information. To unravel the history of such species, we use synchrotron-based scanning X-ray fluorescence. It allows the mapping of elements on the entire otolith at a high spatial resolution. It gives access to precise fish migration history by tagging landmark signature for environmental transition and it also characterises localised growth processes at a mineral level. Freshwater pipefish, which are of conservation concern, have otoliths that are small and fragile. Growth increments are impossible to identify and count; therefore, there is a major lack of knowledge about their life history. We confirm for the first time by mapping strontium that the two tropical pipefish species studied are diadromous (transition freshwater/marine/freshwater). Mapping of other elements uncovered the existence of different migratory routes during the marine phase. Another major breakthrough is that we can chemically count growth increments solely based on sulphur signal as it is implicated in biomineralization processes. This novel method circumvents reader bias issues and enables age estimation even for otoliths with seemingly untraceable increments. The high spatial resolution elemental mapping methods push back limits of studies on life traits or stock characterisation.

Territoriality and dear enemy relationships in ayu (*Plecoglossus altivelis*)

Hayashi, Kota; Sogawa, Syumpei; Kohda, Masanori; Awata, Satoshi

Laboratory of Animal Sociology, Department of Biology, Graduate School of Science, Osaka Metropolitan University, Osaka, Japan

To defend their territory, animals must exert energy. Therefore, many territorial animals are known to have dear enemy (DE) relationships, in which individuals in adjacent territories become more tolerant of each other and reduce aggression when they establish boundaries. This has the benefit of reducing time spent on fighting, energy costs and risk of injury. However, it has not been well studied in fish, except for the cichlid, which has complex social behaviours, such as cooperative breeding. An amphidromous fish, the ayu (*Plecoglossus altivelis*) forms feeding territories to defend its food resource of algae on the river bottom. The ayu is the most famous territorial fish in Japan, but its DE relationship has not been examined due to difficulties of direct observation of their territorial interaction, although territoriality has been studied in the field. In this study, we tested whether ayu formed DE relationships through aquarium experiments. When focal fish were confronted with strangers in an adjacent tank for six days, they exhibited strong aggression towards each other on the first day. However, their aggression decreased from the second day and remained constant thereafter. When the neighbours were replaced by other strangers, the aggression between them increased again. These results suggest that ayu form DE relationships with territorial neighbours and can recognise each other. They also imply that territorial fish may form DE relationships even in a short-term relationships of less than a year regardless of whether they have complex societies.

2.2A Special Session 4: The evolution and ecology of fishes: assessing traits and functions in a changing world, 260-073, November 21, 2023, 10:30 AM - 12:30 PM

Do all fish species have similar body size distributions and why does it matter?

Heather, Freddie[1]; Audzijonyte, Asta[1,2]; Richards, Shane[3]

[1]*Institute for Marine and Antarctic Studies (IMAS), University of Tasmania, Hobart, Australia*

[2]*Centre for Marine Socioecology, University of Tasmania, Hobart, Australia*

[3]*School of Natural Sciences, University of Tasmania, Hobart, Australia*

The body size of a fish is often more important than its species identity with regards to physiology, growth rate, and how it interacts with the environment. The distribution of fish body sizes in a population will determine its resilience, ecological role and is a good indicator of the fishing pressure. Body size distributions seem to obey general ecological rules and it has been suggested that scaled species level body size distributions are relatively conservative across species. Here we use large datasets from underwater visual surveys and other sampling methods, covering hundreds of fish species. We apply Bayesian methods to assess whether there is indeed a universal shape of body size distributions in fish species and whether the properties of this shape (skewness, means) can be predicted based on species or environmental characteristics. Specifically, we test whether water temperature and fishing produce predictable changes in the shape of species size distributions. These predictive models would enable better estimates of fish population baselines and fishing impacts across spatial gradients and allow predictions of how fish populations may respond to increasing water temperatures.

Metabolomics and lipidomics: ‘the last piece of the omic puzzle’

Heim, Sara[1,2]; Gallart-Ayala, Hector[2]; Ivanisevic, Julijana[2]; Salamin, Nicolas[1]
[1]Department of Computational Biology, University of Lausanne, Switzerland
[2]Metabolomics Platform of the University of Lausanne, Switzerland

In the underwater world, one of the greatest challenges remains the understanding of chemical communication between different organisms. Subtle yet so meaningful, this vector of communication is the key behind established interactions such as mutualisms, predation, reproduction, host-microbe interactions, but also on a broader scale, it shapes population structure, community organization and ecosystem function. Metabolomics along with its branch lipidomics, allows for the detection and identification of small molecule metabolites which serve as mediators of chemical interactions. The relevant examples include the deciphering of metabolic cross-talk in mutualistic interactions such as host-microbiome, specific sea cucumber-crab; clownfish-sea anemone, coral-dinoflagellate symbiosis, characterizing unknown molecules that act as cues in fish/coral, reproduction, food foraging, larvae settlement. Depending on the approach (untargeted and targeted profiling, stable-isotope assisted tracing and mass spectrometry-based imaging) metabolite analysis can either provide a snapshot of the metabolic state of an organism at a given time point, inform us about the pathway activity (in different conditions) or spatial localization of a label or labeled metabolite and therefore the organism produces it. As the metabolome represents the phenotype at the molecular level, these analytical approaches can provide additional mechanistic insights to complement findings derived by other upstream omics technologies. The key steps of the metabolomics workflow (from samples to metabolite data and biologically relevant information) and the importance of the experimental design will be described to elucidate how to generate high-quality and robust data, including the remaining challenges with the annotation and identification of unknown molecular features.

Decoding morphological diversity in deep-sea spikefishes (Triacanthodidae: Tetraodontiformes): phylogenetics, genomics, and habitat associations

Heiple, Zach[1]; Arcila, Dahiana[1]; Bemis, Katherine[2,3]; Fujiwara, Kyoji[4]; Ho, Hsuan-Ching[5,6]; Nakae, Masanori[4]; Tyler, James[3]; White, William[7]

[1]*Marine Vertebrate Collection, Scripps Institution of Oceanography, University of California San Diego, 9500 Gilman Drive, La Jolla, CA 92093-0244, USA.*

[2]*National Systematics Laboratory, Office of Science and Technology, NOAA Fisheries, Washington, D.C. 20560, U.S.A.*

[3]*Department of Vertebrate Zoology, National Museum of Natural History, Smithsonian Institution, Washington, D.C. 20560, U.S.A.*

[4]*Department of Zoology, National Museum of Nature and Science, 4-1-1 Amakubo, Tsukuba, Ibaraki 305-0005, Japan*

[5] *Department and Graduate Institute of Aquaculture, National Kaohsiung University of Science Technology, Kaohsiung 811213, Taiwan*

[6]*National Museum of Marine Biology & Aquarium, Pingtung 944, Taiwan*

[7]*CSIRO Australian National Fish Collection, National Research Collections Australia, Hobart, TAS, Australia*

A central goal in evolutionary biology is elucidating the origin of morphological diversity. Among deep-sea fish groups, spikefishes in the family Triacanthodidae (Tetraodontiformes) are typically found on the continental slopes at mesopelagic depths (200-1000m). Members of the group present a fascinating continuum of morphological diversity, from relatively normal-looking deep-bodied species with well-developed dorsal fins, through intermediates, to bizarrely specialized forms with exaggerated long tubular snouts, elongated body plans, and reduced dorsal fins. Here, we examine the phylogenetic relationships of spikefishes, a group comprising 24 extant species in 11 genera. We assembled a genomic matrix comprising 1,105 single-copy exon markers and a new morphological matrix based on 60 characters representing all 24 extant species. Additionally, we estimate a new timeframe for spikefishes diversification by integrating data from fossil and extant species, employing tip-dating and the Fossilized Birth-Death model. Further, we employ high-resolution micro-CT scan and whole-genome sequencing data to link the morphological diversity of spines, body shape, and snout elongation with the underlying genomic signatures of evolution in the group. Lastly, using geographical data from collected specimens, we provide new insights into the potential association of habitats, such as seamounts or continental slopes, and the evolution of extreme morphologies. Using a suite of cutting-edge molecular approaches, we aim to shed light on patterns of diversification in triacanthodids.

Using colouration as a trait to study ecosystems and communities: a case study on coral reef fishes

Hemingson, Christopher[1]; Bellwood, David[2]; Cowman, Peter[3]; Mihalitsis, Michalis[4]

[1]*The University of Texas at Austin's Marine Science Institute, Port Aransas, Texas, USA*

[2]*James Cook University, Townsville, Queensland, Australia*

[3]*Museum of Tropical Queensland, Townsville, Queensland, Australia*

[4]*The University of California, Davis, Davis, California, USA*

Colouration is a key trait that can relay much about an organism or ecosystem. It can provide clues as to how a species behaves, it can reflect the health of an individual, or it can indicate as to when ecosystems may be changing. Historically, colours and patterns have been a difficult trait to study since their description is contingent upon the visual capabilities of the viewer. However, there recently have been numerous novel resources developed that use digital images to study biological colouration. In my talk, I will first cover the utility of some of these resources and show how techniques can be combined from both colour research and community ecology. We showcase how this approach can be used to measure multiple different aspects relating to the appearance of entire communities or ecosystems giving it widespread use in the natural sciences. We then use this technique to assess what habitat features are important for supporting colourful communities of fishes on the Great Barrier Reef. We find that more colourful and vibrant fish communities are directly correlated with the amount of structurally complex corals found within the survey area. As the surveyed habitat transitions to containing substrates that are more typical of degraded reefs, the appearance of the resident fish community becomes more uniform and drabber in appearance. Our findings have implications for the aesthetic value humans place on reefs and how this may be changing in the near future.

Conserving for complementarity: A functional approach to conservation

Henderson, Christopher J.[1]; *Olds, Andrew D.* [1]; *Gilby, Ben L.*[1]

[1]*School of Science, Technology and Engineering, University of the Sunshine Coast, Maroochydore, Queensland, 4556, Australia*

Conservation actions, like protected areas, have been implemented widely to arrest biodiversity declines, but these structural tools are rarely informed by empirical data on the functional characteristics of food-webs, ecological functioning, and resilience. Functional redundancy and complementarity are pivotal characteristics of ecosystems that link biodiversity to ecosystem functioning. High redundancy can help to maintain the delivery of an ecological function through time when significant species are removed or lost. By contrast, high complementarity within food-webs can help to support a diversity of functions, further promoting the resilience of ecosystems to disturbances. Here we highlight four concepts to support tighter integration of functional complementarity into conservation. Firstly, it is crucial that management decisions and actions are informed by data on the rates and distributions of key ecological functions that are demonstrably linked to the maintenance of ecosystem structure and resilience. It is then important to develop and integrate appropriate metrics (e.g. functional diversity metrics) of community change that incorporate the functional composition of food-webs and key ecological functions. Managers should then identify species (e.g. dominant generalists or pests) that could limit the positive outcomes of conservation, and finally monitor, adapt, and set realistic goals for management that focus on diverse functioning.

2.4C Themed Session F: Conservation of Indo Pacific fishes, 260-092, November 21, 2023, 3:30 PM - 4:15 PM

Shortjaw kōkopu distribution, population status and threats in the Northern South Island, New Zealand

Henderson, Anna[1]; **Hunt, Kate[2]**

[1]*Department of Conservation, Wairau*

[2]*Department of Conservation, Motueka*

Shortjaw kōkopu (*Galaxias postvectis*) are a species of freshwater fish endemic to New Zealand. The species is ranked as endangered by the International Union for Conservation of Nature (IUCN), and Threatened – Nationally Vulnerable in the New Zealand Threat Classification System. Shortjaw kōkopu prefer stable, bouldery, forested streams. Habitat loss is thought to be a key driver of decline, with impacts including loss of adult habitat, degradation of water quality, and fish passage barriers preventing access to existing habitat.

Ngā Ika e Heke is a Department of Conservation programme dedicated to increasing the security of four diadromous fish, including shortjaw kōkopu. The initial focus is to assess the state of existing populations and improve understanding of the mechanisms behind their decline. Many sites in the Northern South Island have not been surveyed for at least 20 years. We returned to known sites to determine their current population status. Here we compare updated and previous data to establish long-term population trends.

A 400 m reach was spotlighted in each of the selected waterways. Habitat data was also collected. Waterways were chosen based on historic records and modelled catchments. Of the sites that had been surveyed before, the majority had declined in shortjaw kōkopu numbers. We look at the possible causes, including changes in habitat and the potential impacts of recent storms. The data collected, and the implementation of long-term monitoring, will help inform the management of shortjaw kōkopu, with the ultimate goal of securing stable populations of the species throughout the country.

Long-term biodiversity monitoring reveals few poleward shifts in Australian shallow water reef species

Herrera Fuchs, Yann[1]; Edgar, Graham[1] , Stuart-Smith, Rick[1]

[1]Institute of Marine and Antarctic Studies – University of Tasmania

Numerous projections from historical records predict warming seas to redistribute marine species poleward. Yet evidence from contemporary range shifts is extremely rare, with multiple large reviews emphasizing a distinct lack of observed extirpations from lower latitudes by tropical species. We used a standardized dataset of underwater visual surveys to assess the changes in latitudinal limits of 799 shallow-water reef species in 706 sites around Australia, following periods of warming and cooling over the last decade. Latitudinal shifts are stochastic (median = 0), but average movements (0 – 50 km dec^{-1} ± 10 km dec^{-1}) reveal poleward contractions from warm edges along warming coasts though opposite in direction for cooler edges of tropical species in a cooling coast. This plasticity to temperature cues supports predictions of range shift dynamics; however, with nowhere poleward to retreat and heatwaves altering the direction and speed of species' flux, prioritizing regions of ecological collapse and recovery will be key for safeguarding biodiversity in a warming planet.

A Transcriptome Insight During Larval Settlement of a Coral-Reef Fish

Herrera, Marcela[1]; Reynaud, Mathieu[1,2]; Huerlimann, Roger[3]; Chamot, Zoe[1]; Gairin, Emma[1]; Miura, Saori[1]; Ravasi, Timothy[3,4]; Laudet, Vincent[1,5]; Lecchini, David[2,6]

[1]*Marine Eco-Evo-Devo Unit, Okinawa Institute of Science and Technology Graduate University, Okinawa 904-0495, Japan*

[2]*PSL Université Paris, EPHE-UPVD-CNRS, USR3278 CRIOBE, 98729 Moorea, French Polynesia*

[3]*Marine Climate Change Unit, Okinawa Institute of Science and Technology Graduate University, Okinawa 904-0495, Japan*

[4]*Australian Research Council Centre of Excellence for Coral Reef Studies, James Cook University, Townsville, QLD 4811, Australia*

[5]*Marine Research Station, Institute of Cellular and Organismic Biology, Academia Sinica, I-Lan 262, Taiwan*

[6]*Laboratoire d'Excellence "CORAIL", 66100 Perpignan, France*

Understanding early life events is crucial for predicting the impacts of changing environments in fish metamorphosis, yet, the expression of early developmental genes and regulation of pathways during the most sensitive stages of their life history is still poorly understood. In the present study, we sequenced and generated a high-quality chromosome scale assembly for the convict surgeonfish *Acanthurus triostegus* with the aim of understanding the dynamic molecular regulation of metamorphosis. We characterized the transcriptome of this species at four stages that correspond to concomitant developmental and ecological shifts, from crest captured larvae to 1, 3, and 8 days following their entry in the reef. Significant changes in expression of digestion and vision-related genes that corresponded to dietary and behavioural shifts during this ecological transition were observed. Similarly, changes in genes related to glycolysis, citric acid cycle, and fatty acid biosynthesis indicated a metabolic transition and shift in energy availability during larval settlement. In particular, expression of developmental genes that are associated with organogenesis and morphological changes of the nervous and muscular systems was investigated and special focus was given on thyroid hormone pathways as thyroid hormones have been shown to be critical for triggering and coordinating metamorphosis. These findings improve our understanding of the morphological and physiological changes reef fish experience upon settlement but, most importantly, provide a baseline to further study the mechanisms underlying metamorphosis in the context of changing environments.

Denticle hygiene: examining the viral communities of Elasmobranch skin

Hesse, Ryan[1]; Kerr, Emma[1]; Carlson-Jones, Jessica[1]; Meyer, Lauren[1]; Huveneers, Charlie[1]; Best, Giles[2]; Scott, Mark[3]; Dinsdale, Elizabeth[1]

[1]*Flinders University, Bedford Park, South Australia*

[2]*Flinders University Medical Center, Bedford Park, South Australia*

[3]*Norfolk Island National Park, Burnt Pine, Norfolk Island*

Many marine animals rely on their external microbiomes (resident communities of microbes like bacteria and viruses) to eliminate pathogens before they can reach the epidermis. Viruses and bacteriophages (viruses infecting bacteria) play a critical but understudied role in these marine epidermal microbiome defense systems. Elasmobranchs demonstrate a unique ability to resist epidermal infections despite frequent injury and constant exposure to environmental pathogens. Part of this heightened immunity stems from various innate mechanisms, such as skin morphology, immune responses, and antimicrobial secretions, but the role of the external microbiome in maintaining elasmobranch health is still largely unknown. We sampled the skin microbiomes of elasmobranchs from Norfolk Island in the southwest Pacific Ocean and Gulf St. Vincent in South Australia to investigate the viral communities on their epidermis. A handful of individuals were captured with skin lesions at various healing stages, which were sampled along with nearby undamaged skin. Bacterial and viral counts were estimated using flow cytometry, and enriched viral samples were collected for shotgun metagenomic sequencing. Elasmobranch epidermis had lower microbial abundances than surrounding water and contained higher proportions and greater variability of virus-like particles (VLPs) than the epidermis of other species sampled. Wounded shark skin harbored higher proportions of VLPs than undamaged skin on the same individual, and higher proportions than average undamaged individuals of the same species, while healing skin had intermediate proportions of VLPs. These differences in viral counts suggest that bacteriophages may have a role in facilitating epidermal wound healing in sharks.

Measuring thermal limits of fish heart mitochondria on a shoestring-lockdown projects

Hickey, Tony[1]; Harford, Alice[1]; Riordan, Breana[2]; Johnston, Sheri[2]; Devaux, Jules[1]

[1]*Applied Surgery and Metabolism Laboratory, School of Biological Sciences, University of Auckland, Auckland, New Zealand*

[2]*Zoology Department, University of Otago, Dunedin, New Zealand*

The vertebrate heart appears to be the most sensitive organ to acute increases in temperature, and heart failure results in death. Fish hearts are no exception and over the years my group has shown that the fish hearts likely fail due to mitochondrial failure. ATP synthesis is the primary role of mitochondria, and this is dependent on sustaining an adequate membrane potential that is generated by proton transfer across the inner mitochondria membrane (IMM). The membrane potential then powers proton flow through the ATP synthase to form ATP. The current paradigm is that with rising temperature, the fluidity of the IMM phospholipids increases and that this increases the IMM permeability to protons. This dissipates the mitochondrial membrane potential while increasing mitochondrial oxygen consumption. More importantly, just below to the critical temperature at which the heart fails, mitochondrial ATP synthesis fails, linking membrane potential to mitochondrial collapse.

Typically, measurements of mitochondrial function requires large complicated oxygraphs, and multiple experiments with large amounts of tissue (requiring a big fish or many fish). These are then tested at distinct temperatures. We developed a different approach that permits measurement of temperature mediated changes in mitochondrial membrane potential (and some other parameters) using inexpensive microscopes and purpose-built heaters. Here we can measure changes in mitochondrial stability using less than a milligram of tissue and inexpensive microscopes. This system provides a simple tool to test mitochondrial function in several samples, increasing our potential to more rapidly screen species for their tolerance to acute temperature change.

Laboratory-based comparison of screening materials for excluding New Zealand juvenile freshwater fishes

Hickford, Mike[1]; Jellyman, Phil[1]

[1]*National Institute of Water and Atmospheric Research Ltd, Christchurch, New Zealand*

Growing demand for water requires resource managers to be innovative to minimise impacts on aquatic ecosystems. Abstracting surface waters for irrigation can impact fish communities by altering habitat and disrupting migration and spawning movements. Additionally, if surface water intakes are not properly screened, they can unintentionally damage or remove fish from rivers. Very few studies have examined the effectiveness of different screening materials for excluding New Zealand fishes. New Zealand's unique fish fauna is dominated by small, benthic, and often diadromous species, so criteria for New Zealand fish screens need to be developed for local species rather than adapted from generic principles conceived overseas.

We experimentally tested six screens (50–100 and 100–200 mm rock bunds, 3 mm woven mesh, 1.5, 2 and 3 mm wedge-wire), on two introduced and five native fish species. Juvenile bluegill bully, common bully, Canterbury galaxias and rainbow trout were screened effectively by 3 mm woven mesh and wedge-wire. Juvenile Chinook salmon and īnanga whitebait were excluded by 2 mm wedge-wire, but shortfin elvers penetrated 3 and 2 mm wedge-wire, and glass eels penetrated 1.5 mm wedge-wire. Rock bunds were effective barriers for rainbow trout but were ineffective, and acted as habitat, for bluegill bully, Canterbury galaxias and shortfin eels. We recommend that 1.5 mm wedge-wire screens are used in the tidal zone of New Zealand rivers, 2 mm screens are used beyond this zone with an upstream transition to 3 mm screens dependent on catchment-specific fisheries values.

Conservation of eels in New Zealand: response to reduction of invasive fish biomass

Hicks, Brendan[1,2]; Ling, Nicholas[1]; Özkundakci, Deniz[1]; Rossaak, Andrew[2]; Tempero, Grant[1]

[1]*School of Science, Division of Health, Engineering, Computing and Science, University of Waikato, Hamilton, New Zealand*

[2]*MorphumEnvironmental Ltd, Auckland, New Zealand*

The freshwater eels *Anguilla australis*, shortfin eel and *A. dieffenbachii*, longfin eel are widespread in Aotearoa New Zealand and were named tuna by Māori, the tangata whenua (people of the land). Māori have occupied New Zealand for over 700 years and consider eels to be a taonga (treasured) species. Eels continue to recruit well to rivers and lakes despite habitat change and commercial fishing that have reduced their abundance. The longfin eel is particularly vulnerable to overfishing through commercial fishing because of their long life cycle (about 40 years to maturity for females).

Invasive fish species dominate the Waikato region of the North Island (Te Ika a Māui), Aotearoa New Zealand, where koi carp (*Cyprinus rubrofuscus*) comprise 60-80% of the fish biomass and dietary overlap occurs between invasive fish and eels. Koi carp and eels, for instance, are both primarily benthic carnivores. We removed invasive fish from the 17-ha Lake Ohinewai, reducing koi carp biomass from 308 kg/ha in 2011 to 14 kg/ha in 2014. In response, shortfin eels increased from 8 kg/ha in 2011 to 41 kg/ha in 2016. Longfin eels increased from 0.4 to 1.9 kg/ha over the same period. This demonstrates the impact that invasive fish can have on important indigenous species and the recovery of abundance that is possible when invasive fish biomass is substantially reduced.

Goby spotting: Three new species descriptions and a revised guide to Info-Pacific *Gobiodon* genus

Hildebrandt, Courtney A.[1]; Brodenicke, Ole[2]; Froehlich, Catheline Y. M.[3,4]; Klanten, O. Selma[5]; Möller, Peter R.[6]; Wong, Marian Y. L.[1].

[1] *Centre for Sustainable Ecosystem Solutions, School of Earth, Atmospheric and Life Sciences, University of Wollongong, Wollongong, Australia.*

[2] *Department of Biology, University of Copenhagen, Copenhagen, Denmark.*

[3] *Department of Biology, University of Alabama, Alabama, USA.*

[4] *Dauphin Island Sea Lab, Dauphin Island, Alabama, USA.*

[5] *School of Life Sciences, University of Technology Sydney, Sydney, Australia.*

[6] *Natural History Museum of Denmark, University of Copenhagen, Copenhagen, Denmark.*

Gobiodon is a genus of obligate highly specialised coral dwelling fish species found inhabiting most Indo-Pacific coral reefs. Forming a likely obligate mutualistic relationship with reef building scleractinian corals, they are an important member of the coral reef ecosystem and contribute to maintaining and sustaining healthy coral ecosystems. Despite this, they are often omitted from fish assemblage studies, biodiversity surveys and field guides due to their cryptic nature and confusion regarding species identification. Here we present an updated guide to *Gobiodon* in the Indo-Pacific region, incorporating recent taxonomic changes based on molecular genetics, morphology, and colouration. In addition, we include details regarding IUCN Red-List status, sociality and habitat usage and thereby build upon prior work. We also present a new identification key for species within the Indo-Pacific region based on live colouration and host coral choice. Importantly, we will also provide formal descriptions of three new species found within the Indo-Pacific, two species restricted to Papua New Guinea and one that extends from the southern Great Barrier Reef to Papua New Guinea. These species, like many others are highly specialised and only found in a few coral hosts, thereby vulnerable to climate change, especially threats from coral bleaching and cyclone damage. Formal descriptions such as these are crucial for the conservation of species, a process which relies on accurate taxonomic identification and distribution data. Therefore, with this guide and descriptions, we hope future studies will more accurately identify and include these species in surveys assessing the impacts of climate change.

Preliminary results on the gut plasticity of reef fishes across different feeding strategies in the Tropical Eastern Pacific

Hinojosa, Natasha[1]; Lardinois, Laura[2]; Leray, Matthieu[3]; Mehta, Rita[1]; Sellers, Andrew[2],

[1]*University of California at Santa Cruz*

[2]*McGill University*

[3]*Smithsonian Tropical Research Institute*

For an organism to be successful in a variable environment, it is strategic to exhibit plasticity in morphology, physiology, and behavior. Plasticity in foraging behavior, diet choice, and feeding physiology are particularly important when the environment undergoes a seasonal shift that affects the abundance and composition in species assemblage and flux of nutrient availability. Here, we examine plasticity in the gut of five reef fish families how it responds to the different environments of the tropical eastern Pacific (TEP) and across the Isthmus to its corresponding Caribbean sister species. To account for the breadth of trophic strategies we included six feeding strategies (herbivore, planktivore, corallivore, spongivore, invertivore, and piscivore). Statistical analyses included a T-test and F-test which had 'relative gut length to standard length' ratio (RGL) as a response variable. Preliminary results comparing reef fish sister pairs in the Pacific vs. Caribbean revealed statistically significant differences in RGL mean between *Abudefduf concolor* and *A. taurus, Anisostremus taeniatus* and *A. virginicus*, and *Chaetodon humeralis* and *C. ocellatus*. However, when comparing the degree variance around the mean, there was statistical significance between *Abudefduf troschelii* and *A. saxatilis* and *C. humeralis* and *C. ocellatus*. This suggests three different outcomes depending based on feeding strategies: 1) similar mean RGL but different degrees of plasticity (*Abudefduf* sp.), 2) different mean RGL but similar degrees of plasticity (*Anisotremus* sp.), and 3) different RGL and different levels of plasticity (*Chaetodon* sp.). These preliminary results show the interplay between adaptation and plasticity in TEP reef fish feeding physiology.

Multiple hybrid zones of coastal marine gobies around the Japanese archipelago: natural laboratories for marine hybridization

Shotaro, Hirase[1]; Shuya, Kato[1]; Tomoyuki, Kokita[2]

[1]*Fisheries Laboratory, Graduate School of Agricultural and Life Sciences, The University of Tokyo*

[2]*Faculty of Agriculture, Kyushu University*

Hybrid zones between divergent lineages can play an important role in elucidating the first steps towards allopatric or hybrid speciation. Pleistocene isolation events of the Sea of Japan caused genetic divergence between the Pacific Ocean (PO) and Sea of Japan (SJ) lineages in two coastal gobies of Japanese archipelago, *Chaenogobius annularis* and *Leucopsarion petersii*, and generated two independent hybrid zones in each species.

Individuals from two hybrid zones of *C. annularis* showed excess ancestry of either lineage in many genomic regions, suggesting that they are later-generation hybrids that have mosaic feature of hybrid genomes. We found that significantly more nonsynonymous substitutions occurred in mitogenomes in one hybrid zone, and these substitutions were likely to be caused by mitonuclear incompatibility. However, the other hybrid zone of this species did not show such mitogenome mutations.

The two lineages of *L. petersii* were genetically and phenotypically divergent, and the SJ lineage has a larger body-size and a greater number of vertebrae. Genomic data showed that one hybrid zone was genetically close to the SJ lineage and the other hybrid zone was to the PO lineage. Notably, phenotypic patterns of vertebral number in the two hybrid zones were clearly explained by genotypes but those of body size were not, suggesting selective pressure to body size of hybrids.

These findings demonstrate that hybridization could lead to variable genomic and phenotypic consequences under different environmental settings. Multiple hybrid zones around the Japanese archipelago are important to access the inevitability of the consequence of the hybridization.

Developing solutions to mitigate impacts of fishing trawlers on elasmobranchs, Sabah, Malaysia

Ho, Kooi Chee[1,2]; Manjaji Matsumoto, Bernadette Mabel[1]; Pilcher, Nicolas James[2]

[1]Borneo Marine Research Institute, University Malaysia Sabah, 88400 Kota Kinabalu Sabah, Malaysia

[2]Marine Research Foundation, 88000 Kota Kinabalu Sabah, Malaysia

The seas around Sabah are home to the richest elasmobranch biodiversity in Malaysia. However, many elasmobranch species are caught accidentally by fishing trawlers. These incidental catches of elasmobranchs are one of the greatest threats faced by the species. In Malaysia, elasmobranchs are mainly caught in the commercial fishing industry, especially by demersal trawlers. This has led to changes in their species composition and abundance, and in some cases, drastic population declines. Moreover, there is no information on where and when these capture events occur. To ascertain when and where these species are caught, electronic monitoring cameras were installed on fishing trawlers to capture images of elasmobranchs that were landed on fishing vessel decks. Images of species such as Scalloped Hammerhead Shark, Spottail Shark, Brownbanded Bambooshark, Coral Catshark, Eastern Cowtail Stingray, Longtail Butterfly Ray, and Bottlenose Wedgefish were captured by the electronic monitoring cameras. These images are time- and GPS-stamped, and this provides us with accurate location data for each capture. Images of trawl-caught elasmobranch that were captured by the cameras were identified by using a field guide, and species distribution maps were produced by combining all the location data. These data will be used to investigate the spatial and temporal trends of trawl-caught elasmobranch, that hopefully can be used for future conservation management of the species to address the accidental catches of elasmobranch, such as to establish time-area closure to protect the species in the hotspot areas from trawling during certain months.

Habitat persistence? Phylogeography of mesophotic holocentrids reveals younger than expected populations

Hoban, Mykle[1]; Bowen, Brian[1]; Copus, Joshua[1,2,†]; Kosaki, Randall[3]; Lee, Anne[1]; Pyle, Richard[1]; Toonen, Robert[1]; Walsh, Cameron[1]

[1]*Hawai'i Institute of Marine Biology*

[2]*Bernice Pauahi Bishop Museum*

[3]*Papahānaumokuākea Marine National Monument*

[†]*Deceased*

Mesophotic coral ecosystems (MCEs: ~30 to 100+ m depth) may be older and more stable than shallow coral ecosystems that are more prone to disturbances in both the long term (glacial sea level cycles) and short term (heavy weather and anthropogenic activities). Here, we assess the phylogeography of two MCE fishes, the soldierfish *Myripristis chryseres* (N = 85) and the squirrelfish *Neoniphon aurolineatus* (N = 74), with mtDNA cytochrome oxidase C subunit I. Our goal is to resolve population genetic diversity across the Central and West Pacific and compare these patterns to three shallow-reef species in the same taxonomic family (Holocentridae). Significant population structure ($\Phi_{ST} = 0.148$, $p = 0.01$) was observed in *N. aurolineatus*, while no structure was detected in *M. chryseres* ($\Phi_{ST} = -0.031$, $p = 0.83$), a finding that matches the shallow-water congener *M. berndti* ($\Phi_{ST} = -0.007$, $p = 0.63$) across the same range. Nucleotide diversity in the MCE fishes was low ($\pi = 0.0024$–0.0028) compared to shallow counterparts ($\pi = 0.003$–0.006). Coalescence times calculated for *M. chryseres* (~272,000 years) and *N. aurolineatus* (~284,000 years) are more recent or comparable to the shallow-water holocentrids (~220,000–916,000 years). We conclude that the shallow genetic coalescence characteristic of shallow-water marine fishes cannot be attributed to frequent disturbance and see no evidence from holocentrid species that MCEs are older or more stable habitats.

1.2B Special Session 4: The evolution and ecology of fishes: assessing traits and functions in a changing world, 260-073, November 20, 2023, 2:00 PM - 4:15 PM

Food availability influences life history traits of a widespread herbivorous reef fish

Hoey, Andrew[1]; Matthews, Sam[1]; McClure, Eva[1]; Taylor, Brett[2]

[1]*College of Science and Engineering, James Cook University*

[2]*University of Guam Marine Laboratory*

Variation in life history traits is common among and within animal populations, and is often mediated by environmental conditions. While a growing number of studies have shown that environmental temperature can influence life history traits of fishes, relatively few have investigated the importance of food availability. Using the bluespine unicornfish (*Naso unicornis*) as our model species, we investigate how differences in the availability of their preferred food (foliose and leathery brown algae) across the continental shelf of the Great Barrier Reef influence their diet (stomach content), condition, growth and mortality. There was considerable cross-shelf variation in the diet of *N. unicornis* that broadly corresponded to the availability of various algae. The diet of individuals from inshore reefs was characterised by foliose and leathery brown algae (primarily *Sargassum*, *Hormophyssa* and *Dictyota*), while those from mid- and outer-shelf reefs were characterised by foliose and corticated red algae, and to a lesser extent the foliose brown alga *Lobophora*. This difference in diet corresponded to differences in the life history traits and fitness of *N. unicornis* among shelf positions. *N. unicornis* from inner-shelf reefs exhibited higher initial growth and had greater body condition (fat stores), but higher mortality and reduced maximum age compared to conspecifics from mid- and outer-shelf reefs. Our results highlight the importance of considering resource availability when assessing life history traits, especially for widespread species such as *N. unicornis*, and the potential trade-offs among life history traits that may optimise lifetime fitness.

Geographical barriers and secondary contact shape the phylogeography of a widespread Indo-West Pacific reef fish, the banded sergeant *Abudefduf septemfasciatus*.

Hsu, Ling-Lan[1]; Borsa, Philippe[2]; Chen, Wei-Jen[1]

[1]*Institution of Oceanography, National Taiwan University, Taiwan*

[2]*Institut de recherche pour le développement, France*

Marine geographical barriers and ecological factors drive population structure in the Indo-West Pacific (IWP) reef species, spatially and temporally. We studied the population genetics and historical demography of a widespread egg-brooding damselfish species, the banded sergeant *Abudefduf septemfasciatus*, to investigate the effects of such drivers on speciation in coral reef fishes. Banded sergeants were sampled from four areas across the entire IWP. Two genetic datasets were used: one compiled genome-wide SNPs derived from double digest restriction-associated DNA sequencing, and the other consisted of concatenated mitochondrial DNA sequences. The species was partitioned into two distinct genetic clusters (Indian Ocean, IO vs Pacific Ocean, PO), illustrating the isolating effect of the Indo-Pacific Barrier during the glacial periods. Sharp population structure that may be the consequence of low gene flow was also observed in the PO but not in the IO. High connectivity between the two IO populations and a negative neutrality-test result suggested recent demographic expansion coupled with geographic expansion. An admixture of PO and IO genotypes was observed in Taiwanese waters. Two scenarios were then proposed: (i) recent secondary contact and (ii) ancient polymorphism. Simulated demographic models showed a higher likelihood for scenario (i). The present findings provide insights into how the phylogenomic geography of a widespread reef species is shaped and underlies potential evolutionary mechanisms to explain the high diversity of IWP reef fishes.

Gut microbiome and host molecular response of Malabar grouper (*Epinephelus malabaricus*) exposed to marine heatwaves

Huerlimann, Roger[1,2]; Izumiyama, Michael[1]; Jolly, Jeffrey[1]; Li, Chengze[1]; McMahon, Shannon[1]; Ravasi, Timothy [1,3]

[1]*Marine Climate Change Unit, Okinawa Institute of Science and Technology Graduate University, Onna-son, Japan*

[2]*Centre for Sustainable Tropical Fisheries and Aquaculture, College of Science and Engineering, James Cook University, Townsville, QLD 4811, Australia*

[3]*Australian Research Council Centre of Excellence for Coral Reef Studies, James Cook University, Townsville, Australia*

Marine heatwaves are increasing in frequency, duration, and magnitude due to anthropogenic climate change. This will present a physiological challenge for most marine organisms. Therefore, investigating how marine heatwaves will not only acutely affect marine organisms, but also their ability to recover, is of immediate importance. It has also been shown that intestinal microbiomes provide an important function in the health status and resilience of all organisms; however, it is unclear how quickly the host microbiome will change during marine heatwaves, to what extent, and whether the change is reversible over time. In the present study, we have sequenced the intestinal microbiome as well as tissue level transcriptomes of malabar grouper (*Epinephelus malabaricus*) exposed to a +3°C heatwave for either three days or three weeks. Additionally, fish were sampled again after four weeks of recovery at control temperature. We found that even a short heatwave (three days) can affect the liver and muscle transcriptome, in a similar magnitude to a longer heat wave, and that this effect persists even four weeks after the heat wave. In contrast, the changes in the gut microbiome were less pronounced, but still showed a marked increase in potentially pathogenic *Vibrio* spp. when temperature was elevated for three weeks. This information is not only relevant in an ecological context of predatory grouper living on a coral reef, but also in an aquaculture context, where heat waves will also have a future impact on food security.

Life history traits of the migratory river sculpin in small streams on Sado Island, northern Japan

Iida, Midori[1]; Shirai, Kotaro[2]; Natsukawa, Kosuke[1]

[1]*Marine Biological Station, Sado Island Center for Ecological Sustainability, Niigata University*

[2]*Atmosphere and Ocean Research Institute, The University of Tokyo*

Small insular ecosystems often have unique characteristics, due to their limited geographic extents, compared to continents and large islands. The river sculpin, *Cottus hangiongensis*, which inhabits east Eurasia and northern Japan, exhibits riverine migration in large rivers in northern mainland Japan. Its life history traits may differ in small island streams in response to environmental variation. However, the river sculpin's ecology is totally unknown in small island streams. Therefore, several life history traits of *C. hangiongensis* were examined in light of island effects.

Seasonal riverine distribution patterns and microhabitats were surveyed in 2020–2021 in streams on Sado Island, northern Japan, where we observed gathering in lower reaches in winter and rapid flow utilisation. Egg clutches in streams were surveyed to estimate egg diameter and larval survival in different salinities. Egg diameter (2.0–2.7 mm) and hatching size (7.6–9.7 mm, total length) varied more widely than values previously reported from rivers in mainland Japan. Salinity tolerance of newly hatched larvae was examined. The survival rate was higher in freshwater compared with brackish water. Diadromous migratory patterns were estimated by otolith Sr:Ca ratio (n=20). Almost all individuals apparently moved rapidly to the sea just after hatching, despite higher survival of larvae in freshwater. These characteristics of migratory river sculpins, such as larger egg size, higher survival in freshwater may be an adaptation to short, steep streams on small islands.

Dispersal and evolution in Chatham Island freshwater fish

Ingram, Travis[1]

[1]*Department of Zoology, University of Otago*

Rēkohu/Wharekauri/Chatham Island presents unique opportunities for studying Pacific fish evolution given the presence of numerous lakes on a small isolated island and the lack of introduced fish species. Common smelt (*Retropinna retropinna*) have become landlocked in low-elevation lakes. Morphometric analyses confirm that the landlocked smelt have diverged from diadromous relatives. Analysis of genetic markers from across the smelt genome suggest at least three divergent landlocked groups on Rēkohu, and demographic modeling suggests that these have become landlocked independently. Rēkohu is also home to an endemic mudfish (*Neochanna rekohua*) with an unusual lacustrine habitat. Several mudfish population centres around the island suggest a previously wider distribution. Taken together, these species' distributions suggest important roles for the large central lagoon Te Whanga, as well as Pleistocene sea level fluctuations, in shaping present freshwater fish diversity on Rēkohu. Ongoing work is considering the potential implications of future sea level rise on genetic diversity and ecological communities.

The usefulness of eDNA metabarcoding for monitoring fish fauna in a large lake: the South Basin of Lake Biwa, Japan

Ito Gen[1]; Kuramoto Mao[2]; Kondo Akihiro[2]; Nakamura Masafumi[2]; Ishizaki Daisuke[3]; Taguchi Takashi[3]; Kawase Seigo[4]; Asami Maki[1]; Goto Yuko[1]; Yamanaka Hiroki[1]

[1]*Center for Biodiversity Science, Ryukoku University, Japan*

[2]*Hiyoshi Corporation*

[3]*Shiga Prefectural Fisheries Experiment Station*

[4]*Lake Biwa Museum*

Monitoring fish fauna in large, diverse lakes poses challenges for accuracy. Lake Biwa, Japan's largest lake, hosts a rich freshwater fish population. However, the South Basin has seen an increase in non-native fish since 1980, resulting in only six native species recorded in 2008. While non-native fish numbers are believed to have decreased recently, the status of native species distribution remains unknown. To address this, we used environmental DNA (eDNA) metabarcoding to assess the South Basin's fish fauna. We collected water samples from 30 sites across the basin in 2021 and conducted capture surveys in the same locations. Our eDNA analysis identified 39 species, including 30 native ones, with 16 native species found at over half the sites. The capture survey revealed 13 native species, 12 of which matched the eDNA results at over half the sites. Comparing these findings to the 2008 survey indicated a significant recovery in native species numbers. eDNA analysis proves effective in detecting low-abundance fish species in vast water bodies. Overall, our study provides valuable insights into the current fish fauna of Lake Biwa's South Basin. It demonstrates the potential of eDNA analysis for comprehensive monitoring of aquatic biodiversity in large-scale ecosystems.

Utilizing natural analogs of future oceans to study the adaptive potential of fish communities to climate change

Izumiyama, Michael[1,4]; Agostini Sylvain[2,4]; Jolly Jeffrey[1,4]; Kawaii Erina[1,4]; Moore Billy[1,4]; Rodolfo-Metalpa, Riccardo[3,4] and Ravasi**,** Timothy[1,4]

[1] *Marine Climate Change Unit, Okinawa Institute of Science and Technology Graduate University, 1919-1 Tancha, Onna-son, Okinawa 904-0495, Japan*

[2] *Shimoda Marine Research Center, University of Tsukuba, 5-10-1 Shimoda, Shizuoka, 415-0025, Japan*

[3] *ENTROPIE, IRD, Université de La Réunion, CNRS, IFREMER, 98848, Nouméa, New Caledonia*

[4] *ICONA International CO2 Natural Analogue Network, Shimoda, Japan*

Understanding if and how fishes will adapt to climate change is essential in understanding the future of fish populations. Unique sites such as CO2 seeps provide a natural analog to predicted future ocean conditions under climate change and offer the opportunity to understand how fishes may be able to adapt to these extreme environments. Our study utilized two natural analogs, a CO2 seep in Shikine Island, Japan, and a semi-enclosed lagoon in Bourake, New Caledonia, and examined the brain and gill transcriptome of fishes across different families. We found several differentially expressed genes associated with acid-base regulation and O2 transportation, related to previous studies in natural analogs, suggesting some similarities in the adaptive potential of fishes to ocean acidification (OA). However, there may also be adverse effects of OA, which warrant further investigation and highlights the importance of natural analogs of future oceans to study how fishes will respond to climate change.

4.5A Special Session 5: Larval fishes - solving phylogenetic, life-cycle and ecological questions, 260-051, November 23, 2023, 10:30 AM - 12:30 PM

Ichthyoplankton diversity and distribution in the Straits of Singapore

Jaafar, Zeehan[1]; Koh, Clement[1]; Nelson, Sarah[1]

[1]Department of Biological Sciences, National University of Singapore

In many areas within the Indo-Pacific, coastal habitats experience cumulative impacts from anthropogenic activities and rapid development. Our understanding of the responses to fish communities at such nearshore habitats are overwhelmingly dependent on data from adult fishes, primarily because of limited available data on larval fish communities. Yet, the acute sensitivity of larval stages to biotic and abiotic environmental parameters are often absent from this discourse. We plug this knowledge gap through the study of larval fish community structure along the Singapore Straits, one of the busiest shipping channels globally. Our 13-month study, from August 2020 to August 2021, aimed to characterise the spatial and temporal distributions of larval fishes. Samples were collected using a double-barrelled Bongo net fortnightly, off Pulau Subar Laut and off Pulau Hantu, during new and full moon phases. Data of physico-chemical parameters—surface water temperature, dissolved oxygen, conductivity, and pH—were also recorded. We recovered a total of 6117 specimens comprising 78 fish families. Five families—Leiognathidae, Gobiidae, Bregmacerotidae, Engraulidae, and Pinguipedidae—were the most abundant, making up more than 60% of all specimens. These families show consistent dominance throughout the study except for Bregmacerotidae, whose abundance peaked from February 2021 to July 2021. We found lunar phases to result in significant differences in diversity of larval fishes; while lunar phases, site, and season resulted in significant differences in abundance. Our results demonstrate the importance of incorporating the ecologies of both larval and adult fishes towards informing the conservation and management strategies of this resource.

2.5A Themed Session E: Biology and Conservation of Sharks and Top-predators, 260-051, November 21, 2023, 10:30 AM - 12:30 PM

From undervalued or ignored to luxury products – shark and ray skins in an expanding global market

Jabado, Rima W[1,2,3]; Simeon, Benaya[1,4]; Fahrni Mansur, Elisabeth[1,5]; Tyabji, Zoya[6]; Ali, Ahmed[1]; Chen, Jiajie[1,7, 8]; Fahmi[1,9]; García-Rodríguez, Emiliano[1]; Krajangdara, Tassapon[1,10]; Shea, Stanley[1,11]; Yamaguchi, Atsuko[1,12]; Zhang, Jie[1,13]

[1]*International Union for Conservation of Nature Species Survival Commission Shark Specialist Group, Dubai, United Arab Emirates*

[2] *Elasmo Project, P.O. Box 29588, Dubai, United Arab Emirates*
[3] *College of Science and Engineering, James Cook University, Townsville, Qld 4811, Australia*

[4]*Charles Darwin University, Casuarina - Northern Territory, Australia.*

[5] *Wildlife Conservation Society, Bangladesh Program, Dhaka, Bangladesh*

[6] *Department of Biology, Dalhousie University, Halifax, Nova Scotia, Canada*

[7]*Engineering Research Center of Environmental DNA and Ecological Water Health Assessment, Shanghai Ocean University, 201306, Shanghai, China*

[8]*East China Sea Fisheries Research Institute, Fisheries Science of Chinese Academy, 200090, Shanghai, China*

[9] *Research Center for Oceanography, National Research and Innovation Agency (BRIN), Jalan Pasir Raya, No. 1 Ancol Timur Jakarta, Indonesia, 14430*

[10] *Fishery Science, Senior Professional Level, Phuket Marine Fisheries Research and Development Center, Vichit, Muang, Phuket, Thailand, 83000*

[11]*BLOOM Association Hong Kong and ADM Capital Foundation*

[12] *Institute of Integrated Science and Technology, Nagasaki University, Nagasaki, Japan*

[13] *Institute of Zoology, Chinese Academy of Sciences, Beijing, China*

Globally, sharks and rays are valuable fisheries resources. Demand for fins, meat, and other derivative products, results in species being increasingly retained and widely used. Shark and ray skins, uniquely textured and durable enough for polishing wood and grating spices, have historically been used for a variety of purposes. Tanned skins (‘shagreen’) are favored in fashion for high-end accessories and decorative furniture, in traditional weaponry and armor, and for musical instruments. Thick skins of certain species are considered a delicacy and consumed cooked in curries, soups, or fried as crackers. Despite this diverse usage, it appears that the utilization of shark and ray skins has remained quite localized and trade relatively small compared to other derivatives until the late 1990s. This changed over the past two decades with the implementation of policy frameworks advocating the full utilization of animals, leading to increased retention and targeting, particularly of rays. While in some countries most ray species were regarded as undesirable catch (i.e., discarded or used as trash fish), nowadays their skins, primarily sourced from Asia, are traded regionally and with Europe for use in luxury products. For example, skins from the intricately patterned *Himantura* spp. whipray complex, previously considered of low value and often discarded, are today retained to supply a growing global demand. Considering the alarming population declines of most shark and ray species, and the limited and often undocumented information on the utilization and trade of their skins, this trade needs to be immediately characterized and addressed.

The effects of habitat connectivity and complexity on the distribution of inshore reef fish communities

Jarrett, Alexander[1], Gilby, Ben L.[1], Henderson, Christopher J.[1], Olds, Andrew D.[1]

1. *School of Science, Engineering and Technology, University of the Sunshine Coast, Qld, Australia,*

Fish species occupy different coastal ecosystems throughout their daily movements and life cycle. These movements are to facilitate their need for dispersal, feeding, spawning and refuge. While the influence of inshore coral reef systems on fish species has been vastly explored, the influence of inshore rocky reef systems, particularly those in close proximity to surf zones, is relatively understudied. Furthermore, these ecosystems are a crucial link for species moving throughout coastal ecosystems and for those moving southward due to a changing climate, but these ecosystems currently face a range of threats including recreational fishing. We sampled 13 locations with baited and unbaited underwater camera systems along a 35km stretch of coastline in eastern Australia to determine if the variation in size, connectivity, and composition of rocky reef habitats shape fish community structure and the abundance of functionally important species. We found well connected, complex rocky reef habitats had a high species richness and fish abundance. Sites closest to human disturbance typically contained communities that had a lower overall diversity and abundance of fish and functionally important species. Functional important herbivores were more abundant on reefs that contained a greater coverage of algae and were more complex. Our results highlight the importance of well-connected and complex rocky reef systems. Management must therefore aim to incorporate connectivity and the context of habitats when identifying inshore rocky reef systems that require protection from fishing and that may be hotspots for species moving southwards in the future.

Large-scale larval study reveals fine morphological differences: the case of Sciaenidae

Si-Yeong, Jeong[1]; Hwan-Sung, Ji[2]; Jin-Koo, Kim[1]

[1]*Department of Marine Biology, Pukyong National University, Busan 48513, Korea*

[2]*Fisheries Resources Management Division, National Institute of Fisheries Science, Busan, 46083, Korea*

Sciaenidae larvae were collected from the Korean exclusive economic zone between July 2018 and September 2021 using a bongo net. As a result of molecular analysis of 12 morphotypes, 61 individuals were successfully identified, and most were identified as sciaenid species, except one morphotype being identified as *Jaydia lineatus* in the family Apogonidae. Six species of sciaenid larvae and juveniles were identified in this study, and were collected during the following months: *Pennahia argentata* (July–September), *Johnius grypotus* (August), *Miichthys miiuy* (September–October), *Collichthys niveatus* (July), *Larimichthys crocea* (October–November) and *Johnius belangerii* (July–August). A key to the six sciaenid species during the early life stage were revealed as follows: dots present at the pectoral fin base, dots present at the base of the anal fin, the number and size and the presence of dots on the back of the operculum. *J. lineatus* was distinguished from the six species of sciaenid larvae by having a narrower gap between the anus and anal fin base, and a spine on the occipital part. This study will facilitate an understanding of the early life history of commercially important Sciaenidae.

Shrinking fishes on the world's hottest coral reefs

Johansen, Jacob L[1], Mitchell, Matthew D[2], Vaughan, Grace O[2,3], Ripley Daniel M[2,3], Shiels, Holly A[3], Burt John A[4]

[1]*Hawaii Institute of Marine Biology, University of Hawaii Manoa, Oahu, HI, USA*

[2]*Marine Biology Lab, Science Division, New York University Abu Dhabi, Abu Dhabi, UAE*

[3]*University of Manchester, Manchester, UK*

[4]*Arabian Center for Climate and Environmental Sciences, New York University Abu Dhabi, Abu Dhabi, UAE*

The impact of ocean warming on fish and fisheries is vigorously debated, with major potential consequences for ecosystems and industries. Leading theories project limited adaptive capacity of tropical fishes and 14-39% size reductions by 2050 due to a mass-scaling limitation of oxygen supply in larger individuals. Using the world's warmest coral reefs in the Arabian Gulf (AG) as a natural laboratory for ocean warming, where species have survived +3°C elevations in temperature for over 6,000 years and are estimated to be 14-40% smaller at max size compared to cooler locations, we found two adaptive pathways across 10 metabolic and swimming performance metrics that appear to have facilitated survival at elevated temperatures. Comparing AG populations of *Lutjanus ehrenbergii* and *Scolopsis ghanam* to populations from typical present-day coral reef temperatures in the Gulf of Oman (GO, summer max 32.0°C) across 27.0, 31.5°C and 35.5°C, our data reveals that despite limited adaptive capacity in reef fishes, the species surviving in AG have found pathways to maintain oxygen supply and aerobic performance to 35.5°C. However, our findings challenge the leading theoretical explanations for warming-induced size reductions in fishes as we found no consistent negative consequences of size. Instead, our data support a modified unifying theory encompassing aspects of existing oxygen limitation theories as well as resource limitation and ecological metabolic theory, to explain species-specific responses to ocean warming and why smaller individuals are evolutionarily favored at elevated temperatures.

Suspended sediments and the physiology of a coral reef fish, *Amphiprion ocellaris*

Johansson, Johanna[1]; McMahon, Shannon[1,2]; Ravasi, Timothy[1,2]

[1] *Marine Climate Change Unit, Okinawa Institute of Science and Technology, Onna-son, Okinawa, Japan*

[2] *ARC Centre of Excellence for Coral Reef Studies, James Cook University, Townsville, QLD, Australia*

Anthropogenic pressure on coral reefs is increasing worldwide. While many aspects of this pressure, such as marine heatwaves and ocean acidification, are being rigorously investigated, the effect of terrestrial run-off and increased suspended sediments on coral reef fishes is relatively understudied. Additionally, the intensity and duration of suspended sediment events is expected to increase as a consequence of coastal development and the increased frequency of storms. In areas of the world where fringing coral reefs are dominant these events may have a significant impact on the organisms that inhabit these environments. This is the case in Okinawan coral reefs. With this in mind, we investigated the acute effects of increased suspended sediments on a commercially important species, *Amphiprion ocellaris*. We exposed individuals to acute suspended sediment treatments, to simulate sudden run-off and increased suspended sediment events. Using intermittent-flow respirometry we measured their standard and maximum metabolic rate, excessive post-exercise oxygen consumption, aerobic scope, and recovery time. These measurements were taken before and after suspended sediment treatments to fully gauge the physiological impact of these sudden events. Understanding how coral reefs and their resident organisms respond to increased sedimentation events is important for the future management of these biologically and economically important ecosystems.

The molecular mechanisms underlying environmental resilience

Johnson, Sheri

University of Otago

In a time of rapid environmental change, understanding the potential for adaptive resilience is critically needed. We have used zebrafish (*Danio rerio*) as a model to investigate how paternal hypoxia experience impacts subsequent progeny. We detected 91 differentially expressed genes, including two hemoglobin genes that are significantly upregulated by more than 4-fold in the offspring of males that were exposed to hypoxia for two weeks. Moreover, the offspring which maintained equilibrium the longest showed the greatest upregulation in hemoglobin expression. We conducted whole genome bisulfite sequencing (WGBS) on the sperm of parental males to assess whether changes in progeny phenotype and gene expression are underpinned by changes in DNA methylation. While we observed coupling of methylation levels in the parental sperm and gene expression in progeny overall, we did not detect differential methylation at any of the differentially expressed genes, suggesting that another epigenetic mechanism is responsible for the observed changes in gene expression. Overall, our findings suggest that a ‘memory’ of past hypoxia exposure is maintained and that this environmentally induced information is transferred to subsequent generations, pre-acclimating progeny to cope with hypoxic conditions. More recently, we have been using a New Zealand fish model to elucidate the molecular mechanisms underlying adaptation and resilience to thermal stress. Triplefin species from intertidal habitats have stable and efficient brain and heart mitochondrial function at high temperatures and we are using genomics to reveal the underlying molecular mechanisms that facilitate thermal resilience – I will share some of our preliminary findings.

Safeguarding the threatened: the status of shallow reef species from temperate to tropical Australia

Johnson, Olivia[1]; Edgar, Graham[1]; Heather, Freddie [1]; Stuart-Smith, Jemina[1]; Stuart-Smith, Rick[1]

[1]*Institute for Marine and Antarctic Studies, University of Tasmania, Hobart, Tasmania 7001, Australia*

The identification of threatened species in the marine environment is more challenging than in the terrestrial environment. In particular, collection of population distribution and trend data is logistically difficult for marine species. Many marine species are rare or highly cryptic, hence difficult to find, let alone study, and few species beyond those that are commercially exploited or highly charismatic have been studied in any detail. Given the large range of anthropogenic effects known to threaten marine organisms, including climate change, fishing, habitat degradation, and pollution, a critical need remains to identify the most vulnerable species before they are lost.

In this study, we systematically identify a large range of Australian shallow (<30m) reef species (including fish, invertebrate, algae, and coral) that classify as threatened based on international (IUCN) and federal criteria. Our analysis focuses on recent population trends and geographic distribution as revealed in long-term reef monitoring datasets (Reef Life Survey and the Australian Temperate Reef Collaboration). Shared traits of threatened reef species have been identified, and species most in need of urgent management attention brought to light.

Isolation management to protect threatened native galaxiid fish species: lessons from Aotearoa New Zealand

Jolly, Martha E.[1,3]; Warburton, Helen J.[1]; Bowie, Sjaan[2]; Challies, Edward[1]; Jellyman, Phillip G.[3]; McIntosh, Angus R.[1]
[1]*Te Kura Pūtaiao Koiora, Te Whare Wānanga o Waitaha | School of Biological Sciences, University of Canterbury, Private Bag 4800, Christchurch, New Zealand*
[2]*Te Papa Atawhai | Department of Conservation, 161 Cashel Street, Christchurch 8011*
[3]*Taihoro Nukurangi | National Institute of Water and Atmospheric Research Ltd, P.O. Box 8602, Christchurch, New Zealand*

The use of barriers in freshwater systems to mitigate invasions, known as isolation management, is increasingly implemented as a protection strategy for native fish species. Barriers are crucial for securing vulnerable populations, but much remains unknown about deliberate fragmentation such as risks to isolated populations through extreme events, formation of sink populations, loss or changes in key microhabitat values, and disruption to native species dispersal. In Aotearoa-New Zealand, native non-migratory galaxiid (NMG) fishes are characterised by a disproportionate number of threatened species. Numerous studies have identified introduced salmonids (trout) as a key driver of NMG declines. A qualitative review of barriers protecting NMG in within the South Island of Aotearoa, illustrated varying outcomes and current knowledge gaps with case studies. Barrier types ranged from natural bedrock waterfalls, shallow high velocity chutes and drying reaches to deliberate exclusion barriers. NMG species protected by fragmentation had threat statuses encompassing “least concern” to “critically endangered”. Despite the critical role of the barrier, we also conclude these isolated populations are at risk of stochastic extirpation, invasion, or re-invasion. Overall, the use of exclusion barriers requires managers to assess extinction risk of individual populations by isolation or invasion, often based on incomplete data. Despite well documented benefits to NMG populations, key knowledge gaps such as long-term viability of isolated populations and understanding of key physical characteristics required of both natural and engineered instream structures to prevent incursion by salmonids under differing flow regimes still exist.

5.3B Themed Session B: Ecology of Indo-Pacific Fishes, 260-115, November 24, 2023, 1:30 PM - 3:00 PM

The dark side of the reef: the missing contribution of nocturnal species and biomass to shallow reef communities

Jones, Tyson[1]; Ling, Scott[1]; Denis-Roy, Lara[1]; Johnson, Olivia[1]; Mellin, Camille[2]; Rose, Matthew[1]; Trebilco, Rowan[3]; Edgar, Graham[1]

[1]*Institute for Marine and Antarctic Studies, University of Tasmania, Hobart, Tasmania 7001*

[2]*The Environment Institute and School of Biological Sciences, University of Adelaide*

[3]*CSIRO, Oceans and Atmosphere, Hobart, 7004, Australia*

Sustainable management of reef ecosystems is contingent on systematic understanding and monitoring of species and whole-community dynamics. However, species inventories and our understanding of ecological functioning comes almost exclusively from daytime sampling. Subsequently, possible contributions of rarely sampled nocturnal fauna to reef ecosystem dynamics is scarcely acknowledged and accounted for. Here, we conduct an extensive continental assessment of the contribution of nocturnal reef fauna to the structure and functioning of shallow reef ecosystems. Using paired day and night visual census techniques, nocturnal periods were found to support a rich and unique community and biomass of functional groups not detected during normal daytime sampling. Species exclusive to nocturnal communities were dominated by mobile invertebrates, with more than 67% of tropical and 40% of temperate invertebrates found to only be recorded at night, compared with 18% of tropical fishes and 22% of temperate fishes. Similar patterns in functional composition and community-level diel shifts were observed across both tropical and temperate realms, with reefs exhibiting fish dominance during the day and invertebrate dominance at night. Nocturnal periods revealed substantial increases in invertebrate biomass, whilst fish biomass decreased. Despite being composed of reduced biomass, nocturnal periods yielded unique contributions to fish biomass, attributed to species occurring exclusively or in greater abundances at night, predominantly due to emergence of planktivores. Collectively, we show that accounting for the role of under-sampled nocturnal communities is fundamental for wholistic understanding of reef ecosystem functioning, essential for effective management of these ecosystems which is missed by conventional daytime surveys.

Deriving energy landscapes from stereo-video: Investigating the 3D trajectories of butterflyfishes on a coral reef with a turbidity gradient

Jupp, Emily[1]; Lilkendey, Julian[1]; Zhang, Jingjing[1,2]; Sabetian, Armagan[1]

[1]*Auckland University of Technology (AUT)*

[2] *The New Zealand Institute for Plant and Food Research Limited*

Energy landscapes, which relate to the costs associated with animal movement, provide a valuable framework for studying how ecosystems function amidst global changes. Coral reefs are undergoing modifications in these landscapes due to various degradation processes, including increased turbidity resulting from anthropogenic activities like logging. Elevated levels of turbidity negatively affect coral communities and may influence the foraging behaviours of butterflyfishes. These species, vital to ecosystem functioning and highly reliant on corals, are disproportionately affected by these environmental changes.

We used stereo-video to track the 3D movements and record the foraging behaviour of three butterflyfish species (*Chaetodon vagabundus*, *Chaetodon lunulatus*, and *Chaetodon baronessa*) with varying degrees of dependence on corals in their diet. This was done along a turbidity continuum on the fringing reef of Kolombangara Island, Solomon Islands. By calculating the Overall Dynamic Body Acceleration (ODBA), we inferred the energy expenditure associated with foraging. Our aim was to assess the energetic implications of their adaptive movements in response to changing environmental conditions, which indicate modifications in energy landscapes.

Inferring energy landscapes from the movements of functional key species provides valuable insights for effective ecosystem management. Our research contributes to the understanding of how well coral reefs are functioning by examining the energetics underlying foraging behaviour of corallivorous butterflyfishes. Consequently, our findings are crucial for informing indigenous and local communities that depend on coral reefs for their livelihoods and well-being. Furthermore, they support the establishment of sustainable practices and the mitigation of environmental pressures to conserve these vital ecosystems.

Fish in natural CO_2 seeps imply core transcriptional regulations for ocean acidification acclimation

Jingliang Kang[1]; Ivan Nagelkerken[2], Sean Connell[2], Timothy Ravasi[3,4], Celia Schunter[1,5]

[1]Swire Institute of Marine Science, School of Biological Science, The University of Hong Kong, Pokfulam, Hong Kong SAR

[2]Southern Seas Ecology Laboratories, School of Biological Sciences and The Environment Institute, DX 650 418, The University of Adelaide, Adelaide, SA 5005,

Australia

[3]Marine Climate Change Unit, Okinawa Institute of Science and Technology Graduate University, 1919–1 Tancha, Onna-son, Okinawa 904–0495, Japan

[4]Australian Research Council Centre of Excellence for Coral Reef Studies, James Cook University, Townsville, Queensland, 4811, Australia

[5]State Key Laboratory of Marine Pollution and Department of Chemistry, City University of Hong Kong, Hong Kong, SAR, China

Ocean acidification can affect various physiological and behavioural traits in fishes. However, some fish species seem to benefit, exhibiting increased population densities at natural CO_2 seeps. To investigate the molecular mechanisms underlying this advantage with ocean acidification, we sequenced the brain transcriptomes of four fish species from temperate natural CO_2 seeps and nearby control sites in White Island, New Zealand. All species exhibit significant expression changes in genes involved in circadian rhythm and vision signal perception under elevated pCO_2, and three species displayed expression changes in intracellular pH regulation as a potentially adaptive response to elevated pCO_2. Further adaptive changes, such as transcription factor AP-1 (*JUN*) and heat shock proteins may boost their transcriptional plasticity to elevated pCO_2 and mitigate OA stress. In addition, the two species with double the density under acidified conditions displayed expression changes and unique amino acid substitutions in calcium channels and glutamate receptors, which may have cascading effects on neural signaling genes and allow these species to thrive in acidified conditions. Our study reveals crucial molecular responses across fish species with potential acclimation for fish to cope with ocean acidification.

Can acoustic telemetry be used inside mangrove habitats?

Kanno, Shiori[1]; Heupel, Michelle[2,3]; Simpfendorfer, Colin[1]

[1]*Centre for Sustainable Tropical Fisheries and Aquaculture & College of Science and Engineering, James Cook University, Townsville, QLD 4811, Australia*

[2] *Australian Institute of Marine Science, Townsville, QLD 4810, Australia*

[3] *Integrated Marine Observing System (IMOS), University of Tasmania, Hobart, TAS 7004, Australia*

Acoustic telemetry has been used to monitor the movement of sharks and rays in a broad range of aquatic environments. Despite their importance, mangrove habitats are understudied for spatial ecology of elasmobranchs, with acoustic telemetry rarely used inside mangrove habitats. One reasons may be a general assumption that acoustic signal would not be able to get detected by the receivers in such shallow water, structurally complex, environments. This study tested whether acoustic receivers can be used in mangrove habitats to track the movement of sharks and rays. 38 receivers were deployed in a mangrove system in Pioneer Bay, Orpheus Island, Great Barrier Reef, including inside mangroves, mangrove edges and adjacent reef flat areas. The detection range and receiver performance metrics, such as code detection efficiency, rejection coefficient and noise quotient were examined and tested among habitats.

Results highlighted that the signal from transmitters were successfully detected inside mangrove habitats as well as on the adjacent reef flat. The detection range to get at least 50% of detection was up to 20 m inside mangroves and up to 120 m outside mangroves. The performance metrics of acoustic receiver in mangrove habitat was characterised by low background noise, low rejection rates and reasonably high code detection efficiency. Furthermore, this study tested application of this method on juvenile sharks and rays and demonstrated that it can be used to successfully track animals inside mangrove habitat. This novel method could reveal further information on how sharks and rays are using mangrove habitats.

Revealing the pattern of mangrove use by juvenile sharks and stingrays

Kanno, Shiori[1]; Heupel, Michelle[2,3]; Simpfendorfer, Colin[1]

[1]*Centre for Sustainable Tropical Fisheries and Aquaculture & College of Science and Engineering, James Cook University, Townsville, QLD 4811, Australia*

[2] *Australian Institute of Marine Science, Townsville, QLD 4810, Australia*

[3] *Integrated Marine Observing System (IMOS), University of Tasmania, Hobart, TAS 7004, Australia*

Mangroves are highly productive habitats, supporting a wide variety of organisms by providing shelter, nursery and food resources. However, sampling challenges mean that the importance of mangrove habitats to sharks and rays remains poorly understood. This study investigated movement patterns of juvenile sharks and rays in a mangrove-fringed intertidal system using passive acoustic telemetry over a one-year period. An array of acoustic receivers was designed to track animal's movement inside mangrove stands. Range testing confirmed the method can be used to successfully track animals in this structurally complex habitat. Juvenile blacktip reef sharks *Carcharhinus melanopterus* and mangrove whiprays *Urogymnus granulatus* were equipped with acoustic transmitters and released in Pioneer Bay, Orpheus Island, Great Barrier Reef, between October 2020 and December 2021.

The results demonstrated that both species penetrate deep into complex mangrove habitats than previously thought (80 m from the leading mangrove edge). Sharks often roamed along the mangrove edge and swim deep into the mangrove zones during high tide. Juvenile stingrays remained inside mangrove habitats more regularly than sharks and only left the mangroves when driven out by the receding tide. Aggregating behaviour of juvenile stingrays was examined, revealing the time and tidal heights when aggregations were most common. The present data suggested that juvenile sharks and rays use the structurally complex and tidally influenced mangrove habitats to avoid predation.

Introgression landscape from a ghost extinct lineage in the genome of the coastal intertidal goby in Japan

Shuya, Kato[1]; Seiji Arakaki[2]; Atsushi J. Nagano[3,4]; Kiyoshi Kikuchi[1]; Shotaro, Hirase[1]

[1]*Fisheries Laboratory, Graduate School of Agricultural and Life Sciences, The University of Tokyo*

[2]*Amakusa Marine Biological Laboratory, Kyushu University*

[3]*Department of Life Sciences, Faculty of Agriculture, Ryukoku University*

[4]*Institute for Advanced Biosciences, Keio University*

Most extinct lineages are inaccessible without fossils, but some extinct lineages have left legacies in the genomes of extant lineages through ancient introgressive hybridization. Given that hybridization is an important source of diversity and evolution, it is interesting to characterize the genomic landscape of introgression from extinct lineages. However, it is challenging to locate the traces of unsampled “ghost” extinct lineages without ancient genomes.

In our previous phylogeographic study of *Chaenogobius annularis*, an intertidal goby in Japan, we discovered a lineage that is suspected to have inherited a small portion of its genome from an extinct lineage. Therefore, we conducted population genomic analyses to examine the introgression from the ghost extinct lineage and characterize its introgression landscape.

Combining phylogenetic analysis and demographic modelling, we revealed that the target lineage arose from hybridization with a ghost extinct lineage. We then characterized the introgression landscape by estimating the local rate of introgression using sliding-window approach. Consistent with introgression in extant organisms, there is less survival of extinct lineage in low recombining and functionally important regions, suggesting a role of linked selection that eliminated the extinct lineage in shaping the hybrid genome. Moreover, we found enriched repetitive elements in regions where ghost introgression occurred, which was also observed in the reanalysis of introgression in extant organisms. Our results emphasize that the regions inherited from minor parents are unexpectedly common, even in ghost introgression. We also suggest that coastal fishes of the North-West Pacific provide good material for the study of hybrid evolution.

Nesting and reproductive behaviour of the sand-dwelling goby, *Hazeus ammophilus* (Gobiidae), which constructs a radially aligned ditches surrounded nest

Kawase, Hiroshi

Coastal Branch of Natural History Museum and Institute, Chiba

This study aimed to clarify the nesting and reproductive behavior of the sand-dwelling goby *Hazeus ammophilus*, having a unique spawning bed surrounded by radial ditches. The underwater SCUBA observations revealed that this species is nested year-round on the sandy bottoms at 7–8 m depths at the eastern coast of Okinawa Island, Japan. The males measured 45 mm in total length and held a nest. The bivalves' shells and deciduous leaves of terrestrial plants served as the spawning bed with an average width of 50 mm × 24 mm. The males dug ditches using their fins at varying angles outward from the spawning bed edge, forming radial ditches surrounding nest. The blowing sand sometimes completely buried the nest. The radial ditches' mean width was 187 mm × 146 mm including the nest. The males courted females, lured them to the nest, and spawned in pairs. Subsequently, the females departed, while the males stayed and cared for the eggs near the nest. The spindle-shaped, 0.74 mm × 0.49 mm eggs adhered to the beds with threads. Herein, the relationship between the total length of the male, nest size, number of eggs laid, and relevance of the radially formed ditches surrounding nest is discussed.

The influence of distribution mapping sources on Sustainability Assessment for the Effects of Fishing (SAFE) vulnerability scores for deepwater chondrichthyan species in the Southern Indian Ocean

Keller, Krystle[1]; Emery, Timothy[1]; Timmis, Trent[1]; Fuller, Michael[2]; Hartog, Jason[2]

[1]Australian Bureau of Agricultural and Resource Economics and Sciences, Department of Agriculture, Fisheries and Forestry, Canberra, Australian Capital Territory 2601, Australia

[2]CSIRO Oceans and Atmosphere, Hobart, Tasmania 7000, Australia

Threats to populations of deepwater chondrichthyans (sharks, rays, and chimaeras) from fishing are poorly understood, especially in areas outside national jurisdiction. The lack of catch, effort, and biological information can make the assessment of their vulnerability to fishing particularly difficult. Ecological Risk Assessment (ERA) tools, such as the Sustainability Assessment for Fishing Effects (SAFE) are useful for identifying species that may be vulnerable to fishing-induced mortality when data is limited. Vulnerability in the SAFE is a function of a species' biological attributes (productivity and life-history characteristics) and susceptibility attributes (availability, encounterability, selectivity and post-capture mortality).

This study assessed how the availability attribute (i.e. horizontal overlap between a species distribution and fishing effort) within the SAFE methodology may be sensitive to the underlying distribution mapping sources used through a case study of 94 deepwater chondrichthyan species in the Southern Indian Ocean Fisheries Agreement (SIOFA) area. Vulnerability scores were compared across demersal trawl, midwater trawl, and demersal longline gears using three different species distribution mapping sources: AquaMaps, FAO GeoNetwork and IUCN Redlist. The choice of distribution mapping source was found to have a significant effect on the vulnerability score of chondrichthyan species in the SAFE across all three fisheries, with results using the IUCN Redlist having a greater number of high or extreme risk species than results using the other two mapping sources. These findings highlight the importance of considering the underlying reliability of predicted distributions from these mapping sources when conducting SAFE assessments for fisheries management of deepwater chondrichthyans.

4.2A Special Session 2: Facing environmental changes: what are the genetic and epigenetic mechanisms providing resilience in fishes?, 260-073, November 23, 2023, 10:30 AM - 12:30 PM

Heavy metal and antimicrobial resistance in benthic shark microbiomes

Kerr, Emma[1]; Dinsdale, Elizabeth[1]; Doane, Michael[1]; Edwards, Robert[1]; Hesse, Ryan[1]; Huveneers, Charlie[1]; Martin, Belinda[1]; Meyer, Lauren[1]; Roberts, Chloe[1]

[1]*Flinders University, Adelaide, South Australia*

Microbial genes for heavy metal and antibiotic resistance are selected for simultaneously in environments or hosts with high concentrations of metals. Antibiotic resistance has been linked to the overuse and misuse of antibiotics in both human and animal populations. Antibiotic-resistant bacteria spreads between different organisms and environments, including aquatic ecosystems, through various pathways such as wastewater discharge and aquaculture. Exposure to metals alters the gut microbiota of fish, which has negative effects on their health and immune function. Antibiotics alters the microbial communities of aquatic organisms, leading to an increase in antibiotic-resistant bacteria impacting host microbiomes. Shark microbiomes typically have a higher relative abundance of heavy metal resistance genes than nearby algae or water microbes. The co-selection of heavy metal and antibiotic resistance genes in shark microbiomes could have a direct effect on host health and vulnerability to pathogens. To address how anthropogenic activity impacts shark microbiomes, we collected the skin microbiome of Port Jackson sharks, *Heterodontus portusjacksoni*, at several locations in South Australia with varying human activity. We utilized shotgun metagenomics describe the AMR profile of *H. portjacksoni* microbiomes sampled at different locations. We found a high relative abundance of *Pseudalteromonas* bacteria which are known carriers of antibiotic resistance genes in the marine environment. A metagenome assembled genome (MAG) of *Photobacterium damselae*, a potential shark pathogen, contained four antibiotic resistance genes. We highlight the importance of understanding shark microbiomes and their impact on global environmental health.

Genome-wide SNP discovery and phylogeography of Pacific sand lance (*Ammodytes heian* and *Ammodytes japonicus*) using MIG-seq: Implications for evolution

Kim, Jin-Koo[1]; Lee, Yu-Jin[1]

[1]*Department of Marine Biology, Pukyong National University, Busan 48513, Republic of Korea*

Although Pacific sand lance populations in the Northwest Pacific have been classified as *Ammodytes japonicus* and *Ammodytes heian* by mtDNA, the taxonomy of the East Sea populations is uncertain due to the hybridization by ms. We performed MIG-seq to investigate the genome-wide population structure of the Pacific sand lance in the Northwest Pacific. In total, 48 Pacific sand lances from five locations in the Yellow Sea (Baengnyeongdo, BA), Korea Strait (Tongyeong, TY), East Sea (Gijang, GI and Jumunjin, JU), and Okhotsk Sea (Wakkanai, WA) were analysed. We obtained 99,175,917 raw reads. After filtering low-level reads, 74,195,010 reads remained. On the basis of 10,545 SNPs, FST values were calculated: 0.501 between WA and TY, 0.446 between WA and BA, 0.003 between GI and JU, and 0.014 between GI and WA. Structure analysis based on 45,575 SNPs showed optimal values when K was 5, but two genetic components were dominant. The SNP, mtDNA, and ms analyses showed consistent results among most individuals regardless of genetic markers; however, individuals in the GI and JU populations exhibited different results. Our SNP results indicate that the genetic traits based on SNP are similar to those of mtDNA, but not to those of ms, which may be due to the small number of ms markers or bias. *A. heian* and *A. japonicus* have a close relationship, with the former being adapted to cold waters and the latter to warm waters. Additionally, the Tsushima warm current may act as a physical barrier between the two species.

Engaging with First Nation people through Fisheries Management 101

Kimlin, Eliza., Gardiner, Leah., McPhail, Jonathan., Needham, Evan.,

[1]*Northern Territory Fisheries, Department of Primary Industry, Tourism and Trade*

On 30 July 2008, a High Court ruling known as the Blue Mud Bay decision ruled approximately 80% of the Northern Territory's (NT) intertidal zone as Aboriginal land. This area includes some significant NT commercial fisheries.

First Nations people in the NT have raised concerns about their lack of engagement and understanding of westernised fisheries management. NT Fisheries acknowledges that there are significant data gaps of Aboriginal traditional knowledge in the management of fisheries, as well as limited capacity to engage and understand the spiritual and cultural connection of Aboriginal people with their country.

In 2022, NT Fisheries developed Fisheries Management 101, a pilot program to provide an introduction to how fisheries are managed in the NT. The pilot was designed to build awareness, increase engagement with Aboriginal communities on the fisheries management process, and support two-way learning. The project team presented the pilot to four coastal communities, providing an overview of the six basic components of contemporary fisheries management.

Complementary and previous to this pilot, NT Fisheries has been delivering a certificate II and III in Fisheries Compliance training, empowering Aboriginal Marine Rangers and appointing Fisheries Inspectors to assist with caring for country.

Some of the challenges the project team faced were language barriers and adapting engagement styles to culturally appropriate methods. NT Fisheries are eager to continue engagement to foster relationships and taking the time to listen to First Nations aspirations whilst still upholding the objectives of the Fisheries Act.

Herbivore communities through the lens of ecological processes across Pacific coral reefs

Kindinger, Tye[1]; Adam, Thomas[2]; Baum, Julia[3]; Dimoff, Sean[3]; Hoey, Andrew[4]; Williams, Ivor[1]

[1]*Pacific Islands Fisheries Science Center, National Oceanic and Atmospheric Administration*

[2]*Marine Science Institute, University of California, Santa Barbara*

[3]*Department of Biology, University of Victoria*

[4]*College of Science and Engineering, James Cook University*

Herbivory is often viewed as key to maintaining coral-dominated reefs, and herbivore management is gaining traction as a possible strategy for promoting reef resilience. The functional impact of herbivorous fishes has typically been inferred from total biomass, but robust estimates of ecological processes are needed to better inform management targets. Here, we provide a framework to calculate rates of herbivory across Pacific reefs. We synthesized observations of foraging metrics in relation to fish body size and found considerable variation, even among closely-related species. We then applied these allometric functions to survey data and calculated rates of herbivory for acanthurids and scarines, which make up the vast majority of herbivorous fish biomass in the Pacific. Estimated rates of algal consumption, area scraped, and bioerosion varied across islands by one to three orders of magnitude. We observed non-linear relationships between fish biomass and rates of herbivory. Islands with diverse assemblages of fish species or the largest size classes of herbivores did not consistently have greater rates of processes. The importance of specific herbivores varied across islands and regions, and we identified locations where herbivore processes were dominated by one or two species. Lastly, we highlight gaps in foraging observations and additional work that is needed to further broaden our ability to quantify the functional impact of herbivores.

Soft corals contribute to a mosaic of habitats for fishes on coral reefs.

Kingsford, Michael[1]; Garra, Stephanie[2], Hall April[1, 3], Epstein Hannah[1,4], Moynihan, Jaimee[1,5], Woods, Emma [1, 6]

[1]*Marine Biology an Aquaculture, College of Science and Engineering, James Cook University, Townsville , Australia.*

[2]*Australian Institute of Marine Science, Townsville, Australia.*

[3]*TropWater, James Cook University, Townsville , Australia.*

[4] *School of Life Sciences, University of Essex, Colchester, United Kingdom*

[5]*Tasman District Council, Richmond, New Zealand*

Habitats provide critical resources for fishes on coral reefs. Although it is well recognised that hard corals provide important resources for fishes, soft corals have been largely ignored; this is despite often ranking highly in percentage cover on many reefs. Here we demonstrate, on the Great Barrier reef, that the cover of soft corals generally ranks second to hard coral and at times ranks first. Soft coral is often utilised as habitat and are a source of prey to some fishes. We found that species diversity and abundance was highest where there was a mix of soft and hard corals, rather than in association with one type of coral. Many site attached fishes, especially pomacentrids of the genera Pomacentrus and Chromis, hovered directly above while feeding and sometimes sheltered within colonies. We found evidence that soft corals benefited from associated fishes that excrete nearby or amongst the soft coral. In a natural experiment soft corals with fish had more symbiotic algae and content of protein than colonies with very low numbers of fish. Chaetodontids and damselfishes feed on soft coral and bite marks were commonly found on colonies, but experimental removal of tissue indicated that bites were unlikely to result in mortality. We conclude that the interrelationships between soft coral and fishes require closer attention if we are to understand the resilience of reef fish assemblages to a changing world.

Digging Deeper: uncovering the social structure, population genetics and behaviour of a cryptic fisheries species, *Trypaea australiensis*.

Kirby, Renae[1]; Froehlich, Catheline Y. M.[1,2,3]; Greaves, Samuel[4]; Klanten, O. Selma[5]; Wong, Marian Y. L.[1].

[1]*School of Earth, Atmospheric and Life Sciences, University of Wollongong, Northfields Avenue, Wollongong NSW 2522, Australia*

[2]*Biological Sciences, University of Alabama, Tuscaloosa, AL, USA*

[3]*Dauphin Island Sea Lab, Dauphin Island, AL, USA*

[4] *Genomics and Bioinformatics Cluster, Department of Biology, University of Central Florida, Orlando, FL, United States of America*

[5]*School of Life Sciences, University of Technology Sydney, Sydney, NSW, Australia*

As the largest and arguably most important biome, why are our aquatic ecosystems overfished? Regarding fisheries management, catch regulations are often founded on baseline species ecology without reference to more specialised information namely species behaviour and genetic connectivity. For more informed management decisions, a more holistic approach is therefore needed. One such understudied fisheries species is the cryptic Australian burrowing mud shrimp, *Trypaea australiensis*. Despite current catch regulations, there is a lack of specialised knowledge on *T. australiensis* and no consideration of sex or size on catch limits which could lead to over-exploited populations. Herein, we aimed to 1) quantify *T. australiensis* social structure and its correlates, 2) determine the degree of connectivity using population genomics among three sampled locations along the SE coast of NSW, Australia, and 3) quantify social behaviour using laboratory manipulations. Surprisingly, *T. australiensis* exhibited intraspecific variation in social structures relating to body morphology, seasonality and site. Typically, they were found in solitary arrangements but also frequently in pairs and sometimes groups. Genomic analysis demonstrated a lack of population structure, indicating likely gene flow between the locations. Behavioural manipulations uncovered the temporary nature of pairings. Based on our findings, improved management practises could include establishing/increasing the size of marine parks given the high connectivity between populations, and seasonal closures or body size limits to help juveniles grow and allow larger adults to breed and replenish populations. Together, these findings have the potential to better inform management strategies, ensuring this important ecosystem engineer and fishery is sustained.

Multiple lines of evidence suggest population structure in two small-bodied northern Australian sharks

Kirke, Amy[1,7]; Alves, Fernanda[2]; Banks, Sam[1]; Barton, Diane[3]; Braccini, Matias[4]; Crook, David[5]; Greig, Alan[6]; Harry, Alister[4]; Johnson, Grant[7]; King, Alison[8]; Kyne, Peter[1]; Saunders, Thor[5]; Travers, Mick[4]

[1]*Research Institute for the Environment and Livelihoods, Charles Darwin University, Darwin, Northern Territory, 0909, Australia*

[2]*Australian National University, Canberra, Australian Capital Territory, 2601, Australia*

[3]*School of Agricultural, Environmental and Veterinary Sciences, Charles Sturt University, Locked Bag 588, Wagga Wagga, New South Wales, 2658, Australia*

[4]*WA Fisheries - Department of Primary Industries and Regional Development of Western Australia, PO Box 20, North Beach, WA 6920, Australia*

[5]*NSW Fisheries – Department of Primary Industries, Locked Bag 1, Nelson Bay, New South Wales, 2315, Australia*

[6]*School of Geography, Earth and Atmospheric Sciences, University of Melbourne, Parkville, Victoria, 3010, Australia*

[7] *NT Fisheries - Department of Industry, Tourism and Trade, Fisheries Branch, Northern Territory Government, 33 Vaughan Street, Berrimah, Northern Territory, 0828, Australia*

[8]*CSIRO Research Institute Wodonga, University Drive, La Trobe University, Wodonga Victoria, 3689, Australia*

The small-bodied sharks *Carcharhinus coatesi* and *Rhizoprionodon acutus* are regular bycatch of tropical fisheries across northern Australia and Papua New Guinea (PNG). There is currently little information on the spatial structure of populations of these sharks to guide their conservation and management. We employed a combination of complementary techniques (genetics, vertebral chemistry, and parasite taxa) to assess stock structure using samples collected at three regions in the Northern Territory, Australia. Tissue samples were also obtained from northwest Western Australia and southern PNG to assess genetic connectivity over a broader scale. STRUCTURE analysis provided support for a single genetic population of each species across their distribution, indicating broad-scale connectivity. Vertebral chemistry and parasite taxa provided some support for finer-scale stock structure in *C. coatesi*, whereas there was little evidence of stock structure using any of the approaches for *R. acutus*. Although the vertebral chemistry and parasite taxa analysis suggests limited exchange between regions for *C. coatesi* there is enough mixing between all populations to maintain gene flow across their range.

Ancient DNA techniques applied to formalin-fixed ethanol preserved fish specimens to help answer previously intractable biological questions.

Kitchen, Adam W.D.[1]; Closs, Gerry P.[1]; Oosting, Tom[2]; Stewart, Andrew L.[3]; Rawlence, Nicholas J.[1]; Waters, Jon M.[1]

[1]*University of Otago*

[2]*Victoria University of Wellington*

[3]*Te Papa Tongarewa, National Museum of New Zealand*

Ancient DNA (aDNA) is an established tool that has been used to genetically identify specimens and uncover the phylogenetic relationships of extinct and threatened species. Formalin-fixed ethanol preserved specimens comprise a large proportion of museum natural history collections. These have been previously difficult to extract DNA from due to the crosslinking and fragmentation of. New techniques developed recently have sequenced mitochondrial and nuclear genomes from formalin-fixed specimens. These can be used to answer previously intractable biological questions.

We are undertaking three different projects using state of the art aDNA techniques to sequence mitochondrial genomes from formalin-fixed of the extinct New Zealand Grayling *Prototrochtes oxyrhynchus* to determine if this species was one metapopulation, which would have implications for its mysterious and dramatic extinction. The second is the taxonomic status of three galaxiid individuals from two species (*Galaxias prognathus* and *G. paucispondylus*) collected from the Maruia river catchment. This river drains to the west of the Southern Alps, and comparatively all other populations of these species inhabit rivers draining to the east. Therefore, these could have been from a genetically distinct and isolated population. We aim to detect any remnant of this population using eDNA sampling and electrofishing. The third is reconstructing the evolutionary history of *Acanthoclinus sp.* where some species are only represented by formalin-fixed specimens. *Acanthoclinus* phylogeny is still unresolved, and this work will help clarify its taxonomic status. Described are preliminary results and summaries of the projects as well as the techniques used.

Color patterning in anemonefishes

Klann, Marleen[1], Lee, Fiona[2], Miura, Saori[1], Miyake, Minato[1], Laudet, Vincent[1,2]
[1]*Marine Eco-Evo-Devo Unit, Okinawa Institute of Science and Technology, 1919-1 Tancha, Onna-son, Okinawa 904-0495, Japan*
[2]*Marine Research Station, Institute of Cellular and Organismic Biology (ICOB), Academia Sinica, 23-10, Dah-Uen Rd, Jiau Shi, I-Lan 262, I-Lan, Taiwan*

Color patterning systems are of great interest to understand how changes in developmental mechanisms can lead to a wide variety of patterns. These patterns are often conspicuous, but their origins remain elusive for many fish species. Dismantling a biological system allows a better understanding of the required components and the deciphering of how such complex systems are established and function. Our understanding of color pattern formation and development in fishes is mainly restricted to a single species: zebrafish. It has been shown that zebrafish stripe formation follows a Turing pattern which requires cell-cell interactions between pigment cells. However, not all pigmentation patterns follow this model and thus provide interesting cases to explore color pattern development. One such example are anemonefishes, which display a robust color pattern comprised of 1-3 vertical white bars with a black outline on an orange to reddish body. To elucidate how these iconic bar patterns are established (1) transmission electron microscope (TEM) studies were done to reveal the detailed composition of pigment cells in the skin, (2) time lapse imaging was utilized to investigate how the white bars are formed, (3) pharmacological reagents were used to analyze disruption of the normal developmental processes, and (4) the genetics of a color pattern mutant fish was analyzed in detailed which revealed that cell-cell communication is crucial.

How do cryptic goby species fare in a changing environment?

Klanten, Selma[1]; Froehlich, Catheline[2]; Greaves, Samuel[3]; Kirby, Renae[4]; Wong, Marian[4]

[1] *School of Life Sciences, University of Technology Sydney, Sydney, NSW, Australia*

[2] *Department of Biology, University of Alabama, Tuscaloosa, AL, USA*

[3] *Genomics and Bioinformatics Cluster, Department of Biology, University of Central Florida, Orlando, FL, USA*

[4] *School of Earth, Atmospheric and Life Sciences, University of Wollongong, Australia*

As reefs are experiencing repeated disturbances with increasing frequency, many fish species inhabiting corals are being adversely affected. This is alarming for reefs in general, and essentially to small cryptic species known to be important for the health and biodiversity of coral reefs. One of these taxa are the small, social goby species (genus *Gobiodon*) which live permanently within the branches of *Acropora* corals. Although it has already been demonstrated that these species suffer population declines following cyclone and especially bleaching events, little is known about the population structure and hence their ability to withstand future environmental changes. We sampled goby species from a relatively undisturbed region (Kimbe Bay, PNG), to Lizard Island (northern Great Barrier Reef) pre- and post-disturbances, and to One Tree Island (southern GBR). Applying genomic methods using SNPs, we first established distinct population structure in several goby species across this latitudinal gradient. Moreover, in a baseline study at Lizard Island, we were able to demonstrate the adverse impact of disturbances on the population structure of several goby species. We will present these important preliminary results in the context of environmental changes occurring repeatedly and more destructively into the future.

Widespread genetic population structure in sea chubs (Kyphosidae)

Knudsen, Steen W.[1,2,3]; Clements, Kendall D.[1]

[1]*School of Biological Sciences, University of Auckland, Auckland, New Zealand*

[2]*NIVA Denmark Water Research, Njalsgade 76, DK-2300 Copenhagen, Denmark*

[3]*Natural History Museum of Denmark, University of Copenhagen, Universitetsparken 15, DK-2100 Copenhagen, Denmark*

The kyphosid sea chubs are widely-distributed consumers of macroalgae on tropical and temperate reefs worldwide, but the distribution ranges of species has been confounded by taxonomic confusion. A revision of the phylogeny and taxonomy in this family allows us to examine genetic population structure in five of the most widespread species of *Kyphosus*. The worldwide tropical distributions of four species is most likely partly due to the capacity for juveniles to disperse widely across oceans by rafting, enabling them to cross oceanic barriers. We analysed four mitochondrial gene markers and three nuclear gene markers from individuals of five species of *Kyphosus*. The four worldwidespecies, *Kyphosus bigibbus*, *K. cinerascens*, *K. sectatrix*, and *K. vaigiensis*, displayed genetic differences between populations in the Atlantic and Pacific Oceans, reflecting reduced connectivity between these two oceanic regions. However, there was connectivity between the populations in the Atlantic and in the Indian Ocean, and also between the populations in the Indo-Australian Archipelago and the Pacific Ocean. A fifth species, *Kyphosus sydneyanus* is restricted to temperate Australasia, and displayed no regional population structure between Western Australia, eastern Australia and New Zealand, and can be considered a single panmictic population. All five species have very low genetic diversity and high haplotype diversity, suggesting they all have experienced recent population bottlenecks with subsequent rapid population growth.

Cavefishes across the ocean: evidence for amphidromy in a cavernicolous goby on tropical islands

Kobayashi, Hirozumi[1]; Maeda, Ken[2]; Sato, Mao[3]; Tan, Heok Hui[4]; Shirai, Kotaro[5]; Iida, Midori[6]; Yamahira, Kazunori[1]

[1]*Tropical Biosphere Research Center, University of the Ryukyus*

[2]*Marine Eco-Evo-Devo Unit, Okinawa Institute of Science and Technology Graduate University*

[3]*Department of Zoology, National Museum of Nature and Science*

[4]*Lee Kong Chian Natural History Museum, National University of Singapore*

[5]Atmosphere and Ocean Research Institute, The University of Tokyo

[6]*Sado Marine Biological Station, Niigata University*

Typical cavernicolous creatures are thought to have evolved through physical isolation in caves and currently have a restricted distribution. However, many of aquatic cavernicolous species on tropical islands have wide geographic ranges and their evolutionary processes are unclear. To unveil this, we focus on a cave-dwelling eleotrid goby recorded from several islands in the Indo-Pacific region, which is often confused with the widely distributed amphidromous surface species *Eleotris fusca*. Using genome-wide SNP-based phylogenetics, otolith microchemistry, and morphology, we explore its potential amphidromous origin, migration, and cave adaptations.

We discovered genetic divergence between the cave and surface-dwelling *E. fusca* complexes, suggesting they are distinct species. However, no geographic population structure was evident in the cavernicolous populations across the Indo-Pacific regions, including six Ryukyu islands, Sulawesi, and Christmas Island. This strongly implies retention of the dispersal ability rather than convergent speciation. This migratory nature was further supported by otolith microchemistry analysis. Morphological alterations (i.e., small eye size, enlarged otolith, and unique arrangement of neuromasts) in the cavernicolous lineage indicate specific adaptations to the cave environments.

As amphidromous animals cannot return to the sea once they have settled, the evolution of such a “stygo-amphidromous” species may be triggered by a change in juvenile preference for recruitment habitats, which may have shifted from surface rivers to groundwaters. This could lead to the physical isolation of breeding grounds, acting as an automatic magic trait. This evolutionary model could potentially apply to other widespread cave organisms.

Food provisioning of anemonefish to host sea anemones: what they provide and their effects on the host

Kobayashi, Yuya[1]; Kohda, Masanori[1]; Kondo, Yuki[1]; Awata, Satoshi[1]

[1]*Graduate School of Science, Laboratory of Animal Sociology, Department of Biology, Osaka Metropolitan University, Osaka 558-8585, Japan*

Some organisms are known to provide nutrition to their partners in mutualistic symbiosis. Anemonefish have been found supplying nutrients directly to sea anemones in both artificial and natural settings. Although researchers have been aware of this behaviour since the 19th century, no studies have been conducted to determine the significance of food provisioning in their relationship. We investigated the true nature of this behaviour and its influence on the relationship between sea anemones and Clark’s anemonefish (*Amphiprion clarkii*) through a field experiment. First, for tracing, shrimp with strings attached were given to the clownfish and provided to the anemone. In 17 of 22 cases, the shrimp were transferred to the gastrovascular cavity of the anemone. Second, when the anemonefish were presented with different sizes and types of food (shrimps, fish, bivalves, and seaweeds), they consumed smaller animal scraps and seaweeds but provided larger animal scraps to the host. Third, when small pieces of shrimp were continuously presented to the anemonefish, they initially consumed the food themselves. However, as the number of presentations increased, so did the food supply to the host. Finally, food provisioning by the anemonefish increased the host’s growth rate. These results suggest that anemonefish actively and situationally feed their host in response to the host's feeding habitat and its own condition. Moreover, the anemone-anemonefish relationship may have an aspect of farming that improves the quality of the host.

Diversity and Molecular Phylogeny of Congrid eels (Anguilliformes: Congridae) of Indian Waters

Kodeeswaran, Paramasivam[1]; Ajith Kumar, T. T.[1]; Sarkar, Uttam Kumar[1]

[1]*ICAR-National Bureau of Fish Genetic Resources, Lucknow, Uttar Pradesh, India*

The family Congridae Kaup, 1856 is known as small to large-sized eels, which reside throughout temperate and tropical waters, mainly from the continental shelf or slope of the deep sea, along the world's oceans. Congridae comprises 231 valid species belonging 32 genera under three subfamilies, and very little information is available about their taxonomy, biology, ecology, and precise distribution. The present study aims to document the diversity and molecular evolution of marine congrid eel distributed along Indian waters. Sampling has been done at various major landing centres along the Indian coast during 2020-2022. In this present study, 36 species belonging to 16 genera have been documented. Amongst this, 9 new species and 4 new records have been described and documented. The genus *Ariosoma* dominates diversity with 8 species, followed, *Rhynchoconger* (5), *Bathycongrus* and *Heteroconger* with 3 species each. The genus, *Macrocephenchelys* was recorded for the first time from Indian water based on a specimen from Arabian Sea. Further, the phylogenetic relationship of the family Congridae was inferred using, Bayesian Inference (BI) in Mr. Bayes, which revealed that three monophyletic groups within the family with significant bootstrap support. The phylogenetic analysis also suggests that the genus '*Congromuraena*' distinct from *Gnathophis* as well as *Japonoconger*. Congrid eels are an important fishery resource in terms of utilization and conservation perspective and are less studied due to the existence of taxonomic ambiguity, and rarity in the collection of samples warranting the need to ascertain the diversity of the group.

Male medakas mate with females despite sperm depletion

Kondo, Yuki; Kohda, Masanori; Awata, Satoshi

Laboratory of Animal Sociology, Department of Biology, Graduate School of Science, Osaka Metropolitan University, Osaka 558-8585, Japan

The energy cost of spermatogenesis in sexually reproducing organisms is considerably higher than anticipated, which may limit the reproductive potential of males. Sperm depletion occurs when males cannot maintain the number of sperm released during successive matings, which is a pervasive phenomenon among various taxonomic groups. However, comprehensive studies regarding the number of sperm released, spawned eggs, fertilisation rate, and behaviour during successive matings are limited. In the present study, male medakas (*Oryzias latipes*) were allowed to mate successively with different females until they stopped. We investigated the effect of successive male mating on sperm release, fertilisation rate, and mating behaviours in the absence of male-male competition and nutritional constraints. We found that males mated with an average of 19 females per day (range: 4–27 females per male per day). Male fertility declined over successive matings and days, with more sperm getting invested during the first mating of the day. Consequently, the females experienced reduced fertilisation rates. These results suggest that sperms deplete in males after successive matings. The rapid decline in the number of sperm released and fertilisation rates due to successive matings proves costly for females. This study highlights the dramatic constraints on male reproductive success across mating events, even under optimal laboratory conditions (i.e. without competition for resources or partners), which may cause sexual conflicts over limited sperm availability.

Larvae of three species of the Genus *Plectranthias* (Serranidae: Anthiadinae) with characteristic pigment patterns

Konishi, Yoshinobu

Retired, formerly Seikai National Fisheries Research Institute

The serranid subfamily Anthiadinae is very diverse in the Indo-Pacific region, but their larvae are poorly known due to overlapping fin-ray counts in most genera. This paper describes the larval morphology of three anthiadine species, *Plectranthias sagamiensis*, *P. winniensis*, and *P. longimanus* (or *P. nanus*), based on a total of six specimens (4.4 mm－8.6 mm Standard Length (SL)), two from each species, collected in the East China Sea and its adjacent waters. Identification of the larvae is based on a combination of the meristic data including fin rays, scales and predorsal bones, and on the spiny ornamentation of head bones. The larvae examined have a deep body (BD = 41.1－50.0% SL), large head (HL = 37.5－47.7% SL), and mostly moderate eye (ED = 23.8－32.4% HL). They all have similar spiny ornamentation on some exposed head bones including the supraorbital ridge, posttemporal, supracleithrum, opercle, preopercle, subopercle, and interopercle, but not on the fin spines and scales. Pigment patterns of the larvae are species-specific: a large internal pigment blotch on the snout in *Plectranthias sagamiensis*, widely scattered melanophores on the pectoral and pelvic fins in *P. winniensis*, and laterally on the trunk and tail in *P. longimanus* (or *P. nanus*).

Males of nest-spawn fish lure females using attractants produced by their kidney.

Koya, Yasunori[1]; Nagaya, Miki[2]

[1]*Faculty of Education, Gifu University*

[2]*The United Graduate School of Agricultural Science, Gifu University*

The males of certain teleost species reproduce in a closed space such as underneath a stone or in a nest built by some materials. They are referred to as “nest-spawn fish” in this study. The male nest-spawn fish cannot travel far from his nest during breeding process. However, he must attract a female to his nest to ensure reproductive success. We identified several similarities among male nest-spawn fish: their kidney becomes swollen and produces polysaccharide, and they preserve urine in their urinary bladder. So, we devised and attempted to verify the hypothesis that males nest-spawn fish lure females to their nest using attractants produced by their kidney. Kidney hypertrophy, renal polysaccharide production, and urine retention during nesting have been reported previously and were found by the present study in three taxonomical groups—Gobiidae (*Rhinogobius* and *Tridentiger*), Cottidae (*Cottus, Myoxocephalus*), and Gastrosteidae (*Gasterosteus, Pungitius*). The attraction of females through male urine, water retention by a nesting male, or kidney extracts of mature males have been reported and were confirmed by the present study in five species of the above three taxons (*Neogobius, Rhinogobius, Cottocomephorus, Cottus, Pungitius*). In the nest-spawn species of Siluridae (*Liobagrus*), no changes in the kidney and urinary bladder were detected during the reproductive season. Based on these results, our hypothesis that male nest-spawn fish lure females using attractants produced by their kidney may be applicable particularly in Perciformes.

Investigating shortfin mako migratory patterns through an integrative data approach

Kresge, Colby[1]; Vaudo, Jeremy[2]; McCandless, Cami[3]; Cortés, Enric[4]; Shivji, Mahmood [2]; Wetherbee, Brad [1,2]

[1]*College of Environment and Life Sciences, University of Rhode Island*

[2]*Guy Harvey Research Institute, Halmos College of Arts & Sciences, Nova Southeastern University*

[3]*NOAA Fisheries Northeast Fisheries Science Center*

[4]*NOAA Fisheries Southeast Fisheries Science Center*

The shortfin mako shark (*Isurus oxyrinchus*) is a widely distributed oceanic species frequently caught in commercial and recreational fisheries. Because of declines in mako populations, there is strong interest in reducing fishing mortality to rebuild stocks. One factor that detracts from informed mako shark management is a poor understanding of their migratory patterns. Migratory patterns of mako sharks are poorly understood, which detracts from informed management to assist recovery of some of their populations. Assessment of stock status and migratory pathways of marine fishes relies heavily on fishery-dependent data; however, such information is often biased towards locations where fishing is concentrated. We investigated the migratory patterns of mako sharks in the Western North Atlantic Ocean using data derived from both fishery-dependent and -independent sources, including the U.S. Pelagic Longline Observer Program, Cooperative Shark Tagging Program, Canadian ICCAT data, and satellite telemetry. Each data source has shortcomings for modeling migratory pathways contributing to an incomplete understanding of their migratory patterns, however, an integrated approach based on data combined from all sources provided a more robust model of migration patterns than any single source of data. Mako sharks exhibited seasonal shifts in distribution as well as shifting core areas of habitat occupied throughout the year. For effective global management the insights gained from our integrative approach for characterizing the migratory patterns of mako sharks in the Atlantic Ocean can serve as a valuable tool for investigating the migratory patterns of mako sharks in the Indo-Pacific region.

Ecological variability increases the conservation impact of marine protected areas

Krueck, Nils[1]; Dwyer, Ross[2]; Brock, Danny[3]; Bryars, Simon[3]; Braccini, Matias[4], Clarke, Tom[5]; Dennis, Joshua[5]; Davey, Joshua[5,6]; Drew, Michael[6], Fowler, Anthony[6], Whitmarsh, Sasha[5,7], Huveneers, Charlie[8]

[1]*Institute for Marine and Antarctic Studies, University of Tasmania, Hobart, Tasmania, Australia (nils.krueck@utas.edu.au)*

[2]*School of Science, Technology and Engineering, University of the Sunshine Coast, Maroochydore, Queensland 4556, Australia*

[3]*Department for Environment and Water, South Australian Government, South Australia, Australia*

[4]*Department of Primary Industries and Regional Development, Western Australian Government, Western Australia, Australia*

[5]*Flinders University, South Australia, Australia*

[6]*South Australian Research and Development Institute, South Australian Government, South Australia, Australia*

[7]*Deakin University, Geelong, Victoria, Australia*

[8]*Southern Shark Ecology Group, College of Science and Engineering, Flinders University, Adelaide, South Australia, Australia*

Marine protected areas (MPAs) are an important component of the Global Biodiversity Framework, but even fully protected MPAs do not guarantee the survival of mobile species if resident individuals move between MPAs and fished areas. However, variability in movements and other ecological traits, e.g. maximum age and age-at-maturity, is often considerable and might influence MPA effectiveness. Here, we integrate data from acoustic telemetry and BRUVS into an individual-based model to estimate the survival of 10 ecologically diverse species in MPAs of increasing sizes. We then contrast outcomes based on species-averaged movements and maximum ages to those that consider individual movements and ages at maturity. Assuming a considerable fishing mortality risk outside of MPAs (20% year^{-1}), we find that even largely sedentary species might require 5 km wide MPAs to ensure the lifetime survival of most (>50%) resident individuals. These estimates increased to 10-30 km for more mobile fishes and >50km for wide-ranging fishes, rays, and sharks. In contrast, we find that even just 2 km wide MPAs could be effective in protecting 35-77% of all individuals of investigated fish species if (1) intra-specific variability in movements is considered and (2) survival to reproduction (contribution to population replenishment) rather than maximum age is used as a benchmark for protection. However, achieving protection to reproduction of >50% of individuals for more wide-ranging rays and sharks still required MPAs larger than 10 km and might be impossible in some cases. Our findings provide a new perspective on conservation impact to inform MPA planning.

Contrasting habitat use and growth of two anguillid eels, *Anguilla marmorata* and *A. japonica* in sympatric subtropical rivers

Kumai, Yusuke[1]; Kuroki, Mari[1]; Yamakawa, Takashi[1]

[1] *Graduate School of Agricultural and Life Sciences, The University of Tokyo, Japan*

In the western North Pacific, the tropical Indo-Pacific eel *A. marmorata* and the temperate Japanese eel *A. japonica* coexists in subtropical rivers. Despite their ecological and economic importance, previous studies have primarily focused on their allopatric distribution areas, and the biological and ecological information in their sympatric distribution areas is currently lacking. To acquire the fundamental knowledge necessary for their conservation in these areas, the habitat use and growth of the two species were investigated in the rivers of Yakushima Island, southern Japan by sample collection, visual observation, environmental measurements, and otolith investigation.

The habitat use of the two species was significantly influenced by several environmental parameters, and their habitat was clearly segregated: *A. marmorata* exclusively utilized habitats associated with larger substrate materials, fewer leaf detritus on riverbeds, higher current velocity, and lower turbidity than *A. japonica*. The growth rate of *A. marmorata* (female 35.3 and male 32.9 mm/year) was significantly lower than that of *A. japonica* (female 87.2 and male 89.9 mm/year) and was also lower than its tropical conspecifics. The slower growth rate of *A. marmorata* compared to its tropical conspecifics can likely be attributed to the cool and oligotrophic environment of this subtropical island.

These results indicate that heterogeneous environments must be maintained for their coexistence and conservation in sympatric river systems. *Anguilla marmorata* in subtropical regions might be more sensitive to disturbances and fisheries due to their slower growth compared to their tropical conspecifics and may need prioritized conservation.

Environmental DNA metabarcoding reveals the impact of riverine slope on ichthyofauna in the rivers of subtropical Yakushima Island, Japan

Kumai, Yusuke[1]; Miya, Masaki[2]; Sado, Tetsuya[2]; Yamakawa, Takashi[1]; Kuroki, Mari[1]

[1] *Graduate School of Agricultural and Life Sciences, The University of Tokyo, Japan*

[2] *Natural History Museum and Institute, Chiba, Japan*

Riverine ecosystems are now facing biodiversity decline due to climate changes and human influences, and biomonitoring of these ecosystems is imperative for effective management. An environmental DNA metabarcoding approach provides a powerful tool for this purpose. In Japan, however, it has rarely been applied to subtropical rivers, limiting our understanding of how fish fauna varies within these rivers. Here, we conducted a fish fauna assessment using this approach at a total of 17 stations in 12 rivers on subtropical Yakushima Island, a world natural heritage site, to investigate the relationship between riverine morphology and fish fauna on this island.

A total of 27 molecular operational taxonomic units (MOTUs) were detected, of which 74% were diadromous species, including 17 gobiidae, two anguillids, and ayu *Plecoglossus altivelis*. Three *Rhinogobius* gobies and the Indo-Pacific eel *Anguilla marmorata* were detected above an 88 m waterfall, indicating the remarkable climbing ability of these fishes. Generalized linear models and a non-metric multidimensional scaling analysis indicated that the number of diadromous species in each river decreased with increasing riverine slope, and the diadromous fish fauna was similar among rivers with comparable slopes. In the steepest river, merely four species including three *Rhinogobius* gobies and *A. marmorata* were detected even near the river mouth.

These results suggest that the riverine slope strongly influences the diadromous fish fauna on this island. Since the species diversity was high in relatively low-gradient rivers, these rivers would need prioritized conservation for species diversity maintenance on this island.

A critically endangered Ryukyu-ayu *Plecoglossus altivelis ryukyuensis* in Japan's latest world natural heritage site "Amami-Oshima Island", southern Japan

Kume, Gen[1]; Yonezawa, Toshihiko[2]; Tachihara, Katsunori[3]; Iguchi, Kei'ichiro[4]; Nishida, Mutsumi[3]; Akagi, Isao[1]; Shinomiya, Akihiko[1]

[1]*Kagoshima University, Kagoshima, Japan*

[2]*Kagoshima Environmental Research and Service, Kagoshima, Japan*

[3]*University of the Ryukyus, Okinawa, Japan*

[4]*Nagasaki University, Nagasaki, Japan*

The Ryukyu-ayu *Plecoglossus altivelis ryukyuensis* belongs to the family Plecoglossidae of the order Salmoniformes and is a subspecies of the ayu *Plecoglossus altivelis altivelis*, which is distributed widely from Japan and the Korean Peninsula to northern Vietnam. It has been speculated that the ancestor of *P. altivelis ryukyuensis* was isolated from populations inhabiting the mainland of Japan in the Middle Pleistocene with the formation of the Ryukyu Islands (a chain of islands extending from southwestern Kyushu to northern Taiwan) and then evolved separately for a million years.

Amami-Oshima Island in the Ryukyu Islands was registered as Japan's latest world natural heritage site in July 2021. The Island is the only area where wild populations of *P. altivelis ryukyuensis* are found. The subspecies was designated as critically endangered by the Japanese Ministry of the Environment and the Kagoshima Prefecture, and fishing them has been completely banned since 2004. Although administrative supports contribute to the conservation of the Ryukyu-ayu, the subspecies is continually facing the risk of extinction.

Since 1992, we have conducted monitoring surveys in their main river habitats of the Ryukyu-ayu every year. In addition, researchers regularly practice outreach programs to educate local people on the value of the Ryukyu-ayu and the importance of their conservation. In this presentation, we explain population dynamics of amphidromus *P. altivelis ryukyuensis* and introduce our conservation activities for the subspecies.

The food sources of Anguilliformes leptocephali in the Kuroshio Current and adjacent waters

Kume, Gen[1]; Minagawa, Akinori[2]; Jinno, Satoru[3]; Hirai, Junya[4]; Shiozaki, Kazuhiro[1]; Ichinomiya, Mutsuo[5]; Komorita, Tomohiro[5]; Habano, Akimasa[1]; Kodama, Masafumi[1]; Kobari, Toru[1]

[1]*Faculty of Fisheries, Kagoshima University, Kagoshima, Japan*

[2]*Ecoh Corporation, Fukuoka, Japan*

[3]*Ehime Prefectural Fisheries Experimental Station, Ehime Prefectural Office, Ehime, Japan*

[4]*Atmosphere and Ocean Research Institute, The University of Tokyo, Chiba, Japan*

[5]*Faculty of Environmental and Symbiotic Sciences, Prefectural University of Kumamoto, Kumamoto, Japan*

Information on the feeding ecology of leptocephali is essential for the successful aquaculture of Anguilliformes fishes including Japanese eel *Anguilla japonica*. Generally, fish larvae mainly prey on mesozooplankton such as copepods. Meanwhile, previous studies have shown some evidence that leptocephali feed on particulate organic matters (POM). In the present study, we assessed the diet of early-development-staged leptocephali of dominant Anguilliformes fish in the Satsunan area, southern Japan through morphological and DNA metabarcoding analyses for gut contents and the stable carbon and nitrogen isotope analysis. The purpose is to elucidate which components of POM leptocephali feed on. Samples were collected by an Ocean Research Institute net (diameter: 160cm; mesh size: 335µm) from 2015 to 2022. A total of 284 leptocephali (18 taxonomic group) were used for the present study. A wide variety of eukaryotes (16 taxonomic groups) were detected by DNA metabarcoding analysis for gut contents, supporting the previous implication that leptocephali feed on POM. By electron microscopic observations, zooplankton fecal pellets and amorphous particles that would be components of zooplankton fecal pellets were dominantly observed in their guts. The stable isotope analysis indicated that fecal pellets of calanoid copepods would be a main source of nutrition for leptocephali. In the many regions, copepods are main components of zooplankton. Our study strongly suggests that leptocephali would passively feed on POM such as fecal pellets of copepods occurring abundantly in the ambient environment, which can pass through the space between fang-like teeth.

Application of environmental DNA metabarcoding for detection of non-native fish species in an urban river in Tokyo, Japan

Kuroki, Mari[1]; Zhu, Mengyao[1,2]; Mizuta, Fuki[1]; Yamakawa, Takashi[1]; Sado, Tetsuya[3]; Miya, Masaki[3]

[1] *Graduate School of Agriculture and Life Sciences, the University of Tokyo, Tokyo, Japan*

[2] *Ocean Policy Research Institute of the Sasakawa Peace Foundation, Tokyo, Japan*

[3] *Department of Ecology and Environmental Sciences, Natural History Museum and Institute, Chiba, Chiba, Japan*

The expansion of non-native fish distributions is a critical problem in urban rivers. This study examined the potential of environmental DNA (eDNA) metabarcoding to detect non-native fish species in the Tama River, a large urban river in Tokyo, Japan.

In total, eDNA of about 90 molecular operational taxonomic units (MOTUs, species or a group of species) were detected in monthly water samples taken from 12 mainstream and 7 tributary locations during 2018-2019, of which 17 were non-native fish species (8 domestic species and 9 foreign species). The most frequently detected non-native species was the Amur catfish, a large carnivorous fish whose original distribution was in western Japan. Some cyprinids whose original distribution ranges were in western Japan were also detected, which would have been incidentally transferred through the stocked ayu. Two salmonids were detected in the upper stream and tributaries. These species have been stocked for aquaculture and recreational fishing since the late 1870s, and are now heavily farmed and stocked along the upper stream. Two Chinese cyprinids, which were introduced as food resources in the late 1870s in Japan, were detected in the lower stream. The popular recreational fish species such as the smallmouth bass and Japanese crucian carp were also frequently detected at many sites.

There are concerns that predation, competition, and other interspecific interactions among these non-native and native fish species affect river ecosystems. These results demonstrate that eDNA detection methods can provide invaluable information for monitoring and management of non-native fish species in urban rivers.

Relative growth of southern bluefin tuna (*Thunnus maccoyii*) larvae in the eastern Indian Ocean

Ricardo, Borrego[1]; Jose M., Quintanilla[1]; Patricia, Romero[1]; Teresa, Pérez-Sánchez[1]; Carolina, Johnstone[1]; Estrella, Malca[2,3] Alejandro, Jivanjee[2]; Luke, Matisons[4]; **Lynnath, Beckley[4]**; Rasmus, Swalethorp[5]; David Die[2]; Michael R. Landry[5] and Raúl, Laiz-Carrión[1]

[1]*Instituto Español de Oceanografía (IEO-CSIC), Centro Oceanográfico de Málaga, Fuengirola, Spain*

[2]*Cooperative Institute for Marine and Atmospheric Studies, University of Miami, Miami, FL, USA*

[3]*NOAA Fisheries, Southeast Fisheries Science Center, Miami, FL, USA*

[4]*Environmental and Conservation Sciences, Murdoch University, Perth, WA, Australia,*

[5]*Scripps Institution of Oceanography, University of California San Diego, La Jolla, CA, USA*

Southern bluefin tuna (*Thunnus maccoyii*, SBT) is a commercially important highly migratory species that is widely distributed in temperate regions of the Southern Hemisphere. Mature fish migrate to a single spawning ground located in the eastern Indian Ocean (IO), between Indonesia and NW Australia. Early life stages represent a critical period when fish larvae suffer maximum mortality. Survival during this period is crucial for future recruitment success in which larval growth has a determinant role. As part of the 2nd International IO Expedition, an oceanographic survey was conducted in January-March 2022, coinciding with the SBT spawning peak. Fish larvae were sampled by standard double oblique net tows from 25 m to the surface, using a square-mouth Bongo nets (90-cm) with 0.5-mm and 1-mm mesh. SBT larvae were sampled and identified onboard according to morphological, meristic and pigmentation characters and DNA was extracted from each larva for positive post-cruise genetic identification. A multiplex PCR assay distinguished SBT from yellowfin (*T. albacares),* albacore (*T. alalunga),* bigeye (*T. obesus),* and skipjack (*Katsuwonus pelamis)*. Standard length (SL) and width were measured to the nearest 0.05 mm using the image analysis software Image J., dehydrated in a freeze dryer for 24 h and dry weighed (DW) on a precision microbalance (0.01mg). Relative growth rate was determined by SL *vs* DW relationship, together with larval width. Results are discussed in comparison with other tuna species to assess species-specific differences in relative larval growth patterns. This study is funded by project PID2021/122862NB/100 MCIN/AEI/10.13039/501100011033/FEDER, UE and BLOOFINZ-IO (USA-NSF).

Effects of ocean warming on fish community composition and species-specific dietary shifts

Lamb, Robert W. [1,,2,3]; Munson, Calvin[4]; Perez-Matus, Alejandro[5]; Smith, Franz[3]; Thorrold, Simon[2]; Witman, Jon D.[3]; Zeff, Maya[6]

[1] *Nature Coast Biological Station, University of Florida, Cedar Key, FL 32625*

[2] *Biology Department, Woods Hole Oceanographic Institution, Woods Hole, MA 02543*

[3] *Department of Ecology, Evolution, and Organismal Biology, Brown University, Providence, RI 02912*

[4] *Department of Ecology and Evolutionary Biology, University of California - Santa Cruz, CA 95064*

[5] *Facultad de Ciencias Biológicas, Pontificia Universidad Católica de Chile, Santiago, Chile*

[6] *Department of Biology, California State University - Northridge, CA 91330*

Herbivorous fish diversity and abundance decrease with latitude, which has generated the temperature constraint hypothesis (TCH), suggesting that algal digestion by ectothermic fishes becomes prohibitively inefficient as temperature decreases. We tested the predictions of the TCH across an upwelling gradient in the Galapagos Islands spanning a sea surface temperature (SST) range of 3 °C. We quantified herbivorous fish abundance and diversity and benthic herbivory by each species and collected fish and primary producer tissues to trace dietary pathways. In keeping with TCH predictions, herbivore abundance and species richness were linearly and positively correlated with SST, as were total herbivory rates for most species. Carbon isotope analysis of essential amino acids revealed that herbivores from three different families relied primarily on detrital food webs when upwelling was low and temperatures were high. When upwelling was high and temperatures were low, angelfish and damselfish shifted to planktonic food webs while surgeonfish relied on algal production. The condensed SST gradient in Galapagos provides general support for the TCH, but increases in herbivory rates are driven by greater herbivore abundance, not per capita bite rates. Differential diet switching among herbivore species suggests that bottom-up subsidies and variation in consumer traits likely affect food web functioning more than strict physiological limitation of herbivory at colder temperatures.

Transparency in Sanctuary Zone planning: attribute analysis informed by continental scale meta-analysis

Langlois, Tim[1]; Hamre, Nicole[1]; Navarro, Matthew [1]; Goetze, Jordan [2]

[1]*University of Western Australia*

[2]*Department of Biodiversity Conservation and Attractions*

No-take Sanctuary Zone and Marine Park planning can be a complicated process where government agencies, community representatives, domain experts and interest groups may come together to consider a multitude of options, usually informed by design principles, resulting in multiple maps of zoning options that must be considered.

In larger scale marine park planning with multiple sanctuary zones, this can be a daunting process which can lead to non-optimal outcomes for no-take sanctuary zone placement due the difficulty in choosing which option better meets design principles whilst accounting for impacts on other users.

Using a subset of a national synthesis of baited remote stereo-video data on fish assemblages around Australia (Goetze et al. 2022), we determined two of the most important sanctuary zone attributes, and thresholds, to achieve the design principle of Adequacy. Using these attributes we create an ordination that can be used to characterise and compare how different zone options compare and indicate which individual sanctuary zones meet adequacy thresholds.

This ordination will be a useful tool in any future process to create or rezone marine parks or networks of sanctuary zones.

4.4A Themed Session I: Novel Methods and Techniques Advancing our Understanding of Fish Biology, 260-092, November 23, 2023, 10:30 AM - 12:30 PM

The benefits of multiple methods to survey deep reef fish assemblages: comparison of stereo panoramic drop-camera systems with baited video

Langlois, Tim[1]; **Aston, Charlotte**[1]

[1]*University of Western Australia*

Standard Baited Remote Underwater stereo-Video systems (BRUVs) are increasingly viewed as a standardised cost-effective, non-extractive method for estimating the relative abundance and size-structure of demersal fishes across multiple habitats and depths from 0-250m. Baited video has been shown to sample greater abundance of fished species than other methods, but has some known behavioural biases due to the presence of the bait that can influence the assemblage sampled. Around Australia, BRUVs are being used to successfully characterise fish assemblages across shallow (0-30 m), mesophotic (30-70 m) and rariphotic (70-200) habitats, although the standard 1 hour long deployment period to characterise rariphotic and deeper shelf reef assemblages can be challenging due to strong along shore currents.

Stereo panoramic drop-camera systems, pioneered in California by Rick Starr, do not use bait, and use a much shorter deployment time and may provide a more representative sample of the fish assemblage. We compare the size distribution of fisheries indicator species from both baited and non-baited video systems inside and outside protected areas across tropical, sub-tropical and temperate locations along the Western Australian continental shelf, to illustrate the potential biases and strengths of using multiple data sources and comment on the logistical constraints of each method.

Getting to the bottom of Indian gobioids

Larson, Helen[1]; Murugan, Arumugam[2]

[1]*Museum and Art Gallery of the Northern Territory, Australia*

[2]*United Nations Development Programme, India*

Many Indian gobioids have been misidentified and misunderstood for many years, with over 280 nominal species recorded so far and 25 *incertae sedis*. Today, names are still confused and copied from paper to paper, and there has been no good summary of Indian gobioids overall since Day's 1876 *The Fishes of India*, and Koumans 1941 *The gobioid fishes of India*. We are working on remedying this. Early published work on gobies was mostly done by British and French colonisers from 1803 onward, with most specimens taken back to Europe. The earliest goby descriptions that were not made by a European are in Hora's 1923 work on Chilika Lake fishes. The notorious small size and difficulty of identification of gobioids has made their documentation and verification difficult. Habitats have now been modified in many places and India's coral reef and estuarine habitats are the least studied – and these environments have the greatest diversity. Efforts are in place to improve habitats and the conservation of their fish fauna.

Coral reef fish, hormones and metamorphosis: a tale of adaptation

Laudet, Vincent[1,2]

[1]*Marine Eco-Evo-Devo unit, Okinawa Institute of Science and Technology (OIST), Japan*

[2] *Marine Research Station, Institute of Cellular and Organismic Biology (ICOB), Academia Sinica, Taiwan*

Determining how the plasticity of developmental traits respond to environmental conditions is a challenge that must combine evolutionary sciences, ecology and developmental biology. Developmental plasticity is defined as the ability of an organism to adjust its development depending on environmental signals, thus producing alternative phenotypes precisely adjusted to the environment. Yet the mechanisms underlying developmental plasticity are not fully understood: Determining how plastic developmental changes are coordinated at the physiological, cellular, and molecular levels is a challenge that must combine ecology with developmental biology. The mechanisms that underlie the development of alternative phenotypes are still unclear for many systems and is one major goal of ecological developmental biology or Eco-Evo-Devo.

Coral reef fish are very promising model systems to better understand the role of hormones in the evolution of life history strategies by integrating ecological, evolutionary and developmental components. Using anemonefishes (*Amphiprion* spp.) and the convict surgeonfish *Acanthurus triostegus* and focussing on specific traits that emerge or change during metamorphosis such as pigmentation, metabolism or behavior we explore how hormones fine tune development to suit environmental conditions and how this ultimately impacts the survival, quality and fitness of juveniles and adults.

2.1C Themed session A: Evolution, Taxonomy and Biogeography of Indo-Pacific Fishes, 260-098, November 21, 2023, 3:30 PM - 4:15 PM

Discovery of cryptic species complex within sand diver (*Limnichthys fasciatus*), and it's evolutionary implication

**Lee, Yu-Jin[1]; ** Kim, Jin-Koo[1]

[1]*Department of Marine Biology, Pukyong National University, Busan 48513, Republic of Korea*

Specimens in the genus *Limnichthys* (Family: Creediidae) were collected from the intertidal zone on Moseulpo, Jeju-do Island, Korea, between July 2022 and April 2023 using a scoop net. These specimens were originally identified as *Limnichthys fasciatus* based on morphological traits. However, the cytochrome oxidase subunit I gene of mitochondrial DNA (mtDNA-COI) and 16S rRNA sequences were significantly different from those of Japanese *L. fasciatus*. Subsequently, we conducted a range-wide investigation using *L. fasciatus* specimens collected from Japan, as well as northeastern and southeastern Australia, to clarify the taxonomic entities of the Korean sand diver. As a result, we discovered that *L. fasciatus* was divided into five distinct clades. Comparing the mtDNA COI and 16S rRNA sequences of the clade from the type locality (southeastern Australia) to the other clades of the remaining localities revealed deep divergence in the COI and 16S rRNA sequences as follows: 14.9–15.2%, 10.9–11.9% from Korea, 13.7%, 12.9–13.2% from Japan, and 12.7–24.3%, 7.9–19.6% from northeastern Australia, respectively. The most similar congeneric species, *L. nitidus*, showed a genetic difference of 24.7% in the COI, and 16% in the 16S rRNA sequence from *L. fasciatus*. The present study suggests that *L. fasciatus* comprises at least five species and has undergone independent evolutionary events by locality. Because *L. fasicatus* is known as anti-tropical species, it may have migrated from Australia to the northern hemisphere across the equatorial sea during the glacial period. They may have undergone an allopatric speciation event after the last glacial maximum, resulting from a water temperature barrier. A further comparative study, such as an osteological work, is required to clarify the taxonomic status of the five sand diver clades.

Distribution and habitat characteristics of the juvenile mudskipper, *Periophthalmus modestus* on the Edogawa flood channel

Lee, Yijin[**1**]; Aoki, Shigeru[2], Kaneko, Kenichi[3], Okamoto, Ken[4] , Sakurai, Nobuo[5], Shingo, Tanabe[6]

[1]*Okinawa Institute of Science and Technology*

[2]*The University of Tokyo, asaoki@g.ecc.u-tokyo.ac.jp*

[2]*Municipal Museum of Natural History in Ichikawa, kenichi-kaneko@city.ichikawa.lg.jp*

[4]*The University of Tokyo, okamoto.ken@purple.plala.or.jp*

[2]*Kajima Technical Research Institute, sakurano@kajima.com*

[2]*Inokashira Park Zoo, tanabe@tzps.or.jp*

Coastal development in the 20th century has resulted in the loss of approximately 90% of intertidal flats in Tokyo Bay. However, surviving tidal flats, as well as small-scale artificial tidal flats formed in flood channels, now serve as habitats for benthic organisms. The mudskipper (*Periophthalmus modestus*) is one of the inhabitants in this urbanized environment. Given its amphibious lifestyle, the mudskipper has the potential to serve as a bioindicator for assessing intertidal ecosystems. Therefore, studying the population dynamics of *P. modestus* in Tokyo Bay can provide valuable insights into identifying potential habitats and conserving species. This study aimed to expand current knowledge of *P. modestus* population dynamics by investigating the distribution of the species during its juvenile stage and its relationship with environmental factors. In 13 sites along the Edogawa flood channel, the largest habitat for *P. modestus* in Tokyo Bay, we collected data on the species' distribution and various environmental factors (sediment water contents, sediment gradient, copepod population, chlorophyll a concentration, organic matter content, and vegetation distribution) while the juveniles are active. By employing Generalized Linear Mixed Models, we identified the factors influencing the juvenile distribution. The vegetation distribution (*Phragmites australis*) was the most significant environmental factor influencing juveniles distribution; habitats with complex structure of the vegetation tend to have more juvenile population as the vegetation is used as shelter from predators. Furthermore, we found out that different environmental factors were dominant during certain periods. The present findings will be helpful for artificial tidal flats management and species conservation.

Marine reserves supply half of the larvae to a coral reef fishery

Leis, Jeffrey M.[1, 2]; Bode, Michael[3], Choukroun, Severine[4], Emslie, Michael[5], Harrison, Hugo B.[4], Mason, Luciano B.[4], Williamson, David H.[6], Jones, Geoffrey P.[4]

[1]*Institute for Marine and Antarctic Studies, University of Tasmania, Hobart*

[2]*Australian Museum Research Institute, Sydney*

[3]*School of Mathematical Sciences, Queensland University of Technology, Brisbane*

[4]*College of Science & Engineering, James Cook University, Townsville*

[5]*Australian Institute of Marine Science, Townsville*

[6]*Great Barrier Reef Marine Park Authority, Townsville*

No-take marine reserve networks can deliver impressive increases in the local abundance and size of exploited species, but larval dispersal makes it difficult to estimate their system-wide benefits. Australia's Great Barrier Reef (GBR) contains a network of hundreds of no-take marine reserves, covering 30% of its reef habitat. We combined GBR-wide fish surveys, a biophysical model and catch data to estimate the total ecological and economic contributions of reserves to reproductive output, larval supply, and commercial catch of the GBR's most important line fishery (coral groupers, *Plectropomus* spp). Marine reserves contain half of coral grouper biomass, and generate the majority of their reproductive output (55%). Our modelling shows they are responsible for the majority of GBR larval supply (53%), including 63% of larval supply into marine reserves and 51% of larval supply into fished areas. Finally, given the distribution of the commercial catch, we estimate that almost half of the fishery yield (48%) is made up of individuals spawned within the marine reserve network. On the GBR, dispersal creates mutually-supporting reserves, assuring the reserves are self-sustainable, while also exporting large numbers of larvae to the reefs targeted by the commercial fishing fleet.

Seeing through mud – Using mobile hydroacoustic sonar to monitor environmental watering outcomes

Lewis, Sam[1]; Bond, Nicholas[1]; King, Alison[1,2,3]; McPhan, Luke[1]; Trethewie, John[3]; Watts, Robyn[3]

[1]*Centre for Freshwater Ecosystems, La Trobe University, Wodonga, VIC, Australia*

[2] *Environment, CSIRO, Albury, NSW 2640 Australia*

[3] *Institute for Land, Water and Society, Charles Sturt University, Albury, NSW, Australia*

Since the breaking of the millennium drought (~2010) the Edward/Kolety-Wakool system has experienced several large unregulated flow events resulting in periodic hypoxic blackwater conditions throughout the system. In 2022 and 2023 unregulated flooding throughout the Murray catchment triggered the development of hypoxic blackwater conditions and resulted in localised mortality of fish and crustaceans. Commonwealth environmental water was delivered through Spring and Summer from several Murray Irrigation Limited (MIL) escapes in the Edward/Kolety-Wakool system to create small refuges of higher dissolved oxygen for fish and other aquatic biota. A concurrent contingency monitoring program was instigated to assess the environmental outcomes of the water delivery from two of the larger irrigation escapes; The Edward escape from Mulwala canal, and the Niemur escape from the Northern branch canal.We conducted a novel survey approach for fish abundances and species composition associated with the irrigation escape releases by point sampling the adjacent reaches using a boat mounted hydroacoustic camera (ARIS 1800, Sound Metrics Corp, Bellevue, WA, USA). Generalised linear mixed models showed a significant decline in dissolved oxygen concentration as distance from the release point increased and a positive correlation between large-bodied fish abundance and proximity to the irrigation escape release point. The mobile application of the ARIS1800 sonar offers advantages to other forms of fish survey methods as it allows non-intrusive observation and collection of key metrics while not being limited by light and water clarity making it particularly useful in freshwater environments.

Genetic stock structure of the silky shark *Carcharhinus falciformis* in the Indo-Pacific Ocean

Chia-Yun, Joanne Li[1]; Wen-Pei, Tsai[2]; Ranatunga, R.R.M.K.P. [3]; Munandar, Samidon[4]; Shang Yin Vanson Liu[1*]

[1]*Department of Marine Biotechnology and Resources, National Sun Yat-sen University, Kaohsiung, Taiwan*

[2]*Department of Fisheries Production and Management, National Kaohsiung University of Science and Technology, Kaohsiung, Taiwan*

[3]*Centre for Marine Science and Technology, Department of Zoology, University of Sri Jayewardenepura, Nugegoda, Sri Lanka*

[4]*Department of Marine Science, Teuku Umar University, Aceh Barat, Indonesia*

The silky shark (*Carcharhinus falciformis*) is a cosmopolitan species commonly caught as a bycatch for longline fisheries. However, the genetic stock structure in the Indo-Pacific Ocean is not well-defined yet. Here, we examined 307 individuals of silky sharks from 5 sampling locations across Indo-Pacific to reveal their genetic stock structure and effective population size by using eight microsatellite loci. A major genetic break was found between Aceh and the remaining locations (F_{ST} = 0.0505-0.0828, p = 0.001). A slightly lower effective population estimate (Ne) in the Indian Ocean compared to the Pacific Ocean may be due to the higher fishing pressure in the Indian Ocean. The lowest Ne was found in the Aceh population (Ne= 2.3), which may indicate a small and endemic population. These findings provide valuable information for the conservation and management of silky sharks. We suggested that the population around Aceh waters represents a unique stock and should be managed separately. Further studies on migratory and movement patterns are needed to define the boundaries of different stocks to effectively manage silky sharks in the Indo-Pacific region.

The ripple effect of predator removal: results from a five-year trout removal trial in a mountain stream

Lieschke, Jason[1]; West, Matt[2]

[1]*Arthur Rylah Institute for Environmental Research*

[2]*Wild Research Pty Ltd*

Non-native fish (trout) are regarded as key threat to native freshwater fauna in south-eastern Australia, but their impact on native species has rarely been quantified. In conjunction with a range of partners including the Australian Trout Foundation, a 5-year study was undertaken in small tributaries of Lake Eildon to evaluate the impact of trout removal on the survival of the critically endangered spotted tree frog. Subsequently, this study allowed us to examine native fish and crayfish responses to the removal. In Autumn 2021, 2022 and 2023, the surveys were repeated, but with trout removed from the impact site. Above the impact site trout have been removed for up-to 18 kilometres each year (in autumn 2021-23), resulting in the removal of 14,000 trout.

In 2022, the first year after trout removal at the impact site, an increase of two-spined blackfish recruitment – Young-of-Year fish was observed, whereas the control site had similar abundances and low levels of two-spined blackfish recruitment. Similar recruitment was observed in 2023.

Changes in climate will inevitably lead to a reduction in the range of wild populations of salmonids in Australia. Understanding and capitalising on such responses will be vital in the planning for Fishery and NRM outcomes.

5.2A Special Session 1 Moving beyond home-ranges: how can we harness fish movement ecology to study, understand and manage ecosystem functioning?, 260-073, November 24, 2023, 10:30 AM - 12:30 PM

Assessing ecosystem functioning through 3D AI-enhanced fish tracking: A Red Sea Case Study

Lilkendey, Julian[1]; Barrelet, Cyril[2]; Chaumont, Marc[2,3]; Larbi, Houssam[2]; Meares, Michael[1]; Sabetian, Armagan[1]; Subsol, Gérard[2]; Zhang, Jingjing[1,4]

[1]School of Science, Auckland University of Technology (AUT), Auckland, New Zealand

[2]Laboratoire d'informatique, de robotique et de microélectronique de Montpellier (LIRMM), University of Montpellier/CNRS, France

[3]University of Nîmes, Nîmes, France

[4]The New Zealand Institute for Plant and Food Research Limited, Auckland, New Zealand

Anthropogenic pressures are placing coral reefs, crucial pillars of marine biodiversity, under increasing threat. A key challenge in managing these sensitive ecosystems lies in understanding the fine-scale movement ecology of herbivorous fish. Their grazing behaviour has a significant impact on the health and function of coral reefs.

In this study, we harness the power of AI-driven 3D tracking technologies and stereo-video measurements. We aim to explore the foraging behaviour of two dominant grazers, Brown surgeonfish *Acanthurus nigrofuscus* and Yellowtail tang *Zebrasoma xanthurum*, in a severely degraded coral reef system in Eilat, Israel, Gulf of Aqaba, Red Sea. We reveal complex energy-distance trade-offs between bite distance and feeding intensity. The species optimise their foraging strategies and energy expenditure in accordance with the distribution of grazable substrate patches. Remarkably, despite different foraging strategies, both species maintain similar energy expenditure levels, demonstrating a sophisticated adaptation to spatial resource heterogeneity.

By showcasing the potential of AI and 3D tracking technologies to provide detailed insights into species-specific foraging behaviour, this study enhances our understanding of fine-scale fish movement and ecosystem functioning. Our results underscore the importance of leveraging advanced technologies and interdisciplinary approaches for ecosystem management, highlighting the potential of integrating these tools and knowledge into effective conservation strategies for these at-risk ecosystems.

Genetic barcoding and population biology of diadromous fish, shrimp and snails native to Guam.

Lindstrom, Daniel[1]

[1]*University of Guam, College of Natural and Applied Science, Division of Natural Science, Biology Program*

Guam is an isolated oceanic island separated by great distances from other islands and continents that have freshwater rivers, streams and associated fauna. Freshwater streams on Guam are home to 9 named species of diadromous teleost fishes (anadromous, diadromous, and amphidromous), 19 putative species of amphidromous gastropods and at least 6 amphidromous decapod shrimp which are all presumed to be native. None of these species affinities have been confirmed using genetic barcoding techniques, thus limiting further research and conservation efforts on many fronts. Up to10 individuals of all target species present in several reaches of all 16 of Guam's watersheds were collected, high resolution photo-documented, biopsied, and preserved. Genomic DNA was purified, PCR amplified targeting the Cytochrome-Oxidase I (COI) gene and sequenced to produce genetic barcodes. Barcode sequences were then compared to all other specimens and those in GenBank to confirm or refute species affinities. Additionally, some samples underwent MIG-seq genotyping to further discern species affinities and population structure of species with unclear barcode outcomes and/or contrasting life histories. During these genetic studies on all specimens, several cryptic species were identified, and population structure discerned. Confirmation of all species present in Guam’s streams and their native and/or endemic status is essential before future population genetics, biogeographic research and conservation planning can be executed.

How low can we go? Targeted removal of exotic fish at Lake Tomorata

Ling, Nicholas[1]; Studholme, Belinda[2]

[1]*The University of Waikato, Hamilton, New Zealand*

[2]*Auckland Council, Auckland, New Zealand*

Lake Tomorata is a small, shallow, dystrophic dune lake in northern New Zealand (36°11’37”S, 174 39’00”E). Exotic tench (*Tinca tinca*) and rudd (*Scardinius erythrophthalmus*) were introduced illegally to the lake in 1971. A fish survey in 2019 confirmed that both species were abundant and likely negatively impacting the lake ecology.

Targeted fishing using gill nets of varying mesh sizes aims to significantly reduce exotic fish biomass with the ultimate aim of eradicating both species. An initial removal in 2022 involved 19.4 net night km, with nets spanning the lake at 50 m intervals. Total catch comprised 119 tench and 709 rudd, with removal approximating 75% for tench and 98% for rudd, averaged across 6 different statistical methods. However, all methods underestimated total population size for both species. A second removal in 2023 deploying 11.4 net night km removed 79 tench and 195 rudd. Population estimates in 2023 indicated a much lower population than 2022 but higher than expected. Initial CPUE values for 2023 were only slightly reduced for tench but 87% lower for rudd, compared to 2022. However, CPUE for both species declined significantly with removal estimated at greater than 80% of the residual population for both species.

Tench proved more problematic than rudd due to their tendency to be strongly associated with littoral emergent vegetation. The species ratio (rudd:tench) declined from 5.96 in 2022 to 2.47 in 2023. Subsequent fishing will continue to target these species to attempt eradication and restore the ecology of this lake ecosystem.

New hadal snailfish species represents an independent radiation of vertebrates into the hadal zone

Linley, Thom[1,2]; Canto-Hernández, Jhoann[3]; Fernandez, Vincent[4]; Gerringer, Mackenzie[5]; Glud, Ronnie[6,7,8]; Jamieson, Alan[9]; Ritchie, Heather[10]; Scott-Murray, Amy[4]; Frank Wenzhöfer[6,11,12]; Weston, Johanna[2]

[1]*Museum of Te Papa Tongarewa, Fish Collection, Tory Street Facility, 169 Tory Street, 6011 Wellington, New Zealand*

[2]*School of Natural and Environmental Sciences, Newcastle University, Ridley Building, Newcastle-upon-Tyne NE17RU, UK*

[3]*Jefe de Área Zoología Vertebrados, Museo Nacional de Historia Natural, Santiago, Chile*

[4]*Imaging and Analysis Centre, The Natural History Museum, Cromwell Road, London SW7 5BD, UK*

[5]*State University of New York at Geneseo, Geneseo, NY 14454, USA*

[6]*Nordcee and HADAL, Department of Biology, University of Southern Denmark, 5230 Odense M, Denmark*

[7]*Department of Ocean and Environmental Sciences, Tokyo University of Marine Science and Technology, Tokyo 108-8477, Japan*

[8]*Danish Institute of Advanced Study, University of Southern Denmark, 5230 Odense M, Denmark*

[9]*Minderoo-UWA Deep-Sea Research Centre, School of Biological Sciences and Oceans Institute, The University of Western Australia, IOMRC Building M470, 35 Stirling Highway, Perth, WA 6009, Australia*

[10]*Japan Agency for Marine-Earth Science and Technology (JAMSTEC), 2-15 Natsushima, Yokosuka, Kanagawa 237-0061, Japan*

[11]*HGF-MPG Group for Deep Sea Ecology and Technology, Alfred Wegener Institute Helmholtz Center for Polar and Marine Research, 27570 Bremerhaven, Germany*

[12]*HGF-MPG Group for Deep Sea Ecology and Technology, Max Planck Institute for Marine Microbiology, 28357 Bremen, Germany*

Snailfishes (Liparidae) are among the most rapidly radiating families of marine fishes, resulting in a global distribution from the coastal intertidal to deep subduction trenches. The true diversity and distribution of deepwater snailfishes, particularly at hadal depths (>6000 m) and in the Southern Hemisphere, has yet to be determined due to the rarity of samples. Three hadal snailfishes were observed in the Atacama Trench, which runs along the southwest coast of South America. A single specimen of a novel snailfish species was recovered from 6714 m. The new species represents the first hadal *Paraliparis* and is revealed to be an independent radiation into the ocean's deepest zone. There is evidence that this independent radiation originated from the highly diverse snailfishes of the Southern Ocean. The liparids continue to reveal themselves as a family particularly suited to adapting to life in the hadal zone.

Characteristics of a newly-discovered population of the critically endangered stocky galaxias

Lintermans, Mark[1,2]

[1]*Fish Fondler Pty Ltd,*

[2] *Centre of Applied Water Science, University of Canberra*,

The fish fauna of the upland streams of the Australian Alps are dominated by the alien salmonids Rainbow trout and Brown trout. Salmonids have severely impacted the distribution and abundance of many native fish species, including the Galaxiidae, which generally only persist where trout are absent. The critically endangered Stocky galaxias *Galaxias tantanagara* is one of 14 new species described in 2014 from the Mountain galaxias complex, with 11 of these new species now listed as threatened under Australia's Environmental Protection and Biodiversity Conservation Act 1999. Trout predation is the major threat to all of these newly described and listed species. Until recently, Stocky galaxias was only known from a single, small, headwater stream in the upper Murrumbidgee Catchment upstream of Tantangara dam in the Snowy Mountains, where it was the only fish species present. Serendipitously, a second population was discovered in an even smaller isolated headwater stream in another sub catchment in 2021. This presentation details investigations to determine the extent and size of this new population, and the spatial interactions with another galaxias species present. The new population occurs in <3 km of Sallys Flat Creek at an elevation of ~1345 m ASL where it co-occurs with the Mountain galaxias *G. olidus*. The stream is an isolated headwater above a 25m high series of waterfalls that excludes trout. Stocky galaxias is distributed along the entire length of the creek upstream of the waterfall, but Mountain galaxias are only present across ~50% of this distribution.

What’s on the menu? Elucidating the diet and habitat use of immature white sharks in eastern Australia using biochemical tracers

Lipscombe, Rebecca[1]; Butcher, Paul[1,2]; Butcherine, Peter[1]; Huveneers, Charlie[3]; Meyer, Lauren[3]; Morris, Stephen[2]; Scott, Anna[1]

[1]*Southern Cross University, Australia*

[2]*New South Wales Department of Primary Industries, Australia*

[3] *Flinders University, Australia*

White sharks (*Carcharodon carcharias*) play a crucial ecological role, shaping ecosystems through direct predation, and indirectly through predator-prey interactions. On the east coast of Australia, immature white sharks are broadly distributed, inhabiting a wide range of habitats and ecosystems from temperate regions of southern New South Wales and Bass Strait in summer to tropical regions as far north as the Great Barrier Reef, Queensland in winter. We examined the diet and habitat use of 136 immature white sharks along the east Australian coast using stable isotopes and fatty acids in muscle and plasma, facilitating the assessment of white shark trophic ecology across different timescales from a few weeks up to approximately a year. Biochemistry of muscle samples showed that white sharks predominantly feed at low trophic levels in coastal environments, with demersal elasmobranchs and mullet *(Mugil cephalus*) being the largest contributor to their diet. A seasonal shift in diet was evident, driven by higher proportions of essential fatty acids in muscle tissues in spring and summer compared to other seasons, suggesting that prey items consumed during these seasons are of higher nutritional quality. By combining stable isotope and fatty acid analysis, we gain a comprehensive understanding of immature white shark diet in eastern Australian waters. Our results confirm that these white sharks are generalist predators that adapt to seasonal changes in prey availability. Their high use of coastal habitats reinforces the importance of these areas for foraging, which is crucial for growth and development during this critical life stage.

Optimising and sustaining an integrated biological monitoring program for fisheries in Queensland waters: Focus on Fish and Sharks

Litherland, Lenore[1]

[1]*Fisheries Queensland, Department of Agriculture and Fisheries, Brisbane.*

Long-term monitoring of fisheries is crucial for effective conservation and fisheries management. In Queensland waters, Fisheries Queensland operates a state-wide monitoring program that collects biological data on harvested fish, crustaceans, molluscs, and sharks. This program combines field observations and laboratory analyses to enhance knowledge of fished populations throughout the region.

The multi-decadal program incorporates fishery dependent sampling, including boat ramp surveys, roving shore-based surveys, frame donation programs, fish market surveys, and on-board surveys. Standardized methods ensure integrated representative sampling across different fisheries. Additionally, fishery-independent sampling, including otter trawl, beam trawl, and dilly nets, establish abundance indices for select species. Laboratory techniques encompass otolith extraction for fish aging, DNA barcoding for accurate species identification and high-throughput sequencing for population structure analysis. Quality and efficiency are prioritised through meticulous data recording, organisation, and analysis. Software systems, including electronic data entry, data visualization dashboards, fish aging training programs, and version-controlled data streamlining support these processes.

Integrating species, length, sex, and age data with commercial and recreational catch and effort information and social and economic survey data has proven instrumental in assessing Queensland fish stocks. Insights guide fisheries management by informing harvest strategies, quotas, and spatial management for sustainable exploitation and the preservation of healthy fish populations.

Sustaining monitoring programs presents challenges, including inconsistent funding, methodological drift, stakeholder participation and adaptability to management or environmental changes. This presentation showcases the monitoring of Tailor (*Pomatomus saltatrix*) and sharks, highlighting the program’s diverse approaches, and sharing lessons learned in maintaining a relevant and adaptive monitoring program.

Technical and operational development of MLAI technology for application to electronic monitoring in marine fisheries

Little, L. Richard[1]; Cannard, Toni[2]; Khokher, M. Rizwan[3]; Saqib, Muhammad[3]; Tuck, Geoff[1]; Untiedt, Candice[1]; Wang, Dadong[3]; Yan, Bo[3]; Guan, Xinlong[3]; Yuan, Xin[3]

[1]*CSIRO Environment, Hobart TAS Australia*

[2]*CSIRO Environment, QLD Bioscience Precinct, St. Lucia, QLD, Australia*

[3]*CSIRO Data 61, Marsfield, NSW, Australia*

Fisheries around the world are moving towards electronic-monitoring (EM), and Machine Learning and Artificial Intelligence (MLAI) application to EM is not far behind. There is no doubt that the impact of on-vessel species identification will be large. The wild capture fisheries in Australia are worth $2.5b AUD annually, but globally tuna fisheries alone are worth over $42 billion USD.

Electronic monitoring (EM) cameras are currently deployed to 75 Australian federally managed fishing vessels in four fisheries, with the understanding that this number may increase in the coming years. Current EM reviewing costs to both government and industry alone are high. Automated species identification using MLAI will have a large impact in reducing costs to industry and government regulatory agencies. It will also increase the coverage of the fishery so that an entire fishing fleet is monitored. This will result in better governance and management outcomes of publicly owned resources, as well as better environmental outcomes.

The CSIRO Marine Visual Technologies team (MVT) have been actively developing the application of MLAI technology for fishery management with successfully developed algorithms and techniques. We will show our developed workflow for the process which includes a catch detector (called SNAPPER), a species identification algorithm (called WANDA™) that classifies commercial catch and bycatch on longline vessels, a tracker, video quality improvement techniques and an on-line cloud-based reporting and auditing system.

Poster Function, OGGB Level 0 Foyer, November 21, 2023, 4:15 PM - 6:30 PM

The role of colour patterns in anemonefish species recognition

Locke, Noah

Okinawa Institute of Science and Technology (OIST)

Colour patterns in fish are an important means of visual communication. Anemonefish have a distinctive colour pattern of vertical white bars on an orange, red, or black body, and the number of bars tends to be species specific. Anemonefish are known to inhabit and protect a host anemone, the species of which differs between the species of anemonefish. Cohabitation can be observed in host anemones, usually with fish that have different colour patterns than that of the resident anemonefish. For example if a species of anemonefish with 3 bars was inhabiting a host anemone, there would likely not be cohabitation with another 3 bar species. This tank experiment looked at duration of aggressive behaviours by *Amphiprion ocellaris*, an anemonefish with 3 white bars, towards heterospecific and conspecific intruder fish of genus *Amphiprion* with varying numbers of white bars. Longer durations of aggressive behaviour were displayed by *A. ocellaris* towards conspecific intruder fish, and duration of aggressive behaviours towards *A. ocellaris* was significantly longer than towards *A. sandaracinos*, a species with no bars. Duration of aggressive behaviours towards other species investigated, *A. polymnus* (1 bar) and *A. clarkii* (3 bars), fell between these two extremes. These results suggest colour patterns are utilised by anemonefish for species identification, although number of bars is likely not the only factor, and indicate colour patterns as a key feature for inter- and intra-specific interactions in anemonefish.

Dissemination of knowledge on freshwater fish in remote tropical islands. The example of research in the Solomon Islands

Clara Lord[1], David Boseto[2], Philippe Keith[1]

[1]*Unité Biologie des Organismes et Écosystèmes Aquatiques-BOREA, Sorbonne Université, Muséum National d'Histoire Naturelle, CNRS, IRD, UCN, UA, CP 26, 43 rue cuvier, 75005 Paris, France*
[2]*Ecological Solutions Solomon Islands, Gizo, Western Province, Solomon Islands*

The protection and the implementation of conservation and protection measures are based on the acute knowledge of the species present in their habitat and their geographic distribution. To know which species are present also enables to undertake research on their biology and ecology, which have to be considered while writing conservation plans. For many years now our team has worked on the inventory of freshwater fish of the Solomon Islands. Prior to each field survey, a social assessment plan was written for each island studied to comply with Safeguard Policy on Indigenous Peoples; there was an initial understanding via consultation meetings with local communities of each site visited and actions were taken for the participation and consent of local communities to the project. When in the field, at each site, new meetings were organized before work started, and restitutions were done before departure. During the field trips, local staff from villages was trained in species identification, stream management and ecology of freshwater fauna. Each time, relevant government institutions and community members were involved, providing opportunities for capacity building in taxonomy and life cycle studies. All this work enabled us to publish a guide to freshwater fish of the Solomon Islands (written in English and Pidgin), which was given to government authorities, Solomon Islands National University, schools and village libraries, raising awareness on the stream biodiversity and the importance of protecting it. This work is particularly important in the context of tropical islands, which are threatened by logging and mining activities.

Discovery of parasites of tropical island freshwater fish: a new angle to study migrations of diadromous species.

Lord, Clara[1], Audebert, Fabienne[1], Mathews, Patrick D.[1]

[1]*Unité Biologie des Organismes et Écosystèmes Aquatiques-BOREA, Sorbonne Université, Muséum National d'Histoire Naturelle, CNRS, IRD, UCN, UA, CP 26, 43 rue cuvier, 75005 Paris, France*

Tropical island streams are home to diadromous species. These species migrate between freshwater and seawater during their life cycle. For instance, eels live in freshwater and migrate to the sea to reproduce. Amphidromous gobies, such as Sicydiinae gobies live and reproduce in the river, at hatching larvae migrate downstream to the sea where they spend 3 to 6 months before recruiting back to freshwater. The search for parasites in these freshwater species has seldom been done. Recently, we discovered a new species of cnidarian parasite, *Myxobolus choiseulae* n. sp., on an eel *Anguilla marmorata* from the Solomon Islands. We also discovered the presence of a Digenean (Cryptogonimidae) *Stemmatostoma cribbi* on a cling goby species, *Sicyopterus cynocephalus* from the Solomon Islands, attesting for the first time that this fish species is an intermediate host just as like Eleotridae. The high genetic similarity between the Solomon Islands isolate and the Australian isolate of *S. cribbi* is likely a result of the amphidromous life cycle of the different possible hosts. Therefore, the study of tropical island fish parasites and the geographic distribution of both the parasites and the hosts may represent a new interesting angle to study fish migrations. Finally a comprehensive data set including molecular data and phylogenetic analysis of the many yet-to-be-discovered parasite species from these underrepresented hosts should help understand the processes involved in the colonisation of tropical island rivers.

Resolving the evolutionary relationships of the order Centrarchiformes using genomic data and dense taxonomic sampling

Ludt, William[1]; Bernardi, Giacomo[2]; Chakrabarty, Prosanta[3]; Clements, Kendall[4]; Hobbs, Jean-Paul[5]; Near, Thomas[6]; Sandel, Michael[7]; Unmack, Peter[8]

[1]*Natural History Museum of Los Angeles County*

[2]*University of California Santa Cruz*

[3]*Louisiana State University*

[4]*University of Auckland*

[5]*University of Queensland*

[6]*Yale University*

[7]*Mississippi State University*

[8]*University of Canberra*

The order Centrarchiformes contains approximately 300 species classified into 19 families that are distributed worldwide in both freshwater and marine systems. Many of these fishes occur widely throughout the Indo-Pacific, including familiar families such as the Terapontidae, Kyphosidae, and Cirrhitidae. This order contains many commercially important species, as well as species popular in the aquarium trade. While a variety of centrarchiform fishes are economically important, many also provide essential ecosystem functions. Despite their economic and ecological importance, little is known about the evolutionary history of these fishes, as this order wasn't recognized until the inclusion of molecular data in large-scale fish phylogenetic studies. However, there are considerable differences in the hypothesized phylogenetic relationships of this group among the molecular studies that have included multiple families from this order. Insufficient genomic and taxonomic sampling likely cause these disparities, as most previous studies fail to include representatives from all centrarchiform families, have limited taxonomic sampling within these families, or only sample a handful of loci. Here we take a phylogenomic approach to examine the evolutionary history of this order using approximately 400 ultraconserved elements with dense taxonomic sampling that includes 85% of the accepted centrarchiform genera and 193 species. Relationships from multiple analyses are largely congruent, well-supported and agree with several prior findings. However, difficulty remains in determining the evolutionary relationships among families within the Terapontoidei. We discuss the implications of our findings, and highlight future directions that will further our understanding of this order of fishes.

Functional and taxonomic beta-diversity of freshwater fishes across northern Australia river basins

Luiz, Osmar[1]; Kopf, Keller[1]

[1]*Research Institution for the Environment and Livelihoods, Charles Darwin University, Darwin NT, Australia*

Australia’s freshwater fishes manifest a unique marine signature, diverging from the ostariophysan dominance witnessed on other continents. Despite the global recognition of Australia's distinctive mammal fauna, the fish fauna also exhibits noteworthy singularity. Evolution in a unpredictable environment created a depauperate yet resilient fish fauna, characterized by adaptations to exploit and survive these conditions. However, the relative distinctiveness of Australian fish fauna, compared to other well-studied continents, remains largely unexplored. Employing a functional ecological approach, our study quantified taxonomic and functional beta-diversity of fish communities at the watershed-scale across Northern Australia. Congruencies between diversity facets were assessed, with variation between watersheds quantified using Jaccard’s dissimilarity index. The relationship between alpha and beta diversity for each diversity facet was determined, and the relative contribution of each species to watershed’s alpha taxonomic and functional diversity was gauged. Our findings highlight how tide incursions and estuary influence impact riverine systems, constricting species and trait occurrences, thereby driving patterns of taxonomic and functional turnover. The variability in freshwater fish beta-diversity was shown to be contingent on the proportion of species with saltwater affinity and assemblage composition along estuarine gradients. Functional dissimilarity appeared limited in space and time. This study illuminates the considerable influence of ecological connectivity with the marine ecosystem in promoting local diversity. Despite the influence of myriad environmental factors, the marine linkage emerges as a pivotal component in shaping Australia's unique freshwater fish diversity. This work lays groundwork for future research into understanding the complexities and uniqueness of Australia’s aquatic biodiversity.

Phylogenetic patterns and diversification rates of scalpel morphology and the novel venom delivery system of surgeonfishes (Acanthuridae)

Lungstrom, Linnea[1,2]; Westneat, Mark[1,2]

[1]*University of Chicago, Chicago IL, USA*

[2]*Field Museum of Natural History, Chicago IL, USA*

Coral reef fishes are morphologically and ecologically diverse, providing useful systems for the exploration of structure, function, and behavior. Morphological adaptations for defense often promote the survival and diversification of fishes by aiding in ecological interactions. One such example is that of a venom delivery system (VDS), which has evolved several times in fishes. The surgeonfishes (Acanthuridae) are an ideal family to study the morphology of venom delivery as all acanthurids have modified scales (scalpels) on their caudal peduncles, many of which are capable of venom delivery. Previous research has shown that 6 of the 84 species of surgeonfishes are venomous. Here, we employ a morphological survey of scalpels and venom glands and grooves within a new phylogeny for the surgeonfishes to assess the prevalence of venom glands and compare VDS-related morphology across the Acanthuridae using museum and fresh specimens. Results show that venom production is more prevalent across surgeonfishes than previously thought, especially in the genera *Acanthurus* and *Ctenochaetus*. The effect of venom prevalence and associated morphology on diversification rates was analyzed using state-dependent speciation and extinction models. We conclude that morphological traits and variation in diversification rates are associated with venom production. Understanding how venom production is associated with locomotor structures, morphological traits, and phylogenetic diversification rates reveals the influences of the defensive Acanthuridae VDS on the evolution of this ecologically and economically important clade of coral reef fishes.

1.3A Themed Session: J. Fisheries Management, 260-115, November 20, 2023, 11:15 AM - 1:00 PM

Global drivers of tropical marine herbivorous fish catches

Lutzenkirchen, Lucas[1]; Bellwood, David[1]; Tebbett, Sterling[1]; Yan, Helen[1]

[1] *Research Hub for Coral Reef Ecosystem Functions and College of Science and Engineering, James Cook University, Townsville, Queensland 4811, Australia*

Sustainable food security in the Anthropocene is a critical challenge. Human activities have significantly altered the Earth's ecosystems, including coastal seascapes that are important for fisheries. Recent work found that coral reefs in the Anthropocene may no longer be able to provide ecosystem services, as indicated by a 63% decline in catch per unit effort (CPUE) of reef-associated fishes since the 1990s. Herbivorous fishes play a crucial role in coral reef ecosystems by grazing on algae and other plants, which can help to prevent overgrowth and improve water quality. They also provide a nutritious and sustainable source of protein for human communities. However, global catch patterns and broadscale assessments of potential overexploitation remain elusive. We used reported and reconstructed catch data from the Sea Around Us database to explore potential drivers of herbivore catch. We found that catch per unit effort data of rabbitfishes, as well as parrotfishes and surgeonfishes, suggests global overexploitation, with declines in CPUE exceeding previous estimates. Given the accumulation of stressors due to climate change, the sustainability and resilience of coastal seascape fisheries are in question. Climate change impacts are likely to exacerbate mismatches between the nutritional needs of ever-growing coastal populations and herbivore abundance, with serious potential ramifications for coastal communities, especially in island states.

Assembly rules of coral reef fish communities along the depth gradient

MacDonald, Chancey[1,2,*]; Loss, Ana Carolina[6]; Phelps, Tyler[2,5]; Pinheiro, Hudson[2,3,*]; Quimbayo, Juan Pablo[2,3]; Rocha, Luiz[2]; Shepherd, Bart[4]; Teixeira, Joao Batista[7]

[1]*School of Biology, University of Leeds, Leeds, United Kingdom*

[2]*Department of Ichthyology, California Academy of Sciences, San Francisco, CA, USA*

[3]*Center for Marine Biology, University of Sao Paulo, Sao Sebastiao, SP, Brazil*

[4]*Steinhart Aquarium, California Academy of Sciences, San Francisco, CA, USA*

[5]*Department of Biology, San Francisco State University, San Francisco, CA, USA*

[6]*Instituto Nacional da Mata Atlantica, Santa Teresa, ES, Brazil*

[7]*Departamento de Oceanografia, Universidade Federal do Espirito Santo, Vitoria, ES, Brazil*

[*]*Co-lead authors.*

Coral reefs are home to some of the most studied ecological assemblages on the planet. However, differences in large-scale assembly rules have never been studied using empirical quantitative data stratified along the depth gradient of reefs. Consequently, little is known about the small- and regional-scale effects of depth on coral reef assemblages. Using a large dataset of underwater surveys, we observed that the influence of classic biogeographic drivers on the species richness of coral reef fishes changes significantly with depth, shaping distinct assemblages governed by different rules in mesophotic coral ecosystems. We show that a general pattern of decreased taxonomic and functional richness of reef fish assemblages with depth results from convergent filtering of species composition and trophic strategies on deeper reefs across ocean basins and that at smaller scales deep-reef communities are less influenced by regional factors than shallower reefs.

Morphological diversity of the oral lures of Stargazers (Uranoscopidae: *Uranoscopus*)

MacLeod, Leo[1,2]; Bemis, Kate[2]; Farina, Stacy[1]

[1]*Howard University, Department of Biology, Washington D.C., USA*

[2]*Smithsonian Institute, National Museum of Natural History, Department of Vertebrate Zoology, Washington D.C., USA*

Within the family Uranoscopidae, commonly known as Stargazers, *Uranoscopus* is the largest genus (30 valid species) and inhabits the tropical and temperate waters throughout the Mediterranean, West Africa, and the Indo-Pacific. Stargazers are ambush predators that bury into the sediment until only the eyes and dorsal region of the mouth are visible. While buried, many species of *Uranoscopus* use water flow to flick a lure out of the mouth to entice prey closer. In this study, we examined the extreme morphological diversity in the lures of *Uranoscopus* from across the Indo-Pacific. The lure is attached to a membrane on the inside of the lower jaw and is diverse in size, shape, and colour. For example, some species, the lure is black with a simple thread shape, while in others it is an orange filamentous pompom. We describe the variation both within and between species and discuss use and challenges of the lure as a phylogenetic character.

Decomposing global trade in shark and ray meat

MacNeil, M Aaron[1]; Babcock, Elizabeth[2]; Chapman, Demian[3]; Martins, Ana[1]; Mull, Chris[1]; Tyabji, Zoya[1]

[1]*Department of Biology, Dalhousie University, Halifax NS, Canada*

[2]*Rosenstiel School of Marine, Atmospheric, and Earth Science; University of Miami, Miami FL, USA*

[3]*Mote Marine Laboratory, Sarasota FL, USA*

Understanding trade in marine resources is challenging given the high uncertainty surrounding the species landed, rates of domestic consumption, and mis-reported imports and exports. This challenge is further confounded for sharks and rays that present very different markets for fin versus non-fin commodities – including meat, oil, and cartilage. While the global trade in shark fins is relatively understood, trade in shark meat presents a potentially increasing threat to shark populations, driven in part by elevated demand and the potential emergence of new markets due to “fins attached” policies. Here we decompose global trade in shark and ray meat using a unique modelling approach that identifies key species correlations and integrates expert information, revealing both broad trends in demand as well as the identities of the species involved. We show distinct trade flows for shark meat relative to rays, and highlight potential species of concern. This work establishes a new baseline for monitoring trade in shark meat that will facilitate dynamic understanding the role of regulatory change in addressing demand for shark and ray products.

Migration and distribution patterns of freshwater gobies of the genus *Rhinogobius* in continental rivers and tropical island's streams

Maeda, Ken[1]; Iida, Midori[2]; Kobayashi, Hirozumi[3]; Shirai, Kotaro[4], Palla, Herminie P[5], Tran, Hau Duc[6]

[1]*Marine Eco-Evo-Devo Unit, Okinawa Institute of Science and Technology Graduate University*

[2]*Sado Marine Biological Station, Niigata University*

[3]*Tropical Biosphere Research Center, University of the Ryukyus*

[4]*Atmosphere and Ocean Research Institute, the University of Tokyo*

[5]*Western Philippines University, Puerto Princesa Campus*

[6]*Hanoi National University of Education*

Rhinogobius is a genus of freshwater goby distributed in East and Southeast Asia, and is composed of many species with various migration patterns, including amphidromous species with a marine larval phase, large-egg spawner with direct-developing life cycle, fluvial species with a larval life in the upper reaches, lentic species living in lakes and marshes, etc. They are very unique and interesting material to understand evolution involving a shift of the migration pattern, because it is considered that migration patterns have often changed during their evolution history. While many researches have been conducted on species from temperate and subtropical islands of Japan, knowledge is poor from other regions with different environments, such as continental rivers and tropical islands. What migration patterns evolved under each environmental condition?

In this study, we surveyed distribution of *Rhinogobius* species in continental rivers of Vietnam and tropical island's streams of Palawan, Philippines, and investigated their migration patterns by otolith microchemistry analysis. The profiles of Sr:Ca ratio suggested that nine Vietnamese species examined include both typical amphidromous species and freshwater residents. The amphidromous species have relatively wide distribution range along the coast line. By contrast, two Palawan species are freshwater residents, even though they inhabit small streams near the sea. The two species have been found only in the respective single stream. The results suggested that migration patterns differ depending on the environment. This could be more interesting in future when discussed with population genetics, phylogeny, and life history traits including their egg sizes.

Post-release mortality of line-caught snapper (*Chrysophrys auratus*: Sparidae) depends on hook site and capture depth: results from a controlled field experiment

Maggs, Jade[1]; Evans, Oliver[1]; Hartill, Bruce[1,2]; Holdsworth, John[3]; Lumley, Thomas[4]

[1]*National Institute of Water and Atmospheric Research Ltd (NIWA), Private Bag 99940, Newmarket, Auckland 1149, New Zealand*

[2]*Fisheries New Zealand, MPI Centre, 17 Maurice Wilson Avenue, Mangere 2022, Auckland, New Zealand*

[3]*Blue Water Marine Research, P.O. Box 402081, Tutukaka, Northland 0173, New Zealand*

[4]*Department of Statistics, University of Auckland, 38 Princes Street, Auckland 1010, New Zealand*

Catch-and-release angling is common in recreational fisheries, but mortality may be high among released fish although not readily observable. This cryptic mortality is often overlooked in stock assessments or when changes are made to catch limiting regulations. We conducted a controlled field experiment to estimate the post-release mortality rate on snapper *Chrysophrys auratus* associated with capture depth and anatomical hook site. Volunteer fishers caught 960 treatment snapper across three capture depth strata (shallow, <15 m; medium, 15–25 m; deep, 26–40 m), which were either lip-hooked, foul-hooked on the exterior body surface or gut-hooked (deep hooked in the gills, throat or oesophagus). A bottom longline vessel caught 162 lip-hooked control fish in shallow water. All fish were transported from the capture vessel to one of nine, 15-m deep, holding nets. Overall, 80% of the treatment fish survived. Both hook site and capture depth were significant predictors of post-release mortality. In lip-hooked fish, the probability of mortality was low when capture depth was less than 10 m (<0.02) but increased rapidly as depth increased to 20 m (0.24), at which point the mortality rate stabilised. In foul-hooked fish, mortality increased steadily with capture depth (from 0.05 to 0.65). The highest mortality rates were for gut-hooked fish (0.48–0.98). Notwithstanding a low incidence of gut-hooked fish, and therefore a small sample size for this hook site, the effect of gut-hooking appeared to entirely override the effect of depth. All control fish survived. Potential measures for mitigating post-release mortality are briefly discussed.

Morphology and metabolic traits related to swimming in tāmure/ Australasian snapper (*Chrysophrys auratus*) selected for fast growth

Magnoni, Leonardo J[1]; Black, Suzy[1]; Collins, Selwyn[1,2]; Wellenreuther, Maren[1,3]; Wylie, Matthew J[1]

[1]*Seafood Production Group, The New Zealand Institute for Plant and Food Research Limited*

[2]*Leigh Marine Laboratory, Institute of Marine Science, University of Auckland*

[3]*School of Biological Sciences, University of Auckland*

Swimming is a fundamental activity contributing to the fitness of fish. Changes in body shape are linked to swimming performance and become a relevant aspect in selective breeding programmes aiming to maximise growth. We studied how selective breeding affects fish phenotypes by investigating the relationship between swimming performance and body shape, which is highly relevant for future aquaculture production systems. Critical swimming speed (U_{crit}) was evaluated along with body weight (BW), body length (BL), condition factor (K), and plasma metabolite levels (lactate and glucose) in two snapper populations; one derived from wild broodstock (F_1 generation), the other selected for fast growth (F_4 generation). U_{crit} was determined by implementing eight independent tests per population, and parameters were obtained at the end of the tests (10 fish/test). Selection for fast growth in the F_4 generation produces changes in body shape by increasing K by 5.5%, although this did not change the absolute U_{crit} (0.68 m/s) in fish of equivalent BW and BL (71.7 g and 14.6 cm). The absolute U_{crit} and plasma lactate levels showed no correlation in both populations (R^2 <0.014). The variation in the absolute U_{crit} was similar between both populations (SD <0.06), although plasma lactate levels were consistently higher in snapper from the F_4 population subjected to exhaustive swimming (4.7 vs 2.8 mM for F_1). Taken together, this study suggests that selective breeding modifies the body shape of snapper without an apparent effect on the U_{crit}, changing plasma metabolic traits as well in fish subjected to high-intensity swimming.

Broad scale prioritization of fish barriers across Aotearoa New Zealand

Mahlum, Shad[1]; Baker, Cindy[1]; Franklin, Paul[1]

[1]National Institute of Water and Atmospheric Research, Hamilton, New Zealand

Enhancing riverscape connectivity is a crucial issue that must be addressed to ensure the health of aquatic ecosystems. In response, the New Zealand government has mandated regional councils to formulate a comprehensive Fish Passage Action Plan (FPAP) aimed at re-establishing river connectivity to safeguard the long-term survival of vital ecological and cultural aquatic species. Although methods for measuring river fragmentation have been available for over 15 years, the recent development of open-source tools now enables managers to calculate fragmentation indices across focal catchments. This project quantifies river connectivity at the catchment level across NZ using the Dendritic Connectivity Index and prioritizes fish passage remediation efforts by identifying key instream structures that will yield the greatest gains in connectivity. By assessing connectivity at catchment levels, it will allow managers to identify connectivity baselines and set target goals for restoration actions. These tools have been implemented in the Barrier Assessment and Reporting Tool (BART), a user-friendly web-based shiny app with an interactive geospatial interface. The tool will assist stakeholders in allocating resources effectively and help to generate region specific reports that can be directly used to meet the annual reporting requirements for fish passage under NZ's National Policy Statement for Freshwater Management. The outcomes of this project have implications beyond NZ, as they contribute to the global understanding of riverscape connectivity and provide practical tools and approaches that can be adapted and applied in diverse aquatic ecosystems worldwide.

Structural variation in clownfishes’ adaptive radiation

Marcionetti, Anna[1]; Salamin, Nicolas[1]

[1]*Department of Computational Biology, University of Lausanne, Lausanne, Switzerland*

Clownfishes are a complex of 28 species that rapidly diversified following the acquisition of mutualism with sea anemones around 15 MYA. While the genomic mechanisms behind this adaptive radiation have started to emerge, little attention was given to structural genomic variations (SV; i.e., deletions, insertions, duplications, translocations, and inversions). For example, recent phylogenomic studies suggested two large inversions on chromosome 18 in clownfish, but the presence and role of these inversions were not formally tested. Yet, SV can disrupt gene function and regulation or alter gene dosage, and a central role of SV in adaptive evolution and species diversification has been demonstrated in multiple taxa.

Here, we investigated the number, type, and role of SV in clownfish genomes. Using long PacBio reads, we obtained high-quality genomes for several clownfish species spanning the main lineages identified in the genus. We found a large number of insertions, deletions, duplications, and inversions that occurred during clownfish diversification. We were able to reconstruct and date their evolutionary history and we confirmed the presence of large inversions on chromosome 18 while identifying additional large chromosomal rearrangements. These large inversions likely disrupted recombination, possibly playing a role in speciation and hybridization events in the clownfish group.

This study provides the first evidence of considerable SV in clownfish genomes, despite the fast evolution of the group. It also provides new, high-quality, valuable genomic resources for pursuing research on this iconic group of coral reef fishes and their adaptation to sea anemones.

3.3B Themed Session B: Ecology of Indo-Pacific Fishes, 260-115, November 22, 2023, 2:30 PM - 3:30 PM

Big fish have big mouths: is snapper predation on urchins determined by mouth size?

Marinovich, Jessica[1]; Parsons, Darren[1,2]; Shears, Nick[1]

[1]*University of Auckland*

[2]*National Institute of Water and Atmospheric Research (NIWA)*

Understanding the role of fished predators is essential to managing the indirect impacts of fishing, such as the commonly observed ecosystem shift from kelp forest to ‘urchin barren’ after overexploitation of sea urchin predators on temperate rocky reefs. Snapper (*Chrysophrys auratus*) are widely considered an important predator of the sea urchin or kina (*Evechinus chloroticus*) on north-eastern New Zealand reefs, yet limited information exists on the frequency and size of kina in snapper diet. To determine this, and how these factors vary with snapper size, we collected gut contents from recreationally caught snapper from north-eastern New Zealand shallow rocky reefs. Kina was a key component of snapper diet across the full snapper size range sampled (30-80cm), found in approximately one-third of snapper sampled and was the most important identifiable taxa group (~19% of total gut contents). However, while found across the entire snapper size range sampled, kina contributed significantly to the largest snapper size class and the maximum size of kina eaten was strongly correlated to snapper fork length, appearing to be limited by gape height. This implies that while all snapper occupying rocky reefs likely contribute to maintenance of kina populations, large individuals are required to remove the largest urchins with the greatest grazing capacity and likely have the most significant role in reversing ecosystem shifts on rocky reefs (i.e., from urchin barrens to kelp forest). Therefore, to promote macroalgal recovery on rocky reefs via trophic cascades, fisheries management must prioritize the protection of larger, more influential snapper.

New learnings in tidal interface fish passage: insights from a cone fishway at Manns Weir, Boyne River, Queensland

Marsden, Tim[1]; Scanlon, Melinda[1]; Battey, Nathan[1]

[1]*Australasian Fish Passage Services Pty Ltd: Fern Bay NSW*

Sampling from a newly constructed cone fishway at Manns Weir, located at the tidal interface of Boyne River in Queensland has uncovered significant findings relating to fish passage at tidal barriers. The study aimed to assess the effectiveness of the fishway in facilitating fish movement during spring tides. Sampling was conducted across multiple tidal cycles at the entrance and exit of the fishway. Fish ranging from 10 to 300mm were captured, with observations including the presence of eel leptocephali at the peak of the tide, shedding light on their migration patterns.

Small fish displayed a collective behaviour, approaching the fishway in clusters for safety. If individuals did not ascend with a group, they waited for the next group and joined that to ascend. Whereas adult fish such as bream freely moved between fresh and brackish water environments, but showed reluctance towards moving when traps were in place. Fish actively utilized the fishway during the early stages of the tide, but their movement ceased soon as the tide turned. Unsuccessful individuals retreated to the downstream pool.

The fishway successfully passed thousands of fish, however highlighted the limited window for fish movement within tidal fishways. These findings emphasize the importance of considering tidal dynamics and fish behaviour in designing effective fish passage solutions. Understanding fish movement patterns at the tidal interface contributes to maintaining healthy fish populations and ecological balance in similar environments. These new learnings offer valuable insights for the development of strategies to improve tidal interface fish passage.

3.2A Themed Session C: Fisheries and Aquaculture in the Indo-Pacific, 260-073, November 22, 2023, 10:30 AM - 12:30 PM

Depleted striped trumpeter (*Latris lineata*) stocks and fisheries management in Tasmania

Marshell, Alyssa[1]; Coulson, Peter[1]; Krueck, Nils[1]; Tracey, Sean [1]

[1]*Institute for Marine and Antarctic Studies, University of Tasmania*

Striped trumpeters (*Latris lineata*) are large and long-lived fish inhabiting temperate rocky reefs. Juveniles live in shallow, inshore reefs, while adults migrate offshore to deeper, exposed reefs. Fishers primarily use hook methods (e.g., handlines, droplines, and longlines) to catch them offshore around Tasmania. The commercial catch of striped trumpeters has declined from 111 tonnes in 1990/91 to 49 tonnes in 2000/01 and reached a historic low of eight tonnes in 2020/21. Recreational fishers accounted for 67% (29 tonnes) of the total catch in Tasmania in 2017/18. Striped trumpeter stocks have been classified as depleted in recent annual stock assessments, particularly on south-east coasts. Key concerns for the stock include a current minimum size limit set below estimated size at maturity, and highly variable recruitment success. Current fisheries management measures include trip and size limits, and a spawning closure. Despite historically low commercial catches, combined fishing pressure from commercial and recreational sectors and recruitment variability continue to hinder stock recovery. The latest stock assessment (2020/21) revealed no evidence of stock recovery. Therefore, current catch levels risk further depleting the spawning stock and recruitment potential, and stock recovery in Tasmania. Encouragingly, the Department of Natural Resources and Environment Tasmania (DNRET) are proposing striped trumpeter fisheries management rule changes through a wider Tasmanian Scalefish Fishery Rules Review process. The proposed changes will ideally support the recovery of depleted and depleting species to ensure the long-term sustainability of the fishery.

Innovative approaches to fish passage: Harnessing the potential of Tube Fishways

Martino, Jasmin C[1,2]; Cox, Reilly X[1]; Farzadkhoo, Maryam[1]; Felder, Stefan[1]; Jeremy, Yoel[1]; Kammanankada, Hiruni[1]; Kingsford, Richard T[2]; Nolan, Samuel[1]; Suthers, Iain M[2]

[1] *Water Research Laboratory, School of Civil and Environmental Engineering, UNSW Sydney, Manly Vale, NSW 2093, Australia*
[2] *Centre for Ecosystem Science, School of Biological, Earth and Environmental Sciences, UNSW Sydney, Kensington, NSW 2052, Australia*

Freshwater fish populations worldwide are facing dramatic declines, significantly attributable to human-constructed dams and weirs acting as formidable barriers to migration and disrupting vital connectivity. To tackle this pressing challenge, we are developing various tubular fishway systems as cost-effective and efficient fish-passage solutions for river and wetland ecosystems. By integrating hydraulic engineering with fish biology and ecology, we have established a multidisciplinary approach for restoring fish passage for Australian species.

Our key design for the Tube Fishway involves harnessing a downward momentum of water within a closed conduit system to surge fish at atmospheric pressure up and over a barrier. Our laboratory experiments with native species demonstrated successful attraction and safe lifting up 4 and 8 m. Our ongoing experiments are resolving critical aspects such as injury thresholds and volitional passage performance through pipe contractions, expansions and bends, in addition to investigating alternative siphon mechanisms. Furthermore, we have deployed the Tube Fishway at various weir sites to evaluate performance under natural and variable conditions. Complementing these field studies, our project includes the analysis of long-term size and movement data of PIT tagged fish through conventional slotways to ascertain the needs for upstream and downstream migrations.

The combination of ongoing laboratory trials and insights from field performance reinforces the reliability and effectiveness of Tube Fishways as a viable solution for facilitating successful fish passage. By developing these innovative systems, we strive to make meaningful contributions to address the critical needs for improving distribution and abundance of native freshwater fish.

Impact of cattle disposal on tiger shark behaviour at Norfolk Island, Australia

Matley, Jordan[1]; Barnett, Adam[2]; Dinsdale, Elizabeth[1]; Doane, Michael[1]; Harasti, David[2]; Hoopes, Lisa[3]; Huveneers, Charlie[1]; Meyer, Lauren[1]; Scott, Mark[4]

[1]*Flinders University*

[2]*James Cook University*

[3]*NSW DPI*

[4]*Georgia Aquarium*

[5]*Norfolk Island National Park*

Tiger sharks are a wide-ranging generalist species and considered dangerous to humans. At Norfolk Island, a small remote Australian island in the middle of the Pacific, tiger sharks are regular visitors along the shores. Farming cattle is one of the main industries on Norfolk Island, as is tourism. Given the limited space, offal from cattle is regularly disposed of into the ocean from a remote site, creating concern that tiger sharks have become accustomed to this provisioning. While there is a move to limit this practice in the future, community members are concerned that sharks may search elsewhere for food instead, such as beaches visited by locals and tourists. This study tracks the movements of tiger sharks with acoustic and satellite telemetry to understand general area-use patterns, but also to determine how periods of offal disposal affect the behaviour of sharks. Sampling is ongoing but several years of collected data show little difference in movements between disposal and non-disposal days. Nevertheless, sharks are consistently detected near the disposal site more than anywhere else on the island, highlighting that provisioning cannot be ruled out as an attractant, although other possible reasons for their presence exist. Overall, this project explores an important Indo-Pacific human-shark relationship integrating both ecological and social concerns.

Systematics of the scorpionfish genus *Neomerinthe* Fowler, 1935

Matsumoto, Tatsuya[1]; Motomura, Hiroyuki[2]

[1] *The United Graduate School of Agricultural Sciences, Kagoshima University, Kagoshima, Japan*

[2] *The Kagoshima University Museum, Kagoshima, Japan*

The scorpionfish genus *Neomerinthe* (Scorpaenidae) is one of the most taxonomically confusing genera in the family. The genus consists of 10 valid species from the Indo-Pacific Ocean and three from the Atlantic Ocean, but the validity and characteristics of each species have been unclear for many years. A comprehensive taxonomic review of the Indo-Pacific species in the genus *Neomerinthe* during this study showed that recognition of six undescribed species and *N. procurva* Chen, 1981, previously considered a valid species, as a junior synonym of *N. bucephalus* (Alcock, 1896). A key to all species of the genus *Neomerinthe* from the Indo-Pacific is provided in this study. In addition, molecular genetic and morphological analyses revealed that *Neomerinthe* can be divided into three genera. The true *Neomerinthe* consists only of two species, *N. hemingwayi* Fowler, 1935 and *N. folgori* (Postel and Roux, 1964), which are distributed in the Atlantic Ocean, while *N. beanorm* (Evermann and Marsh, 1900) (Atlantic Ocean) and 15 other species (Indo-Pacific Ocean) each are considered to be classified in a separate genus. These three genera are defined by morphological features such as the presence or absence of swimbladder and scales on the snout, and the shapes of the spines on the head.

1.2B Special Session 4: The evolution and ecology of fishes: assessing traits and functions in a changing world, 260-073, November 20, 2023, 2:00 PM - 4:15 PM

Plasticity in foraging behaviour of *Ctenochaetus striatus* linked to sedimentation, with implications for cryptic functional vulnerability

McAndrews, Ryan[1,2]; Bejarano, Sonia[2]; Ford, Amanda[2,3]; Eich, Andreas[2,4]; Ferse, Sebastian[2]

[1]*National Emerging Infectious Diseases Laboratories (NEIDL), Boston University, Boston, MA, USA*

[2]*Leibniz Centre for Tropical Marine Research (ZMT), Bremen, Germany*

[3]*University of the South Pacific (USP), Suva, Fiji*

[4]*Ecole Pratique des Hautes Etudes (EPHE), CRIOBE, French Polynesia*

We sought to investigate the removal of benthic sediment from a fish perspective, using behavioural traits as to investigate mechanistically how functional provision by species and individuals might vary with sedimentation in otherwise similar environments. We aimed to build upon previous experiments and observations suggesting that even natural carbonate sediment loads deter benthic herbivory. Lab-based feeding trials agreed, detritivorous surgeonfishes (*Ctenochaetus striatus*) and scraping parrotfishes preferred fine silicates sediments over coarse carbonates. The resulting expectation is that fishes would respond positively to increasingly terrestrially influenced sediment loads, preferring high organic content and finer grain size delivered by coastal runoff. Spanning coarse/carbonate to fine/silicate sedimentation regimes on a fringing reef in Fiji, these expectations were validated *in situ* by *Ct. striatus*, but not for parrotfishes, which stopped foraging altogether under fine/silicate sedimentation. This contrast in functional provision was not expected and might not have been apparent without behavioural observations.

Most taxa preferred foraging on vertical over relatively coarse/carbonate-laden horizontal surfaces. Interestingly, *Ct. striatus* foraging behaviour was plastic, with no obvious preferences at coarse/carbonate sites, but solely foraging on horizontal surfaces at fine/silicate sites. These results provide an example of the limitations and power of *in situ* observations vs. lab-based experimentation in explaining functionally relevant behaviour. By quantifying the targeted surface orientation and behavioural traits (bites/foray, bites/second, and distance/foray) and considering other functionally relevant phenotypic traits, we were able to represent intra-specific variation in the behavioural expression of functional traits in multivariate space (and compare functional effectiveness/plasticity among variation in sedimentation).

5.3B Themed Session B: Ecology of Indo-Pacific Fishes, 260-115, November 24, 2023, 1:30 PM - 3:00 PM

Does habitat and continental shelf position influence reef fish assemblage response to major disturbance?

McClure, Eva[1]; Hoey, Andrew[1]; Richardson, Laura[2]

[1] *College of Science and Engineering, James Cook University, Townsville, Australia*

[2] *Bangor University, School of Ocean Sciences, Menai Bridge, United Kingdom*

Environmental gradients operating across a range of spatial scales are known to shape distinct reef fish and benthic communities on coral reefs. However, relatively little is known of how these distinct communities respond or reassemble following major disturbances. Here we investigate the short- and longer-term (6 months and 6 years, respectively) effects of multiple major disturbances (two category 4 cyclones and mass coral bleaching events) among reefs spanning the continental shelf, and among distinct habitats within a mid-shelf reef system on the Great Barrier Reef, Australia. Six months after disturbance, the previously distinct fish and benthic assemblages of the inner-, mid- and outer-shelf had dramatically changed. Benthic composition saw an 81-95% relative reduction in live coral cover across the shelf, with significant increases in macroalgae inshore, and algal turfs and pavement on mid- and outer-shelf reefs. Short-term responses in the herbivorous fish assemblages varied, with each shelf position sharing fewer species and becoming dominated by different species and groups than prior to disturbances. Longer-term responses indicate that while coral cover did not return to pre-disturbance levels, changes in benthic composition may be shelf-position dependent, with mid-shelf reefs appearing more consistent with pre-disturbance composition across multiple groups (e.g., hard and soft coral cover, and biomass of grazing and browsing fishes), than inner- and outer-shelf reefs. We further discuss short- and long-term disturbance-response dynamics, by focusing on the benthic and fish assemblage structure of five taxonomically distinct habitats of a mid-shelf reef system, to elucidate whether pre-disturbance configurations help determine post-disturbance outcomes.

The influence of oil and gas infrastructure on marine community structure, connectivity, and fish productivity: Bass Strait, south-east Australia

McLean, Dianne[1]; Birt M[1]; Case M[1]; Claisse J[2]; Colquhoun J[1]; Driessen D[3]; Galaiduk R[1]; Greer D[4]; Ferreira L[1]; Fullwood L[3]; Harvey E[3]; Jaworski S[1]; Macreadie P[5]; Mc Cormack S[1]; Speed C[1]; Travaglione N[1]; Treml E[1,5]; Wyatt M[1]

[1]*Australian Institute of Marine Science*

[2]*California State Polytechnic University*

[3]*Curtin University*

[4]*eCoast Marine Consulting and Research*

[5]*Deakin University*

Understanding the influence of oil and gas structures on marine ecosystems is important for informing decisions regarding their removal to achieve optimal environmental outcomes. Initial findings are presented for south-east Australia documenting: 1) seasonal patterns in marine communities on infrastructure and in natural and surrounding habitats; 2) fish production on platforms and in natural habitats; 3) connectivity dynamics on infrastructure and natural rocky reefs; and 4) potential impacts of different decommissioning end states on marine communities.

Jewel anemones (Cnidaria) are the dominant colonising biota on platforms but are replaced by a diversity of sponges at the base of platforms. Sponges are prevalent on pipelines, while offshore natural habitats comprise mostly sand, mud, and gravel with patchy occurrences of shells and sponges. Fish communities on platforms are characterised by schooling pelagic and bentho-pelagic species, and demersal reef-associated species, with marked differences across depths, platforms, and, to a lesser extent, across seasons. Sand-affiliated fish species characterise offshore natural habitats. Fish production on platforms is higher than surrounding natural habitats and similar to platforms off southern California. Natural reefs in the nearshore region are responsible for most of the regions metapopulation connectivity for studied fish and invertebrate species. The impact of full and partial removal of platforms or complete removal of pipelines on metapopulation dynamics of the study species differs according to the species and location of the infrastructure. Initial research findings are presented in the context of informing decommissioning decisions but also inform the development of offshore renewable energy in Australia.

2.3A Themed Session B: Ecology of Indo Pacific Fishes, 260-115, November 21, 2023, 10:30 AM - 12:30 PM

The effects of marine heatwaves on the physiology of a coral reef snapper

Shannon J. McMahon[1,2], Philip L. Munday[2], Timothy Ravasi[1] & Jennifer M. Donelson[2]
[1]*Marine Climate Change Unit, Okinawa Institute of Science and Technology, Onna-son, Okinawa, Japan*
[2]*ARC Centre of Excellence for Coral Reef Studies, James Cook University, Townsville, QLD 4811, Australia*

The increasing frequency and intensity of marine heatwaves (MHWs) pose a significant threat to marine organisms, especially those evolved to live in relatively stable thermal environments, such as coral reefs. However, while there is extensive research into how MHWs cause mass coral bleaching and mortality, there is little known about how MWHs directly affect fishes living on coral reefs. In this study we investigated how MWH conditions affect whole-organism physiological traits and associated biochemical markers in the blood of a coral reef mesopredator, *Lutjanus carponotatus*. Specifically, we exposed mature adults to two different MWH intensities, +1°C (29.5°C) and +2°C (30.5°C), and tested how their physiological performance was effected at two and four weeks exposure, and then at two weeks post-exposure. We found that MWH conditions had a direct physiological costs on adult coral reef snapper with elevated metabolic rates, blood lactate, hemoglobin, and also increased time to recover from capture stress. Interesting, we also found that while individuals mostly recovered at 2 weeks post-exposure there was evidence of ecologically relevant residual effects. These findings provide new insight into the effects of MWHs on the physiological performance of coral reef fishes. By expanding out understand of how coral reef mesopredators fare under MHW conditions we can hope to better manage these important and valuable populations.

Engineering *Drosophila melanogaster* to produce carbohydrase enzymes for aquaculture.

McNab, Justin, M[1,2]; Maselko, Maciej[2]; Williamson, Jane, E[1]

[1]*School of Natural Sciences, Macquarie University, NSW, 2109, Australia*

[2]*School of Applied Biosciences, Macquarie University, NSW, 2109, Australia*

A priority of aquaculture worldwide is the supplementation of fishmeal with other more sustainable alternatives, namely a combination of plant materials that would need to be equal in essential nutrients and oils. Plant material however is often difficult to digest and contains anti-nutritional factors such as phytic acid or non-starch polysaccharides (such as hemicelluloses) that negatively impact the growth of fish. One way of reducing anti-nutritional factors is by dietary supplementation with carbohydrase enzymes, this group of enzymes hydrolyses non-starch polysaccharides into more accessible sugar forms that fish can successfully digest and this improves their growth. The production of these enzymes currently relies on a variety of sources and can be costly, as such there is a need for a simpler host organism that could maximise production. Here, we demonstrate the production of several carbohydrase enzymes within a single host organism, *Drosophila melanogaster*. Using synthetic biology techniques, genetic constructs related to several carbohydrase enzymes are engineered into *D. melanogaster* and the effectiveness of these enzymes are tested by commercial assay. Successfully expressing these enzymes in *D. melanogaster* allows us to adapt these genetic constructs into other insect host species in order to further focus on sustainability or upscaling production. Further studies will involve the testing of these products in an aquacultural setting and will assess the viability of this method of enzyme production.

That’s a lot of fish! Daily fish movement revealed using an imaging sonar, in an Australian estuary.

McSpadden, Kristen[1]; Raoult, Vincent[1,2], Bennett, Mark[1], Gaston, Troy[1]

[1]*School of Environmental and Life Sciences, The University of Newcastle, NSW, 2258, Australia*

[2]*School of Environmental and Life Sciences, Deakin University, Victoria, 3125, Australia*

Estuaries are widely regarded for their economic, environmental, and social importance. There have been multiple studies examining the role estuaries play in supporting fisheries, particularly as a nursery ground for juvenile fish. Despite this, there is limited research on the daily movement of fish within these systems, the exchange between ocean and estuaries and how this varies throughout the day. Estuarine environments often present sampling challenges, particularly for optical surveys, as visibility is highly variable between systems. Here we used an imaging sonar to quantify fish movement at 4 sites through an important commercial fishing estuary in New South Wales, Australia, across diurnal and nocturnal sampling periods. We examined the size of fish, their movement patterns and the biomass flux occurring within this estuary. We found that fish were highly active throughout this estuary, with > 66,200 fish counted and measured, amounting to ~15,500 kg over 60 hours of processed footage. Of this, fish were observed to be highly active at night, with activity occurring primarily at the estuary mouth. The imaging sonar’s field of view was set to 10m, thus, to determine the true quantity of fish moving throughout the channel, fish biomass was extrapolated to channel width. The maximum quantity of fish moving through a channel ranged to 47 tons h^{-1}. These results reveal the high productivity of estuaries, offer insight into the ecological patterns of fish behaviour, and provide rational for further fine scale studies of fish movement within these environments.

Internal organs and body tissues of free-swimming whale sharks (*Rhincodon typus*) imaged using underwater ultrasound

Meekan, Mark[1]; Thompson, Farand[2]; Brooks, Kim[3]; Matsumoto, Rui[4]; Murakumo, Kiyomi[4]; Lester, Emily[1]; Dove, Alistair[5]; Hopper, Belinda[6].
[1]*Oceans Institute, University of Western Australia, Western Australia 6009, Australia*
[2]*Mira Mar Veterinary Hospital, Mira Mar, Western Australia, 6330, Australia*
[3]*Australian Institute of Marine Science, Perth, Western Australia 6009, Australia*
[4]*Okinawa Churaumi Aquarium, Ishikawa, Motobu, Okinawa 905-0206 Japan*
[5]*Georgia Aquarium, Atlanta, Georgia USA*
[6]*Animalius, Bayswater, Western Australia, 6053, Australia*

Ultrasound imaging can be used to measure the reproductive status and condition of sharks. This usually requires restraint of the subject, which is not feasible in the wild when the target species is of conservation concern and very large, as is the case for whale sharks. Our study invoked a behavioural response in free-swimming whale sharks that allowed snorkellers to image internal organs and structures using a submersible ultrasound scanner linked to an iPhone in an underwater housing. We were able to reliably locate and monitor the heart and other internal organs inside the body cavity and the brain inside the head and image skin and muscle in the dorsal surface of the sharks. We evaluate the technique as a means for assessing the condition and reproductive status of free-swimming whale sharks.

Population Genetics of the Catadromous Eel, *Anguilla marmorata*, in the Indo-Pacific

Mejia, Karina[1]; Lindstrom, Daniel[2]

[1]*University of Guam*

Anguilla marmorata is the most common freshwater eel in the Indo-Pacific. Little is known about details of its's life history, making sustainable management challenging. Anguillid eels are catadromous, living as juveniles and adults in freshwater and spawning in the marine environment. There is some evidence for multiple spawning grounds, one to the southeast and the other west of Micronesia. In this study, the population structure of *A. marmorata* on Guam and the Indo-Pacific were investigated through otolith microchemistry and phylogeographic genetic analysis to pinpoint geographic and temporal patterns of spawning, dispersal and recruitment. New recruits (glass and elver stage eels) were collected at multiple stream mouths throughout the year. Genomic DNA was extracted from biopsied tissue and subjected to PCR amplification and bar-code sequencing of the mitochondrial control region (D-loop). Multiplexed ISSR genotyping (MIG-seq) further resolved geographic origin and population structure. This technique identified individuals to their spawning cohort. Each specimen had otoliths extracted and polished to reveal the otolith core and daily rings to age specimens. Laser ablation of otolith core and ring material was used to analyze for chemical makeup and likely spawning location(s). This method found a correlation between genetic clustering and otolith microchemistry. The correlation indicates genetics differences within the eels. Future work will compare otolith microchemistry to ocean water chemistry from likely spawning locations. The determination of geographic/oceanographic location and temporal patterns of spawning will provide information key to the effective conservation and sustainable harvest of this important resource.

Unravelling the physiological, ecological, and genomic origins of endothermy in fishes

Melendez-Vazquez, Fernando[1-2]; Arcila, Dahiana[1-2]; Betancur, Ricardo[1-2]; Lucaci, Alexander[3]; Rincon, Melissa[4]; Santaquiteria, Aintzane[4]; Selberg, Avery[3]

[1]*Scripps Institution of Oceanography, 8622 Kennel Way, La Jolla, CA*

[2]*University of California, San Diego, 9500 Gilman Dr, La Jolla, CA*

[3]*Temple University, 1801 N Broad St, Philadelphia, PA*

[4]*University of Oklahoma, 660 Parrington Oval, Norman,OK*

Contact information (in the order presented above): fernando.melendez1@upr.edu, dkarcila@ucsd.edu, betanri@gmail.com, alexander.lucaci@temple.edu, melissa.rincon.sandoval@ou.edu, a.santaquiteria@ou.edu, avery.selberg@temple.edu

Endothermy has been identified as a key adaptation in the survival of many of the present vertebrate lineages. However, in fishes, only around 38 out of the roughly 35,000 species are endothermic, including the Tunas, Billfishes, Opahs, and some Elasmobranchs. Past studies addressing the origins and advantages of endothermy have been mostly restricted to terrestrial vertebrates, while marine-focused experiments have suffered from low taxonomic sampling and limited physiological, ecological, and molecular data integration. We present an in-depth look at the evolutionary drivers of endothermy in marine organisms using phylogenomic data (1,050 species of ray-finned fishes and 13 other endothermic marine vertebrates) to provide a comprehensive analysis integrating physiological, ecological, and genomic factors, to further understand the origins of this trait in the marine realm. In ray-finned fishes, we observed a strong relationship between body length and endothermy, indicating that size might play a critical role in developing this trait, yet no relationship was observed in any of the other physiological factors studied. Using a novel paleoclimatic evolutionary model, we found no patterns of increased evolutionary rates, suggesting that the origins of endothermy in marine organisms are not tied to past climatic events as previously thought. Comparative genomic analyses of 833 candidate genes of endothermic marine organisms identified signals of convergence between endothermic ray-finned fishes and other marine endotherms in genes related to fatty acid oxidation and deglutamylation. This study analyses various factors thought to have driven the evolution of endothermy in marine organisms while addressing long-standing hypotheses about its advantages.

Glow in the dark party: new records and evolutionary implications of biofluorescence in deep-sea fishes

Melo, Marcelo R. S. [1]; Gallano, Margherita[1,2]; Galeazzo, Gabriela A.[1]

[1] Instituto Oceanográfico, Universidade de São Paulo, São Paulo, SP, Brazil, melomar@usp.br, margherita.gallano@physik.uni-muenchen.de, gabriela.galeazzo@usp.br

[2] Ludwig-Maximilians-Universität, München, Germany

Biofluorescence occurs when an organism absorbs high-energetic electromagnetic radiation (*i.e.*, UV or blue light) from the environment, and re-emits light at a longer, lower-energetic wavelength (green, yellow, or red). In oceanic waters, the sunlight is rapidly attenuated at shallow depths (< 50m), resulting in a spectrally restricted, blue-shifted illumination (450–480 nm) that reaches the dim twilight zone (200–1,000m). Our collections were made onboard the Brazilian N/Oc *Alpha Crucis* in depths between 150 and 1,500 meters using bottom trawling. To simulate the natural conditions, soon after the collection, the specimens were brought into a dark room and exposed to a 470 nm wavelength blue light. Then, if present, biofluorescence was recorded using an Ocean Optics Flame spectrometer and the specimens were photographed. Biofluorescence was observed in species collected up to 900 meters, including two synodontids and two chlorophthalmids (Aulopiformes), a bembropid, a serranid and a setarchid (Perciformes), a mullid (Mulliformes), a centriscid (Syngnathiformes), and two scyliorhinid sharks (Carcharhiniformes). Only green biofluorescence was observed, with peaks ranging from 501 to 523 nm, in structures such as the eye iris and crystalline lens, and the skin. The unique lightening conditions of the twilight zone drove the independent evolution of biofluorescence in fishes that are capable to transform the ambient blue-light into wavelengths otherwise absent in the environment. Funding FAPESP (2017/12909-4).

Taxonomic revision of the perciform genus *Acanthistius* (Günther 1859) with resolution of the identity of *Acanthistius paxtoni*

Menkara, Younis[1]; Gill, Anthony[2]; Ho, Simon[1] and Tea, Yi-Kai[3].
[1]*School of Life and Environmental Sciences, University of Sydney, NSW, Australia*
[2]*Chau Chak Wing Museum, University of Sydney, NSW, Australia*
[3]*Ichthyology Department, Australian Museum Research Institute, NSW, Australia*

The Serranidae is a large and diverse family of marine fishes that has been subject to extensive phylogenetic contention. The serranid genus *Acanthistius* is particularly problematic and has been regarded as *incertae sedis*, partly due to poor taxon sampling. The genus, with 11 species, is exclusively distributed in the Southern Hemisphere, with Australia and New Zealand accounting for nearly half of the global diversity. Of particular interest is the enigmatic Australian endemic *A. paxtoni*, the Orangelined Wirrah, which was described in 1982 and is only known from two formalin-fixed type specimens. I hypothesise that *A. paxtoni* might be the hybrid offspring of the two other East Australian species of *Acanthistius*: *A. ocellatus*, the Eastern Wirrah, and *A. cinctus*, the Yellowbanded Wirrah. To resolve the identity of *A. paxtoni*, I will employ an integrative taxonomic approach that combines morphological, osteological, and molecular data. Preliminary results indicate that specimens of *A. paxtoni* exhibit intermediate morphology between the two other East Australian species. I will also sequence three mitochondrial and three nuclear DNA markers from each species of *Acanthistius*, to infer a global phylogeny and produce a robust estimate of the evolutionary relationships within the genus. Where fresh or alcohol-fixed tissue is not available, I will attempt to extract viable DNA from formalin-fixed specimens. These results will provide the foundation for further phylogenetic studies at the familial level, as well as population genetic studies for the conservation and management of potentially threatened species of *Acanthistius*.

1.1A Themed Session: A. Evolution, Taxonomy and Biogeography of Indo-Pacific Fishes, 260-098, November 20, 2023, 11:15 AM - 1:00 PM

A DNA reference library for New Caledonian freshwater fish: challenges and prospects

Mennesson, Marion Isabelle[1*]; Charpin Nicolas [2]; Keith Philippe [1]

[1] *UMR Biologie des organismes et écosystèmes aquatiques (UMR BOREA 8067), MNHN, CNRS, IRD, SU, UCN, UA, 57 rue Cuvier CP26, 75005 Paris, France [keith@mnhn.fr]*

[2] *Association Vie d'Ô Douce, 3090 bis route de la Corniche, Mont Dore Sud, 98876 La Coulée, Nouvelle-Calédonie [charpin.nicolas@gmail.com]*

*Corresponding author: marion.mennesson@mnhn.fr

Several research projects on the taxonomy and ecology of New Caledonian freshwater fish have been conducted between 1999 and 2009. Theses studies, based on classic taxonomic methods, highlighted the difficulty to identify some species belonging to the Gobiidae, Eleotridae or Syngnathidae families. With the coming of Next-Generation Sequencing (NGS), and more precisely with integrative taxonomy, new species have been discovered (cryptic ones) leading to new protocols for the species identification. The description of new species now relies on the study of old (Type specimens) and recent specimens using a combination of morphomeristic and molecular data. With this method, since 2019, we implemented the first DNA reference library for New Caledonian freshwater fish. Our work was based on several field missions (2019-2023): the specimens were added to the National Museum of Natural History of Paris collection and morphomeristic analyses were undertaken, a part of the mitogenome (*mt*DNA) was sequenced for at least 3 individuals per species and when possible, pictures of live specimens were taken. When morphomeristic analyses were complicated we tried to sequence old Type specimens to validate or not a species name.

Our aim is to give access to clear species identification with morphmeristic and molecular data linked to a specific specimen, we created a DNA reference library with partial 12*S* non-coding gene (for eDNA studies) and partial *COI* gene (commonly used for barcoding), each sequence being linked to a correct and reliable species identification. Our database is available on the Barcode Of Life Data system (BOLD).

Initiatives to improve national guidance for water intake management to ensure safe passage for freshwater fish in New Zealand.

Meredith, Adrian[1]; Bowie, Sjaan[2]; Gabrielsson, Rasmus[3]; Hickford, Mike[4]

[1]*Canterbury Regional Council*

[2]*Department of Conservation*

[3]*North Canterbury Fish and Game Council*

[4]*National Institute of Water and Atmospheric Reseach*

Water intake structures are used throughout New Zealand to supply irrigation, hydro-electric generation, drinking water and industrial water needs. Abstracting surface waters can impact fish communities by altering fish habitats and disrupting fish migration and spawning movements.

The regulatory agencies responsible for protecting fish populations and/or approving surface water infrastructure in New Zealand recognise that there are still a wide range of unresolved issues affecting fish at water intakes in New Zealand. In 2019, the Ministry for Primary Industries funded a collaborative research project to develop good practice national guidance on water intake design. New Zealand guidelines previously identified seven design criteria necessary for effective and efficient fish screening. Subsequently, upstream fish passage has been added as an eighth criterion. The eight key criteria must be implemented sufficiently if water intakes are to minimise or eliminate the possibility of fish being damaged or removed from waterways. The Fish Screen Guidance Tool provides a further method to support selection of preferred design elements to be developed into effective conceptual intake designs. The success of good practice national water intake guidance relies on implementation of these criteria and tools that are first and foremost focussed on fish biology and protecting the needs of the fish community. This paper highlights the tools developed and challenges being faced in achieving the implementation of fish centric intake designs and design criteria for water intakes in New Zealand.

Spatio-temporal variability in occurrences of tropical, subtropical and rare marine fishes in Aotearoa New Zealand

Middleton, Irene[1,2]; Aguirre, J. David[1]; Anderson, John[3]; Carney, Mary[3]; Cox, Nathan[3]; Duffy, Clinton[4]; Francis, Malcolm[2]; Hemstalk, Stephen[3]; Herbert, Blair[3]; Johnston, Craig[3]; Liggins, Libby[1,5]; Middleton, Crispin[2,3]; Oldfield, Tim[3]; Robinson, Richard[3]; Sheath, Chris[3]; Skipworth, Ian[3]; Stancich, Jakson[3]; Struthers, Carl[6]; Trnski, Thomas[5]; Whittington, Hope[3]

[1]*School of Natural Sciences, Massey University, Albany Campus, Auckland 0745, New Zealand*

[2]*National Institute of Water and Atmospheric Research, Wellington office, Haitaitai, Wellington 6021, New Zealand*

[3]*WhatsthatfishNZ working group, Auckland 0745, New Zealand*

[4]*Department of Conservation, Te Papa Atawhai, Auckland office, Auckland 1010, New Zealand*

[5]*Tāmaki Paenga Hira Auckland Museum, Parnell, Auckland 1010, New Zealand*

[6]*Museum of New Zealand Te Papa Tongarewa, Te Aro, Wellington 6011, New Zealand*

Climate change is driving poleward range shifts and the increasing abundance of rare species in marine systems. We examine spatio-temporal patterns in the occurrences of tropical, subtropical and rare marine fishes in New Zealand, with the purpose of characterising biodiversity change and to set a baseline for future monitoring of climate change impacts. We consolidated 50 years of unpublished records of tropical, subtropical, and rare fishes to develop a focal species database for NZ. We identify geographic hotspots of focal species and examine the spatio-temporal variation in hotspots in relation to focal species lifestage, habitat, and taxonomic family.

We present 17 new-to-NZ marine fishes, and a new-to-NZ family. Focal species now account for 6.5% of known pelagic fishes and 17.3% of all benthic fishes in NZ. Northeastern NZ was a consistent hotspot of focal species, but hotspots of mature and pelagic fish occurrences appeared further south than juvenile and benthic species. Focal families with tropical affinities (Labridae, Pomacentridae) were restricted to northeastern NZ whereas focal families with more temperate affinities (i.e., Cheilodactylidae), extended further south.

Tropical, subtropical and rare fishes are a major component of the fish biodiversity in NZ, and their occurrences and diversity has increased over the past half-century. Northeastern NZ consistently has the highest occurrence rate and diversity of focal species, and the patterns of species occurrences in this area could inform future biodiversity shifts. Our study demonstrates the value in consolidating citizen scientist observations to inform current baselines and future monitoring of climate-related biodiversity change.

Integrating computer vision into the collection of fish measurement data for stock assessment

Middleton, Sam[1]; Middleton, David[1]

[1]*Pisces Research Ltd*

The collection of data on the length composition of harvested fish is a routine activity undertaken in support of fish stock monitoring and stock assessment. However, this activity is time consuming and labour intensive, and automation using computer vision is desirable.

Fish length can be estimated automatically from images but previous approaches have typically identified a bounding box associated with the total length of a fish, whereas fork length is often measured when data are collected for stock assessment. To use computer vision to measure fork length, we focussed on identifying keypoints rather than bounding boxes. Using Torchvision’s human keypoint detection model we trained a Region-based Convolutional Neural Network to detect the nose and tail fork of a fish. Conversion from pixel measurements was implemented by the detection of known checkerboard patterns, and also using depth cameras.

In order to implement computer vision in real world collection of fish length data it is necessary to have methods to detect when the keypoint detection has failed. We consider various statistics that can indicate poor detections; however, manual oversight of the performance of the algorithm is also worthwhile, enabling screening of poor images, poor detections, and the periodic re-training of the model with additional labelled images.

While the current focus is on fish-by-fish measurements alongside manual sampling, we consider the potential for scaling up to measurement of fish on conveyors in a processing setting.

Exploring the capabilities and limitations of AI in developmental stage categorization and length extraction from images of tropical fishes.

Mihai, Alexandru[1]; Moore, Billy[1] and Ravasi, Timothy[1]

[1]*Marine Climate Change Unit, Okinawa Institute of Science and Technology (OIST)*

This study delves into the current capabilities and limitations of machine learning algorithms(AI) within the realm of fish developmental stage categorization and length prediction. The research encompasses two projects: one focusing on machine learning for developmental stage and temperature treatment categorization and the other on image analysis for length extraction. In the first project, a neural network algorithm implemented using PyTorch was trained on a pre-collected dataset of fish images, categorized by different developmental stages and temperature treatments. The trained model was then employed to automatically classify new *Amphiprion ocellaris* microscopy images based on their developmental stage and temperature treatment. In the second project, utilizing the same microscope images, a self-contained script was developed to extract quantitative traits, such as length and height. A mathematical model was proposed to minimize length prediction errors, enhancing the accuracy of measurements. By comparing the results from both projects, this work provides an understanding of the capabilities and limitations of AI in fish developmental stage categorization and length prediction. While AI can aid in the characterization of qualitative traits or make predictions regarding environmental conditions, direct image processing and classical algorithms prove to be more useful in extracting quantitative data. The findings emphasize that while AI is a powerful tool, it is not universally applicable. This research contributes to the ongoing debate surrounding the appropriate and effective implementation of AI and machine learning algorithms in scientific research, promoting informed decision-making and facilitating the utilization of these technologies in a manner that maximizes their potential.

4.3B Themed Session B: Ecology of Indo-Pacific Fishes, 260-115, November 23, 2023, 1:30 PM - 3:00 PM

The feeding kinematics of a surgeonfish (*Acanthurus leucosternon*) and the associated functional implications

Mihalitsis, Michalis[1]; Wainwright, Peter[1]

[1]*Department of Evolution & Ecology, University of California, Davis, 95616, California, USA*

Benthic-feeding coral reef fishes display an impressive degree of morphological and functional diversity. While the ecological outcomes of such feeding have been studied in detail, the morphological adaptations and mechanisms required to carry out benthic feeding have only been sparsely studied. Here, we use high-speed video to show how a surgeonfish (*Acanthurus leucosternon*) uses its morphology during feeding (i.e., detachment of filamentous algae). We quantified cranial, body, and pectoral fin components, and how they function during a bite. After gripping mouthfuls of attached algae in its teeth, this species used quick dorsoventral rotation of the jaws to detach the algae, facilitated by an intra-mandibular joint. This motion occurred in conjunction with the retraction of ventral elements between the neurocranium, pelvis, and pectoral girdle, followed by a lateral head flick. This previously undescribed mechanism of removing algae from reefs, employs in novel ways the intra-mandibular joint, as well as cranial elevation and pectoral girdle retraction, two motions primarily employed during suction feeding by teleosts. Ventral rotation of the jaws may represent a more efficient method of detaching benthic algae, that does not require the same additional forces delivered by lateral body bending and a head flick. Overall, our results provide novel insights into functional traits related to cropping, a function with significant implications to the process of herbivory on coral reefs.

Formalin-fixed paraffin-embedded (FFPE) samples help to investigate potential lamprey disease

Miller, Allison[1]; Baker, Cindy[2]; Brosnahan, Cara[3;] Dowle, Edwina[1]; Gemmell, Neil[1]; Geoghegan, Jemma[1]; Kitson, Jane[4]; Pande, Anjali[3]

[1]*University of Otago*

[2]*National Institute of Water and Atmospheric Research Limited*

[3]*Animal Health Laboratory, Ministry for Primary Industries*

[4]*Kitson Consulting Ltd*

Infectious diseases impact numerous organisms. Knowledge of host-pathogen interactions and host responses to infection is crucial for conservation and management. Obtaining this knowledge quickly is made increasingly possible by a variety of genomic approaches, yet, for many species the bottleneck to understanding this, remains access to appropriate samples and data. Lack of sample availability has also limited our understanding of how pathogens and the immune responses of hosts change over time. Archival materials may provide a way to explore pathogen emergence and host responses over multiple—possibly hundreds—of years. Here, we tested whether formalin-fixed paraffin-embedded (FFPE) tissue samples could be used to understand an unknown pathology, lamprey reddening syndrome (LRS), affecting pouched lampreys (*Geotria australis*). Our differential expression analyses of dermal tissues from four unaffected lampreys and eight affected lampreys collected in 2012 alluded to potential agents associated with LRS. Interestingly, the pathways associated with viral infections were overrepresented in affected versus unaffected lamprey. Gene ontology analyses of the affected and non-affected lampreys also provided new insights into the largely understudied immune responses of pouched lampreys. Our work confirms that FFPE samples can be used to infer information about the transcriptional responses of a wild fish species affected by unknown historical pathologies/ syndromes. In addition, the use of FFPE samples for transcriptomics offers many opportunities to investigate the genomic responses of fishes to a variety of environmental changes. We conclude with a discussion about how to best sample and utilize these unique archival resources for future wildlife transcriptomic studies.

A novel phylogenomic hypothesis of Eupercaria, the new bush at the top

Miller, Elizabeth[1]; Álvarez-Carretero, Sandra[2]; Arcila, Dahiana[1,3]; Baldwin, Carole[4]; Betancur-R, Ricardo[1,3]; Carnevale, Giorgio[5]; Evans, Kory[6]; Faucher, Rose[6]; Hughes, Lily[7]; Ortí, Guillermo[8]; Santaquiteria, Aintzane[1]; Troyer, Emily[1]; West, JoJo[6]; Westneat, Mark[9]

[1]*Department of Biology, University of Oklahoma*

[2]*School of Earth Sciences, University of Bristol*

[3]*Marine Biology Research Division, Scripps Institution of Oceanography*

[4]*Department of Vertebrate Zoology, National Museum of Natural History, Smithsonian Institution*

[5]*Dipartimento di Scienze della Terra, Università degil Studi di Torino*

[6]*Department of Biosciences, Rice University*

[7]*Section of Research and Collections, North Carolina Museum of Natural Sciences*

[8]*Department of Biological Sciences, George Washington University*

[9]*Department of Organismal Biology and Anatomy, Biological Sciences Division, University of Chicago*

Here, we present novel phylogenomic hypotheses for Eupercaria, a clade within the spiny-rayed fishes (Acanthomorphata) with similar diversity to passerine birds or placental mammals. The systematics of this group have long been plagued with uncertainty, largely due to short internodes associated with early rapid radiations (hence the ‘new bush at the top’). Using >1000 exons obtained through target capture approaches, we built concatenation- and species-coalescent trees comprising 1,051 species. Our taxonomic sampling covers 80% of families, 40% of genera and 20% of species in Eupercaria (of 171 families and ~5,000 species total). We accommodated uncertainty in relationships and divergence times by generating additional trees from independent gene subsets. We time-calibrated the resulting trees based on a comprehensive list of 46 well-justified fossil and 15 geologic calibrations. We present inferences of relationships among major lineages, which include reef fishes such as groupers, wrasses, butterflyfishes, surgeonfishes and pufferfishes; deep-sea fishes such as anglerfishes; coldwater groups such as icefishes, eelpouts, and sculpins; and freshwater groups such as darters and basses. We will discuss which clades are stable and which relationships remain uncertain even with the use of genome-wide approaches. These trees form the backbone of a re-evaluation of the classification of orders and families in Eupercaria, the timescale of evolution of major lineages, and a comparison of evolutionary rates among groups.

Comparison of juvenile morphology and assessment of ontogenetic morphological changes in three species of seahorses *Hippocampus* spp. from south-eastern Australia

Miskiewicz, Tony [1,2]; Parkinson, Kerryn [2]; Short, Graham [2,3]

[1] *School of Biological, Earth & Environmental Sciences, University of New South Wales, Sydney, NSW, 2052, Australia*

[2] *Ichthyology Department, Australian Museum Research Institute, Australian Museum, Sydney, NSW,2010, Australia*

[3] *California Academy of Sciences, San Francisco, CA 94418 USA*

Seahorses are a charismatic component of the fish fauna in estuarine and coastal marine water. In addition to their unique morphology and reproductive strategy, they are threatened by habitat degradation. The taxonomy of seahorses has been problematic with many species misidentified in museum collections. This poster will describe the morphology of newly hatched juveniles and ontogenetic changes with juvenile growth of three species of seahorses, *Hippocampus whitei*, *H. abdominalis* and *H. breviceps* from south-eastern Australia. We will describe and compare differences in morphological characters of juveniles, such as the number and location of spines on the body and the structure of the coronet on the head, which are important features for identification of adults of different species. The ontogenetic changes in morphology of the juveniles will also be compared with the adult morphology of the three species.

4.5A Special Session 5: Larval fishes - solving phylogenetic, life-cycle and ecological questions, 260-051, November 23, 2023, 10:30 AM - 12:30 PM

The identification of flathead larvae (F. Platycephalidae) and their seasonal and spatial distribution off south-eastern Australia

Miskiewicz, Tony [1,2]; Appleyard, Sharon [3]; Baylis, Noah [1]; Reilly, Indiana [1,2]; Shilling, Hayden [4]; Suthers, Iain [1]

[1] *School of Biological, Earth & Environmental Sciences, University of New South Wales, Sydney, NSW, 2052, Australia*

[2] *Ichthyology Department, Australian Museum Research Institute, Australian Museum, Sydney, NSW,2010, Australia*

[3] *CSIRO Australian National Fish Collection, National Research Collections Australia, Hobart, TAS, 7000, Australia*

[4] *NSW Department of Primary Industries, Port Stephens Fisheries Institute, Taylors Beach Road, Taylors Beach, NSW, 2316, Australia*

Platycephalidae is an iconic family of flathead fishes exploited by recreational and commercial fisheries around southern Australia. Despite this, species-specific characteristics of flathead reproduction such as larval distribution and seasonality remain largely unknown, as most flathead larvae could only be identified to family-level. Using a methodology integrating C01 barcoding of morphotypes and subsequent detailing of morphological and pigmentation characters, 10 species of larval flatheads were identified in monthly ichthyoplankton samples collected between 2014–2021 at three oceanographic monitoring stations near Brisbane (27°S), Sydney (34°S) and Hobart (43°S) off eastern Australia. Seasonal water temperature significantly influenced the larval distributions, with distinct taxa characterising the larval assemblages of each site. Species-specific larval abundances were analysed with coincident oceanographic data to elucidate spawning seasonality and preferred environmental conditions for each species across latitudes. The paper will describe the temporal and spatial distribution of different species of flathead larvae across the three NRS sites based on adult distributions and reproductive patterns.

Ecological drivers and pigmentation changes underlying adult colour pattern formation in the anemonefish, *Amphiprion frenatus*

Mitchell, J. Laurie[1]; Zwahlen, Jann[1]; Hayashi, Kina[1]; Miura, Saori[1]; Laudet, Vincent[1]

[1]*Okinawa Institute of Science and Technology, Onna-son, Okinawa, Japan*

Anemonefishes (genus *Amphiprion*) are an iconic group of reef fishes and marine fish model in eco/evo/devo research. Interspecies variation in anemonefish colour patterns show a strong phylogenetic signal in the number of white bars (zero to three), that are mainly comprised of iridophore pigment cells and develop in a strict anterior-to-posterior order. Interestingly, the ontogenetic loss of bars in the juveniles of nine species (e.g., *Amphiprion frenatus*) has occurred at least five times independently during evolution, suggesting a developmental constraint in colour pattern formation. This variation in bar number is a major source of phenotypic diversity among sympatric species. Previous research has focused on the formation of white bars during metamorphosis but has not addressed the external drivers and internal processes underlying bar loss in the post-metamorphic stage of some species.

We investigated the influence of environment on the timing of bar loss in the anemonefish, *A. frenatus*. The timing of bar loss appears to be strongly reduced when captive-raised with a host anemone than without (unpublished data). Moreover, it is postulated that having a different number of bars from adults may be important to juvenile settlement success. We will present preliminary experimental findings which quantify the effect that a host anemone (*Entacmaea quadricolor*), and the presence of adult congeners have on the timing of bar loss in *A. frenatus*. Finally, results from differential gene expression analysis and the in-situ examination of skin pigmentation cells using TEM reveal the internal changes that facilitate this ontogenetic transition in colour pattern.

A preliminary assessment of the distribution of small pelagic fish within Cockburn Sound using acoustic methods

Mitchell, Peter[1]; Yeoh, Daniel[1]; Scoulding, Ben[2]; West, Lisa[1]; Seymour, Josh[1]; Norriss, Jeffrey[1]

[1] *Department of Primary Industries and Regional Development, Hillarys, Western Australia*

[2] *Oceans and Atmosphere Flagship, Commonwealth Scientific and Industrial Research Organisation, Hobart, Tasmania*

The marine embayment of Cockburn Sound (CS) in the Perth metropolitan region supports a multitude of recreational, commercial, industrial and military activities, yet remains a diverse and ecologically important area. Following the State Government's recent plans to develop a new port for Perth within CS, a collaborative research program was initiated to provide data and information for an environmental impact assessment. A key knowledge gap identified was the spatio-temporal distribution of small pelagic species, in particular, scaly mackerel *Sardinella lemuru*, Australian sardine *Sardinops sagax* and Australian anchovy *Engraulis australis*. By weight, the small pelagic fishery is the largest commercial fishery operating within CS, and these species are important prey for a range of higher trophic levels, from teleost fishes to seabirds and marine mammals. However, there are limited information on how small pelagic fishes use CS and whether any potential port developments would impact key areas or habitats used by these species.

To determine the spatial and temporal distribution of small pelagic fish schools, monthly acoustic surveys of CS were conducted for one year using a Simrad wideband transceiver (WBT) with a Simrad 38/200 combi C transducer (38 kHz, three sector split-beam and 200 kHz single-beam, 18° beamwidth). Acoustic signals resembling schools were regularly cross-validated with drop cameras to provide species identifications. While acoustics are widely applied elsewhere globally to survey small pelagic fishes, within Australia these methods have been comparatively underutilised. This presentation outlines initial results and discusses the challenges and successes encountered during the development of this research program.

Diversity, distribution and evolution of colour patterns in three reef fish families

Mittelheiser, Laurent[1]; Baurain, Denis[2]; Frédérich, Bruno[1]

[1]*Laboratory of Evolutionary Ecology, FOCUS, University of Liège, Liège, Belgium*

[2]*Unit of Eukaryotic Phylogenomics, InBioS, University of Liège, Liège, Belgium*

Reef-associated teleosts are well-known for their phenotypic diversity, including colour patterns. Studies revealed that patterns of colour markings diverged rapidly and are under ecological and sexual selection. However, the geographical distribution of this diversity was never investigated and thorough comparative analyses among fish families are lacking.

Here, we aim to compare the distribution and the evolution of colour patterns in three reef fish families: the angelfishes (Pomacanthidae) which are exclusively reef dwellers, and the goatfishes (Mullidae) and the snappers (Lutjanidae) which are associated with reefs and other coastal habitats including mangroves, sandbanks and seagrass beds.

Fish colour patterns were described by a combination of binary traits translating the presence/absence of various markings (*e.g.* stripes, spots, blotches…), and then summarized using Principal Coordinates Analyses. Geographic data were recorded for each species, and they were assigned to five main regions. Our taxon sampling reached 70% of the species of each family

Here, we firstly showed the diversity of colour patterns is similar and equally distributed among regions in the three fish families. Functional richness was correlated to species richness, supporting the hypothesis of a relationship between the divergence in colour patterns and speciation. High functional divergence suggests a crucial influence of colour patterns in species phenotypic differentiation. Secondly, by combining our data with time-calibrated phylogenies, we confirmed a great evolvability of colour patterns in reef fishes. Finally, we revealed that a high level of colour pattern diversity was produced recently in major subclades of the three fish families.

Seeing stripes: using the optomotor response to investigate differences of visual acuity between coral reef fishes

Moad, Claire [1], Cheney, Karen [1]

[1] *School of Biological Sciences, University of Queensland*

Coral reef fishes are a highly diverse group and occupy a variety of different ecological niches. Due to this ecological diversity, visual systems amongst reef fishes are also highly variable. For many coral reef fish species, we still have incomplete information regarding their visual system (including spectral sensitivities, visual acuity, visual specialisations) to accurately model how they perceive their visual environment. Spatial vision and visual acuity are related to the level of detail an animal can perceive in a scene. Understanding visual acuity is important to key ecological processes such as foraging, mate selection and predator avoidance. It is also important for understanding how changes in the visual environments of coral reefs (due to events like coral bleaching, algal blooms and run off) may influence reef fishes. One method of investigating visual acuity is using the optomotor response. This is an innate behavioural response of many animals to wide-field visual stimuli. To elicit an optomotor response, the fish is placed into an arena surrounded by a rotating drum holding a stimuli composed of alternating vertical black and white stripes. We measured the optomotor response of several reef fish species (including *Rhinecanthus aculeatus*, *Chromis viridis*, *Pseudochromis fuscus*, *Zoramia leptacantha*, *Amphiprion akindynos*, *Neoniphon sammara*) in order to investigate how visual acuity varies between different reef fish ecologies. This research significantly increases the number of reef fish species for which we have visual acuity estimates, expanding the pool of species available for visual modelling and help us understand how reef fish perceive their complex environment.

Environmental DNA based insights of fish diversity associated to oil platforms in the Arabian Gulf

Sørensen, Johan M. [1,2]**;** Araujo, Gonzalo[2]; Basseres, Anne[4]; Ben-Hamadou, Radhouan[2]; Carara, Mathieu[4]; Chapman, Constance F.[2]; Faulkner, Lauren[3]; Godina, Alexei[4]; Knudsen, Steen W.[1]; Lowe, Christopher G.[3]; Møller, Peter R. [1]; Range, Pedro[2]; Torquato, Felipe[2]

[1]*University of Copenhagen*

[2]*Qatar University*

[3]*California State University*

[4]*TotalEnergies*

In the Arabian Gulf, a removal of natural reef habitats has caused a decrease in the marine fish diversity. Simultaneously, offshore manmade structures, like oil and gas platforms, could harbor great conservational value as potential artificial reefs. A presences of a broad diversity of fishes associated to these structures has been indicated by previous studies. The world's largest whale shark aggregations is also observed in close proximity of such offshore platforms in the central Arabian Gulf. Still it remains to be answered which species benefits from these artificial reefs and if the observed whale shark aggregations also causes a unique associated fish diversity.

Environmental DNA was extracted from water samples collected around oil platforms and related whale shark aggregations in the Arabian Gulf. Using the MiFish primers, mitochondrial DNA of both elasmobranches and bony fishes are amplified and sequenced.

From all survey sites, a total of 97 fish species was detected. Fish diversity was significantly higher in close proximity of the platforms compared to just a few hundred meters away. The observed species differed between platform sites and reference sites, and an exchange in the species assemblages was also observed at different depths near the platforms. The seasonal whale shark aggregations within a Qatari oil field was followed by a unique species assemblage of fishes.

These early results clearly shows that the platforms is acting as reefs and creates local biodiversity hotspots. This indicates the conservational value of such structures for marine fishes in the Arabian Gulf.

Physiological and Transcriptomic Response of Early-Life Stage Clownfish to Future Ocean Warming

Moore, Billy[1]; Jolly, Jeffrey[1]; Izumiyama, Michael[1]; Kawai, Erina[1]; Ryu, Taewoo[1]; Ravasi, Timothy[1]

[1]*Marine Climate Change Unit, Okinawa Institute of Science and Technology Graduate University, 1919-1 Tancha, Onna-son, Okinawa, 904-0495 Japan.*

Increasing ocean temperatures have a range of negative impacts on coral reef fishes, however, despite many studies of juvenile/adult reef fish, studies of how early developmental stages respond to ocean warming remain limited. As the persistence of reef fish populations is dependent upon the development, settlement and survival of early-life stages, further assessments of how these stages respond to future ocean warming are required. Here, in an aquaria-based study we investigate how temperatures associated with future warming and present-day marine heatwaves (+3°C) impact the growth, metabolic rate, and transcriptome of larval, post-larval and juvenile clownfish (*Amphiprion ocellaris*). Physiological results indicate that larvae will grow and develop faster, reaching key developmental stages sooner at +3°C, whilst metabolic rates of larval and juvenile clownfish will increase at +3°C. The genetic data presented here consists of developmental-stage specific (6 stages) larval transcriptomes, tissue-specific (4 tissues) post-larval transcriptomes and tissue-specific (7 tissue) juvenile transcriptomes, and thus represents a comprehensive assessment of the molecular response of clownfish to elevated temperatures. Clownfish exhibit a strong developmental-stage specific and tissue-specific molecular response to elevated temperature, with a high number of differentially expressed genes throughout development at +3°C. These differentially expressed genes vary throughout development and encompass a range of biological pathways such as metabolism, heat-stress, epigenetic reprogramming, neural development and function, liver damage and oxygen transport. Overall, the strong physiological and molecular response of multiple early-life stages to +3°C, indicate that the development, settlement, and overall fitness of clownfish will be strongly affected by future climate change.

1.4A Themed Session: K. General Session, 260-057, November 20, 2023, 11:15 AM - 1:00 PM

Are parrotfishes the primary drivers of dead coral colony erosion?

Morais, Juliano[1]; Bellwood, David[1]; Morais, Renato[1,2] ; Tebbett, Sterling[1]

[1] Research Hub for Coral Reef Ecosystem Functions, College of Science and Engineering, James Cook University, Townsville, Queensland 4811, Australia [2]Institution

[2] Paris Sciences et Lettres Université, École Pratique des Hautes Études, EPHE-UPVD-CNRS, USR 3278 CRIOBE, University of Perpignan, 66860 Perpignan, France

Carbonate budgets describe the dynamic production and loss of calcium carbonate ($CaCO_3$) on coral reefs. To sustain or expand the coral reef framework, $CaCO_3$ production must be higher than erosion. Although parrotfishes are widely recognized as the primary reef bioeroders, this estimated bioerosion rates exhibit marked spatial variability across depths, habitats, and exposure levels. However, these values are based on estimates of removal, using proxies e.g. fish abundances. Our understanding of the links between potential bioerosion (via proxies) and the disappearance of dead coral skeletons is in its infancy. Here, we followed the fate of 143 recently dead coral colonies of complex growth forms at Lizard Island for up to 5 years, to investigate dead coral colony erosion rates. We also estimated parrotfish-driven bioerosion, to assess the adequacy of the current methods in estimates erosion in dead coral colonies. We revealed rapid erosion of dead coral colonies, with an average of 79.7% of dead colonies completely disintegrating within 60 months. The predicted half-life of a dead coral colony was just 40 months, with limited variation among wave exposure levels. Remarkably, we found no effect of estimated parrotfish bioerosion, wave exposure, nor coral growth form, on observed erosion rates. Overall, based on these results, I will highlight how our understanding of the erosion of dead corals, the role of corals with complex growth forms in reef growth, and, more importantly, the role of parrotfishes in reef erosion may be more limited than previously thought.

Sustained productivity and the persistence of coral reef fisheries

Morais, Renato[1,2]; Smallhorn-West, Patrick[3,4,5]; Connolly, Sean R[5,6]; Ngaluafe, Poasi F[7]; Malimali, Siola'a[7]; Halafihi, Tu'ikolongahau[7]; Bellwood, David R[2,5]

[1]*Université Paris Sciences et Lettres, École Pratique des Hautes Études, CRIOBE, Perpignan, France*

[2]*Research Hub for Coral Reef Ecosystem Functions, James Cook University, Townsville, Australia*

[3]*WorldFish, Bayan Lepas, Malaysia*

[4]*Wildlife Conservation Society, New York, USA*

[5]*College of Science and Engineering, James Cook University, Townsville, Australia*

[6]*Smithsonian Tropical Research Institute, Balboa, Republic of Panama*

[7]*Tonga Ministry of Fisheries, Nuku'alofa, Tonga*

Fishing-induced biomass depletion is common on coral reefs. Yet, fisheries persist, maintaining the livelihoods of millions of fishers. Understanding this persistence is key to sustained reef fisheries in a time of global changes. Here we combine snapshot fish surveys and individual models of growth and mortality in a novel framework to evaluate potential reef fisheries productivity across a whole Pacific country (Tonga) spanning a major fishing pressure gradient. We provide empirical evidence of compensatory ecological responses triggered by fishing on coral reefs. High fishing exploitation drove biomass declines, yet, for a given exploitation level, productivity was consistently larger than expected from the remaining biomass. This buffering response provided, on average, an extra ~20% or 0.24 kg ha^{-1} d^{-1} of target fish production—a sizeable proportion of reported coral reef fisheries yields. Such 'buffering productivity' was strongest in wave-exposed, shallower, benthic-diverse and structurally complex areas. Consequently, a reef's capacity to deliver these responses is conditional on where it is located (that is, some habitats have higher propensity to support strong responses) and on its disturbance history (for example, episodic coral mortality that reduces structural complexity and benthic diversity). Thus, while compensatory buffering production may help explain persistent yields in biomass-depleted coral reef fisheries, the sustainability of these yields may be jeopardized by the impacts of climate change.

5.3B Themed Session B: Ecology of Indo-Pacific Fishes, 260-115, November 24, 2023, 1:30 PM - 3:00 PM

Animal biomass on Earth's ecosystems: are coral reefs any special?

Morais, Renato[1]; Narvaez, Pauline[1]; Parravicini, Valeriano[1]

[1]Université Paris Sciences et Lettres, École Pratique des Hautes Études, CRIOBE, Perpignan, France

Animal biomass is distributed unevenly across Earth, with some ecosystems concentrating much more of it than others. In deserts and the open ocean, animals are rare; in savannahs, polar seas and coral reefs, animal communities often form dense aggregations of biomass. Among these, coral reefs are touted as particularly productive, harbouring high animal diversity and abundance, particularly of fishes. However, how animal biomass on coral reefs compares with other highly productive ecosystems remains unresolved. Global analyses have provided detailed estimates of the living mass of Earth, yet these studies mostly focused on the contribution of distinct taxonomic groups or on differences between geographic regions, regardless of ecosystem type. We compiled 402 quantitative food webs including producer, invertebrate and vertebrate biomass and biomass production from 14 ecosystem types in terrestrial, freshwater, estuarine and marine systems to evaluate which ecosystem holds the highest animal biomass density. As predicted by theory, standardising variables by ecosystem volume (i.e., t km^{-3}) revealed a strong positive relationship between primary production and consumer biomass across the dataset. However, remarkable deviations indicated fundamental primary-production independent differences between ecosystems. Combining these two effects allowed comparing animal biomass density (also positively and strongly related to biomass production) among ecosystems. This revealed that coral reefs host between 2.4 and 430 times more animal biomass than the second most productive (rocky/kelp reefs) and the least productive (open ocean) ecosystems, respectively. Thus, we provide evidence that coral reefs host uniquely dense animal biomass among Earth's ecosystems, begetting the question: how?

The Design of Fish Screen Facilities at River Intakes – Lessons Learnt

Morgan, Paul[1]

[1]*Riley Consultants Ltd*

This presentation will focus on some of the key challenges in the design, construction and operation of fish screen facilities based on the experience of work at many sites with a variety of screen types.

In New Zealand there are guidelines that include eight criteria for the design of an effective fish screen facility. River intakes have several functions which include flow control, flood protection, sediment and debris management, safety of river users and operators, social and cultural needs. A fish screen needs to be integrated within the overall operation of an intake so an understanding of the interactions between these functions is a key part of the design process.

I will cover what has worked well, what the problems have been and some ideas on how we can improve the approach for future designs. Some of these issues relate to the design and construction but others link to the regulatory processes.

Early gonadal development, maturation and sex change in diandric protogynous red-belted anthias, *Pseudanthias rubrizonatus*

Moritoshi, Emma[1]; Dewa, Shinichi[2]; Kume, Gen[1]; Matsumoto Haruka[1]; Matsuoka, Midori[1]; Sunobe, Tomoki[3]

[1]*Faculty of Fisheries, Kagoshima University, Kagoshima, Japan*

[2]*Umiannai Diving Service, Kagoshima, Japan*

[3]*Tateyama Station, Tokyo University of Marine Science and Technology, Chiba, Japan*

Pseudanthias rubrizonatus belongs to the family Serranidae, and has been considered monandric protogyny. *P. rubrizonatus* is a dominant coastal species in Kagoshima Bay, Japan. However, the sexual pattern still remains unclear. The life history of this species was studied using histological observations of the gonads (n=426) and otoliths (n=376). This study not only revealed the process from sexual differentiation to the maturation of this species but also discovered the existence of bisexual juveniles and primary males. The spawning season was estimated as May to October. All juvenile gonads developed an ovarian lumen before sexual differentiation. Some juveniles underwent bisexuality; Spermatocytes were found with primary-growth stage oocytes in juveniles between 22.6 and 46.9 mm SL, ≦ 1 yr (n=24). Most differentiated to females with a minimum and maximum size of 38.0 mm and 77.0 mm SL, respectively (1 to 3 yrs, n=197), then changed sex to secondary males (52.0-79.3 mm SL, 2 to 3 yrs, n=14). However, nine small males aged 1-year-old (50.2-65.5 mm SL), considered primary males, were collected. Ovarian lumen was observed in all testes (50.2-95.1 mm SL, 1 to 5yrs, n=83). Therefore, this species is diandric protogyny, with two ways of becoming a male. Some individuals undergo bisexuality during the juvenile stage and differentiate to primary male. This sexual pattern is unprecedented in the subfamily Anthiadinae.

The effect of group size on mating system and sexual pattern of red-belted anthias, *Pseudanthias rubrizonatus*, Kagoshima Bay, Japan

Moritoshi, Emma[1]; Dewa, Shinichi[2]; Kume, Gen[1]; Matsuoka, Midori[1]; Sunobe, Tomoki[3]

[1]*Kagoshima University, Kagoshima, Japan*

[2]*Umiannai Diving Service, Kagoshima, Japan*

[3]*Tokyo University of Marine Science and Technology, Chiba, Japan*

Pseudanthias rubrizonatus has been considered polygyny and monandric protogyny. In this study, we investigated the mating systems and sexual patterns of this species in different-sized groups in Kagoshima Bay, Japan. The effect of group size on the mating system was studied using SCUBA, and the sexual pattern was studied using histological observations of the gonads. Two medium (50-100 individuals) and one large group (6,700-10,500 individuals) were observed in the study site of Kagoshima Bay. The large group had a unique group structure, with dominant males (n≒1,200) establishing territories near the female aggregation (sex ratio of female:male = 7:1), and the subordinate males (n≒800) establishing territories at the deeper site. The medium and large groups had the same mating system: pair-spawning. However, the sexual pattern differed among group sizes: monandric protogyny in medium groups and diandric protogyny in the large group. The difference in the sexual pattern would be caused due to the interaction between individuals. Males performed the pre-courtship behaviour toward bisexual juveniles and females throughout the year, even outside the breeding season (May to October). This behaviour is considered to suppress sex differentiation in juveniles and sex change in females. Under the female-biased sex ratio, not every female can receive an equal amount of pre-courtship; thus, primary males (n=9) were only found in the large group. Therefore, group size would affect the mating system and sexual pattern of this species.

2.2A Special Session 4: The evolution and ecology of fishes: assessing traits and functions in a changing world, 260-073, November 21, 2023, 10:30 AM - 12:30 PM

Exploring patterns in the phenotypic diversity of individual growth across a fish species' range

Morrongiello, John[1]; Fobert, Emily[1]; Ng, Zhong Wang Clement[2]

[1]*School of BioSciences and Oceania Institute, University of Melbourne, Australia*

[2]*Asian School of the Environment, Nanyang Technological University, Singapore*

Rapid environmental change necessitates we investigate the adaptive capacity of species to respond to a warmer future. Importantly, species and populations comprise of individuals, each of which may respond to its environment in its own way. Several hypotheses have been proposed to describe patterns of individual phenotypic diversity and plasticity across a species' range. First, populations that experience the greatest environmental variability (often at higher latitudes due to increased seasonality) are expected contain individuals with high levels of plasticity in traits adaptive in those conditions. Conversely, individuals inhabiting stable environmental conditions should express less plasticity. Second, it has been predicted that core and margin populations will differ significantly in phenotypic expression and plasticity patterns, as genetic structure and selection pressures related to environmental heterogeneity vary along the distribution range of a species. Third, phenotypic patterns may reflect a trade-off between overall performance under a set of conditions and the capacity of individuals to plastically modify their phenotype. Here, we compile an extensive dataset of individually resolved growth thermal reaction norms for pink snapper, collected over 15 degrees of latitude along the Australia's east coast. We use this data to provide an empirical test of three contrasting hypotheses that explain trait variability in response to spatio-temporal patterns of warming across a species' range, and explore the potential of other stressors, such as fishing, to erode phenotypic portfolios. We discuss our findings in the context of the capacity of species across their natural range to withstand or adapt to continuing warming.

Scavenger richness and functional diversity modify carrion consumption in the surf zone of ocean beaches

Mosman, Jesse[1]; Borland, Hayden[1]; Gilby, Ben[1]; Henderson, Christopher[1]; Olds, Andrew[1]; Rummell, Ashley[1]

[1]*School of Science, Technology and Engineering, University of the Sunshine Coast, Sippy Downs, Queensland 4558, Australia*

Ecological functions are linked to the condition and stability of coastal ecosystems. Quantifying how human disturbance and seascape context influence biodiversity and how different forms of diversity (i.e. species richness and functional diversity) influence ecological functioning is important in managing coastal ecosystems. We measured if the rates of carrion consumption by fish and crustaceans were influenced by scavenger richness and functional diversity or the abundance of key scavenger species, and which environmental factors shaped carrion consumption in surf zones at 20 beaches eastern Queensland, Australia. Carrion consumption was positively correlated with scavenger richness and functional diversity, and the abundance of two species; weeping toadfish (*Torquigener pleurogramma*) and ornate wobbegong (*Orectolobus ornatus*). Carrion consumption was highest at sites that were near rocky headlands (<1km) and shark control program equipment (<1km) and was also characterised by functional complementarity as weeping toadfish consumed more carrion at sites with a smaller area of reef nearby (<0.1 km2) whilst ornate wobbegong consumed more carrion at sites with a larger area of reef nearby (>0.3 km2). We highlight the importance of scavenger richness and functional diversity in shaping carrion consumption in surf zones, particularly when the species performing the function do this in spatially distinct areas.

Preliminary review of the interstitial gobiid genus *Luciogobius* Gill, 1859 in the Ryukyu Archipelago, Japan

Motomura, Hiroyuki[1]; Koreeda, Reo[2]; Maeda, Ken[3]

[1]*The Kagoshima University Museum, Kagoshima, Japan*

[2]*The United Graduate School of Agricultural Sciences, Kagoshima University, Kagoshima, Japan*

[3]*Marine Eco-Evo-Devo Unit, Okinawa Institute of Science and Technology Graduate University, Kunigami, Japan*

The earthworm-like goby genus *Luciogobius* is known to consist of 16 described species and more than 20 possible undescribed species from East Asia. Most of them inhabit the interstitial spaces between rocks and/or gravels in the intertidal zone on the rocky coasts or river mouths in Japanese temperate area. However, taxonomy of *Luciogobius* in subtropical regions has poorly been known. In the Ryukyu Archipelago (subtropical area of Japan), eight species, including six undescribed species, have been reported, although five of them are known only as larvae or juveniles. In this study, we investigated ichthyofauna of the archipelago focusing on the interstitial species and found 15 species of *Luciogobius* on the islands from the Tokara to Yaeyama. The genus *Luciogobius* consists of five species complexes defined by morphological characters, all of which occurring in the Ryukyu Archipelago. Each species differs in meristic counts (including total of, or ratio of abdominal and caudal vertebrae), position of the anus, fin shapes, and coloration. Many species were found from interstitial habitats in/around river mouths or freshwater springs, but their microhabitats vary among the species, and four species also inhabit environments not affected by fresh water, such as within dead coral sediments along the coastline. Diagnostic features, geographic distributions, and habitat of all species from the Ryukyu Archipelago are provided here with a key to the species.

Local habitat composition and complexity outweigh seascape effects on fish distributions across a tropical seascape

Moustaka, Molly[1,2,3]; Bassett, Tahlia J[4]; Cuttler, Michael VW[2,5]; Evans, Richard D[1,3]; Hyndes, Glenn A[6]; Kendrick, Gary A[1,2]; O'Leary, MJ[2,7]; Wilson, Shaun K[2,3]

[1] *School of Biological Sciences, The University of Western Australia, Perth, WA, 6009, Australia*

[2] *The Oceans Institute, The University of Western Australia, Perth, WA, 6009, Australia*

[3] *Marine Science Program, Biodiversity and Conservation Science, Department of Biodiversity, Conservation and Attractions, Kensington, WA, 6151, Australia*

[4] *School of Molecular and Life Sciences, Curtin University, Perth, WA, 6102, Australia*

[5] *Oceans Graduate School, The University of Western Australia, Perth, WA, 6009, Australia*

[6] *Centre for Marine Ecosystems Research, School of Science, Edith Cowan University, Perth, WA, 6027, Australia*

[7] *Centre for Energy Geoscience, School of Earth Sciences, The University of Western Australia, Perth, WA, 6009, Australia*

The distribution of animals is influenced by a complex interplay of landscape, environmental, habitat, and anthropogenic factors. While the effects of each of these forces on fish assemblages have been studied in isolation, the implications of their combined influence within a seascape remain equivocal. We assessed the importance of local habitat composition, seascape configuration, and environmental conditions for determining the abundance, diversity, and functional composition of fish assemblages across a tropical seascape. Underwater stereo-video was used to quantify fish assemblages in coral, macroalgal, mangrove, and sand habitats throughout the Dampier Archipelago, Western Australia. A full-subsets modelling approach that incorporated data from benthic habitat maps, a hydrodynamic model, *in situ* measures of habitat composition, and remotely-sensed environmental data was used to evaluate the relative influence of biophysical drivers on fish assemblages. Measures of habitat complexity were the strongest predictors of fish abundance, diversity, and assemblage composition in coral and macroalgal habitats, with seascape effects playing a secondary role for some functional groups. Proximity to potential nursery habitats appeared to have minimal influence on coral reef fish assemblages. Consequently, coral, macroalgal, and mangrove habitats contained distinct fish assemblages that contributed to the overall diversity of fish within the seascape. Our findings underscore the importance of structural complexity for supporting diverse and abundant fish populations and suggest that the value of structural connectivity between habitats depends on local environmental context. Our results support management approaches that prioritise the preservation of habitat complexity, and that incorporate the full range of habitats comprising tropical seascapes.

Assessing mechanisms of vulnerability in sharks occupying different marine environments

Mukherji, Sushmita [1]; Simpfendorfer, Colin[1]; Dowling, Natalie[2] and Krueck, Nils [1]
[1] *Institute for Marine and Antarctic Studies, University of Tasmania, Hobart, Tasmania, Australia*
[2]*Commonwealth Scientific and Industrial Research Organisation (CSIRO) – 3 - 4 Castray Esplanade, Hobart, Tas. 7004, Australia*

The threatened status of shark species as recognized by their IUCN Red List classifications, is a function of exposure to fishing mortality and intrinsic life history traits. Given that life history traits, such as reproductive strategies, are known to evolve and adapt in concert with complex interactions between environmental conditions, the vulnerability of shark species might also be predicted by the marine environment (herein habitat) occupied by the species. Although reproductive strategies of sharks have been intensively studied, the relationship between these strategies and key life history traits in different habitats are not well understood. We aimed to investigate 1) the prevalence of reproductive strategies across depth gradients and major habitats (i.e. shelf, pelagic and deep sea) and 2) the association between reproductive strategies and key life history traits that predict the vulnerability of shark species. Distribution of reproductive strategies varied among habitats. Shelf habitats were dominated by placental viviparous species, that rarely reside in other habitats. Oviparous species were less selective with their habitat preference and reside equally in shelf and deep sea, but were not found in pelagic environments. Oviparous species also showed significantly different life history traits compared to other reproductive strategies. Additionally, threatened shark species were found to be mainly associated with shelf habitats. Therefore, under current fishing scenarios it can be hypothesised that placental viviparous species may be more vulnerable in comparison to oviparous species. However, with fisheries moving deeper, results from this study provide important insights into the vulnerability of sharks occupying different habitats.

Estimating the species composition of global shark and ray fisheries

Mull, Christopher [1]; Babcock, Elizabeth [2]; Barbosa Martins, Ana Paula [1]; Warwick, Luke[3]; Chapman, Demian [4]; Andorra, Alex; MacNeil, M. Aaron [1]

[1] *Integrated Fisheries Lab, Dalhousie University*
[2] *Department of Biology, University of Miami*
[3] *Wildlife Conservation Society*
[4] *Mote Marine Laboratory*
[5] *PyMC Labs*

Shark and ray fisheries landings have decreased over the past decade. While more than 300 species are caught in global fisheries, reliable species-specific landings information is scarce as statistics are often reported as aggregate categories (e.g. “sharks, skates, and rays, nei”). Aggregate data masks important species-specific trends, complicating stock assessment efforts and obscuring the ecological footprint of fishing. Generating reliable species-specific landings estimates across the globe is critical for effective fisheries management. Here, we present an estimate of species-specific landings across more than 100 countries from 2012 to 2019 based on the FAO Fisheries Capture Production Database. Aggregate landings were allocated to species based on taxonomy, FAO Major Fishing Area, and estimates of fishing pressure. Unsurprisingly, blue sharks dominate global landings though batoids represent a greater proportion than expected. Our results provide species-specific trends in fisheries landings and will assist with estimating biological reference points across all landed shark and ray species globally. These refined landings estimates will improve stock assessments and strengthen the implementation and enforcement of conservation initiatives such as CITES.

Otolith chemistry improves age estimation and reveals movement history of catadromous barramundi (*Lates calcarifer*)

Munpholsri, Nut[1]; Gardiner, Naomi[1]; Leahy, Susannah[2]; Waltham, Nathan[1,3]

[1]*College of Science and Engineering, James Cook University, Townsville, QLD 4811.*

[2]*Department of Agriculture and Fisheries, Cairns QLD 4870.*

[3]*Centre for Tropical Water and Aquatic Ecosystem Research (TropWATER), James Cook University, Townsville, QLD 4811*

Barramundi (*Lates calcarifer*) is a facultative catadromous species that hatches in seawater, can grow in brackish and freshwater before returning to reproduce in seawater. Only some barramundi migrate, but juveniles that move to freshwater grow faster than those that remain in saltwater. Our study aims to understand the proportion of migrants at each life stage and factors that trigger this facultative migration.

To achieve this, we obtained otolith chemistry (LA-ICP-MS) of 593 fish from commercial and recreational samples on the northeastern coast of QLD. Fish age was estimated by counting and comparing increment rings with microchemical signatures. We quantified changes in mean Sr:Ca ratio as a proxy of movement between salinity gradients using a change-point analysis. The magnitude and direction of Sr:Ca changes were then correlated with environmental data to determine movement cues.

Patterns in Mg:Ca, P:Ca, and P:Mg closely matched placement of increment formation. Incorporating these ratios can resolve challenges in increment determination. Reconstructed movement history using the Sr:Ca signature showed that only 121 fish (20.4%) experienced a freshwater environment ($Sr:Ca < 1.5\ mmol.mol^{-1}$) at some point in their lives. The changing salinity events primarily occurred during the first two years of life, with a higher proportion observed in years with high rainfall and increased river flow. Our results indicate that freshwater availability is a major driver of freshwater usage in barramundi. These findings have important implications for the allocation of freshwater resources and improvements in habitat connectivity to encourage barramundi migration and its subsequent benefits to the fishery.

5.4A Themed Session G: Long Term Monitoring of Indo-Pacific Fishes, 260-092, November 24, 2023, 10:30 AM - 12:30 PM

Meta-analysis reveals weak associations between reef fishes and corals

Muruga, Pooventhran[1,2,3]; Siqueira, Alexandre C.[1,2,3]; Bellwood, David R. [1,2,3]

[1]*Research Hub for Coral Reef Ecosystem Functions, James Cook University, Townsville, QLD 4811, Australia*

[2]*College of Science and Engineering, James Cook University, Townsville, QLD 4811, Australia*

[3]*James Cook University, Townsville, QLD 4811, Australia*

Tropical, shallow water coral reefs are renowned for their abundance and diversity of life, most notably in reef fishes and corals. It is widely believed that on coral reefs, there is a clear, strong, and positive relationship between fishes and the predominant coral form: hard coral. This belief is underpinned by multiple studies that document a decline in fishes following coral loss. However, only a small proportion of reef fish species are regarded as being ecologically reliant on corals. With coral reefs continuing to experience environmental disturbances, it remains prudent to scrutinise the nature of this relationship, and specifically, to examine the nature of association between fishes and corals. Here, we perform a rigorous meta-analytic review, screening 4653 individual studies across 2 databases. Following a robust screening criteria, we synthesise 720 effect sizes spanning 74 empirical studies that quantify reef fishes and coral cover, utilising their correlation coefficient as a measure of association. Remarkably, there appears to be no consistent pattern of correlation at a global scale; evidenced by positive yet weak correlations ($r < 0.4$) across common fish metrics (abundance, biomass, and species richness). Notably, we also find that apart from obligate corallivores, all reef fish trophic groups and families are characterised by weak correlations with coral cover, including the families, Pomacentridae and Chaetodontidae. These findings highlight the need for caution when generalising the notion of more coral = more fish?

Homoploid hybrid speciation in Torpedo scad *Megalaspis cordyla* in the western Pacific

Muto, Nozomu[1]; Babaran, Ricardo[2]; Ghaffar, Mazaln Abd.[3]; Hata, Harutaka[4]; Nguyen, Van Quan[5]; Su, Yong Chao[6]; Vilasri, Veera[7]

[1]*Kitasato University, Japan*

[2]*University of the Philippines Visayas, The Philippines*

[3]*Universiti Malaysia Terengganu, Malaysia*

[4]*Smithsonian Institution, USA*

[5]*Vietnam Academy of Science and Technology, Vietnam*

[6]*Kaohsiung Medical University, Taiwan*

[7]*National Science Museum, Thailand*

Homoploid hybrid speciation (HHS) is a fascinating phenomenon in evolutionary biology, where new species arise through hybridization without changes in chromosome number. Although documented in various organisms, convincing cases of HHS in pelagic marine fishes have been lacking. Our study presents evidence for HHS in Torpedo scad *Megalaspis cordyla* based on genome-wide SNP analysis. A Principal Component Analysis identified three distinct clusters (species) in western Pacific samples. STRUCTURE analysis indicated admixed ancestry for one species, with asymmetric genomic contributions from the other two species. The admixed ancestry was also supported by multiple statistical methods for hybrid detection. Moreover, model-based demographic inference favored a hybrid speciation scenario over introgression. Estimated divergence times for the three species align with the Pleistocene. The hybrid species is restricted to the coasts of Taiwan and Japan, where all three species coexist. The parental species are additionally found in lower latitudes such as the coasts of the Philippines, Vietnam, Thailand, and Malaysia, where they exhibit non-overlapping distributions. We propose that Pleistocene glacial cycles drove allopatric divergence, latitudinal range shifts, and secondary contact of the parental species, leading to the formation of the hybrid species. Our findings shed light on HHS in pelagic marine fishes and emphasize the impact of historical climate changes on speciation. Additionally, we provide taxonomic implications for the three species based on comprehensive morphological examinations.

3.5A Themed Session E: Biology and Conservation of Sharks and Top-predators, 260-051, November 22, 2023, 10:30 AM - 12:30 PM

What's on the menu?: analysing stingray vomit shows species-specific resource partitioning within an intertidal nursery

Myers, Jaelen[1]; Crook, Kevin[1,2] Barnett, Adam[1], Bradley, Michael[1], Mattone, Carlo[1], Sheaves, Marcus[1]

[1]*College of Science and Engineering, James Cook University Townsville, QLD 4814*

[2] *Marine Science Program, Department of Biodiversity, Conservation and Attractions, Kensingston, WA 6151*

Intertidal flats provide abundant foraging opportunities for juvenile rays, and studying the diets of species that inhabit these ecosystems is necessary for understanding their unique feeding ecologies. Rays are often generalist feeders that consume a range of benthic invertebrates, but differences in habitat preferences and foraging strategies may drive dietary variability between species. At Lucinda Beach in N. QLD, drone surveys show that two stingray species (Australian whipray, *Himantura australis* and cowtail stingray, *Pastinachus ater*) feed in different habitats within the sandflat boundary and exhibit different foraging behaviours. This suggests each species may be targeting different prey items that are unevenly distributed across available habitat. To investigate this hypothesis, I used non-lethal gastric lavage to extract stomach contents from juvenile Australian whipray, cowtail stingray, and a third resident species, the giant shovelnose ray, *Glaucostegus typus*. Results showed that although juvenile rays consumed several invertebrate taxa, composition of the diet varied by species. The cowtail stingrays were more generalist, consuming more polychaetes, gastropods, and bivalves than Australian whiprays or giant shovelnose rays, which primarily consumed small portunid crabs and penaeoid prawns. These findings, combined with existing data on their foraging behaviours, are evidence of resource partitioning within the nursery. Efforts are currently underway to map invertebrate distributions, which will allow for further investigation on how prey availability influences prey choice. Studies that integrate information on diet, foraging behaviours, and environmental prey will continue to have strong implications for understanding habitat use of elasmobranchs in productive coastal habitats.

Functional beta diversity of New Zealand fishes: Characterising morphological turnover along depth and latitude gradients, with derivation of functional bioregions

Myers, Elisabeth[1]; Anderson, Marti J[1,4], Eme, David[1]; Harvey, Euan S.[2]; Liggins, Libby[1]; Roberts, Clive D.[3]

[1]*Massey University, Albany, Auckland, New Zealand*

[2]*Curtin University, Bentley, Western Australia*

[3]*Museum of New Zealand Te Papa Tongarewa, Wellington, New Zealand*

[4] *PRIMER-e, Massey University, Albany, Auckland, New Zealand*

Here, we describe patterns in functional beta diversity for New Zealand marine fishes versus depth and latitude, including broad-scale delineation of functional bioregions. We derived eight functional traits related to food acquisition and locomotion and calculated complementary indices of functional beta diversity for 144 species of marine ray-finned fishes occurring along large-scale depth (50–1200m) and latitudinal gradients (29°–51°S) in the New Zealand EEZ. Morphological traits were calculated directly from in-situ Baited Remote Underwater Stereo-Video footage and museum specimens. We found that functional changes were primarily structured by depth followed by latitude, and that latitudinal functional turnover decreased with increasing depth. Functional turnover among cells increased with increasing depth distance, but this relationship plateaued for greater depth distances (>750m). In contrast, functional turnover did not change significantly with increasing latitudinal distance at 700–1200m depths. Shallow functional bioregions (50–100m) were distinct at different latitudes, whereas deeper bioregions extended across broad latitudinal ranges. Fishes in shallow depths had a body shape conducive to efficient propulsion, while fishes in deeper depths were more elongated, enabling slow, energy-efficient locomotion, and had large eyes to enhance vision. Environmental filtering may be a primary driver of broad-scale patterns of functional beta diversity in the deep sea. Greater environmental homogeneity may lead to greater functional homogeneity across latitudinal gradients at deeper depths (700–1200m). We suggest that communities living at depth may follow a ‘functional village hypothesis’, whereby similar key functional niches in fish communities may be maintained over large spatial scales.

Does nest-building glue secreted by the kidney of male stickleback attract females?

Nagaya, Miki[1]; Yambe, Hidenobu[2]; Koya, Yasunori[3]

[1] *The United Graduate School of Agricultural Science, Gifu University*

[2] *Faculty of Bioindustry, Tokyo University of Agriculture*

[3] *Faculty of Education, Gifu University*

Male sticklebacks (*Gasterosteus* belonging to Gasterosteidae) produce an adhesive substance, “spiggin,” from their kidney epithelial cells. They utilize this substance to build spawning nests with vegetative fragments. Spiggin primarily consists of polysaccharides that are released mixed with urine. A similar substance has been reported in freshwater sculpins (*Cottus* belonging to Cottidae), where they spawn eggs in the nest underneath a stone. The swollen male kidney produces the substance containing polysaccharides, and the male fish preserve its urine in their urinary bladder during the breeding season. In sculpins, the secretions of the kidney are assumed to be released with the urine to attract the female to their nest. Based on the physiological similarity in kidneys of sticklebacks and sculpins, we hypothesized that spiggin might play a vital role in attracting the females to their spawning nest. Using a Y-maze, the proposed hypothesis was evaluated through a series of behavioral experiments conducted on nine-spined stickleback (*Pungitius* sp.1 belonging to Gasterosteidae). Ovulating females are consistently attracted to male kidney extracts rather than female kidney extracts. The high molecular weight fraction (<3000 mol.wt.) of male kidney extracts attracted the ovulating females compared to low molecular weight fractions (>3000) that were separated through a dialysis membrane. The current study suggests a high possibility that the substance that attracts females is spiggin, so additional experiments need to be conducted using newly built nests (aggregated vegetative fragments by spiggin).

Fish assemblages reshuffle in response to resource alteration due to the indirect effects of climate change

Nagelkerken, Ivan[1]; Cipriani, Vittoria[1]; Agostini, Sylvain[2]; Harvey, Ben[2]; Hayes, Chloe[1]; Izumiyama, Michael[3]; Kawai, Erina[3]; Jolly, Jeffrey[3]; Spatafora, Davide[2]; Wada, Shigeki[2]; Ravasi, Timothy[3]

[1]*Southern Seas Ecology Laboratories, School of Biological Sciences, The University of Adelaide, DX 650 418, Adelaide, SA, 5005, Australia*

[2]*Shimoda Marine Research Center, University of Tsukuba, 5-10-1 Shimoda, Shizuoka, 415-0025, Japan*

[3]*Marine Climate Change Unit, Okinawa Institute of Science and Technology Graduate University, 1919–1 Tancha, Onna-son, Okinawa 904–0495, Japan*

Climate change is forecast to alter the distribution and composition of fish communities globally, yet we still have little empirical evidence of what future communities might look like in the wild. We used a natural laboratory of climate change in temperate waters of Japan (volcanic CO_2 vent and natural warming hotspot) to investigate the effects of ocean warming and acidification on an assemblage of tropical range-extending fishes. The direct effects of these stressors on fish physiology were generally minimal to absent (e.g. reproduction, antioxidants), although one species showed increased oxidative damage and reduced energy storage at its cold-water leading edge. Indirect effects of these stressors were reflected through altered resource availability and composition (i.e. food and habitat). Prey abundance was lower under warming and acidification compared to present-day conditions, whilst the prey communities differed amongst all three treatments. In response, fishes altered their trophic niches (stomach content and stable isotope signatures). Benthic habitat composition also changed in response to climate stressors, with stony corals dominating at the warming site and turf algae at the vent site. Fishes showed altered abundances under warming and acidification, probably associated with their plasticity in habitat use. We here show that whilst some fishes experience direct impacts on their physiology under ocean acidification and warming, the indirect effects of resource alteration appear to be more important in structuring their communities. We conclude that species that are flexible in their resource use will likely be best adapted to adjust to future ecosystem modifications under climate change.

Testing a new method for assessing mirror self-recognition in three-spined sticklebacks

Nakano, Shota[1]; Awata, Satoshi[1]; Funeno, Nana[1]; Mori, Seiichi[2]; Kohda, Masanori[1]; Sogawa, Shumpei[1]

[1]*Laboratory of Animal Sociology, Department of Biology, Graduate School of Science, Osaka Metropolitan University, Osaka, Japan*

[2]*Department of Academics, Gifu Kyoritsu University, Oogaki, Japan*

Mirror self-recognition (MSR), the ability to recognise one's own mirror image as the self, is considered evidence of self-awareness and has been reported in a variety of animals, including the great apes, crows, and cleaner fish. The mark test is a well-known method for examining MSR, but it is unsuitable for animals that do not pay attention to the mark. To address this challenge, we developed a versatile method for testing MSR and applied it to assess the MSR capacity of the territorial three-spined stickleback *Gasterosteus aculeatus*, a model organism for animal behaviour. Firstly, we exposed focal fish to a mirror and neighbour fish for four days. Then, we exposed them to three photographs, of themselves, familiar fish, and unfamiliar fish, for 15 minutes each. We hypothesised that if the focal fish recognised their own mirror image as another familiar individual, they would show similar levels of aggression towards their own photograph and the familiar individual's photograph. However, if the focal fish were capable of MSR, they would be less aggressive towards their own photograph than the photographs of others. We found that focal fish showed different aggression levels: minimum against own photographs, medium against familiar photographs, and maximum against unfamiliar photographs. The results clearly show that they distinguished between their own, familiar, and unfamiliar photographs and thus could recognise their own mirror image as themselves. This new method for testing MSR will be applicable to many territorial species, even those for which the classical mark test is unsuitable.

Integrating movement data and behavioural observations to assess the functional role of reef fishes

Narvaez, Pauline[1]; Morais, Renato[1]

[1] Université Paris Sciences et Lettres, École Pratique des Hautes Études, CRIOBE, Perpignan, France

The ecosystem role of mobile organisms is intimately linked with the way they use space. However, explicitly incorporating movement data in functional assessments of marine fishes has yet to become a common procedure. Here, we combine behavioural observations with detailed short term movement data from GPS tracks of 20 individuals from two related and sympatric reef fish species, the cleaner wrasses *Labroides dimidiatus* and *L. bicolor,* in an East Africa location. We reveal how these complementary sources of information may help to clarify the functional roles of species. In support of previous literature, we found that these two species differ sharply in their overall cleaning behaviour (e.g., number and identity of clients inspected, effective interactions). Expanding from this, we also found that their movement trajectories, including swimming speeds and step lengths, differed considerably. Small and large *L. dimidiatus* both established cleaning stations in relatively small areas and cleaned predominantly small client species. *L. bicolor* exhibited contrasting size-specific cleaning strategies. While small *L. bicolor* displayed cleaning station behaviour similar to *L. dimidiatus*, large individuals roved over much larger areas and cleaned primarily larger client species. Interestingly, despite vastly different areas explored, the cumulative distance swum by both species had a similar magnitude. This indicates that these two distinct ecological strategies, stationary and roving cleaning behaviour, could have similar energetic demands and consequences for the individuals engaging in them. Overall, our study case showcases the opportunities and implications of including movement in the assessments of the functional role of species more generally.

Evolution of substrate use across global assemblages of the goatfishes (Family Mullidae)

Nash, Chloe[1,2]; Lungstrom, Linnea[2]; Westneat, Mark[2]

[1]*Marine Macroevolution Unit, Okinawa Institute of Science and Technology, Japan*

[2]*Committee on Evolutionary Biology, University of Chicago, USA*

Tropical marine fishes offer a spectacular case study on how the evolution of specialized ecological niches can effect rates of phylogenetic, morphological, and distributional change. The goatfishes (Mullidae) are diverse in body form and foraging behavior, yet remain relatively unexplored in their evolutionary ecomorphology and biogeographic patterns. The synapomorphy that unites the goatfishes is the presence of chemosensitive hyoid barbels, which enable goatfishes to access otherwise inaccessible food within benthic substrates. Goatfishes preferentially forage on different substrate types, which results in habitat partitioning across reef systems. In this study, we integrated a recently published phylogeny of the goatfishes with a robust morphological dataset, ecotype trait analyses, and global assemblage delineations to test hypotheses about the evolution of ecomorphological and biogeographical associations with substrate preference. We performed a comprehensive geometric morphometric analysis on various morphological subsets across 72 goatfish species and we curated over 300,000 georeferenced records to identify goatfish-specific bioregions in shallow marine waters throughout the world. We find evidence that body shape, head shape, and fin profiles are significantly associated with substrate preference across the family. In particular, we show that preferential foraging on hard substrates evolved relatively recently within the genus *Parupeneus* and that rates of morphological diversification are significantly faster in hard substrate species. Additionally, we find that the presence of hard substrate species is consistent across Indo-Pacific, although there is species turnover within this niche. In conclusion, we find robust evidence for an evolutionary relationship between substate preference, morphological diversity, and global distribution of the goatfishes.

Social and economic dimensions of Australia's no-take marine sanctuaries

Navarro, Matt[1]; Hamre, Nicole[1]; Spencer-Cotton, Alaya[1]; Langlois, Tim[1]

[1]*The UWA Oceans Institute and School of Biological Sciences, The University of Western Australia, 35 Stirling Highway, Crawley, WA 6009, Australia*

No-take Sanctuary Zones within marine parks are critical to Australia's biodiversity conservation efforts, but relatively little is known about their social and economic dimensions. This presentation draws on Australian national surveys with recreational users of marine parks conducted between 2018 and 2023, as well as a large national survey of the Australian general public to distil insights about changes in Knowledge, Attitudes and Practice (KAP) that have occurred over time and across jurisdictions. We find overwhelming evidence of high levels of support and positive attitudes towards no-take sanctuary zones in marine parks amongst all groups, including the general public, recreational fishers and non-fishing recreational users of marine parks. We also show increases in awareness and support for marine parks over the 5-year time span of our survey data. These results contrast with media and key user group portrayals of attitudes towards no-take sanctuary zones in marine parks, instead highlighting overwhelming positive attitudes, especially in the medium to long term.

3.5A Themed Session E: Biology and Conservation of Sharks and Top-predators, 260-051, November 22, 2023, 10:30 AM - 12:30 PM

The evolution of contemporary population structure in white sharks. A story of sea level change, food availability, movement and sex.

Naylor Gavin[1]; Cliff, Geremy[2]; Corrigan Shannon[3]; Fedrigo, Olivier[4]; Gay Elise[5]; Hoyos Mauricio[6], Laso-Jadart Romuald[5]; Lee Adrian[1]; Lesturgie, Pierre[5]; Lowe, Christopher G[7]; Lyons Kady[8]; Mona Stefano[5]; Sato Keiichi[9], Skomal, Gregory, [10] Tomita Taketeru[9] and Yang Lei[1]

[1]*Florida Museum of Natural History*

[2]*Natal Sharks Board*

[2]*Minderoo Foundation*

[4]*Vertebrate Genomes Project*

[5]*Paris Museum*

[6]*Pelagios Kakunja*

[7]*California State University Long Beach*

[8]*Georgia Aquarium*

[9]*Okinawa Churaumi Aquarium*

[10]*Massachusetts State Fisheries*

The white shark (*Carcharodon carcharias*) is a globally distributed species that occurs in temperate and coastal waters. We established a high quality reference genome for the species and re-sequenced whole genomes for 14 individuals from 5 aggregation sites around the world. We subjected a further 283 individuals from localities throughout the species range to exon capture for 1,200 target genes and whole mitochondrial genome sequencing. Coalescent modelling revealed that the world's white sharks once comprised a panmictic population whose numbers diminished gradually until about 10,000 years ago, at which point they split into the three separate populations that are seen today: one in the North Atlantic, one in the North Pacific and one in the region that spans the Indian Ocean & Australia. The formation of these three populations was likely driven by changes in sea level. Fidelity to a "home ocean basin" may have been driven by the establishment of seasonal feeding aggregation sites which likely provided both a reliable source of food and an opportunity to mate, factors that were probably influential in shaping contemporary population structure.

Poster Function, OGGB Level 0 Foyer, November 21, 2023, 4:15 PM - 6:30 PM

Examining Biogeographic Variation in a Fish-Bacteria Bioluminescent Symbiosis

Neff, Emily[1,2]; Gould, Alison[1]

[1]*Institute for Biodiversity Science and Sustainability, California Academy of Sciences, San Francisco, CA*

[2]*Department of Biology, San Francisco State University, San Francisco, CA*

Siphamia is a genus of symbiotically bioluminescent cardinalfish. There are currently 25 recorded species of *Siphamia*, but none are as broadly distributed as *S. tubifer*. To date, most studies of *S. tubifer* have been based in Okinawa, Japan, so relatively little is known about the diversity of these fish and their symbiotic association across their broad range. Within Okinawa it appears that the fish only associates with a specific sub-species of *P. leiognathi* called *P. mandapamensis*, but it is still unclear whether this holds true throughout the host's Indo-Pacific distribution. To understand this symbiotic association further, we are examining the genetic diversity of the host and symbiont from several locations, including the Philippines, India, and the Red Sea using low-coverage whole genome sequencing on light organ DNA. Characterizing patterns of genetic differentiation across the hosts' range will help us understand population connectivity patterns of *S. tubifer*. We can characterize light organ symbionts from these new locations to determine the degree of specificity of the symbiosis over the host's broad range. Our preliminary analysis of more than twenty thousand single nucleotide variants indicate that *S. tubifer* populations in the Philippines and Japan are highly connected, which is most likely due to the Kuroshio current. Further, fish from the Philippines also associate with *P. mandapamensis*, indicating a high degree of specificity regarding this bioluminescent symbiosis. Overall, this reduced-complexity system can help us understand how specificity and stability of host-microbe associations are maintained over space and time, even in highly connected marine environments.

3.2B Themed Session C: Fisheries and Aquaculture in the Indo-Pacific, 260-073, November 22, 2023,
2:30 PM - 3:30 PM

Parenteral hormone administration induces spawning in redclaw, *Cherax quadricarinatus*

Nesa, Nur Un[1, 2]; Elliott, Lisa[3]; Paris, Damien B. B. P.[1]; Jones, Rhondda[1]; Zeng, Chaoshu[2, 4]; Nankervis, Leo[2, 4]; Cavalieri, John[1]

[1]*College of Public Health, Medical and Veterinary Sciences, James Cook University, James Cook Drive, Townsville, QLD 4811, Australia*

[2]*Centre for Sustainable Tropical Fisheries and Aquaculture, James Cook University, James Cook Drive, Townsville, QLD 4811, Australia*

[3]*Australian Crayfish Hatchery, 21 Everett Street, Mount Saint John, QLD 4818, Australia*

[4]*Discipline of Marine Biology and Aquaculture, College of Science and Engineering, James Cook University, James Cook Drive, Townsville, QLD 4811, Australia*

Redclaw, *Cherax quadricarinatus* is a tropical freshwater crayfish with numerous favourable attributes for commercial aquaculture. However, the ability to produce juveniles in industrial hatcheries is constrained by suboptimal fertility and erratic spawning of female redclaws. The current study examined the effects of intramuscular injection of methyl farnesoate (MF), serotonin (5-HT) and naloxone on redclaw ovarian maturation. A total of 168 redclaw were housed in vertical circulating systems and a dose response study was conducted for selection of optimal concentration. Afterwards, the females were injected with crayfish saline solution as control, MF, 5-HT, and naloxone at optimised concentrations for 3 to 5 times up to 20 days. The 5-HT and naloxone treated animals exhibited greater GSI and oocyte diameter compared to the control and MF treated animals. The odds of survival were less in the animals treated with MF but similar between other treatments. The odds of spawning were greater and the interval to spawning was shorter in crayfish treated with 5-HT and naloxone compared to the control and MF treated animals. The odds of moulting were greater and the mean interval to moulting was shorter in crayfish treated with MF compared to those treated with other treatments. The mean number of eggs/female and fecundity and hatching rate were significantly greater in the 5-HT and naloxone treated crayfish compared to those treated with control and MF. In conclusion, parenteral administration of MF increased mortality in female redclaw, whereas 5-HT and naloxone boosted egg production in an indoor hatchery.

Crossed saws: Evidence of hybridisation between Australian sawsharks

Nevatte, Ryan[1]; Gillings, Michael[1]; Williamson, Jane[1]

[1]School of Natural Sciences, Macquarie University, North Ryde, New South Wales, Australia, 2109

Hybridisation is the creation of viable offspring between two taxa and has been widely recognised in both marine and freshwater fishes. The occurrence of hybridisation between chondrichthyans, however, is a relatively recent discovery and has only been documented in a few species. Here we provide evidence of hybridisation between two species of sawshark – the common (*Pristiophorus cirratus*) and southern (*Pristophorus nudipinnis*) sawshark – which co-occur in the waters of southern Australia.

Specimens of both species collected throughout Australia were subject to mitochondrial DNA analysis, with the majority producing sequences corresponding to their field identification. One individual from north-east Tasmania, however, had a mismatch in its field identification (identified morphologically as *P. nudipinnis*) and molecular identity (possessed *P. cirratus* mitochondrial DNA). To resolve species identity, genotyping with nuclear single nucleotide polymorphisms was performed. Our analyses show that this individual represents a first-generation hybrid between the two sawshark species. Morphometric data indicate that this female had grown to adult size and may have been sexually mature. This shows that hybrid offspring can survive to adulthood in the wild. Molecular data also show that the hybrid was produced through the mating of a female *P. cirratus* and a male *P. nudipinnis*. These results provide new insights into the reproductive biology of this understudied group of sharks and adds to the number of chondrichthyan species known to be capable of hybridisation.

The evolution of dietary diversity in coral reef fishes

Ng, Isabelle[1]; Bellwood, David[1]; Siqueira, Alexandre[1]
[1]*Research Hub for Coral Reef Ecosystem Functions and College of Science and Engineering, James Cook University, Townsville, Queensland 4811, Australia*

Diet is a key aspect of fish ecology and has been shown to influence reef fish lineage diversification. However, the diversification of diet itself has yet to be investigated over evolutionary timescales for reef fishes. Diet is often classified into crude, univariate categories (e.g. trophic guilds) – with minor consideration to the amounts or types of prey – thus overlooking species dietary niche breadths. Here, we address this issue by applying a novel comparative method which models multivariate ecological trait evolution by combining both phylogenies, and the proportion of prey items, to infer dietary states based on information from extant species. Using the largest reef fish gut content dataset and the most complete ray-finned fish phylogeny to date, we investigate the conservatism, transitions, and diversification of dietary states among coral reef fishes through evolutionary time. Our findings reveal that dietary states and rates of prey switching are, in most cases, conserved within each family. We also found that among all prey types, transitions to and from zooplankton were the most common. Finally, two pulses of diet diversification were detected: one at the end-Cretaceous; and another at the end-Eocene. The Cretaceous–Paleogene mass extinction event likely provided the initial ecological landscape for coral reef fish diets to diversify. The subsequent establishment of modern families and their morphologies during the Eocene then paved the way for the second wave of dietary expansion. Altogether, our findings showcase the value of investigating diet across macroevolutionary scales.

A taxonomic review of central Indo-west Pacific lantern sharks (Etmopteridae: *Etmopterus*)

Shing-Lai, Ng[1]; Nicolas Straube[2]; Kwang-Ming, Liu[3,4,5]; Shoou-Jeng, Joung[1,4]

[1]*Department of Environmental Biology and Fisheries Science, National Taiwan Ocean University, Keelung, Taiwan*

[2]*Department of Natural History, University Museum Bergen, Bergen, Norway*

[3]*Center of Excellence for the Oceans, National Taiwan Ocean University, Keelung, Taiwan*

[4]*George Chen Shark Research Center, National Taiwan Ocean University, Keelung, Taiwan*

[5]*Institute of Marine Affairs and Resource Management, National Taiwan Ocean University, Keelung, Taiwan*

The lantern shark genus *Etmopterus* Rafinesque, 1810 is the most diverse group of extant sharks, containing at least 42 species. They are widely distributed from tropical to subboreal oceans, with its majority occurring in the Indo-west Pacific. Although the intrafamilial phylogeny is well resolved, several ambiguous taxonomic relationships within the genus remain unresolved, pending a comprehensive revision. The present study aims at reviewing the taxonomy of lantern shark species of the genus *Etmopterus* in the central Indo-west Pacific, by using an integrated taxonomic approach. Our dataset comprises 100 morphological characters as well as DNA sequence analysis of the mitochondrial NADH2 gene (1044 bp). We examined a total of 275 specimens of 28 species, including six potentially undescribed species. Based on our results, we suggest the following taxonomic revisions: resurrection *E. abernethyi* Garrick, 1957 for specimens hitherto assigned to *E. lucifer* in the southwestern Pacific; resurrection of *E. schmidti* Dolganov, 1986 for specimens hitherto assigned to *E. molleri* in the northwestern Pacific; and synonymizing *E. burgessi* Schaaf-Da Silva & Ebert, 2006 with *E. lucifer* Jordan & Snyder, 1902 in the northwest Pacific. We further provide updates ongeographical distributions of species, and conclude that *Etmopterus* are morphologically conservative, thus several characters such as the lateral flank-marking shape and length, as well as the body coloration, are quite variable within species, and should be used cautiously for species identification.

5.3A Themed Session B: Ecology of Indo-Pacific Fishes, 260-115, November 24, 2023, 10:30 AM - 12:30 PM

Varying importance of environmental variables on tropical snapper growth from the equatorial Indo-Pacific region

Ng, Zhong Wang Clement[1]; Gonzalez, Julio Guazzelli[1]; Newman, Stephen John[2]; Ong, Joyce Jia Lin[1]; Saleh, Muhammad Faiq[1]; Wakefield, Corey Brion[2]

[1]*Asian School of the Environment, Nanyang Technological University, Singapore*

[2]*Western Australian Fisheries and Marine Research Laboratories, Department of Primary Industries and Regional Development, Government of Western Australia, North Beach, Western Australia, Australia*

Climate change is a threat to the survival of tropical marine fish populations, many of whom are at the threshold of their thermal tolerance limits. Despite their importance to food production, there remains a knowledge gap on how changing ocean conditions will influence tropical fish stocks. The analysis of growth increments in otoliths can provide insights to past environmental conditions on fish populations to inform how future warming might affect species performance. The aim of our study was to establish the importance of demographic and environmental drivers on the annual growth expression of two tropical snappers, *Lutjanus johnii* and *L. malabaricus*, from the tropical Indo-Pacific region. Using mixed-effects models, we reconstructed more than four decades of growth chronologies spanning 26 degrees of latitude across the equator. We found that the growth of both species was explained by the mean annual sea surface temperature from the previous year. However, the relationship between growth and temperature varied between life stages. Observed trends were consistent with the Metabolic Theory of Ecology along a temperature gradient; fish from lower latitudes grew faster than those from higher latitudes. The intensity of the Indian Ocean Dipole, the primary mode of climate variation across the Indian Ocean, also had a positive effect on the growth of *L. malabaricus*, irrespective of life stages, and juvenile *L. johnii*, potentially associated with changes in ecosystem productivity. Our results contribute to our understanding of how changing ocean conditions might affect fish populations from an important yet understudied part of the world.

2.3B Themed Session B: Ecology of Indo-Pacific Fishes, 260-115, November 21, 2023, 1:30 PM - 3:00 PM

A role for encrusting, endolithic sponges in the feeding of Indo-Pacific parrotfishes (Labridae, Scarini)?

Nicholson, Georgina[1]*; Clements, Kendall D.* [1]

[1] *School of Biological Sciences, University of Auckland, Auckland, New Zealand*

Coral reef parrotfish display significant variation in trophic cranial morphology, yet these parrotfishes are described as generalist herbivores. Conventional gut content analysis for parrotfishes is problematic as these report mostly unidentifiable calcareous material. Therefore parrotfish dietary assignments typical rely on behavioural observations and the functional categories of scrapers, browsers and excavators.

Testing the recent hypothesis that most parrotfishes target micro-photoautotrophs requires high resolution, fine-scale analysis. We devised a non-invasive benthic substrata extraction method to investigate the dietary targets of parrotfishes and examine trophic partitioning. Fifteen syntopic species of Indo-Pacific parrotfish were followed on snorkel until repeated biting was observed. A 22mm x 20mm reef core was extracted around the bite. We identified and quantified bite core biota by scraping 1mm off the surface of the bite cores for microscopy and 16S/18S small subunit rRNA metabarcoding. Consistent bite core biota for the fifteen parrotfish species included micro-photoautotrophs, particularly Nostocales. We identified species-specific differences in targeted substrata including reef taphonomy, turf height and cover of crustose coralline algae. We investigated the possibility of spongivory in these parrotfishes including the presence of sponge-associated microbiota as suggested by the microphage hypothesis. The presence of encrusting and/or endolithic sponge taxa and sponge-associated microbiota provided a new axis of trophic partitioning with varying levels of spongivory amongst these parrotfish species.

This study provides further evidence that parrotfishes are specialised feeders that partition benthic trophic resources, and our findings provide a nutritional explanation for their bioerosion of carbonate substrata.

4.2C Special Session 8 Fish sensory ecology: new techniques and approaches, 260-073, November 23, 2023, 3:30 PM - 5:15 PM

Comparison of hearing abilities in three species of sharks

Nieder, Carolin[1]; Gibbs, Brendan[2]; Montgomery, John[1] ; Radford, Craig[1] ; Rapson, Jimmy[1]

[1] *The University of Auckland, Institute of Marine Science*

[2] *The University of Florida, Whitney Laboratory for Marine Bioscience*

Elasmobranchs (sharks, rays, and skates) are an ancient, diverse group of fishes, representing a basal stage in the evolution of vertebrate hearing. Yet, our understanding of physiological measures of hearing abilities in sharks is limited. In this study we assessed hearing abilities in the New Zealand carpet shark (*Cephaloscyllium isabellum*), rig shark (*Mustelus lenticulatus*), and school shark (*Galeorhinus galeus*). Specifically, the auditory evoked potential (AEP) technique was used in combination with two modes of stimulation: underwater speaker, providing pressure and particle motion stimuli; and shaker table, providing acceleration stimuli only. The results show differences in hearing abilities, mainly with respect to bandwidth rather than sensitivity. The speaker (pressure and acceleration) derived thresholds showed that hearing was least developed in the benthic carpet shark (upper limit: 300 Hz, best hearing: 40-100 Hz) and was superior in the benthopelagic rig and school sharks (upper limit: 800 Hz, best hearing: 100 Hz for school shark, and 150 Hz for rig). The shaker table (accelerations) derived thresholds showed that the strictly bottom-dwelling carpet shark is equally sensitive to acceleration in the vertical (z-axis) and head-to-tail (x-axis) directions. In contrast, the two benthopelagic species, the rig and school shark are more sensitive to accelerations in the vertical (z-axis) direction. These results indicate that sharks may differ in their directional hearing and potentially sound localization abilities. Habitat preferences and feeding strategies likely contribute to the differences in bandwidth and directional hearing in these sharks, but additional factors may be involved.

Determining species diversity and spatio-temporal distributions of larval fishes in Cockburn Sound, Western Australia

Nilsen, Jake[1]; McIlwain, Jennifer[1]; Strzelecki, Joanna[2]; Yeoh, Daniel[3]

[1] *School of Molecular and Life Sciences, Curtin University, Bentley Campus, Bentley, WA 6102, Australia*

[2] *CSIRO Oceans and Atmosphere, Indian Ocean Marine Research Centre, Crawley, WA 6009, Australia*

[3] *Department of Primary Industries and Regional Development Western Australia, Western Australia Fisheries and Marine Research Laboratories, North Beach, WA 6025, Australia*

Information on the abundance and distribution of fish larvae is critical for identifying spawning times and early-life habitat associations of fishery species or those of conservation interest. Fish larvae are typically highly sensitive to environmental perturbations, making them useful indicators of ecosystem health. Cockburn Sound (CS) is a diverse and ecologically important marine embayment in the Perth metropolitan region which is utilised for numerous recreational, commercial, industrial, and military activities. A broad range of environmental research projects funded by the Western Australian State Government are currently underway to better understand how fish use CS and identify potential impacts of any future infrastructure developments on fish and their habitats. As part of this program, two-years of monthly ichthyoplankton sampling was conducted with oblique towed bongo nets (500 µm mesh) to determine the diversity and spatio-temporal distributions of larval fishes. More than 23,000 individual larvae were identified, representing 48 families and at least 120 unique taxa. Dominant families (by total abundance) included Monacanthidae, Callionymidae, Terapontidae, and Gobiidae. Larval abundance, diversity, and community composition differed significantly over space (sites and regions) and time (months, seasons and years). Fishery important taxa were also well represented, including members of Clupeidae, Sillaginidae, Carangidae, and Sparidae, with marked temporal changes in their larvae aligning with existing biological knowledge of key species. This study provides a deeper understanding of how larval fishes use CS and provides an important baseline for monitoring the impacts of environmental change and future urban developments.

First report of schooling behavior, social structure, and spawning in *Canthigaster margaritata*

Nunes Peinemann, Viktor[1]; Cadiz, Ronald[1]; Coker, Darren J.[1]; Justo, Micaela Sofia dos Santos[1]; Pombo-Ayora, Lucía[1]; Berumen, Michael L.[1]

[1]*King Abdullah University of Science and Technology, Red Sea Research Center, Reef Ecology Lab*

Tobies, *Canthigaster* spp., are small-bodied, demersal pufferfishes inhabiting tropical coral reefs. They typically occur in low densities and can be both visually and behaviorally cryptic, swimming close to or within the matrix of a reef. For all species in which the social structure has been described, both males and females are territorial. Large males maintain a haremic territory encompassing several smaller female territories. Spawning occurs in a male-female pairing, where the female will lay demersal, adhesive eggs, on a nest of turf algae. Here, we provide the first description of the social structure and spawning in the Red Sea endemic *Canthigaster margaritata*. We report similar behavior as in other species of *Canthigaster* spp., with both males and females maintaining territories and depositing benthic eggs in single male-female pairings. Encounters at the border of territories result in territorial threat displays. Notably, however, we also report a behavior that starkly contrasts with the typical behavior of *Canthigaster* spp. In September of 2022, we observed a school of over 450 adult individuals of *C. margaritata* swimming in a coordinated manner several meters above the matrix of the reef. To the best of our knowledge, this has never been reported in *C. margaritata*. We discuss several potential explanations for this unusual behavior, including possible links to previously unreported seasonal population fluctuations.

Re-evaluation of the generic diagnoses of the family Samaridae (Pleuronectiformes) with comments on the phylogeny of the family

Obata, Kota[1]; Imamura, Hisashi[2, 3], Kawai, Toshio[2]

[1]*Chair of Marine Biology and Biodiversity, Graduate School of Fisheries Sciences, Hokkaido University, 3-1-1 Minato-cho, Hakodate, Hokkaido 041-8611, Japan*

[2]*Laboratory of Marine Biology and Biodiversity, Faculty of Fisheries Sciences, Hokkaido University, 3-1-1 Minato-cho, Hakodate, Hokkaido 041-8611, Japan*

[3]*Fisheries Science Center, The Hokkaido University Museum, 3-1-1 Minato-cho, Hakodate, Hokkaido 041-8611, Japan*

The flatfish family Samaridae is composed of four genera and about ca. 35 species distributed in shallower to deeper waters in the Indian and Pacific oceans. We examined the morphology of Samaridae in detail and re-evaluated the diagnostic characters of each genus based on about 350 specimens of ca. 35 species. We recognized *Samariscus* Gilbert, 1905 and *Plagiopsetta* Franz, 1910 are separable from other two genera by absence of extreme prolongation of anterior dorsal- and pelvic-fin rays on ocular side, absence of longer nasal tube in posterior nostril on ocular side, and presence of nostril on blind side (vs. presence, presence and absence in *Samaris* Gray, 1831), and having head depth lower than body depth and larger scales on body (vs. higher and smaller in *Samaretta* Voronina and Suzumoto, 2017). In contrast, it was revealed that *Samariscus* and *Plagiopsetta* cannot be clearly separated from each other by their diagnoses previously suggested: i.e., numbers of pectoral-fin rays (4–6 in *Samariscus* vs. 6–10 in *Plagiopsetta*) and abdominal parapophyses (5–6 vs. 6); sensory pore of supraorbital canal on blind side (presence vs. presence or absence) and scales on eye (presence or absence vs. absence); distributional patterns of intermuscular bones (presence or absence of epimeral, and hypomeral on posterior caudal vertebrae vs. absence). Therefore, they were considered to be inappropriate as the generic diagnoses. The phylogenetic analysis based on the anatomical characters suggested that *Samariscus* and *Plagiopsetta* are closely related with each other.

Identifying and conserving seascape nurseries on the Great Barrier Reef

Olds, Andrew[1]; Bradley, Michael[2]; Borland, Hayden[1]; Carter, Alex[2]; Ceccarelli, Dani[3]; Emslie, Mike[3]; Henderson, Chris[1]; Smith, Tim[2]

[1]*University of the Sunshine Coast*

[2]*James Cook University*

[3]*Australian Institute of Marine Science*

Many juvenile reef fish use alternative habitats as nurseries, but despite decades of research on nursery function, these habitats and their interconnections are often overlooked in coastal conservation. This is because coastal habitats are largely studied in isolation, and there are little data to identify and describe key seascape linkages at scales that are relevant to management. This project addresses these shortcomings by surveying juvenile fishes in the full diversity of inshore habitats on the Great Barrier Reef. It is one component of the wider Integrated Reef Fish Monitoring Program for the GBR, and has been designed and implemented with Traditional Owners to integrate their perspectives on seascapes nurseries. Fish are surveyed with stereo Remote Underwater Video Stations, and on each survey event we complete 900 deployments along 200km of coastline. The survey program has revealed diverse fish assemblages from a range of habitats on the inshore GBR, many of which had not been surveyed previously, and provides a platform that delivers hands-on training for local Sea Rangers. We have identified habitats, and seascape connections, that are critical for the juveniles of species that are of high fisheries, conservation and cultural significance. Our findings illustrate how the functions of nursery habitats depend on their ecological condition, conservation status and spatial context in wider coastal seascapes. We suggest that a deeper understanding patterns of seascape nursery use is needed to better support coastal management decisions for fish and fish habitats.

Environmental DNA (eDNA) based biomonitoring of fish and coral assemblages in changing environments under coastal development.

Açıkbaş Oshima, Ayşe Haruka[1]; Narisoko Haruhi[2]; Huerlimann Roger[1]; Nishitsuji Koki[2]; Satoh Noriyuki[2]; Reimer James Devis[3]; and Timothy Ravasi[1]

[1]*Marine Climate Change Unit, Okinawa Institute of Science and Technology Graduate University, 1919-1 Tancha, Onna-son, Okinawa, 904-0495 Japan.*

[2]*Marine Genomics Unit, Okinawa Institute of Science and Technology Graduate University, 1919-1 Tancha, Onna-son, Okinawa, 904-0495 Japan.*

[3]*Department of Biology, Chemistry, and Marine Science, Faculty of Science, University of the Ryukyus, Okinawa 903-0213, Japan.*

Environmental DNA (eDNA) metabarcoding has seen an increasing use in biomonitoring with promising findings, but its capabilities in long-term monitoring and its ability to assess anthropogenic disturbances have not been fully explored yet. Here we present and discuss the findings from two eDNA biomonitoring of fish assemblages with different spatiotemporal scopes. First is the Ogasawara Islands, a highly isolated oceanic island in the Pacific Ocean where we conducted the first ever spatially resolved eDNA surveys of both fish and Scleractinia coral assemblages to address the lack of recent multi-site surveys and the implications of relatively recent coastal development. We found differing biodiversity hotspots for the two groups, and we detected a total of 125 unique taxa of fish and 38 genera of Scleractinia corals, confirming that these islands host a unique and rich variety of coral and fish fauna. Second is the temporally resolved monthly survey of the Apogama beach, a popular diving spot in the Okinawa Island known for its high biodiversity with an ongoing hotel construction project on its shore, where we characterized the baseline seasonal patterns of fish assemblages over a year, to use it in the assessment of the impacts of coastal development on coral reefs. Overall, we underline the strength of eDNA based surveys in obtaining targeted multi-taxa data with low sampling effort that do not require in situ taxonomic expertise and we anticipate that continued biomonitoring using eDNA with adequate sampling effort will add to and complement the body of knowledge regarding species distributions, biodiversity patterns and their changes caused by anthropogenic disturbances.

Spatial distribution and habitat use of Dottybacks (Pseudochromidae) and color morph plasticity in *Pseudochromis flavivertex*.

Palacios-Narvaez, Stephania[1], Coker, Darren[1], Justo, Micaela[1], Majoris, John[2], Berumen, Michael[1]

[1]Red Sea Research Center, Division of Biological and Environmental Science and Engineering, King Abdullah University of Science and Technology, Thuwal, Saudi Arabia.

[2]Department of Marine Science, The University of Texas at Austin Marine Science Institute, Port Aransas, Texas, USA

Coral reef fish communities are influenced by benthic composition and topographic characteristics through the provision of habitat and food, and mediating predator-prey interactions. Dottybacks (Family: Pseudochromidae) are a diverse group of small reef predators that display a color variation within several species. In the Red Sea, this family has the highest rate of endemism with some species common across reef habitats while others appear to be habitat specialists; however, knowledge about their habitat use and the function of color variation within species is still limited. To enhance our understanding of this group, abundance, distribution pattern, habitat use, and color variation, were recorded on reefs across a distance from shore and depth gradient, and with different wave exposure in the Central Red Sea. We found differences in habitat use among Pseudochromis species and color morphs within a species, influenced by benthic composition. Further, we found two color morphs of Pseudochromis flavivertex of four reported for the Red Sea. Based on an aquaria experiment with individuals of two color morphs of *P. flavivertex* placed in contrasting habitat types (live, bleached, and dead coral), we determined that habitat composition influences color change. The morph commonly found in healthy reef habitats changed to the morph commonly found in degraded habitats. This study highlights the influence of benthic composition on coral reef fish distributions and provides information to predict how changes in habitat characteristics will affect their diversity on reef ecosystems, and if color morph plasticity allows these species to adapt to changing habitat conditions.

Ecological Assessment of the Siganid Fishery in Calapan City, Oriental Mindoro, Philippines

Panahon, Marius L.[1]

[1]*University of the Philippines Los Banos*

The siganid fishery in Calapan City, Oriental Mindoro, Philippines was assessed in terms of its ecological status. A total of 23 fish species from 19 families were identified in the study site, with majority being native and having a least concern conservation status. The population trend of most species was unknown, while some were not assessed. Among the identified species were *Siganus fuscescens, Siganus guttatus, Chanos chanos, Mugil cephalus,* and *Caranx sexfasciatus*. The assessment aimed to provide information on the status of the siganid fishery and its potential for sustainable use. Results of the study may be used for the development of management strategies that will ensure the conservation and sustainable use of the fishery resources. This study is relevant in promoting biodiversity conservation and sustainable development in the Philippines.

Ocean Genomes – A comprehensive high-quality reference genome library for marine vertebrates

Parata, Lara[1]; Ayad, Marcelle [2]; Bayer, Philipp[1,2]; Bennett, Adam[2]; Burnell, Steve[1,2]; Corrigan, Shannon [1,2]; De Jong, Emma [1]; Depiazzi, Anna[1]; Doran, Adrianne[1]; Edwards, Richard [1]; Goncalves, Priscilla [1,2]; Fraser, Matthew[1,2]; Hogan, Hayley[1]; Huet, Lauren[1]; Missen, Laura[1]; Pearce, Jessica[1,2]; Peirce, Tyler[1]; Raes, Eric [1,2]; Rauschert, Sebastian[1,2]

[1] Minderoo OceanOmics Centre at UWA, Oceans Institute, University of Western Australia, Perth, Australia

[2] Minderoo Foundation, Perth, Australia

The world's oceans play a vital role in supporting life on Earth. Ocean acidification, rising global temperatures, pollution and poor fishing practices are placing major stresses on marine life. These threaten the survival of species and ecosystems, creating a marine biodiversity crisis. The Minderoo OceanOmics program seeks to revolutionise how we measure, understand, and protect life in our oceans by advancing genomic tools to improve the conservation of marine biodiversity and sustainable management of marine species. Marine vertebrates are of particular interest because of their ecological roles, cultural significance, and commercial importance.

Environmental DNA (eDNA) is a method of choice for documenting marine biodiversity and monitoring change. eDNA is extracted directly from seawater samples for high throughput sequencing, and species composition established by matching eDNA sequences against taxonomically identified reference sequence databases. Unfortunately, existing reference DNA sequence databases are insufficiently curated, notoriously error prone and have substantial gaps in species and genome coverage, particularly for non-model organisms. These inadequacies present huge roadblocks for eDNA based research of marine organisms. Furthermore, high-quality reference genomes have proven themselves as indispensable foundations for understanding the evolution, adaptability and population genomics of specific species.

Here, we introduce 'Ocean Genomes'. We are building a comprehensive high-quality reference genome library of all Australian marine vertebrates in partnership with the Vertebrate Genomes Project, major sequencing providers, and a broad network of scientific and research organisations. We will introduce the main goals, tools, and workflows of the project, along with its progress to date and opportunities for collaboration.

Comparison of juvenile morphology and assessment of ontogenetic morphological changes in three species of seahorses Hippocampus spp. from south-eastern Australia

Miskiewicz, Anthony[1,2]; Parkinson, Kerryn[1]; Short, Graham[1, 3]

[1]*Australian Museum, NSW 2010*

[2] *University of NSW 2500*

[3] *California Academy of Science*

Seahorses (*Hippocampus* spp.) are a charismatic component of the fish fauna in estuarine and coastal marine waters. There are approximately 41 species worldwide and at least 18 species in Australian waters. In addition to their unique morphology and reproductive strategy, seahorses are threatened by fishing and habitat degradation, with all species listed in Appendix II of CITES. The taxonomy and nomenclature of seahorses is problematic, with multiple names for the same species. Juveniles of many species are also often confused due to variability at size, with few suitable resources to accurately identify specimens. In this study, meristic, morphometric, and key diagnostic morphological characters were compared in three species of juveniles seahorses *H. whitei*, *H. abdominalis* and *H. breviceps*, housed in the larval fish collection of the Australian Museum and collected from Lake Macquarie (NSW), Port Phillip Bay, (VIC), the Tamar River (TAS) and Gulf St Vincent (SA). Specimens were photographed using a Leica M205A Z-stacking microscope and a series of meristic counts and morphological measurements were recorded using Image-J. Specific specimens were examined via x-ray microcomputed tomography (µCT) using a Nikon XTH225 scanner. Examination revealed significant differences in size, pattern of body and head spines, and coronet size and shape, which alter with ontogenetic growth in the three seahorse species. Further research is required to determine if these differences exist in additional juveniles from other locations in south-eastern Australia based on other museum collections.

Predators and habitat association of post-settlement snapper (*Chrysophrys auratus*)

Parsons, Darren[1,2]; Gublin, Yann[1]; Hughes, Richard[1]; Middleton, Crispin[1]; Levell, Demi[1]; Taylor, Rikki[1]

[1]*National Institute of Water and Atmospheric Research, New Zealand*

[2]*The University of Auckland, New Zealand*

Structured habitats play an important nursery role during the crucial early juvenile or post-settlement stages of many fish species. Predominantly, the utility of structured habitats to juvenile fish is thought to be associated with the provisioning of food or as a refuge from predation. Snapper (*Chrysophrys auratus*) in New Zealand have a strong affinity for structured habitats during their post-settlement phase, but the role of predation in determining habitat association is unknown and there are potential alternative explanations relating to energetic sheltering. Here we investigated potential predators of post-settlement snapper by remotely observing interactions of restrained post-settlement snapper with potential predators and investigating the diet of potential predators. We also conducted tank experiments with a potential predator, both with and without the presence of structure. Restrained snapper were infrequently approached by predators, but two new nocturnal predators were identified. No snapper were observed in the diet of potential predators, although two piscivores were identified as potential candidates. No predation occurred during tank experiments, but there was a non-significant indication that under threat of predation post-settlement snapper may use habitat when it is present and aggregate together when it is not. The findings suggest that the pulsed nature of predation may have made it difficult to observe given the methods employed and that the threat of predation may be sufficient to drive the habitat selection of post-settlement snapper. Investigating the significance of predation via methods that do not require direct observations may therefore be more appropriate given this context.

High vulnerability of coral reef food web and energy fluxes to global change

Paul Costesec, Emma[1,2]; Brandl, Simon[3]; Casey, Jordan[3]; Danis, Bruno[1]; Delecambre, Zoe[2]; Floeter, Sergio[4]; Friedlander, Alan[5]; Morais, Renato[2]; Nunes, Lucas[4]; Parravicini, Valeriano[2]; Schiettekatte, Nina[6]

[1]*Marine Biology Lab (CP 160/15), Université Libre de Bruxelles, Brussels, Belgium*
[2]*PSL Université Paris: EPHE-UPVD-CNRS, Université de Perpignan, Perpignan, France*
[3]*Department of Marine Science, Marine Science Institute, The University of Texas at Austin, Port Aransas, TX, USA*
[4]*Departamento de Ecologia e Zoologia, Universidade Federal de Santa Catarina, Florianopolis, Santa Catarina, Brazil*
[5]*Pristine Seas, National Geographic Society, Hawai'i Institute of Marine Biology, University of Hawai'i, HI, USA*
[6]*Hawai'i Institute of Marine Biology, University of Hawai'i at Mānoa, Kāne'ohe, HI, USA*

Coral reefs are the most diverse marine ecosystem on Earth but are nowadays threatened by pervasive stressors, including coral bleaching, ocean acidification, overfishing and pollution. While the influence of these stressors on static community variables such as standing fish biomass or coral cover are well studied, trophic interactions are often overlooked. Hence, it is largely unknown how food webs and the energy fluxes that fuel coral reefs will respond to global changes.

Here, we combine the largest empirical global database of reef fish trophic interactions with fish-centric bioenergetic modelling and visual censuses to create, at a global scale, a coral reef weighted bipartite trophic networks database. Using this database, we delineate patterns of coral reef food webs structure and trophodynamics at a global scale and we explore how energy fluxes are impacted by environmental and anthropogenic pressures.

We found that the architecture of reef fish food webs are not homogeneous across oceans. First, we show that complex (i.e. species-rich) systems are more vulnerable, more compartmentalized and less connected than depauperate communities. On the other hand, sea temperature, coral cover, wave exposure and fishing intensity were all major determinants of reef fish food web architecture. Using Bayesian modelling, we eventually show that food web architecture is remarkably correlated with coral reef trophodynamics and regulates the amount of energy input from internal or oceanic production.

To conclude, our work sheds light on how reef fish food webs may evolve under global changes.

Neurogenomic patterns social and asocial learning of cooperative rules in cleaner fish

Paula, José Ricardo [1,2,3]; Pereira, Beatriz[2], Court, Melanie [2], Schunter, Celia[1]
[1]*Swire Institute of Marine Science, School of Biological Sciences, The University of Hong Kong, Pokfulam Rd, Hong Kong SAR*
[2]*MARE – Marine and Environmental Sciences Centre & ARNET – Aquatic Research Network, Laboratório Marítimo da Guia, Faculdade de Ciências Universidade de Lisboa, Av. Nossa Senhora do Cabo, 939, Cascais, Portugal*
[3]*Departamento de Biologia Animal, Faculdade de Ciências Universidade de Lisboa, Campo Grande, 1749-016, Lisbon, Portugal*

Cleaner wrasses, such as *Labroides dimidiatus*, engage in cooperative cleaning interactions to remove ectoparasites, dead skin, and mucus from other reef fishes (so-called clients). However, cleaners prefer to eat the protective mucus from their clients rather than parasites, which is considered cheating. Juvenile cleaners can socially learn the consequences of cheating, and social learning has been proposed as a potential mechanism for the evolution of cooperation. We used an experimental paradigm derived from cleaners' cooperative interactions with client fish to investigate the neuro-molecular mechanisms of social vs asocial learning of cooperation rules in cleaner wrasses. In this paradigm, juvenile cleaners had to experimentally learn to behave more cooperatively with client models using social information (adult cleaner demonstrator) or by themselves. Here, using transcriptomics in three brain regions (forebrain, midbrain, and hindbrain), we show that, although cleaners were equally able to learn socially or asocially, social learners elicit a higher transcriptional response in the forebrain while asocial learners respond in the hindbrain. Our results suggest a localized activation of social learning with transcriptional changes in social decision-making network-related regions (forebrain), while asocial learning is localized in a region related to associative learning (hindbrain).

3.3A Themed Session B: Ecology of Indo-Pacific Fishes, 260-115, November 22, 2023, 10:30 AM - 12:30 PM

Cleaner fish presence provides a ‘safe-haven’ from predation

Paula, José Ricardo[1,2,3]; Grutter, Alexandra S.[4]; Warner, Robert[5]; Madin, Joshua[1]; McCormick, Mark I.[6]; Meekan, Mark G.[7]; Bshary, Redouan[8]; Madin, Elizabeth M.P.[1]

[1] *Hawai‘i Institute of Marine Biology, University of Hawai‘i at Mānoa, Kāne‘ohe, HI 96744, USA*

[2] *MARE – Marine and Environmental Sciences Centre & ARNET – Aquatic Research Network, Laboratório Marítimo da Guia, Faculdade de Ciências, Universidade de Lisboa, Av. Nossa Senhora do Cabo, 939, 2750-374 Cascais, Portugal*

[3] *Departamento de Biologia Animal, Faculdade de Ciências, Universidade de Lisboa, Campo Grande, 1749-016 Lisboa, Portugal*

[4] *School of Biological Sciences, The University of Queensland, St. Lucia, QLD 4072, Australia*

[5] *Department of Ecology, Evolution, and Marine Biology, University of California, Santa Barbara, Santa Barbara, CA 93106, USA*

[6] *Coastal Marine Field Station, School of Science, University of Waikato, Tauranga 110, New Zealand*

[7] *Australian Institute of Marine Science, The Oceans Institute, University of Western Australia, Crawley, Western Australia, Perth, Australia*

[8] *Institute of Biology, University of Neuchâtel, Emile-Argand 11, 2000 Neuchâtel, Switzerland*

Cleaning mutualisms are ubiquitous interactions where cleaner fish remove and consume ectoparasites from other (‘client’) fish. Although cleaning stations attract many predatory clients, cleaners benefit from immunity to predation by using tactile stimulation to manipulate piscivorous partners. However, little is known about the behavioral impacts of perceived predation risk by bystanders near cleaning stations, nor its community-level implications. Our study sought to fill this gap by investigating how the proximity to cleaning services, provided by the cleaner wrasse *Labroides dimidiatus*, affects the risk-taking behavior of bystander prey, specifically the damselfish *Pomacentrus moluccensis.* To do so, we measured prey foraging excursion distance from reefs with or without cleaners in response to different levels of predator density and to a transient model predator (coral trout, *Plectropomus sp*.). Proximity to cleaning services was compared within a set of patch reefs around Lizard Island (Australia), of which half had all cleaners experimentally removed for 10 years. Prey fish residing near cleaning stations exhibited less risk-averse behavior than those living far from cleaning stations. Prey also decreased their excursion distance with increasing model predator proximity, but those living on reefs with cleaners generally exhibited less risk-averse behavior via larger excursion distances. Our findings suggest that cleaners indirectly reduce the risk of predation by reducing attack likelihood and that bystanders living within cleaning stations benefit through increased foraging area and, therefore, presumably greater access to food. By creating such ‘safe-havens’, cleaning mutualisms may play an even greater role in structuring reef communities than previously documented.

Chronic oxygen loss but not warming increase dishonesty in cleaner wrasses

Pereira, B. P.[1]; Oliveira, R.[1]; Martins, M.D.[1]; Marques, M.C.[1]; Rosa, R.[1,2]; Paula, J. R.[1,2]

[1] *MARE – Marine and Environmental Sciences Centre & ARNET – Aquatic Research Network, Laboratório Marítimo da Guia, Faculdade de Ciências Universidade de Lisboa, Av. Nossa Senhora do Cabo 939, 2750-374 Cascais, Portugal*

[2] *Departamento de Biologia Animal, Faculdade de Ciências Universidade de Lisboa, Campo Grande, 1749-016, Lisbon, Portugal*

Anthropogenic emissions are driving several challenges to marine life such as oxygen loss and ocean warming. Yet evidence for repercussions on mutualistic interactions is limited. In coral reefs, cleaning mutualisms are crucial for ecosystem health by removing parasites and dead skin from their client fish. However, a major conflict arises as cleaner wrasses prefer eating the protective mucus from their clients instead of parasites, which constitutes cheating and challenges the stability of this mutualism. Here we aimed to address the effects of oxygen loss and ocean warming on cleaning mutualism stability. To do so, we exposed cleaner wrasses (*Labroides dimidiatus)* and their clients (*Naso elegans*) to predicted future scenarios of ocean deoxygenation, warming, and a combination of both stressors for 20 days. We then assessed the resilience of the mutualistic interaction using social interaction tests and cooperativeness tests. Our results showed that cleaners exposed to deoxygenation, but not warming, were more motivated to initiate interactions (+17%) and were more dishonest (+169%), but their ability to learn to feed cooperatively remained unaffected. This suggests that under lower oxygen conditions, the decrease in cleaners' honesty is not due to cognitive impairments (i.e. disruptions in the ability to learn cooperative rules) but rather a decrease in inhibition. Our findings suggest that impending oxygen loss could affect the honesty of mutualistic interactions, which could lead to mutualism breakdown and significantly impact coral reef ecosystems.

Challenges and opportunities in evaluating fish community composition for reefs under restoration at unprecedented scales

Pereira, Pedro Henrique Cipresso[1]; Goergen, Elizabeth A.[1]; Suggett, David[1]; Gonzalez Martinez, Karla P.[1]; Forsman, Zac H.[1]; Moore, Tom D.[1]

[1] *King Abdullah University of Science and Technology, Thuwal, KSA – Kaust Reefscape Restoration Initiative (KRRI)*

Coral restoration is accelerating worldwide in efforts to stem ever-deteriorating reef health. However, despite recent growth towards more standardized and networked restoration activity, a step-change in scale is needed to reach ambitious global targets in extent of restored ecosystem targets by 2030. A recent project initiated in the northern Red Sea – KAUST's Reefscape Restoration Initiative (KRRI) represents the largest restoration footprint to date, providing opportunity to develop and implement complex monitoring protocols. Across the 100 ha reefscape area, restoration activity spans rehabilitating existing reef, introduction of new substrates, and large-scale coral propagation nurseries. Within the monitoring program, fish community diversity not only represents outcomes of the reefscape but potentially underpins activity success; for example, where fish are a key performance indicator of site health and aesthetics for ecosystem service values, but fundamentally critical to reduce coral space competitors such as algae that regulate restored coral survivorship. We present the framework for monitoring fish communities over space and time across this ambitious project, through the initial baseline data from across the reefscape. We identify how critical interdependencies with operations – including site zonation – potentially govern development of fish communities over time, and this add further complexities to monitoring. We discuss how fish community monitoring contributes to cost-(in)efficiencies of restoration, and outline steps needed to move activity towards more autonomous practices spanning data collection, processing and curation that are central to decision making. In doing so, we provide a roadmap that restoration projects will likely need in place as they continue to scale.

Exploring movement patterns of coastal reef fishes: insights for management and conservation

Pérez-Matus, Alejandro[1,2,3]; Beldade, Ricardo[3]; Bollmann, Isabella[1]; Fernández-Cisternas, Ítalo[1,2]; Gelcich, Stefan, Godoy, Natalio, González-But, Juan Carlos[1]; Winkler, Gabriela [1]

[1]*Millennium Nucleus for the Ecology and Conservation of Temperate Mesophotic Reef Ecosystem (NUTME), Las Cruces, Chile*

[2]*Subtidal Ecology Laboratory and Marine Conservation Center, Estación Costera de Investigaciones Marinas, Pontificia Universidad Católica de Chile, Santiago, Chile*

[3]*Estación Costera de Investigaciones Marinas, Facultad de Ciencias Biologicas, Departamento de Ecología, Pontificia Universidad Católica de Chile, Santiago, Chile*

[4] The Nature Conservancy, Santiago Office

[5] *Instituto Milenio en Socio-Ecología Costera (SECOS) and Center for Applied Ecology and Sustainability (CAPES), Pontificia Universidad Católica de Chile, Santiago 8331150, Chile*

Effective management of marine metapopulations for fisheries and/or conservation requires matching suitable habitat patches with the population biology and movement behavior of target species to maintain connectivity. Animal movement is a fundamental characteristic of life, as animals must move to find mates, acquire food, avert predators, and avoid harsh environments. Lack of individual movement and connectivity data is often a major weakness in MPA planning. Recent technological developments have greatly contributed to refined tracking of individual movement and behavior in marine systems. Here, we assessed the animal movement patterns such as daily activity patterns, residence index, distance travelled and home range on 55 individuals from 5 species with contrasting functional identities. Using 10 acoustic receivers we found a high percent of detections after tagging and release at catch sites (inside MPA. Results indicate that the daily activity patterns vary among species grouped as diurnal (mainly herbivores), crepuscular (mobile invertivore feeders) and nocturnal species (generalist carnivores). Those species that have similar trophic demands have contrasting activity patterns which promotes niche partitioning. We found that movement pattern correlates with reproductive season. Residence index indicates that the mean presence for all species is higher within the MPA than in the adjacents open access areas revealing high site fidelity. This is confirmed by the restricted home ranges observed for most species, showing that patterns of movement increase in the MPA. We conclude that the restricted movement of species supports the creation of small protected coastal marine areas in central Chile's coastal reef ecosystems.

Exploring the potential benefits of partially protecting the ocean in Australia

Phillips, Genevieve[1,2]; Barrett, Neville[1,2]; Dutton, Ian[2,3]; Hartmann, Klaas[1]; Krueck, Nils[1]; Ogier, Emily[1,2].

[1]*Institute for Marine and Antarctic Studies, The University of Tasmania*

[2]*Centre for Marine Socioecology, The University of Tasmania*

[3]*Department of Natural Resources and Environment, Tasmania*

Theoretically, no-take marine protected areas (MPAs) provide biodiversity, social, and economic benefits to a particular region (triple bottom line management), including boosting fisheries productivity. Partially Protected Areas (PPAs) are spatial zones within MPA networks that allow for some resource extraction – such as commercial or recreational fishing. Currently these areas are considered within MPA target figures for the IUCN 30x30 goals. Other Effective area-based Conservation Measures (OECMs) are spatial zones that provide biodiversity benefits through means other than MPAs. Some examples of marine OECMs are fisheries management tools such as spatial or temporal closures, gear or sector exclusions, and habitat restoration projects.

In this project we have assessed PPA implementation across Australia through a systematic literature review of peer-reviewed publications, and legislative documentation. The review outlines the types and forms of partial protection used in Australia, including OECMs, and the factors affecting the likelihood of attaining mutually beneficial outcomes for all marine users.

In this talk we present the results of our review and outline plans for a spatially based quantitative decision-support tool for marine resource managers. The tool is being developed in consultation with resource managers, industry representatives, recreational fishers, and subject matter experts, and we hope that it will allow informed decision-making when implementing protected area management strategies for marine areas within and near zones of high natural value in Australia. We welcome constructive feedback on our results and recommendations to marine resource managers, particularly inputs that will help ensure this tool can be used in management decision-making.

A decade of ichthyological research from Australia's Research Vessel *Investigator*

Pogonoski, John[1]; Appleyard, Sharon[1]

[1]*Australian National Fish Collection, National Research Collections Australia, Commonwealth Scientific and Industrial Research Organisation, Hobart, PO Box 1538, Tasmania, 7001, Australia*

The Research Vessel *Investigator* has conducted biological and taxonomic research in the Australian region since early 2015 with participation and collaboration from ichthyology staff of most Australian fish collections. A range of collection methods (mostly beam trawl, fish trawl and sled but also midwater trawls, towed video and eDNA) are deployed to help characterise the species compositions of areas surveyed. Studies thus far have focused on Western Australia (North West Shelf and Gascoyne regions), South Australia (Great Australian Bight), the eastern Australian shelf, slope and abyss (Tasmania, Victoria, New South Wales and southern Queensland) and the Christmas and Cocos Islands region in the eastern Indian Ocean. Collections have been made from large bathymetric ranges (inshore shelf waters down to the abyssal depths >5000m) and specimens have been curated into most Australian fish collections for ongoing taxonomic research. Several new species and dozens of newly recorded Australian species have been discovered with assistance from the international taxonomic community. Most species have been freshly photographed with contemporary genetic samples collected and often barcoded for the mtDNA COI gene. A summary of the collection activities to date, highlights of significant discoveries and areas and taxa in need of further investigation will be presented.

1.2A Special Session 4: The evolution and ecology of fishes: assessing traits and functions in a changing world, 260-073, November 20, 2023, 11:15 AM - 1:00 PM

Identifying traits for inferring potential ecosystem functions of cryptobenthic reef fishes

Pombo-Ayora, Lucía[1]; Berumen, Michael[1]; Coker, Darren[1]; Peinemann, Viktor[1]

[1]*King Abdullah University of Science and Technology*

Even though cryptobenthic reef fishes (CRFs) can represent up to 40% of all fish species on a coral reef, they are often overlooked in biodiversity assessments. As such, we know very little about the importance of their presence, abundance, and diversity in coral reef functioning. Trait diversity is a widely used approach to infer ecosystem functions from species characteristics. Six traits (body size, diet, position in the water column, diel activity, mobility, and gregariousness) have been used in several studies of standard fish communities by creating "functional" entities and building ordination plots. However, these traits commonly used for non-cryptic reef fishes do not provide adequate resolution to segregate CRFs species and do not reflect their potential ecosystem functions. For example, fishes can be placed into multiple size categories, while all CRFs fall within the same size category (<5cm); the same applies to the position in the water column and mobility, whereby all CRFs are benthic-associated and have relatively small movement patterns. In addition, little is known about their diets, gregariousness, and diel activities. The uncertainty around assigning correct traits to each species and the lack of resolution of some traits make applying standard traits to the CRFs communities unsuitable. Here we aim to identify which traits and trait sub-categories best represent CRF communities and reflect their potential ecosystem functions on coral reefs. We expect these new traits to be applied to studies that aim to understand coral reef functioning either exclusively using CRF or in combination with the wider fish community.

Social hierarchical formation and individual recognition in the protogynous New Zealand spotty wrasse (*Notolabrus celidotus*)

Quertermous, Haylee M.[1]; Kamstra, Kaj[1]; van der Burg, Chloe A.[1]; Todd, Erika V.[2]; Jasoni, Christine L.[1]; Muncaster, Simon[3]; Brown, Culum[4]; Gemmell, Neil J.[1]

[1]*University of Otago, Dunedin, New Zealand*

[2]*Deakin University, Melbourne, Australia*

[3]*University of Waikato, Tauranga, New Zealand*

[4]*Macquarie University, Sydney, Australia*

Sex change, or sequential hermaphroditism, in teleost fishes is a remarkable example of phenotypic plasticity. Changes in the social environment can trigger the transformation of sexual phenotype, such as the loss of the dominant male in the group leading the dominant female to change their sex. It is still uncertain how this change in social environment initiates the drastic transformation of behaviour, histology, and morphology. While it is well accepted that social dominance plays an important role in sex change, how females establish their social position in a hierarchy, its influence on their ability to change sex, and when and how they commits to sex change are not well understood. In our current research, we investigate the behaviour of females in a protogynous (female-to-male) sex changing wrasse (*Notolabrus celidotus*) to determine their position within their social hierarchy. We conducted behavioural assays on group formation and disruption to analyse their social behaviour. We hypothesize that groups of New Zealand spotty wrasse establish a linear hierarchy and employ individual recognition of group members. This research is intended to enhance future work on the behavioural and molecular processes influencing social dynamics and sexual plasticity among these wrasses, as well as other sequentially hermaphroditic fishes.

What inner ear anatomy can tell us about hearing in elasmobranchs

Radford, C.A.[1]; Sauer, D[1].; Yopak, K.[2]

[1]*Institute of Marine Science, Leigh Marine Laboratory, University of Auckland, New Zealand*

[2]*Department of Biology and Marine Biology and the Center for Marine Science, University of North Carolina Wilmington, USA*

Fishes possess the largest diversity in auditory anatomy among any vertebrate group. However, data come largely from bony fishes, while comparatively little is known about inner ear morphological variation in elasmobranchs (sharks, rays, and skates). Elasmobranchs are thought to exhibit high interspecific variation in inner ear morphology, although comparative assessment across a range of species is rare. In the present study, we used magnetic resonance imaging (MRI) to characterize the inner ears of elasmobranchs, and analysed morphological variation in the inner ears of 26 species, including nine batoids and 17 sharks. Inners ears were imaged in situ on either a 9.4T Bruker Biospec small animal scanner or a Siemens Magnetom 7T whole body MR scanner, using contrast-enhanced, T1-weighted MR imaging. The inner ear end organs (saccule, lagena, utricle, macula neglecta), semi-circular canals (horizontal, anterior, and posterior), and endolymphatic duct were segmented from MR data. Using phylogenetically informed multivariate analyses, we assessed inner ear structure as it relates to body size, diet, and primary habitat, and found that variation in inner ear organization correlates with ecological parameters, and may reflect differences in the hearing capabilities of elasmobranchs. Findings establish a morphological foundation for comparative studies on the inner ears of elasmobranchs, and suggest that, like other sensory systems in elasmobranchs, variation in morphology of the auditory system may reflect differences in auditory specialization.

Cleaner gobies' cognitive performance is linked with their ecology

Ranucci, Maddalena[1]**;** Court, Mélanie[1], Pereira, Beatriz[1]; Romeo, Daniele[2]; Paula, José Ricardo [1,3]

[1]MARE – Marine and Environmental Sciences Centre & ARNET – Aquatic Research Network, Laboratório Marítimo da Guia, Faculdade de Ciências Universidade de Lisboa, Av. Nossa Senhora do Cabo, 939, Cascais, Portugal

[2]Swire Institute of Marine Science, School of Biological Sciences, The University of Hong Kong, Pokfulam Rd, Hong Kong SAR

[3]Departamento de Biologia Animal, Faculdade de Ciências Universidade de Lisboa, Campo Grande, 1749-016, Lisbon, Portugal

Cleaner gobies provide an essential function for marine ecosystem dynamics through their cleaning service. In Central America's Pacific and Atlantic coasts, cleaner gobies remove ectoparasites, dead tissue, and mucus, providing them an essential service for their well-being. Their dependence on cleaning interactions for food varies, with some being primarily dependent on cleaning (dedicated cleaners), while others are not (facultative cleaners). Although evidence for partner choice is present from natural observations, contrarily to their cleaner wrasse counterparts from the Indo-Pacific, their capacity to solve social decision-making tests remains unknown. Our study aimed to fill this knowledge gap by investigating if the ability to make social decisions varies among different cleaning goby species based on their cleaning dependency and ecological relevance. To do so, we used five cleaner gobies species, two dedicated (*Elacatinus oceanops*, *Elacatinus evelynae*), two facultative (*Elacatinus puncticulatus*, *Elacatinus figaro)*, and one non-cleaner (*Tigrigobius macrodon*), and evaluated their capacity to solve a biological market task using different test cues (size, side & color) with different levels of ecological relevance. Our findings suggest that species differences in performance are related to test cue ecological relevance. Namely, dedicated cleaner gobies excelled in solving tasks where the cue was size-dependent (simulating larger predators), but no differences were found in other tasks. Since cleaning gobies are known to prioritize larger predatory clients, this further demonstrates the role of ecology in modulating cognitive performance and, lastly, the brain.

How much fisheries benefit can there be from blue carbon restoration projects?

Raoult, Vincent[1,2]; Heimhuber, Valentin[3]; Glamore, Will[3]; Gaston, Troy F[1]; Taylor, Matt D[4]

[1]*School of Environmental and Life Sciences, University of Newcastle, Ourimbah, NSW Australia*

[2]*Blue Carbon Lab, Deakin University, Burwood, VIC Australia*

[3]*Water Research Laboratory, School of Civil & Environmental Engineering, UNSW Sydney, NSW Australia*

[4]*Port Stephens Fisheries Institute, New South Wales Department of Primary Industries, Locked Bag 1, Nelson Bay, NSW, Australia*

Blue carbon ecosystems and the ecosystem services they provide have declined globally. In response, ecosystem restoration has increased but the scale and urgency of these activities has been limited by the lack of economic drivers. Here we demonstrate a multidisciplinary approach that links hydrologic restoration with ecologic outputs to highlight the economic potential of restoring a drained floodplain. Stable isotope models were used to predict the productivity of Eastern School Prawn per habitat. Hydrologic models were then used to determine the area of saltmarshes and mangroves that could be potentially restored via tidal introduction. Together, these results show that restoration projects can provide millions AUD per year to commercial fisheries via increased prawn production alone. Given that this approach excludes other values that would be gained, such as other species of fisheries value, carbon sequestration, biodiversity, and flood control, it likely represents a conservative financial estimate. Overall, we highlight the scale of fisheries co-benefits from tidal restoration projects, and how business cases for large-scale blue carbon ecosystem restoration projects could be developed using multidisciplinary approaches.

The epigenetic landscape of coral reef fish acclimation and adaptation to climate change

Ravasi, Timothy[1,2]; Ryu, Taewoo[1]; Munday Philip[2]

[1]*Marine Climate Change Unit, Okinawa Institute of Science and Technology Graduate University, 1919–1 Tancha, Onna-son, Okinawa 904–0495, Japan*
[2]*Australian Research Council Centre of Excellence for Coral Reef Studies, James Cook University, Townsville, Queensland, 4811, Australia*

The Earth’s climate is changing rapidly mostly due to anthropogenic disturbances. The average temperature of the ocean is projected to increase up to 3°C by the end of the century, and the oceans are progressively becoming more and more acidic. This will pose a serious threat to the survival of many aquatic species. To persist, populations will either need to shift their geographic distributions or adapt through genetic evolution or phenotypic plasticity.

It is unclear if and how marine species, such as tropical fishes, will adapt to these rapid changes in ocean temperature and acidity. Although many organisms are susceptible to future climate changes, some species shows remarkable ability of acclimation after generations. In my talk I will discuss our latest research that by mean of an integrative genomics analysis, identified molecular pathways responsible for transgenerational acclimation of reef fish to climate stressors and shown that selective epigenetics regulation serves as a central mechanism mediating transgenerational acclimation to climate change.

Enhancing adoption of modern fish-protection screens: insights from stakeholder engagement

Rayner, Thomas[1]; Boys, Craig[1]; Conallin, John[2]; Price, Rodney[1]

[1]*New South Wales Department of Primary Industries – Fisheries, Australia*

[2]*Charles Sturt University, Australia*

Modern fish-protection screens offer significant benefits for Australia's water management practices. The Commonwealth and New South Wales (NSW) governments have invested over $30 million to incentivise early adoption by water users. However, successful adoption requires understanding the motivations and abilities of water users, as well as strategies to overcome barriers. We present four practices used in NSW to strengthen stakeholder understanding and encourage participation in incentive programs. Applying social learning concepts to screening programs fosters collaboration and knowledge sharing. Evaluating stakeholder needs ensures incentives align with priorities. Identifying and mapping stakeholders enhances engagement strategies, enabling targeted outreach. Integrating science in communication facilitates informed decision-making. Analysing motivations and abilities of water users revealed three key drivers: cost savings, fish protection, and reputation improvement. Barriers to adoption varied significantly. We collate identified barriers and respective strategies used in NSW. These stakeholder engagement methods can improve screening technology uptake in other jurisdictions and help maximise outcomes of conservation efforts in aquatic ecosystems.

Asynchrony of intra-specific growth responses to climate and environmental variables along a latitudinal gradient in a coral-reef fish

Reed, Erin[1,2]; Fobert, Emily[3]; Taylor, Brett[4]

[1] *Cooperative Institute for Marine and Atmospheric Research, University of Hawaii, Honolulu, HI, United States, 2*

[2] *Pacific Islands Fisheries Science Center, National Marine Fisheries Service,*

Honolulu, HI, United States

[3] *School of BioSciences, University of Melbourne, Parkville, VIC 3010, Australia*

[4]*University of Guam Marine Laboratory, Mangilao, Guam*

Understanding how environmental stressors impact fisheries productivity is imperative for the sustainable management of our marine resources. Synchrony in individuals' growth patterns within populations has been identified across large spatial scales, both within and among species in the same region. This synchrony indicates a detectable and common sensitivity to changes in climatic or environmental conditions. Baseline information remains elusive for most commercial fisheries on smaller spatial scales, especially tropical coral reef fisheries. We explored environmental and climatic variability along a latitudinal gradient using inter-annual otolith growth rates in a tropical coral reef fish, *Naso unicornis*. Dendrochronology techniques were applied to otolith increments to remove growth effects and extract a high frequency variability signal indicative of environmental change year-to-year. Using linear mixed models, we identified significant predictors responsible for the variation in growth along a latitudinal gradient in the Northern Mariana Islands. We found different growth responses between two adjacent latitude subsets for the years 2000-2013 and 2005-2017. Fish inhabiting the northernmost islands had a positive response to increased annual average sea surface temperature (SST). The adjacent southern latitudes had a negative response to warmer winter SST and El Niño climatic conditions predicted by the El Niño Modoki Index. This is the first evidence of intra-specific asynchrony in growth responses across a latitudinal gradient and the first evidence of the impact of a different "flavour" of ENSO event on growth. We provide information on how climate and environment have impacted past growth with implications for future fisheries productivity.

IBRtools: an R package that integrates biomarker-based assessments and radarchart creation

Resende, Anna[1]; Pereira, Diego[2]

[1]*Marine Ecology and Ecosystem Modelling Lab, School of Biological Sciences, Victoria University of Wellington, Wellington, New Zealand*

[2]*Carl Peter von Dietrich Glycobiology Laboratory, Biochemistry Department, Federal University of São Paulo, São Paulo, Brazil*

Evaluating environmental stress and its subsequent biological effects in fish has been receiving great emphasis. Key enzymes, or biomarkers, are often measured as early warning signals in fish metabolism before severe environmental degradation occurs. Multibiomarker studies are common to evaluate physiological stress responses in fish, and their unified responses are often assessed through two common indexes, IBR and IBRv2, along with a *radarchart* graphic representation. Despite the importance and common use of the IBR and IBRv2, there was not yet an open-source package that allowed for the calculation and graphic representation of both indexes. We developed the R package IBRtools to allow users to calculate IBR and IBRv2 correctly with all biomarkers that are being evaluated at once and perform a *radarchart* with the output using the *fmsb* package. The package includes: (i) functions to calculate the indexes IBR and IBRv2 (ii) functions to calculate the standardized values of each index (iii) functions to generate good data visualization through a *radarchart* (iv) 3 datasets to be used as examples. We aim to describe the main algorithms involved in IBR and IBRv2 calculations, a description of the novel package and illustrate a workflow using data examples available on the package to guide the user on how to accurately acquire the values for either the IBR index or the IBRv2 index. The IBRtools package provides a user-friendly platform to obtain IBR index and IBRv2 values, making it straightforward even for large datasets.

Ngā Ika e Heke - Conserving migratory fish species in Aotearoa

Richarson, Marine[1]; Bowen, Jane[1]; Goodman, Jane[1]

[1] *Department of Conservation*

The freshwaters of Aotearoa New Zealand host a wide range of species with migratory life cycles, which require a landscape-level management approach to ensure they can access, occupy, and move between, the full range of habitats needed during their lives. Launched in 2018 by the Department of Conservation, Ngā Ika e Heke is a programme dedicated to the conservation and management of four native diadromous species that present concerning trends in their population status: Shortjaw kōkopu *Galaxias postvectis* (classified as Threatened—Nationally Vulnerable), Īnanga *Galaxias maculatus*, Longfin eel *Anguilla dieffenbachii* (At Risk—Declining) and Pouched lamprey *Geotria australis* (Threatened—Nationally Vulnerable). Its key focus is to deliver species-specific conservation measures that integrate ecological requirements across different life stages and the associated responses to anthropogenic pressures. Implementing Ngā Ika e Heke relies on filling critical knowledge gaps on the ecology of the focal species, delivering a national vision that is adaptive to local contexts and situations, and developing and nurturing partnerships with stakeholders, local communities, and iwi/hāpu/whānau. This talk will provide an overview of the programme and provide some examples of projects conducted under its umbrella.

The contribution of mitochondria to thermal resilience in the endemic triplefins of New Zealand

Riordan, Breana[1]; Hickey, Tony[2]; Johnson, Sheri[1]

[1]*Department of Zoology, University of Otago*

[2]*School of Biological Sciences, University of Auckland*

Temperature is a major stressor within marine environments, acting to modify the physiological and biochemical parameters of organisms. The capacity to respond to shifting thermal conditions, such as those in the context of climate-mediated ocean warming, is crucial for the persistence of marine ectothermic species. In fish, mitochondria exhibit great sensitivity to suboptimal temperature deviations and are considered to play a pivotal role in determining the thermal tolerance limits across fish species. Using a novel fluorescent approach, we examined brain mitochondria (mt) following warm acclimation in two closely related endemic New Zealand triplefins, to compare thermal resilience. We exposed the common triplefin (*Forsterygion lapillum*) and the estuarine triplefin (*F. nigripenne*) to four temperatures (10, 14, 18 and 22°C) over 4-weeks before assessing the performance of membrane potential and ATP production in brain mt under acute thermal ramping scenarios. Additionally, we measured the activities of enzymes citrate synthase (CS) and lactate dehydrogenase (LDH) as indicators of aerobic and anaerobic potential, respectively, in the acclimated fish. We found that both the common and estuarine triplefin from warm-acclimated treatments tended to display enhanced maintenance of mt function at higher temperatures compared to fish from cooler treatments, though only apparent ATP production was significantly enhanced. Enzyme activity levels exhibited a decrease with acclimation temperature for the estuarine triplefin but was less consistent for the common triplefin. Overall, at least for southern populations of both species the plasticity in mitochondrial performance indicates resilience for these species against future warming.

Inconsistent patterns of phenotypic evolution among canonical 'living fossil' lineages

Rivero-Vega, Rafael A.[1]; Berv, Jacob S.[1,2]; Clarke, John T. [3-6]; Friedman, Matt[1]

[1]*Museum of Paleontology and Department of Earth and Environmental Sciences, University of Michigan, Ann Arbor, Michigan, U.S.A.*

[2]*Department of Ecology and Evolutionary Biology, University of Michigan, Ann Arbor, Michigan, U.S.A.*

[3]*GeoBio-Center, Ludwig-Maximilians-Universität München, Munich, Germany*
[4]*Department of Earth and Environmental Sciences, Paleontology & Geobiology, Ludwig-Maximilians-Universität München, Munich, Germany*

[5]*Department of Ecology and Biogeography, Nicolaus Copernicus University in Toruń, Toruń, Poland*

[6]*Department of Zoology, Institute of Ecology and Earth Sciences, University of Tartu, Tartu, Estonia.*

Coelacanths, lungfishes, and holosteans represent three emblematic living fossil lineages, thought to be united by similar patterns of phenotypic change through time. Past work suggests a variety of evolutionary patterns for these groups, but it is unclear whether these reflect biological differences or stem from contrasting analytical approaches. Here, we examine these lineages under a common framework to assess variation in the evolution of both discrete traits and shape, with the goal of testing whether living fossils show comparable patterns of anatomical change. For each clade, we inferred a Bayesian phylogeny under the fossilized-birth death model to estimate rates of discrete character evolution over time. Additionally, we fit a series of explicit models of phenotypic evolution using a subset of taxa in each group for which body shape data are available. We find that these living fossils have disparate patterns of morphological evolution over geological timescales. For lungfishes, rates in discrete characters are highest in the Devonian and monotonically decline over time. Coelacanth rates show multiple early rate peaks, followed by a decline toward the recent. Holostean rates show modest peaks but are, on average, consistent, showing no secular increase or decline. Body shape evolution also differs between clades but shows similarities to inferred patterns for discrete characters within groups. Our results illustrate how the process of evolutionary change has been idiosyncratic even among traditional examples of living fossils and indicate a need to explicitly quantify patterns of change rather than apply informal, often qualitative, macroevolutionary classifications.

Life in the fast lane: revisiting the fast growth – high survival paradigm during the early life stages of fishes

Robert, Dominique[1]; Shoji, Jun[2]; Sirois, Pascal[3]; Takasuka, Akinori[4,5]; Catalán, Ignacio A.[6]; Folkvord, Arild[7]; Ludsin, Stuart A.[8]; Peck, Myron A.[9]; Sponaugle, Su[10]; Ayón, Patricia M.[11]; Brodeur, Richard D.[12]; Campbell, Emily Y.[13]; D'Alessandro, Evan K.[14]; Dower, John F.[15]; Fortier, Louis [16]; García, Alberto G.[17]; Huebert, Klaus B.[18]; Hufnagl, Marc[19]; Ito, Shin-ichi[20]; Joh, Mikimasa[21]; Juanes, Francis[15]; Nyuji, Mitsuo[4,22]; Oozeki, Yoshioki[23]; Plaza, Guido[24]; Takahashi, Motomitsu[25]; Tanaka, Yosuke[26]; Tojo, Naoki[27]; Watari, Shingo[4,26]; Yasue, Naotaka[28]; Pepin, Pierre[29]

[1] *Canada Research Chair in Fisheries Ecology, Institut des sciences de la mer de Rimouski, Université du Québec à Rimouski, Rimouski, Québec G5L 3A1, Canada*

[2] *Department of Marine Science and Technology, Fukui Prefectural University, 1-1 Gakuen-cho, Obama, Fukui 917-0003, Japan*

[3] *Research Chair in Exploited Aquatic Species, Université du Québec à Chicoutimi, Chicoutimi, Québec G7H 2B1, Canada*

[4] *National Research Institute of Fisheries Science, Japan Fisheries Research and Education Agency, 2-12-4 Fukuura, Kanazawa, Yokohama, Kanagawa 236-8648, Japan*

[5] *Department of Aquatic Bioscience, Graduate School of Agricultural and Life Sciences, The University of Tokyo, 1-1-1 Yayoi, Bunkyo, Tokyo 113-8657, Japan*

[6] *Instituto Mediterráneo de Estudios Avanzados (IMEDEA) - Consejo Superior de Investigaciones Científicas / Universitat de les Illes Balears, C/Miquel Marques 21, 07190, Esporles, Illes Balears, Spain*

[7] *Department of Biological Sciences, University of Bergen, Post box 7803, N-5020 Bergen, Norway, and Institute of Marine Research, N-5817 Bergen Norway*

[8] *Aquatic Ecology Laboratory, Department of Evolution, Ecology, and Organismal Biology, The Ohio State University, 222 Research Center, 1314 Kinnear Road, Columbus, Ohio 43212, USA*

[9] *Department of Coastal Systems, Royal Netherlands Institute for Sea Research, PO Box 59, 1790 AB Den Burg, Texel, The Netherlands*

[10] *Department of Integrative Biology, Oregon State University, Hatfield Marine Science Center, 2030 SE Marine Science Drive, Newport, Oregon 97365, USA*

[11] *Instituto del Mar del Perú, Esquina Gamarra y General Valle S/N, Chucuito Callao, Apartado 22, Callao, Perú*

[12] *Northwest Fisheries Science Center, NOAA Fisheries, Hatfield Marine Science Center, 2030 SE Marine Science Drive, Newport, Oregon 97365, USA*

[13] *State Water Resources Control Board, Division of Water Rights, 1001 I St. Sacramento, CA 95814, USA*

[14] *Rosenstiel School of Marine and Atmospheric Science, University of Miami, 4600 Rickenbacker Causeway, Miami, Florida 33149, USA*

[15] *Department of Biology, University of Victoria, Victoria, British Columbia V8W 2Y2, Canada*

[16] *Département de Biologie, Université Laval, Pavillon Vachon, Québec, Québec G1V 0A6, Canada*
†Deceased

[17] *Instituto Español de Oceanografía, Centro Oceanográfico de Málaga, Puerto de Fuengirola, s/n 29640 Fuengirola, Málaga, Spain*

[18] *CSS, Inc., 2750 Prosperity Avenue, Suite 220, Fairfax, Virginia 22031, USA*

[19] *Institute of Hydrobiology and Fisheries Science, Center for Earth Systems Research and Sustainability, University of Hamburg, Olbersweg 24, 22767 Hamburg, Germany*

[20] *Atmosphere and Ocean Research Institute, The University of Tokyo, 5-1-5 Kashiwanoha, Kashiwa, Chiba 277-8564, Japan*

[21] *Mariculture Fisheries Research Institute, Hokkaido Research Organization, 1-156-3 Funami-cho, Muroran, Hokkaido 051-0013, Japan*

[22] *Fisheries Technology Institute, Japan Fisheries Research and Education Agency, 1551-8 Taira-machi, Nagasaki, Nagasaki 851-2213, Japan*

[23] *Headquarters, Japan Fisheries Research and Education Agency, 1-1-25 Shin-Urashimacho, Kanagawa, Yokohama, Kanagawa 221-8529, Japan*

[24] *Escuela de Ciencias del Mar, Facultad de Recursos Naturales, Pontificia Universidad Católica de Valparaíso, Avenida Altamirano 1480, Casilla, 1020, Valparaíso, Chile*

[25] *Fisheries Resources Institute, Japan Fisheries Research and Education Agency, 1551-8 Taira-machi, Nagasaki, Nagasaki 851-2213, Japan*

[26] *Fisheries Resources Institute, Japan Fisheries Research and Education Agency, 2-12-4 Fukuura, Kanazawa, Yokohama, Kanagawa 236-8648, Japan*

[27] *International Education Office, Faculty of Fisheries Sciences, Hokkaido University, 3-1-1 Minato-cho, Hakodate, Hokkaido 041-8611, Japan*

[28] *Wakayama Prefectural Fisheries Experimental Station, 1557-20 Kushimoto, Kushimoto, Higashimuro, Wakayama 649-3503, Japan*

[29] *Northwest Atlantic Fisheries Centre, Fisheries and Oceans Canada, PO Box 5667, St. John's, Newfoundland and Labrador A1C 5X1, Canada*

Early life survival is critical to successful replenishment of fish populations, and hypotheses developed under the Growth-Survival Paradigm (GSP) have guided investigations of controlling processes. The GSP postulates that recruitment depends on growth and mortality rates during early life stages, as well as their duration, after which the mortality declines substantially. The GSP predicts a shift in the frequency distribution of growth histories with age towards faster growth rates relative to the initial population because slow-growing individuals are subject to high mortality (via starvation and predation). However, mortality data compiled from 387 cases published in 153 studies (1971-2022) showed that the GSP was only supported in 56% of cases. Selection against slow growth occurred in two-thirds of field studies, leaving a non-negligible fraction of cases showing either an absence of or inverse growth-selective survival, suggesting the growth-survival relationship is more complex than currently considered within the GSP framework. Stochastic simulations allowed us to assess the influence of key intrinsic and extrinsic factors on the characteristics of surviving larvae and identify knowledge gaps on the drivers of variability in growth-selective survival. We suggest caution when interpreting patterns of growth selection because changes in variance and autocorrelation of individual growth rates among cohorts can invalidate fundamental GSP assumptions. We argue that breakthroughs in recruitment research require a comprehensive, population-specific characterization of the role of predation and intrinsic factors in driving variability in the distribution and autocorrelation of larval growth rates, and of the life stage corresponding to the endpoint of pre-recruited life.

A catalog of Indo-Pacific fish eggs from US public aquaria

Rocha, Claudia[1]; Lev, Kylie[1]; Rocha, Luiz[1]; Shepherd, Bart[1]

[1]*California Academy of Sciences*

Reef fish eggs and larvae are mostly found in the open ocean and have very few described diagnostic morphological characteristics. Moreover, collecting fertilized eggs from broadcast spawners in complex natural habitats is difficult, and will often produce a large volume of eggs from a variety of species which are hard to identify. When well cared for, reef fishes often spawn in large public aquaria, and that provides a unique opportunity to more easily collect their eggs. Originally developed in 2010 by Roger Williams University and the New England Aquarium, DNA barcoding and photo-documentation of eggs from public aquariums was used to create an Open-sources Marine Fish Egg Catalog. In 2021, through an Association of Zoos and Aquariums (AZA) Conservation grant, this work expanded to include additional collaborators. Today there are nine AZA institutions currently collecting, photo-documenting, and submitting eggs for DNA barcoding from marine fishes spawning in their aquaria, including the California Academy of Sciences. We have collected, photographed, and sequenced the DNA barcode gene (COI) of 238 fertilized fish eggs samples, of which 134 are represented in the catalog. So far, we have a list of 38 species in 12 families. Being able to accurately distinguish eggs allows facilities to strategically select and prioritize fish species to support research and sustainability goals.

Taxonomy, phylogenetic affinities, and conservation of recently discovered mesophotic fishes

Rocha, Luiz[1]; MacDonald, Chancey[2]; Pinheiro, Hudson[3]; Shepherd, Bart[1]

[1]*California Academy of Sciences*

[2]*University of Leeds*

[3]*University of Sao Paulo*

In the past decade several new species of fish have been added to the mesophotic fauna worldwide. This is likely a result of the increasing number of researchers exploring mesophotic coral ecosystems (MCEs) between 30 and 150m using a variety of methods, including technical rebreather diving, submarines, and remotely operated vehicles. In general, these fishes belong to families that are also found in shallow reefs (especially Serranidae and Pomacentridae), and a minority are in families more typically found at deeper depths (e.g.: Callanthiidae). Patterns of phylogenetic affinities are also varied: some groups, like *Chromis*, are mostly composed of shallow species with mesophotic species distributed through the phylogeny, whereas others, like *Pseudanthias*, seem to be mostly mesophotic with fewer species in shallow reefs. Because these depths are still unsampled in most locations, biogeographic patterns are hard to infer, but some generalizations are emerging. Along with the distinctiveness of its fauna, our team has consistently observed several human impacts reaching down to 150m. Plastic pollution (both coming from land and sea through fishing debris) is very common, and in most places MCEs are not included in marine protected areas. Therefore, their uniqueness and lack of protection suggest these ecosystems should be a priority for conservation efforts worldwide.

Baiting and citizen science: a comparative study of BRUVs and eDNA surveys throughout estuaries in New South Wales.

Roe, Sebastian[1]; Price, Amina[2-4]; Rees, Matt[3], & Tout-Lyon, Jessica[1-2]

[1] School of Agricultural, Environmental and Veterinary Sciences, Charles Sturt University, Birpai Country, Port Macquarie, NSW, Australia

[2] Gulbali Institute, Wiradjuri Country, Albury, NSW, Australia

[3] NSW DPI Fisheries, Department of Regional, NSW, Australia

[4] School of Agricultural, Environmental and Veterinary Sciences, Charles Sturt University, Wiradjuri Country, Albury, NSW, Australia

The monitoring of fish assemblages is fundamental to fisheries research and Baited Remote Underwater Videos (BRUVs) have traditionally been used as the method of choice for a non-destructive approach to conducting fish surveys. The use of environmental DNA (eDNA) to study fish assemblages is an emerging technique increasing in popularity. The application of eDNA in aquatic ecosystems is revolutionising the detection of biodiversity, and is proving to be a cheaper, quicker, more sensitive and a citizen-science friendly approach. eDNA is proving to be a powerful complementary technique enabling enhanced sampling capacity previously unattainable by scientists alone. Previous research in estuaries demonstrates an increase in fish species richness from eDNA samples when compared to traditional BRUVS surveys. Our research will fill a knowledge gap by expanding the method comparison of detecting fish assemblages using BRUVs and eDNA across multiple estuaries throughout NSW, and the results will inform the design of biomonitoring programs of estuaries in NSW. Furthermore, our work will investigate the latitudinal distribution and potential range shifts of fish assemblages throughout estuaries in NSW. This research will play an important role in demonstrating the importance of involving citizen-scientists in the collection of water samples for eDNA analysis. The integration of citizen-scientists into the collection of samples is fundamental to expanding and developing longitudinal datasets that are required to improve our understanding of the issues facing aquatic ecosystems, how these systems respond to changes and will ultimately inform on ground conservation and management approaches.

2.3C Themed Session B: Ecology of Indo-Pacific Fishes, 260-115, November 21, 2023, 3:30 PM - 4:15 PM

Molecular pathways underlying cleaning behaviour: a study in the wild

Romeo, Daniele[1]; Ramirez-Calero, Sandra[1]; Ravasi , Timothy[2]; Rudolfo-Metalpa, Riccardo[3]; Schunter, Celia[1]

[1]*Swire Institute of Marine Science, School of Biological Sciences, The University of Hong Kong, Pokfulam Rd, Hong Kong SAR*

[2]*Marine Climate Change Unit, Okinawa Institute of Science and Technology Graduate University, Onna-son, Japan*

[3]*IRD Institut de Recherche pour le Développement, Nouméa cedex, New Caledonia*

In coral reefs, the balance of the ecosystem is affected by the interaction of hundreds of species. One crucial interaction for the health of the fish communities is cleaning behaviour defined as an interaction between a cleaner and a client where the first removes and consumes ectoparasites and other particles from the latter. Despite its importance, we know little about the molecular drivers involved in this complex social behaviour especially in the wild. Through an *in-situ* interaction experiment at a coral reef in New Caledonia, we analysed the neural transcriptome involved in cleaning behaviour in the cleaner wrasse *Labroides dimidiatus*. The cleaners and clients (*Abudefduf saxatilis*) were collected on SCUBA and placed into aquaria underwater close to the reef. Five cleaners were left to interact with the client while five were not presented with a client. The behaviour was recorded by cameras for 40 minutes and showed that cleaners spent 27% of the time interacting with the client. Directly after the behavioural trial the brain was dissected out. RNA was extracted and sequenced and the transcriptomes revealed 23 differentially expressed genes in cleaners that interacted with the client. Among these genes were the histamine receptor 1 related with memory and learning processes, and Urocortin related with cortisol and hormonal activity. Understanding the neuro-molecular drivers behind sophisticated behaviours such as cleaning is vital for comprehending their evolution and the essential role they play in maintaining fish biodiversity.

How global and local stressors interact to impact coral reef mutualisms

Rueger, Theresa[1]; Buston, Peter[2]; Versteeg, Melissa[1]

[1]Dove Marine Laboratory, School of Natural and Environmental Sciences, Newcastle University, UK.

[2]Department of Biology and Marine Program, Boston University, Boston, MA, USA.

Major goals of twenty first century coral reef ecology are to understand i) how global and local stressors interact to impact coral reef populations, and ii) how variation in population interactions such as herbivory or mutualism influence resilience (resistance and recovery) to these stressors. At our study site in Kimbe Bay, Papua New Guinea, the latest El Niño caused a severe marine heatwave, with water temperatures regularly surpassing the average for April/May by 2-4 degrees. Also associated with the El Niño were large amounts of rain, causing flooding, which created large variation in abiotic conditions across the 15 reefs that we work on. Here, we study the iconic mutualism between anemones and anemonefishes. In our study population, there is substantial variation in the characteristics of both partners, e.g., anemone body size and fish group size, that influences the strength of the mutualistic interaction. This confluence of events created the perfect opportunity to tackle two major goals of coral reef ecology. The overarching objective of this project was to capitalize on the unfolding El Niño to understand i) how global and local stressors interact to impact anemone and anemonefish populations, and ii) how variation in the mutualistic interaction influences resistance to and recovery from the stressors. Here, we present preliminary results, showing the large variation between reefs and individual groups in intensity of abiotic stressors, and how changes in group stability, recruitment, reproduction and behaviour through disturbance events depend on the quality of the mutualistic partner for both anemones and anemonefish.

Newborn and juvenile reef sharks in a changing world

Rummer, Jodie L.[1]

[1]*College of Science and Engineering, James Cook University, Townsville, QLD 4811, Australia*

With 450 million years of evolutionary history, elasmobranchs are some of the most successful vertebrates; yet, one-third face extinction due to overfishing and, more recently, climate change. However, to date, fewer than 50 studies have directly assessed climate change impacts on elasmobranchs, representing a massive knowledge gap and call to action whilst prioritising research in the Anthropocene. Our research emphasises newborn and juvenile reef sharks because: 1) early life involves different energetic requirements and vulnerabilities than adulthood, 2) newborns and juveniles often occupy shallow, coastal nursery habitats that present challenging environmental conditions, and 3) tropical species are predicted to be most impacted by climate change because they are adapted to much narrower temperature ranges than temperate species. Based in French Polynesia, the largest shark sanctuary (4.8 million km^2) to date, we can investigate climate change stressors on shark populations in the absence of fishing pressure. Over ten years, we have annually sampled, across ten nurseries around the island of Moorea, five evenings per week during pupping months (October-February), representing >3000 hours of field sampling, to document newborn blacktip reef (*Carcharhinus melanopterus*) and sicklefin lemon (*Negaprion acutidens*) shark habitat use. Specifically, we have been investigating birth timing/size, growth/condition, genetic structure, home-range, site fidelity, temperature preference, environmental limits for physiological performance traits, stress biomarkers, and nutritional/immune status, adding countless hours of laboratory experiments/analyses to our fieldwork. This represents the critical foundation for local and international communities and researchers to reach a common goal of protecting future generations of sharks into the Anthropocene.

Earliest of athletes: How changes in physiological performance over early ontogeny in coral reef fishes facilitates dispersal and connectivity

Rummer, Jodie L.[1]; Downie, Adam[2]; Prescott, Leteisha[4,5]; Nilsson, Göran[3]; Lefevre, Sjannie[3]

[1]*College of Science and Engineering, James Cook University, Townsville, QLD Australia*

[2]*School of Biological Sciences, University of Queensland, Brisbane, QLD Australia*

[3]*Department of Biosciences, University of Oslo, Norway*

[4]*Institute for Marine and Antarctic Studies (IMAS), University of Tasmania, Hobart, TAS Australia*

[5]*Blue Economy Cooperative Research Centre, Cawthron Institute, New Zealand*

Successful dispersal and connectivity of coral reef fish populations depends on physiological adaptations and performance during early life. We investigated the intricate relationship between gill development, oxygen uptake rates, and ionoregulatory systems during embryogenesis in two coral reef damselfish species, *Acanthochromis polyacanthus* and *Amphiprion melanopus,* and continued investigating *Am. melanopus* larvae throughout their pelagic larval phase until settlement. Key gill structures develop rapidly in early embryos in both species. Notably, ionoregulatory cells appear on gill filaments 3-4 days post-fertilization (dpf), increasing in density while diminishing from cutaneous locations. The primary respiratory tissue – lamellae – emerged 5-7dpf, coinciding with a peak in embryonic oxygen uptake rates. Surprisingly, oxygen uptake remained unaffected by phenylhydrazine across all pre-hatching stages, indicating that, even though the heartbeat and blood flow are detected by 2-3dpf, haemoglobin may not be necessary for oxygen uptake until hatching. Immediately post-hatch, however, larval *A. melanopus* are elite swimmers and exhibit the highest mass-specific oxygen uptake rates of any species studied. Transitioning between "physiological extremes", however, oxygen uptake rates decrease midway through the pelagic larval phase, which correlates to enhanced hypoxia tolerance, a switch in haemoglobin gene expression patterns, and increased expression of other oxygen-binding proteins (myoglobin, cytoglobin, neuroglobin), potentially crucial for life on hypoxic reefs. Understanding early-life physiological adaptations, such as rapid gill development and shifts in swimming performance and gene expression patterns, is crucial for comprehending dispersal and connectivity patterns of coral reef fish populations and therefore better predicting their vulnerability and reef health in a changing world.

Transposable elements landscape of transgenerational plasticity to ocean acidification in reef fish

Ryu, Taewoo; Dauyey, Kaisar; Mihai, Alexandru; Ravasi, Timothy

Marine Climate Change Unit, Okinawa Institute of Science and Technology Graduate University, Okinawa, Japan

Ocean acidification caused by rising atmosphere CO_2 levels disrupts ecological processes in many marine organisms. Exposure to elevated CO_2 levels can affect the physiology and behaviour of reef fishes, but the extent of this impairment varies among individuals (sensitive vs. tolerant). We utilized a unique multigenerational rearing experiment coupled with genomic techniques in order to identify the genomic landscape of mobile genetic elements that confer distinct acclimation capacity among individual coral reef fish, *Acanthochromis polyacanthus*, in response to acidic seawater. We reared two fish families showing different CO_2 sensitivity in four different conditions (control, acute, developmental, and transgenerational). We then sequenced 232 fish genomes and identified insertion and deletion status of transposable elements in each fish. We identified significant differences of transposable elements (TEs) mobilization pattern between sensitive and tolerant individuals. Higher number of insertions and deletions of TEs in pairwise comparisons of treatments were observed in tolerant fishes, indicating tolerance to CO2 is determined by genetic basis. Moreover, significant TE insertions and deletions were only identified between transgenerational vs. other three treatments, indicating phenotypic plasticity achieved in the second generations might be related to the mobile genetic elements. Genes associated with significantly mobilized TEs were involved in brain development, learning, and behaviours, which may explain abnormal behaviour of fish exposed to CO_2. Our study demonstrate that TEs may shape the genomic architecture associated with transgenerational acclimation to ocean acidification.

The Cenozoic collapse of the West Tethyan biodiversity hotspot: a test using the fish otolith fossil record

Saad, Hadeel[1,2]; Friedman, Matt[1,2]

[1]*Department of Earth and Environmental Sciences, University of Michigan, Ann Arbor, USA*

[2]*University of Michigan Museum of Paleontology, University of Michigan, Ann Arbor, USA*

Marine biodiversity hotspots have disproportionately greater species richness than surrounding regions. The locations of these hotspots are thought to have changed throughout the Cenozoic—transitioning from the West Tethys in the Eocene to the Arabian Peninsula during the Oligocene and finally arriving in the modern-day Indo-West Pacific (IWP) in the Miocene. Despite extensive research that has examined the geographic shifts in the marine invertebrate biodiversity throughout the Cenozoic, direct paleontological investigation of patterns for teleost fishes remains unexplored. Given the sparse skeletal fossil record of marine teleost fishes, the record of teleost otoliths represents a possible tool to test for the hypothesized collapse of the West Tethyan hotspot. Published otolith records from the Paleocene through the Miocene provide data for over 100,000 individual otolith specimens, typically reported as assemblages. Since the relative abundance of otoliths within assemblages is known, local richness can be standardized and compared between sites. Preliminary investigation of standardized local richness values does not show a clear decline from the West Tethys during the Paleogene to Miocene. However, gamma/global richness does show a decline in richness during the Paleogene to Miocene. Increased paleontological searches are needed to confirm the migration of reef fishes from the West Tethys to the IWP.

5.2B Special Session 1 Moving beyond home-ranges: how can we harness fish movement ecology to study, understand and manage ecosystem functioning?, 260-073, November 24, 2023, 1:30 PM - 3:00 PM

Unveiling movement patterns across habitats and time: insights from Continuous Otolith Microchemistry data

Sabetian, Armagan[1*]; Zhang, Jingjing[1,2,]; Hegg, Jens[3]; Raby, Harrison[1]; Campbell, Matthew[4,5]; Tromp, Monica[6]; Walter, Richard[6]; Reid, Malcolm[7]; Lilkendey, Julian[1]

[1]School of Science, Auckland University of Technology, Auckland, New Zealand

[2]The New Zealand *Institute for Plant and* Food *Research Limited, Auckland, New Zealand*

[3]Department of Biology, Gonzaga University, Spokane (Washington), USA

[4]Anthropology Department, University of Auckland, New Zealand

[5]CFG Heritage Ltd, Auckland, New Zealand

[6]Southern Pacific Archaeological Research, School of Social Sciences, University of Otago, Dunedin, New Zealand

[7]Centre for Trace Element Analysis, Department of Chemistry, University of Otago, Dunedin, New Zealand

Effective fisheries and coastal ecosystem management necessitate understanding the large-scale movements of functionally important fish species. Traditional analytical techniques do not usually provide high-resolution information from continuous movement profiles. In this study, we applied time series analysis techniques - Behavioural Change Point Analysis (BCPA) and Dynamic Time Warping (DTW) - to otolith element profiles of New Zealand snapper (*Chrysophrys auratus*) collected from archaeological, 20th century, and contemporary specimens. Our innovative methodology helped uncover significant differences in snapper movement patterns pre- and post-industrial times and draw inferences about residency, nursery usage, migration, and coastal habitat clustering. We detected a decrease in nursery areas over the past 600 years, signalling shifts in historical fish habitat use. Additionally, we identified distinct cluster groups mainly characterized by samples from different periods. As a result, we gained key insights into the long-term impacts of anthropogenic environmental changes on snapper movements and habitat use. Our research integrates time series analyses with movement analysis, proposing a novel ecological indicator for ecosystem health assessment and conservation. The results underscore the importance of understanding habitat use and fish population resilience amidst anthropogenic disturbances and environmental changes.

Environmental drivers of non-commercial reef fisheries in Guam

Sablan, Leilani[1]; Houk, Peter[2]

[1] *University of Guam Sea Grant*

[2] *University of Guam Marine Laboratory*

Overexploitation of Guam's reef-associated fishery is a long-standing issue, with evidence of targeted species and overall landings in decline for over two decades. Non-commercial reef fisheries are prevalent and essential for society and culture, yet it remains poorly understood when compared to its commercial counterpart. This study examined the variable influence of season, geography, and lunar phase on harvested biomass, catch composition, and landed size of reef-associated landings from Guam's dominant non-commercial fishing methods. Creel surveys were conducted over a one-year snapshot period from 2021 to 2022, sampling 5474 fishes. Hierarchical regression trees for environmental factors show season was the most important predictor of landings, where summer and fall (associated with calm periods of the year in Micronesia) were predicted to yield the most kg/day. Lunar phase was a secondary predictor of landings. Catch composition differed across seasons and geographic regions with higher effect by geography. Species with habitat preferences characteristic of the windward coast (i.e., wave-exposed, shallow reefs) became more exploited as winds and surf fell during the calm periods of the year. Lunar phase was the top predictor of size within the spearfishing sector, whereas season best predicted size for bottom fishing. Beyond environmental predictors at a method level, regression trees were also generated for top species. Species-level analyses highlight the interplay of phenology and fisheries, with fish behaviour presumed to be dictating the success of fisheries in space and time. Results from this study aim to guide and improve ongoing fisheries management strategies in Guam.

3.1C Themed session A: Evolution, Taxonomy and Biogeography of Indo-Pacific Fishes, 260-098,
November 22, 2023, 4:00 PM - 6:00 PM

Host use drives convergent evolution in clownfish and disentangles the mystery of an iconic adaptive radiation

Salamin, Nicolas[1]; Fitzgerald, Lucy[1]; Gaboriau, Théo[1]; Garcia Jimenez, Alberto[1]; Marcionetti, Anna[1]; Titus, Benjamin M[2]

[1]*Department of Computational Biology, University of Lausanne, Lausanne, Switzerland*

[2]*Department of Biological Sciences, University of Alabama, Alabama, USA*

Clownfish (Amphiprioninae) are a fascinating example of marine adaptive radiation. From a central Pacific ancestor, they quickly colonized the coral reefs of the Indo-Pacific and diversified independently on each side of the Wallace line. The association with the venomous sea anemone is often thought to be the key innovation that allowed the clownfish radiation. However, this intuition has little empirical or theoretical support given our current knowledge of the clade. Our synthetic work aims at filling this gap by testing the influence of anemone host use on gene selection and on genetic and phenotypic divergence. We gathered multiple in-situ pictures of clownfish individuals in their host for each clownfish species, from which we estimated variation in colouration patterns, morphology and host use. We significantly updated known clownfish-host associations based on this new data. We also sequenced whole genomes for each clownfish species and reconstructed the most up-to-date phylogenetic tree for the Amphiprioninae. In light of this new data, we found robust evidence for convergent evolution of morphology and colouration driven by differential host use. Clownfish colonized the same hosts in parallel in different regions and evolved the same phenotype in both replicates of similar events. We also identified several genes under positive selection during host shifts events. We provide empirical evidence of adaptive radiation triggered by a key innovation and isolate genetic markers involved in this mechanism.

How do larval reef fishes find reefs and the right settlement sites on them?

Sale, Peter F.[1]

[1]*University of Windsor (Emeritus)*

In the beginning they were ichthyoplankton, drifting on the ocean. Jack Randall's chance observation of larval manini (*Acanthurus triostegus*) swimming against the falling tide as they entered the Ala Wai Yacht Harbor one evening ca 1953 told us they were active swimmers, capable of deciding where to go to find a juvenile habitat. If manini were active swimmers on their last night as larvae, maybe other reef fishes were active too, and for a greater proportion of larval life. Thus began 70 years of study and we still do not know how they do it. In this talk I briefly review the challenges reef fishes face in finding their way back to coral reefs, and the still limited evidence for how they deal with challenges such as how to know where to settle. I point to now largely forgotten papers that gave glimpses of what reef fishes are capable of and limited insight into how they do it. Those innovative but preliminary studies are now being followed up but major gaps in understanding remain, especially for species who begin life as fertilized eggs afloat on the ocean. I suggest novel behavioral, physiological and ecological investigations that could build a fuller picture of the lives of these amazing creatures. We will need much deeper understanding of how reef fishes get back to reefs if we hope to help them continue to prosper in a changing world.

Poster Function, OGGB Level 0 Foyer, November 21, 2023, 4:15 PM - 6:30 PM

Unexpected increase in recreational fishing catches during the Covid-19 pandemic

Saleh, Muhmmad Faiq[1;] Ng, Ying Xuan[1]; Ong, Joyce Jia Lin[1]

[1]*Asian School of the Environment, Nanyang Technological University, Singapore*

Gathering data on recreational fisheries can be difficult due to the costs, time, and logistics needed. To overcome this, researchers can tap on publicly available digital data via social media to facilitate an efficient and discreet method to survey anglers' catches. We investigated the biodiversity of recreational fishing before, during, and after the Covid-19 pandemic by utilising YouTube videos and conducting on-site surveys in Bedok Jetty, a popular fishing spot in Singapore. A total of 202 videos were examined from 2018 to 2022 using the YouTube API and 98 anglers surveyed. We recorded 1021 individual catches that spanned 117 unique species across the five years. The number of videos and species richness peaked in 2021, suggesting that the Covid-19 pandemic may have helped to get more people engaged in the activity and post their catches online. We found that the group of fishes that were most frequently caught were similar across both the video data and the on-site survey. In general, the fishes most frequently caught were tamban (genus: *Sardinella*), queenfish (genus: *Scomberoides*) and trevallies (subfamily: Caranginae). Our work illustrates the value of digital data associated with recreational fishing to provide us with a better representation of fish diversity in Singapore as a result of the pandemic. It is possible to apply this approach to monitor recreational fisheries and assess fish diversity in other parts of the Southeast Asia region, where such activities are less monitored and understudied.

Local and regional environmental drivers of growth in *Lutjanus erythropterus* in Western Australia

Saleh, Muhmmad Faiq[1]; Gonzalez, Júlio Guazzelli[1]; Ng, Clement Zhong Wang[1]; Wakefield, Corey B.[2]; Newman, Stephen J.[2]; Ong, Joyce Jia Lin[1]

[1]Asian School of the Environment, Nanyang Technological University, Singapore

[2]Western Australian Fisheries and Marine Research Laboratories, Department of Primary Industries and Regional Development, Government of Western Australia

Tropical marine fish and fisheries are under threat to the effects of anthropogenic climate change. Despite its significance in global food production, there is still a knowledge gap regarding the impact of changing ocean conditions on tropical fish stocks. Increments developed from otolith biochronologies have been successful in identifying the factors contributing to fish growth. We applied the methodology to the crimson snapper, *Lutjanus erythropterus*, a reef-associated, commercially important species found throughout the Indo-Pacific region. Our study sought to determine the differences in growth of *L. erythropterus*, and the respective factors influencing it, at two adjacent sites in Western Australia: Pilbara and Kimberly. Otoliths from 100 fish ranging from 390 mm to 633 mm in standard length, with ages between 4 and 35 years old were collected at both sites in 2016. Using a series of mixed-effects models, we tested if growth was related to several intrinsic and extrinsic factors. Intrinsic factors used to explain *L. erythropterus* growth included age and site; whereas extrinsic factors included localised sea surface temperature (SST), and precipitation (PPT), as well as different regional climate indices, such as the El Niño Southern Oscillation (ENSO), Pacific Decadal Oscillation (PDO), and Dipole Mode Index (DMI). We hypothesised that there will be differences in growth between the sites and SST will be one of the major factors influencing growth. Preliminary results indicate that the interaction of both intrinsic factors—age and site—influenced growth. Our research highlights the growth drivers and potential impact of changing ocean conditions on marine fish populations.

The Successive Evolution of Giant Marine Filter-Feeders Over Macroevolutionary Time

Sallan, Lauren[1]

[1]*Macroevolution Unit, Okinawa Institute of Science and Technology*

In Modern oceans, baleen whales are the largest animals and the largest ever vertebrates, while whale sharks are the largest “fishes.” These giants feed on some of the smallest prey (krill, small fishes, etc), enabled by convergent changes in feeding morphology such as the evolution of filtering apparati, long, fast-closing jaws, and the reduction and even loss of oral teeth. Here I show that, based on a survey of the repeated evolution of these traits across many groups over the last 500 million years, modern giant filter feeders are only the latest species to emerge from a long-standing macroecvolutionary phenomenon. Starting with arthropods (Dinocariids) in the Ordovician, and continuing with newly identified jawless stem-gnathostomes (“Armored Agnathans”), the largest predatory clades have repeatedly given rise to large filter feeders. These species are identifiable from shared functional features arising from disparate traits, and are inevitably the largest (and often nearly the last) members of their respective groups. The exceptional relative size of these marine filter feeders may be attributable to two factors. First, their initial evolution seems to be an epiphenomenon of warm, stable periods, given that such forms are seemingly absent from unstable and cold periods. Second, their change in diet, which collapses the trophic ladder, may lead to an increase in biomass through greater energy availability. In a zero-sum “diversity dependence” scenario, this implies that the evolution of giant filter feeders should have effects on the viability of their large predator relatives, and perhaps influence marine ecosystem structure.

Predatory and large-bodied fishes depleted on Western Indian Ocean coral reefs

Samoilys, Melita[1]; Osuka, Kennedy[2]; Roche, Ronan[3]; Koldewey, Heather[4]; Chabanet, Pascale[5]

[1]*CORDIO East Africa*

[2]*University of York*

[3]*Bangor University*

[4]*Zoological Society of London*

[5]*UMR ENTROPIE (IRD, UR, CNRS, IFREMER, UNC)*

Predatory and large-bodied coral reef fishes have fundamental roles in the functioning and biodiversity of coral reef ecosystems. These fishes include sharks, groupers, Napoleon wrasse and Bumphead parrotfish, which are vulnerable to overfishing. Despite global concerns of the status of these fishes, data on their populations is largely lacking in the western Indian Ocean (WIO).

We developed a rapid timed SCUBA swim for estimating the density of large-bodied reef fishes and assessed the effectiveness of marine protected areas (MPAs) in maintaining these species' populations across seven regions in the western and central Indian Ocean and Gulf of Aden, including two reference locations where fishing is prohibited. Species came from eight families across three categories: pelagic, demersal and exceptionally large-bodied single species.

Carcharhinidae were absent in five of the seven regions, observed only in Mozambique and the Chagos Archipelago. Scombridae and Sphyraenidae were rarely observed with zero observations in Madagascar, Djibouti and Iles Glorieuses. *Epinephelus lanceolatus* was absent in all regions, *Cheilinus undulatus* was absent in Comoros and Iles Glorieuses, while *Bolbometopon muricatum* was only observed in Tanzania. MPAs were not effective in protecting the single species, or the four pelagic families, except for Carcharhinidae in the highly protected reference locations. However medium protection MPAs were effective for demersal families, notably Epinephelidae.

Understanding whether zero observations are true or false and the applicability of a ZINB model for data with multiple zeros informed our interpretations. The results strongly suggest local extirpation of these large-bodied fishes on many WIO coral reefs.

3.1B Themed session A: Evolution, Taxonomy and Biogeography of Indo-Pacific Fishes, 260-098, November 22, 2023, 2:30 PM - 3:30 PM

Evolutionary history of extant and fossil acanthuriforms and the genomic bases of trophic transitions

Santaquiteria, Aintzane[**1**]; Arcila, Dahiana[2]; Betancur-R., Ricardo[2]; Carnevale, Giorgio[3]; Evans, Kory[4]; McGee, Matthew D.[5]; Meléndez-Vazquez, Fernando[2]; Ortí, Guillermo[6]; Rincón-Sandoval, Melissa[1]; Tyler, James C.[7]; Westneat, Mark W.[8]; White, William T.[9]

[1]Department of Biology, The University of Oklahoma, 730 Van Vleet Oval, Norman, OK 73019, USA
[2]Marine Vertebrate Collection, Scripps Institution of Oceanography, University of California San Diego,
San Diego, CA, USA
[3]Dipartimento di Scienze della Terra, Università degli Studi di Torino, via Valperga Caluso 35, 10125, Torino, Italy
[4]Department of Biosciences, Rice University, Houston, TX 77005, USA
[5]School of Biological Sciences, Monash University, Melbourne, Victoria, Australia
[6]Department of Biological Sciences, George Washington University, 2029 G St. NW, Washington, DC 20052, USA
[7]Department of Vertebrate Zoology, Smithsonian National Museum of Natural History, 10th St. & Constitution Ave. NW, Washington, DC 20560, USA
[9]Department of Organismal Biology and Anatomy, The University of Chicago, Chicago, IL 60637, USA
[8]CSIRO Australian National Fish Collection, National Research Collections of Australia, Hobart, Tasmania, Australia

Independent and recurrent transitions from benthic to pelagic habitats are often associated with the evolution of novel morphologies and trophic strategies. Due to their exceptional fossil record, relatively small genomes, and well-studied ecological life histories, surgeonfishes and allies (Acanthuriformes) provide an opportunity to investigate the evolutionary outcomes of these transitions by integrating paleontological and neontological data. Using phylogenetic and comparative genomic analyses, we examined the independent evolutionary transitions from non-planktivory to planktivory among fossil and extant acanthuriforms by combining genomic data for 81 species (94% of extant diversity) with morphological characters for 32 fossil taxa, as well as diet and tooth morphology data collected from both fossil and extant species. We used these datasets to construct a time-calibrated tree that incorporated both extant and extinct species. Additionally, we estimated the ancestral ranges and the evolution of trophic regimes and tooth morphology. Our analyses show that acanthuriforms originated 63 million years ago in the aftermath of the K-Pg mass extinction event. We found a total of 7-9 transitions to planktivory from non-planktivory lineages followed by 5 reversals to a non-planktivory dietary condition. Most of these transitions occurred in the Indo-Pacific, or the ancient Tethys Sea. While tooth morphology showed no correlation with diet, tropical paleoclimate temperatures did influence acanthuriform's diet transitions. We also generated a chromosome-level genome and shotgun genomes for 45 species to identify candidate genes underlying these trophic transitions. This study represents an important step towards understanding the genetic bases of transitions along the benthic-pelagic axis in marine fishes.

Host sharing and territorial aggression in anemonefishes: investigating the formation of mixed-species groups around Lizard Island, GBR.

Santiago, Carl[1]; Cheney, Karen; Cortesi, Fabio; Hobbs, Jean-Paul.

[1]*School of Biological Sciences, University of Queensland*

Anemonefishes are an iconic and diverse group that is reliant on a critical habitat (anemones) which has declined significantly in recent years – primarily due to mass bleaching events. Disenfranchised anemonefishes may relocate to already colonised anemones after their host dies and the available habitat is limited. Sometimes multiple species may end up coexisting together in what are called ‘cohabiting’ or ‘mixed-species’ groups. Aggressive interactions normally prevent different anemonefish species from cohabiting – thus, the observation of stable cohabiting groups indicates a decrease in the territorial aggression that usually keeps species separate. Cohabitation can then lead to interbreeding between anemonefishes, which has implications for biodiversity. While cohabitation does not always result in hybridization, it is the first in a series of deliberate choices that facilitate this outcome. Therefore, it is of interest to investigate the mechanisms enabling these groups to form.

The overarching objective of this behavioural study was to explore whether reducing the availability of host anemones drives the changes in territorial aggression seen in cohabiting anemonefish groups. It focuses on two species known to form cohabiting groups in colonies of the bubble-tip anemone (*Entacmaea quadricolor*) around Lizard Island, GBR; the Great Barrier Reef anemonefish (*Amphiprion akindynos*) and the Red-and-Black anemonefish (*Amphiprion melanopus*). Territorial defence scenarios were simulated using tank experiments, where the aggression of resident anemonefishes towards conspecific and heterospecific intruders were compared before and after reducing the number of anemones within their territory. I will also present the results of field surveys characterizing cohabitation in anemonefishes around Lizard Island.

Attention-guided counting of seabirds in the wild for compliance of conservation

Saqib, Muhammad[1]; Untiedt, Candice[2]; Wang, Dadong[1]; Tuck, Geoffrey N.[2]; Little, Richard[2]

[1]*Data61, CSIRO, Marsfield, New South Wales, Australia*

[2]*Environment, CSIRO, Hobart, Tasmania, Australia*

Seabird counting is an important task that has received a great deal of attention from researchers in the field of ecology. This problem has practical applications in understanding how fisheries influence seabirds, which is a significant issue that requires attention from both conservation and compliance perspectives, as many seabird species are at risk due to fishing activity. In this paper, we present an attention-guided network for seabird counting in longline fisheries, which can operate in challenging environments that are prone to occlusion and variable lighting conditions. The proposed network consists of convolution blocks with dilated kernels to increase the receptive field and capture discriminative features. Every two convolution blocks are followed by channel attention and pixel attention blocks to guide the features for more accurate seabird estimation. The network is fully end-to-end trainable and can understand complex scenes and perform accurate count estimation. To evaluate the performance of the network, we have created a dataset of seabirds and labelled it with dot annotations for density-based counting and box-based annotations for detection-based counting. We demonstrate the effectiveness of our approach on this dataset, achieving around 2% lower Mean Absolute Error (MAE) than the previous state-of-the-art method.

Examination of the function and evolutionary process of cleaner fish mimicry

Sato, Hajime[1]; Sakai, Yoichi[2]; Kuwamura, Tetsuo[3]

[1]*Graduate School of Integrated Sciences for Life, Hiroshima University, Japan, hsato98@outlook.jp*

[2]*Graduate School of Integrated Sciences for Life, Hiroshima University, Japan, sakai41@hiroshima-u.ac.jp*

[3]*Institute for Research in Social Science, Advanced Collaborative Research Organization of Chukyo University, Japan, kuwamura@lets.chukyo-u.ac.jp*

Cleaning symbiosis of the bluestreak cleaner wrasse *Labroides dimidiatus* (Labridae) is the best-known example of mutualism in Indo-Pacific fishes. Cleaner wrasse acquires ectoparasites and mucus as food by providing cleaning services, making it immune from predation. The false cleanerfish *Aspidontus taeniatus* (Blenniidae) precisely mimics the body color and shape of the bluestreak cleaner wrasse. For the function of cleaner fish mimicry, two hypotheses have been proposed: aggressive mimicry and protective mimicry, but remain inconclusive. We examined these hypotheses to discuss the evolutionary process of mimicry based on field observation on coral reefs of Okinawa, Japan. The false cleanerfish forages on fish fins, demersal eggs of damselfishes, and benthic animals such as tubeworm tentacles and clamshell mantles. A comparison of the frequency of fin-biting in multiple areas in Okinawa revealed that it increased when other prey was scarce, suggesting that aggressive mimicry is important in such situations. For protective mimicry, field observations revealed that the false cleanerfish was occasionally attacked by piscivorous lizardfishes (Synodontidae). We also found that hungry predators (the honeycomb grouper: Serranidae) attacked not only the false cleanerfish but also the cleaner wrasse in the aquarium condition. Furthermore, the false cleanerfish did not copy the dancing behavior of the cleaner wrasse. These results suggest that cleaner fish coloration by itself does not always inhibit predation. From our examination of these functional hypotheses, we conclude that false cleanerfish mimicry evolved primarily as aggressive mimicry to increase the success rate of fin-biting.

3.5B Themed Session E: Biology and Conservation of Sharks and Top-predators, 260-051, November 22, 2023, 2:30 PM - 3:30 PM

Long-term incubation and successful delivery of lantern shark embryos using an artificial uterus

Sato, Keiichi[1,2]; Tomita, Taketeru[2,1]; Kaneko, Atsushi[1]; Toda, Minoru[1]; Murakumo, Kiyomi[1]; Yano, Nagisa[1]; Nakamura, Masaru[2]

[1]*Okinawa Churaumi Aquarium*

[2]*Okinawa Churashima Foundation Research Institute*

The reproductive modes of elasmobranchs are highly diverse and complex. The intrauterine environment of viviparous species, in particular, remains poorly understood. We have studied the function of the shark uterus and have developed an extra-uterine life-support system (artificial uterus) for elasmobranch embryos. The system uses an artificial incubation fluid containing urea to maintain the salinity and osmotic pressure at levels comparable to those seen in shark plasma. We have used this system to maintain two embryos of the slendertail lantern shark (*Etmopterus molleri*) for five months. Once development has been completed in the artificial uterus, the embryos must be primed for artificial delivery and their subsequent life in seawater. To facilitate this transition we developed a protocol that involves a series of stepwise shifts from the initial internal uterine environment to a seawater environment prior to delivery. The system we have developed provides a novel option for the medical treatment of premature embryos for captive viviparous elasmobranchs. The specimens subjected to the protocol survived for more than seven months after delivery, the longest captive record for the species. We anticipate that the technique will be relevant for conservation breeding at public aquaria. During the experiment, we unexpectedly detected bioluminescence of the lantern shark embryos in the artificial uterus. This observation suggests that lantern sharks produce luciferin in utero. This contradicts recent suggestions that lantern sharks can only derive the luciferin they use for bioluminescence from the food they eat.

Reef fish community shifts in the Kuroshio Current region over 10-15 years under ocean warming

Sato, Masaaki[1]; Nakamura, Yohei[2]

[1] *Fisheries Technology Institute, Japan Fisheries Research and Education Agency (FRA)*

[2] *Graduate School of Integrated Arts and Sciences, Kochi University*

Over the last several decades, the world's oceans have warmed substantially as a result of global climate change. The ocean warming can lead to range expansion of tropical fishes to higher latitudes. On the contrary, this has triggered the degradation of corals, which may reduce the associated fishes that inhabit there. Because the ocean warming rate over the western boundary currents is faster than the global mean, the associated shift in reef fish communities is expected to be detected in a short term. Therefore, we examine changes in reef fish communities and abundance of fish functional groups from 2005-2010 to 2020-2022 across tropical (24° N) to temperate reefs (33° N) in a region of the Kuroshio Current, which is one of the major western boundary currents. By 2020-2022, coral covers have largely declined at one tropical reef (24° N) and temperate reef (33° N) due to heatwave in summer and extreme cold event in winter, respectively. The underwater visual surveys found that fish communities shifted these sites, which were associated with decrease in tropical benthivores and corallivores and increase in herbivores. Fish communities also changed at subtropical reefs (26 and 28 ° N), resulted mainly from increase in tropical planktivores and omnivores. Our results suggest that instability of local coral habitats in the tropical and temperate reefs and range expansion of tropical fishes into the subtropical reefs contributed to fish community shifts over 10-15 years in the Kuroshio Current region.

The impact of Green Tape on Barrier Remediation Projects: lessons from Queensland, Australia

Scanlon, Melinda[1]; Marsden, Timothy[1]

[1]*Australasian Fish Passage Services*

The Green Tape revolution has significantly contributed to environmental protection by imposing rigorous requirements on proponents of in-stream barrier developments. However, when the same regulatory processes are applied to assess barrier remediation projects, including fishway installation and barrier removal, it can lead to challenges in terms of project budgets and timeframes. This study presents two examples from Queensland, Australia, highlighting the impacts of this system.

The first example examines the complexities and financial costs of securing approvals and engaging in prolonged departmental consultation for a fishway installation project at the tidal interface. Delays and unforeseen costs resulted from the regulatory process, severely impacting project timelines and budgets. The second example delves into the regulatory hurdles encountered for a barrier removal project, where timelines and costs expanded to comply with green tape requirements, ultimately leading to the failure of the project.

These case studies demonstrate how restoration projects focused on remediating environmental damage, are subject to the same rigorous regulatory processes as instream barrier developments that harm the environment, often for commercial benefit. It highlights the need to adopt a balanced and efficient regulatory process in order to guarantee barrier remediation project success for the restoration of waterways and fish habitats into the future.

Improving regional and temporal comparisons in fish life history

Schemmel, Eva[1], Donovan, Mary[2]

[1]*National Oceanic and Atmospheric Administration, NMFS Pacific Island Fisheries Science Center, USA*

[2]*Center for Global Discovery and Conservation Science, Arizona State University, USA*

Regional and temporal comparisons of life history (age, growth, and reproduction) are rare yet extremely valuable for understanding fishery effects and environmental and climate drivers of fish biology. However, many issues can arise making across study comparisons difficult, which we propose can be resolved through proper sample selection and increased simultaneous reporting of multiple life history parameters such as physiological and functional size and age at reproductive maturity. Additionally, modelling advances such as the use of Bayesian Models can improve between population comparisons while incorporating environmental drivers and fishery effects. We investigated these sampling, reporting, and modelling approaches across multiple Pacific fishes to develop recommendations for improving regional and temporal comparisons of fish life histories. Similarly, adding information on environmental drivers (e.g., variation in temperature) and fishing effects revealed that life histories can vary considerably within relatively fine spatial scales (i.e., within archipelago). Revealing multiple sources of variability in fish life history underscores the importance of accounting for spatial and environmental variation for fisheries management.

1.2B Special Session 4: The evolution and ecology of fishes: assessing traits and functions in a changing world, 260-073, November 20, 2023, 2:00 PM - 4:15 PM

Biological traits and their effect on individual-level processes and ecosystem-level functions

Schiettekatte, Nina[1]; Barneche, Diego[2,3]; Brandl, Simon[4]; Casey, Jordan[4]; Villéger, Sébastien[5]; Parravicini, Valeriano[6]

[1]*Hawai'i Institute of Marine Biology, University of Hawai'i at Mānoa, Kāne'ohe, HI, USA*

[2]*Australian Institute of Marine Science, Crawley, Western Australia, Australia.*

[3]*Oceans Institute, The University of Western Australia, Crawley, Western Australia, Australia.*

[4]*Department of Marine Science, Marine Science Institute, The University of Texas at Austin, Port Aransas, TX, USA*

[5]*MARBEC, Université de Montpellier, CNRS, IFREMER, IRD, Montpellier, France.*

[6]*PSL Université Paris: EPHE-UPVD-CNRS, Université de Perpignan, Perpignan, France*

Consumers play an important role in biogeochemical cycles through the consumption and release of essential elements such as carbon (C), nitrogen (N), and phosphorus (P). A large proportion of consumed elements are rapidly released back into the environment in inorganic (i.e., excretion) or organic form (i.e., egestion). On coral reefs, fishes represent a large part of the consumer biomass and thus play a key role in the recycling of nutrients. On the individual level, ecological and physiological traits will determine how fishes contribute to the storage and flux of C, N, and P. On the community level, the species composition and size distribution affect ecosystem functions. Here, we demonstrate how traits (e.g. size, diet, absorption efficiency, and activity level) affect individual-level processes (e.g. consumption, growth rate, nutrient flux) using a bioenergetic models. We further quantify five key functions—nitrogen and phosphorus cycling, biomass production, herbivory, and piscivory—mediated by reef fishes across the world's tropical oceans. We demonstrate that critical trade-offs exist among functions (e.g. biomass production and phosphorous cycling), and that no reef fish community worldwide can sustain maximum values for all five functions simultaneously. Moreover, we demonstrate that the N and P release is higher in fish egestion compared to excretion for most species and communities. Our findings introduce a challenge for coral reef conservation, in that we cannot maximize all functions simultaneously, so we stress the need for quantitative assessment of multiple functions to make informed management decisions.

2.4C Themed Session F: Conservation of Indo Pacific fishes, 260-092, November 21, 2023, 3:30 PM - 4:15 PM

Integrating thermal tolerance with population genetics to reveal the thermal landscape of a coral reef fish (*Acanthochromis polyacanthus*)

Schmidt, Elliott[1]; Donelson, Jennifer[1]; Torda, Gergely[1]

[1]*College of Science and Engineering, James Cook University, Townsville, 4811, QLD*

Differences in populations' responses to ocean warming can defined by spatial patterns in thermal adaptation. These performance patterns are shaped by evolutionary processes over spatial and thermal gradients, creating a heterogenous thermal landscape across species' distributions, that can be used to determine populations' vulnerability to ocean warming. To reveal species' thermal landscapes both phenotypic plasticity and genetic differentiation need to be understood at the population level. Genetics cannot infer vulnerability, and phenotypic plasticity cannot explain potential mechanisms behind divergences between populations. The coral reef damselfish (*Acanthochromis polyacanthus*) is widespread throughout the Indo-pacific and Great Barrier Reef (GBR), however, populations isolation via the lack of larval dispersal limit gene flow between populations. Thermal performance curves from common garden experiments were used to identify thermal variation between fish from two different geographic regions; central (i.e., core region; summer average temperature of 28.5°C) and southern (i.e., leading edge region; summer average temperature of 27°C) GBR. Samples from each region consists of fish originating from three different populations. Region based thermal performance curves were created for aerobic physiology (i.e., maximum, standard, and net metabolic rate), and cellular enzymes (i.e., lactate dehydrogenase and citrate synthase) to explore evidence for local thermal adaptation. Genetic samples from fish that were tested for physiological metrics were sequenced via shallow whole genome sequencing to identify genetic differences between regions as well as begin to explore putative mechanisms driving thermal differences in physiological traits.

How does environmental change affect the brain and behaviour in coral reef fishes?

Schunter, C.[1], Sourisse M. J.[1], Kang J. [1], Ramirez, S.[1], Paula J.R.[1,2,3]
[1] Swire Institute of Marine Science, The School of Biological Sciences, The University of Hong Kong
[2] MARE – Marine and Environmental Sciences Centre & ARNET- Aquatic Research Network, Laboratório Marítimo da Guia, Faculdade de Ciências da Universidade de Lisboa, Cascais, Portugal
[3] Departamento de Biologia Animal, Faculdade de Ciências da Universidade de Lisboa, Lisboa, Portugal

Anthropogenic activities are causing the global climate to change at an unprecedented rate, and such rapid environmental changes in aquatic ecosystems can have severe consequences on crucial behaviours. We have been investigating the impacts of environmental change on the neurobiology and genomic regulations in marine organisms with the ultimate goal of understanding adaptive potential and resilience to climate change. We focused on the systematic study of the effects of ocean acidification on the behaviour and the underlying nervous system adjustments. Through transgenerational exposure to ocean acidification conditions, we saw changes in chemical alarm cue response behaviour and deciphered developmental as well as parental effects on the molecular signatures in a coral reef fish brain. In addition, collections in the wild at CO_2 seeps allowed to understand the common and variable responses in brains across fish species and revealed different levels of brain transcriptional plasticity and adaptive potentials owing to evolutionary rates and expression of long non-coding RNAs. Further crucial behaviours, such as cooperative social interactions in fish are affected by ocean acidification associated with transcriptional reprogramming in different brain regions in cleaner fish. Lastly, as working with more ecological models is complex, we use the marine sea hare *Aplysia* and evaluate more fine mechanistic response in a neuro system with pH changes associated with the tail withdrawal reflex. These studies reveal the importance of the response of the neurobiological system in the maintenance of key behaviours and resilience of marine organisms in a changing world.

Fossil marine gobies

Schwarzhans, Werner[1]

[1]*Zoological Museum University of Copenhagen, Denmark*

Gobies (Gobiidae) are the most diverse extant marine fish family. In contrast, their fossil record has been rather meager for a long time but much progress has been achieved during the last decade and ongoing research. Here I present recent advances in the understanding of the evolution of the Gobiidae from a paleontological perspective.

The Gobioidei (and Gobiidae) are a young group with the first fossil records about 50 Ma (early Eocene) all represented by pan-Gobioidei. A first pulse of diversification is observed at about 33 Ma (Oligocene) but only during the Miocene (20 Ma) the Gobiidae seem to have entered into a phase of accelerated radiation and have remained in that mode ever since. All major groups of the Gobiidae are known since 20–15 Ma in Europe, the Indo-West Pacific and tropical America. The fossil record is dominated by otoliths. The evolving fossil record and lineage persistence is presented for the European/Indo-West Pacific region, highlighting implications for the shift of biotic centers and rapid speciation and endemic adaptation observed in gobies under ecological stress.

Poster Function, OGGB Level 0 Foyer, November 21, 2023, 4:15 PM - 6:30 PM

Why and how the small males occur in the polygamous mating groups of the protogynous goby *Fusigobius neophytus* (Gobiidae)

Seiwa, Ryoga[1]; Sakai, Yoichi[1]

[1] *Graduate School of Integrated Sciences for Life, Hiroshima University, Higashi-Hiroshima, Hiroshima, Japan*

The common fusegoby *Fusigobius neophytus* inhabits the shallow waters of the Indo-Pacific Ocean. In Kuchierabu-jima Island, southern Japan, this species exhibits a male-territory visiting polygamous mating system with uniparental egg care by males in open nests and protogynous sexuality. As seen in various protogynous fish, territorial males of *F. neophytus* (mostly 55-60 mm TL) tend to be larger than females (30-55 mm TL). In addition, it has been known that a few smaller males co-occur in the goby population. However, it remains unclear how small males appear and what kinds of reproductive advantages they have. Our histological observations of gonads showed that all immature individuals (≤ 40 mm TL, $n = 15$) had ovariform gonads, suggesting the possibility of pre-maturational sex change. Of the 23 spawning events observed in 2022, parasitic spawning did not occur; however, a small male (39 mm TL) was observed conducting pair spawning and egg care, as shown in large territorial males. After the territorial male disappeared, large females (48-55 mm TL, $n = 3$) only conducted sex change to take over mating territories. Small males may have undergone sex changes triggered by other social events. In this study, we discuss the life history tactics of small males of the goby based on our field observation data.

Insights into the residency of oceanic manta rays at cleaning stations on coral reefs in the Bird's Head Seascape, Indonesia

Setyawan, Edy[1]; Beale, Calvin[2]; Erdmann, Mark[3]; Hasan, Abdi[4]; Izuan, Muhamad[4]; Mofu, Imanuel[5]; Putra, Mochamad[6]; Sianipar, Abraham[2]

[1]*Institution of Marine Science, The University of Auckland, Auckland, New Zealand*

[2]*University of Murdoch, Perth, Western Australia, Australia*

[3]*Conservation International Aotearoa, Auckland, New Zealand*

[4]*Konservasi Indonesia, Sorong, Papua Barat, Indonesia*

[5]*BLUD-UPTD Pengelolaan Kawasan Konservasi Perairan di Kepulauan Raja Ampat, Waisai, Papua Barat, Indonesia*

[6]*Konservasi Indonesia, Jakarta Selatan, DKI Jakarta, Indonesia*

The globally endangered oceanic manta ray *Mobula birostris* is generally believed to spend more time in the open ocean than in coastal areas. The Bird's Head Seascape (BHS) in eastern Indonesia hosts a large population of this species (>1200 individuals), where it is frequently sighted at cleaning aggregation sites. Little is known about the movements and habitat use of this wide-ranging species on shallow coral reefs. Here we report results of an initial passive acoustic telemetry study on the use of cleaning stations on coral reefs by M. birostris. Forty-one *M. birostris* were acoustically tracked from February 2016 to August 2019 using 28 receivers deployed across the Raja Ampat, Fakfak, and Kaimana regions of the BHS. A total of 5,932 detections were recorded by 17 of these 28 acoustic receivers from 37 tagged individuals. The tagged individuals demonstrated various degrees of residency, ranging from 0.2 to 427 mins (mean ± SD = 46 ± 67 mins) in close proximity to acoustic receivers. Most (94%) of these detections occurred during the daytime, reaching a peak at 11am. Additionally, the tagged *M. birostris* frequently moved locally between adjacent acoustic receivers separated by only 5-12 km. More than half of all movements (n = 166) occurred between neighbouring cleaning stations in southern Raja Ampat. Some long-distance movements were recorded, including the longest between two cleaning stations in Kaimana and central Raja Ampat separated by ~500 km. Our study provides preliminary insights into the residency and local movements of *M. birostris* at cleaning aggregation sites on coral reefs.

Wandering the ocean: movements of an oceanic manta ray satellite tracked for 10 months in the Southwest Pacific

Erdmann, Mark[1]; Duffy, Clinton[2]; Green, Lydia[4]; Setyawan, Edy[4]

[1]*Conservation International Aotearoa, Auckland, New Zealand*

[2]*The Department of Conservation, Auckland, New Zealand*

[3]*Manta Watch Aotearoa New Zealand, Auckland, New Zealand*

[4]*Institution of Marine Science, The University of Auckland, Auckland, New Zealand*

Despite being found circumglobally in tropical and temperate waters, little is known about the movement ecology of the endangered oceanic manta ray (*Mobula birostris*) in the Southwest Pacific. The waters in northern New Zealand (NZ) are known to serve as summer foraging grounds for this species. Here we report the movements of a mature female satellite tagged on 23 February 2022 while foraging in the Hauraki Gulf (HG), New Zealand. After tagging, the ray spent several weeks in northern NZ waters before leaving northwards on 20 March 2022. The ray was tracked for 310 days, moving a total distance of 9,206 km and ranging up to ~2,500 km to the northeast of its tagging position (easternmost: W 163.675º; northernmost: S 22.65º). A state space model (SSM) indicated that while offshore in temperate waters, the ray showed traveling behaviours (high move persistence index). Over the tracking period, the ray recorded four dives deeper than 1,000 m (up to 1,273 m at the deepest), and spent most of its time in shallow water (mean: 35.3 m depth). It also experienced temperatures ranging from 3.5 to 28.3ºC (mean: 21.1ºC). After 7 months offshore, the ray returned to NZ waters on 8 October 2022, eventually reaching the HG in early November. While in NZ waters, the SSM showed low move persistence index, indicating that the ray was likely foraging. This study highlights the broad movements of *M. birostris* in the Southwest Pacific and its fidelity to NZ waters as an important seasonal foraging ground.

1.4A Themed Session: K. General Session, 260-057, November 20, 2023, 11:15 AM - 1:00 PM

The effects of climate change on seafood nutritional quality

Shalders, Tanika C.[1,2]; Benkendorff, K.[1]; Champion, Curtis[1,2]; Coleman, Melinda A.[1,2]

[1]*National Marine Science Centre, Southern Cross University, Coffs Harbour NSW*

[2]*Fisheries Research, NSW Department of Primary Industries, Coffs Harbour NSW*

Climate change is increasingly impacting marine ecosystems, global fisheries and marine resource use, whilst concomitantly, global reliance on seafood as a source of nutrition is increasing. In addition to a broad range of economic, social and cultural benefits, harvested marine resources provide essential contributions to nutrient security and human health. In an emerging research frontier intersecting climate change ecology and fisheries science, we investigated the impacts of current and near-future climate change on the quality, availability and distribution of nutrients derived from harvested marine resources. Here, we present insights from our recent review of this emerging topic and primary data from experimental and field-based assessments of environmental change on the nutritional quality of key fisheries species. We experimentally demonstrate that marine heatwaves and elevated temperatures reduce the harvestable biomass and increase toxic metal content, with longer exposure significantly altering nutritional responses in an estuarine crustacean. We also use field-based sampling and statistical modelling to show spatial and temporal changes in the nutritional quality of an important demersal fish. Specifically, omega-3 fatty acids are predicted to decrease under future global climate models. Combined, these results show that the quality and availability of nutrients can change within and between species and across spatial and temporal distributions. Overall, our research supports the growing body of evidence that climate-driven environmental change can impact the content of important nutrients within marine species and therefore availability to marine ecosystems and consumers, with potentially negative implications for nutrient security, human health, and sustainable fisheries.

Larval freshwater fish and parasites in Australia – an update

Barton, D.P.[1,2]; Thiem, J.D.[3]; Shamsi, S.[1, 2]

[1] *School of Agricultural, Environmental and Veterinary Sciences, Charles Sturt University, Wagga Wagga, New South Wales, Australia*

[2] *Gulbali Institute, Charles Sturt University, Wagga Wagga, New South Wales, Australia*

[3] *NSW Department of Primary Industries, Narrandera, New South Wales, Australia*

Freshwater fish in Australia are known to have a diverse, yet largely undescribed, parasite fauna. However, little is known about the dynamics of these parasitic infections, including at what size fish start to become infected and by which particular parasites. This study is examining larval and juvenile fish from waterways within the Murray Darling Basin to determine levels of infection in these groups of fish. Larval and juvenile fish across a range of native and introduced species have been dissected with parasites collected, primarily from the introduced carp. Monogenean parasites, found on the gills of the fish, have been the predominant type collected, due to their direct life cycle, and independence of the need for the fish host to ingest infective stages. Identification of the species of monogenean is ongoing. This study provides the first detailed examination of the parasites of larval and juvenile freshwater fish in Australia.

Aquatic Parasites in a Changing World: Emerging Threats to Fisheries Resources

Shokoofeh Shamsi[1]

[1] *Gulbali Institute, Charles sturt University, Australia*

The dynamic nature of our world, driven largely by human activities, has raised numerous concerns about the impact of parasites on aquatic ecosystems and fisheries resources. This presentation focuses on the emerged threats posed by parasites to our valuable fish populations, highlighting case studies where parasites have infiltrated native species and remained undetected by professionals in relevant fields. Human activities, e.g., trade, and demand for exotic culinary preferences have accelerated significantly, leading to significant changes in parasite populations and rise of certain parasite species and the decline of others. Importantly, some parasites have managed to enter new regions through human-mediated activities, establishing themselves within native fish populations. Through case studies, we will examine instances where parasites have been introduced through the importation of exotic fish species, bypassing quarantine measures and affecting the health and dynamics of native fish populations. One of the challenges we face is the hidden nature of these parasites and losing expertise. Despite their potential impacts, they often go unnoticed by veterinarians, health professionals, and conservation scientists. This lack of attention stems from limited surveillance programs, diagnostic complexities, and the intricate life cycles of parasites. Recognizing the implications of overlooking these hidden threats, we will discuss strategies to improve detection and management. Ongoing research and monitoring are essential to adapt to the evolving challenges posed by parasites in our changing world. It is concluded that by understanding the challenges and exploring potential solutions, we can work towards preserving the health and sustainability of our fisheries in the face of a changing world.

Short-term plasticity of an anemonefish (*Amphiprion ocellaris)* visual system in response to anthropogenic changes to the light environment.

Shaughnessy, Abigail[1,2]; Mailer, Chelsea[1]; Cortesi, Fabio[1,2]; Cheney, Karen[1]
[1]*Queensland Brain Institute, the University of Queensland, Brisbane, Queensland, 4072, Australia*
[2]*School of Biological Sciences, the University of Queensland, Brisbane, Queensland, 4072, Australia*

Coral reef fishes are exposed to fluctuations in their prevailing light environment as conditions can change naturally with diurnal cycles, seasons, depth, or more stochastically due to anthropogenic events such as sediment run-off. Previous research has indicated that some reef fishes can alter their visual (opsin) gene expression under different light conditions. However, whether and how changes in gene expression translate to visual performance remains untested. In this study, we examined the capacity of the ocellaris clownfish (*Amphiprion ocellaris*) visual system to adapt to short-term light environment changes. The chosen induced light environments reflect ecologically relevant stressors found on the Great Barrier Reef: enhanced sediment runoff and algal blooms. Firstly, we showed the ability of adult *A. ocellaris* to shift their opsin expression within 10 days of having a different light environment. Secondly, we used behavioural experiments to explore if the changes at a molecular level would alter the threshold at which two colours can behaviourally be distinguished. We found that the largest changes in opsin expression and colour discrimination thresholds occurred in the green algal-simulated light environment. Overall, our results show the potential for short-term plasticity both on a molecular and behavioural level and thus clownfish likely have the capacity to quickly alleviate the effects of environmental change.

Global shortfall in the management of major shark and ray fisheries

Sherman, C. Samantha[1,2,3]; Matsushiba, Jay H.[2]; Digel, Eric D.[2]; Zubick, Patrick[2]; Eged, Jonathan[2]; AHaque, Alifa B.[4,5]; Arnold, Amanda[2]; Sant, Glenn[3,6]; Dulvy, Nicholas K.[2]

[1]*School of Life and Environmental Sciences, Deakin University, Geelong, Victoria, Australia*

[2]*Earth to Ocean Research Group, Department of Biological Sciences, Simon Fraser University, Burnaby, British Columbia, Canada*

[3]*TRAFFIC International, Cambridge, United Kingdom.*

[4]*Nature-based Solutions Initiative, Department of Zoology, University of Oxford, UK*

[5]*Department of Zoology, University of Dhaka, Bangladesh*

[6]*Australian National Centre for Ocean Resources and Security, University of Wollongong, NSW, Australia*

Fisheries management is essential to guarantee sustainable capture of target species, and to avoid undesirable impacts on incidentally caught species. A key challenge is to assess the status of species and the degree to which management is sufficient to avoid declines in relatively data-poor fisheries. While ecological risk analyses focus on intrinsic ‘productivity’ and extrinsic ‘susceptibility’, one would ideally understand the third axis of ‘fisheries management’. Currently, there is no single management evaluation that can be applied to a range of data-poor fishery types. Here, we outline a management risk (M-Risk) framework for sharks, rays, and chimaeras that can be used to evaluate a species’ risk to overfishing resulting from insufficient management. We evaluated whether management of individual species was sufficient for their relative sensitivity by combining the management risk score for each species with their intrinsic sensitivity to determine a final overall M-Risk score. This framework can be applied to determine which species face the greatest risk of overfishing and be used by fisheries managers to identify effective management policies by replicating regulations from countries with lower risk scores. This presentation will explain the M-Risk framework and discuss results of 3,210 completed assessments of 387 species in 31 countries and all 4 tuna RFMOs.

Spawning phenology and offspring sex: Do protogynous hermaphrodites spawn on new moons to make males?

Shima, Jeff[1]; Osenberg, Craig[2]; Noonburg, Erik[3]; Alonzo, Suzanne[4]; Swearer, Steve[5]

[1]*Victoria University of Wellington*

[2]*University of Georgia*

[3]*A boat in Puget Sound*

[4]*University of California, Santa Cruz*

[5]*University of Melbourne*

Parents should spawn at times that maximize their own fitness, even if this does not maximize the fitness of their offspring. In many protogynous mating systems, large males monopolise female harems to achieve greater reproductive success. Consequently, fitness-payoffs for parents can vary dramatically with offspring sex. We consider the perplexing spawning phenologies of the sixbar wrasse (*Thalassoma hardwicke*). Parents spawn disproportionately around the new moon, even though this sets up most offspring to fail. Is this a strategy to make reproductive winners? We address this question with otolith-based demographic reconstructions of 884 fish spanning a range of ages. We quantify residual growth histories through the larval stage to infer birthdates on a lunar calendar. We estimate selection on lunar birthdates from spawning through to settlement, and sexual maturation to females or males. We speculate that spawning at seemingly inopportune times (i.e., new moons) may reflect a strategy to produce fitness winners.

Overlooked mortality in the longface emperor *Lethrinus longirostris* by the didymozoid parasite infection

Shimose, Tamaki[1]; Kanaiwa, Minoru[2]; Katahira, Hirotaka[3]

[1]*Fisheries Resources Institute, Japan Fisheries Research and Education Agency, Japan*

[2]*Faculty of Bioresources, Mie University, Japan*

[3]*School of Life and Environmental Science, Azabu University, Japan*

The longface emperor *Lethrinus longirostris* is a large lethrinid fish species commercially exploited in Okinawa Prefecture, southern Japan. The species is frequently infected with a didymozoid parasite in its muscle. The present study focuses on negative impact of this parasite infection on the mortality of the host fish species. A total of 117 fish specimens (269–761 mm fork length) were purchased from the Yaeyama fish market in Okinawa, and examined for parasite infection. Age was determined by annual ring count using sectioned otoliths. Didymozoid parasite infection was recorded in 25 individuals (0–5 years old) and was often found near the dorsal pterygiophores. Tube-shaped brown structures, regarded as remains of the didymozoid parasite after death, were also observed near the dorsal pterygiophores in other 26 individuals (1–17 years old). The parasite and the remains were recorded more in younger individuals and medium age individuals, respectively. These age-biased occurrences imply that; 1) the mortality of infected host fish is higher than that of uninfected fish, 2) some individuals of the parasite die and leave remains in the host muscle, and 3) the mortality of fish recovered from the parasite infection is still higher than that of uninfected fish. Simple simulations assuming different survivorship in three conditions of fish were applied to explain the age-biased occurrences. The survivorship was estimated to be 63%/year for uninfected fish, 41%/year for infected fish, 61%/year for recovered fish, respectively. The results suggest that the didymozoid parasite infection increases the mortality of *Lethrinus longirostris*.

1.1B Themed Session: A. Evolution, Taxonomy and Biogeography of Indo-Pacific Fishes, 260-098, November 20, 2023, 2:00 PM - 4:15 PM

Spine locking apparatus in vertical and paired fins of fishes from Japan

Shinohara, Gento[1]

[1]Department of Zoology, National Museum of Nature and Science, 4-1-1 Amakubo, Tsukuba, Ibaraki 305-0005, Japan

Fish systematics and functional morphology play important roles in other research fields such as fish biology, fisheries science, and biomimetics. Some ray-finned fishes have a spine locking apparatus (SLA) in the dorsal, anal, pectoral and/or pelvic fins. The SLA mechanism has been studied in detail for several taxa, including two percomorph families Leiognathidae (Ponyfishes) and Acanthuridae (Surgeonfishes). Different types of SLA have been reported in families belonging to the orders Siluriformes, Zeiformes, Beryciformes and Tetraodontiformes. In addition to the use of anatomical techniques and radiographs, a micro-CT scanning survey of the SLA diversity and mechanisms was made of the actinopterygian fishes of Japan. In particular, the family Oplegnathidae (Knifejaws) are reported here to have a newly discovered SLA design in the dorsal fin. This SLA is located in the anterior part of the dorsal fin and the locked condition results from interaction between the first and second spines supported by connective tissues and muscles. A similar design has also been partially found in the dorsal fin spines of some species in the family Scorpaenidae (Scorpionfishes). This paper discusses the diversity and classification of the SLA across more than 20 families.

Poster Function, OGGB Level 0 Foyer, November 21, 2023, 4:15 PM - 6:30 PM

Larval fish assemblage from the French EEZ in the southwestern Indian Ocean

Shiroza, Akihiro[1], Bonhommeau, Sylvain[1], and Chevrier, Thomas[1]

[1]IFREMER Indian Ocean Delegation. Rue Jean Bertho BP 60, 97822 Le Port Cedex, La Réunion

Our knowledge about the early life history of large pelagic, demersal, and reef fishes and the connectivity of these populations in the Indian Ocean is still very limited but critical for a better management of these stocks. Very few larval surveys have been conducted in this ocean over the last decades. The main larval surveys have been conducted between 1956–1981 and only occasionally thereafter. Ichthyoplankton surveys were conducted in January 2022 and March 2023, from the French EEZ of Tromelin Island and the Mozambique Channel, respectively. Tromelin survey was conducted during the peak spawning of albacore and patches of larvae were discovered west of Reunion Island. Survey in the Mozambique Channel revealed abundance of reef and demersal ichthyoplankton, notably fusilier (Family Lutjanidae), around stations near seamounts.

Based on the preliminary finds from these pilot studies, Project Larvaguedom, a series of projects investigating on: 1) the spatio-temporal variances of local reef and demersal ichthyoplankton abundances around Reunion Island, 2) larval albacore abundances and distribution from the western IO spawning ground between 10–30°S and 50–70°E, and 3) the spatio-temporal study of ichthyoplankton abundance around a neighboring seamount, La Pérouse, are planned.

Through these projects, we intend to monitor and evaluate the effectiveness of the current Marine Protected Areas and advise the local fisheries managers for the better management and the protection of local fisheries resource. Prolonged studies would collect adequate dataset of fisheries independent data for development of ecological indices, which can then be integrated into stock assessment models.

Taxonomic revision of the seahorse genus *Hippocampus* (Syngnathidae): hidden diversity in the pygmy seahorses

Short, G.[1,2]; Hamilton, H.[3]
[1]*Australian Museum, Sydney NSW, Australia*
[2]*California Academy of Sciences, San Francisco California, United States*
[3]*Marine Conservation Institute, California, United States*

Seahorses are members of the family Syngnathidae, which includes pipefishes, pipehorses, seadragons, and pygmy pipehorses, and are characterized by male brooding, a unique body plan, including a fused jaw, and morphological adaptations for crypsis. With a total of 46 described species, the Indo-Pacific region harbors the highest level of species diversity. Seahorses range in size from the tiny 12 mm pygmy seahorse *Hippocampus satomiae* to the large 35 cm *H. abdominalis*. While sharing synapomorphies, such as an angled head, the presence of a coronet, and a prehensile tail, the eight Indo-Pacific pygmy seahorse species differ in the number of gills and location of male egg-brooding in the body. Although exhibiting notable external morphological differences, pygmy and non-pygmy seahorses are currently classified under a single genus, *Hippocampus*. Recent phylogenetic studies of Syngnathidae recovered a globally distributed and well-defined clade, with sampled species segregated into pygmy and non-pygmy lineages exhibiting significant evolutionary distances, thereby highlighting the need for a revision of the genus. The aim of this study was to assess the proposed revision of the genus using a taxonomic approach that utilized micro-computed tomography imaging to identify unique skeletal characters that could provide morphological evidence to support the phylogenetic data. Comparisons of skeletal features revealed strong evidence for the erection of three nominal genera within the pygmy seahorses based on novel neurocranial apomorphies distinct from the non-pygmies and a surprising evolutionary twist between the pygmy and non-pygmy seahorses. Implications for the conservation and management of the proposed taxonomic revision are discussed.

When and where: How seascape context and site maturity influences fauna in restored seagrass

Sievers, Michael[1]; Connolly, Rod[1]; Flindt, Mogens[2]; Nielsen, Benjamin[2]; Rasmussen, Jasmine[1]; Steinfurth, Rune[2]

[1] *Coastal and Marine Research Centre, Australian Rivers Institute, School of Environment and Science, Griffith University, Gold Coast, QLD 4222, Australia*

[2] *Department of Biology, University of Southern Denmark, DK-5230, Odense M, Denmark*

As restoration efforts accelerate around the world, understanding the drivers of how actions benefit fauna can inform future restoration projects. Seagrass is restored, in part, to provide habitat for fauna, particularly fishes and crustaceans. Fauna also play vital roles in maintaining ecosystem persistence and resistance, and their presence is thus critical to restoration success. Although the potential for multi-habitat restoration and the benefits of considering the seascape are gaining traction, empirical examinations, particularly at scales relevant to most current restoration projects, of how these concepts affect fauna remain scarce. We surveyed mobile fauna within 133 sites in Vejle fjord, Denmark. These point locations were within natural seagrass, on bare sand, and in restored seagrass that was transplanted 1, 2, 3, or 4 years ago. These sites also varied in terms of their distance to a nearby restored boulder reef and restored mussel beds. A diverse faunal community, including fish, crustaceans and gastropods, colonised all restored patches – and at similar abundance to natural sites – despite very low seagrass density in newly restored areas. Early results regarding seascape context highlight potential benefits of multi-habitat restoration, with more sophisticated analyses underway. We will also present data on the metabolome of two key species, the lesser pipefish and Baltic prawn, revealing potential differences in the health of individuals occupying sites with different characteristics. Our findings support multi-habitat seascape restoration at small spatial scales to enhance faunal communities, with a suite of potential benefits across environmental, social and economic realms.

Growth aspects of *Mugil cephalus* Linnaeus, 1758 from Kilifi creek, Kenya

Sigana, Dorcus A.[1]

[1]*Department of Biology, University of Nairobi, P. O. Box 30197-00100, Nairobi, Kenya*

Grey mullet *Mugil cephalus* (Linnaeus, 1758) were collected from eight sites within Kilifi creek from October 2002 to September 2004 using monofilament gillnets and a nylon cast net. Each fish had the total length (mm), total weight (g) recorded, then ventral side of fish was slit open and sex identified. Length-weight, condition factor and age and growth were studied on 765 specimens obtained. In 537 males length and weight ranged between 57mm TL weighing 3g and 480mm weighing 1169.3g with the regression line fitted for length on weight being Log_{10} W = 1.7457 + 2.8658 Log_{10} L. The length–weight ranged between 61mm weighing 3.8g and 507mm weighing 1385g in 228 females with the regression line fitted for length on weight being Log_{10} W = 1.7973 + 2.8955 Log_{10} L**.** Low variations in the monthly relative condition factors between the sexes as well as during the different seasons were observed, however, the males had higher relative condition factors than females. Asymptotic length was calculated for *M. cephalus* at each site with largest fishes caught at Sea Horse, Nkoma, Fumbini and Mazioni while the smallest fishes were at Kombeni and Kidundu. In females, the asymptotic length (VBGE) L_∞ (51.48 cm) is higher than in males (48.3 cm) and no notable difference was in K (growth coefficient) between females (0.83) and males (0.79) respectively. Kilifi creek is pristine and needs conservation as source of juveniles for stocking in ponds for future culture.

Reducing taxonomic lag via convolutional neural nets

Sih, Tiffany[1]; Unmack, Peter [1]; Hammer, Michael[2]; McGee, Matt[1]

[1]*Monash University*

[2]*Museum and Art Gallery of the Northern Territory*

The ability to discriminate and describe a species' characteristics is a fundamental step in taxonomy. Meristics, the quantification of features such as fins and scales, and morphology, the relative comparison of shape and structure, are important aspects of classifying a species compared to congeners. These steps can be time-consuming and require attention to detail, and due to the limited number of experts in this field can create a 'taxonomic lag'. Computer vision combined with machine learning techniques can help to alleviate this problem by efficiently identifying features in images. Radiographs (x-rays) offer unique insight to several internal characteristics commonly used in ichthyology, for instance, shape and placement of skeletal elements. If we could harness computer vision methods, we could reduce the time spent on meristic counts by allowing experts to rapidly quantify these traits. Here we present a machine learning procedure for identifying features of interest and providing vertebral counts from radiographs of *Retropinna* (Retropinnidae, smelts) using object detection. We produced models using several popular computer vision frameworks to identify individual specimens and provide counts of individual vertebral elements using bounding boxes, which are then reviewed by a human observer. This supervised classification algorithm can reduce mental fatigue, inhibit observer bias, and has broad applications in taxonomy, functional ecology and beyond. Similar models can be used to aid in the identification of species, which can be applied for taxonomic or biosecurity needs.

Assessing the Impact of Introduced Perch through non-lethal Sampling Methods of Native Threatened Eels

Nathan Silcock[1]; Corey Denham[1], Mark Lokman[1], Travis Ingram[1]

[1]*University of Otago*

New Zealand's freshwater systems are globally recognised as biodiversity hotspots, providing habitat for multiple native fish, plant and bird species. However, multiple species have been introduced for angling purposes or by accident, resulting in increased predation pressures, interspecific competition and habitat alterations within native freshwater ecosystems. Observing and analyzing these impacts on our native and even threatened species often involve lethal methods. This study aims to investigate the impacts of introduced European Perch (*Perca fluviatilis*) on the diet and population structure of native longfin (*Anguilla dieffenbachii)* and shortfin eels (*Anguilla australis*) through the further development of non-lethal sampling methods. A total of 10 ponds that varied in perch population structures were observed throughout Te Nohoaka o Tukiauau (Sinclair Wetlands), Dunedin. Mucus excreted from the eels were sampled with stable carbon and nitrogen signatures analyzed to observe trophic position when competing with different populations of perch. Blood samples were collected from the eels to compare hematology characteristics (Triglycerides, Phospholipids, Total Cholesterol) and describe the health of eels across ponds. The knowledge and methods developed from this study will support a better understanding of the relationship between introduced perch and native eel species, while assisting in future eel conservation efforts.

The evolution of fast-growing coral reef fishes

Siqueira, Alexandre C.[1]; Yan, Helen F.[1]; Morais, Renato A.[1,2]; Bellwood, David R.[1]

[1]*Research Hub for Coral Reef Ecosystem Functions, College of Science and Engineering, James Cook University, Townsville, QLD 4811, Australia*

[2]*Paris Sciences et Lettres Université, École Pratique des Hautes Études, EPHE-UPVD-CNRS, USR 3278 CRIOBE, Perpignan, 66860, France*

Individual growth is a fundamental life history trait, yet its macroevolutionary trajectories have rarely been investigated for entire animal assemblages. Here, we analyse the evolution of growth in a highly diverse vertebrate assemblage, coral reef fishes. We combined state-of-the-art extreme gradient boosted regression trees with phylogenetic comparative methods to detect the timing, number, location, and magnitude of shifts in the adaptive regime of somatic growth. We also explored the evolution of the allometric relationship between body size and growth. Our results show that the evolution of fast growth trajectories in reef fishes has been considerably more common than the evolution of slow growth trajectories. Many reef fish lineages shifted towards faster growth and smaller body size evolutionary optima in the Eocene (56-33.9 Ma), pointing to a major expansion of life history strategies in this Epoch. Of all lineages examined, the small-bodied, high-turnover cryptobenthic fishes shifted most towards extremely high growth optima, even after accounting for body size allometry. In concert, these results suggest that the high global temperatures of the Eocene and subsequent habitat reconfigurations might have been critical for the rise and retention of the highly productive, high-turnover fish faunas that characterise modern coral reef ecosystems.

Nine species in one: evidence of hidden species diversity in the Zambezi grunter (Siluriformes, Auchenoglanididae) in southern and south-central Africa

Sithole, Yonela[1,2]; Bragança, Pedro[1]; Chakona, Albert[1,2]; Musschoot, Tobias[3]; Vreven, Emmanuel[1,3,4]

[1]*National Research Foundation - South African Institute for Aquatic Biodiversity (NRF-SAIAB), Makhanda, 6139, South Africa*

[2]*Department of Ichthyology and Fisheries Science, Rhodes University, Makhanda, 6139, South Africa*

[3]*Vertebrate Section, Ichthyology, Royal Museum for Central Africa (RMCA), Tervuren, B-3080, Belgium*

[4]*Laboratory of Biodiversity and Evolutionary Genomics, KU Leuven, Leuven, 3001, Belgium*

There is increasing evidence from recent integrative taxonomic studies that many species of freshwater fishes considered to have wide geographic distribution ranges potentially harbour undocumented species diversity. The Zambezi grunter, *Parauchenoglanis ngamensis*, as currently recognised, is distributed across four river systems in southern and south-central Africa: the Okavango, upper Zambezi, Kwanza and Kasai (sub)basins. The present study used a combination of molecular, colour pattern, and morphological data to explore the possible existence of hidden species diversity within what is currently referred to as *P. ngamensis*. Molecular phylogenetic analysis based on the mitochondrial COI sequences recovered seven distinct lineages (>0.97 Bayesian posterior probabilities) with a substantial genetic divergence between them (>1.6%). These candidate species exhibited a combination of consistent colour pattern and morphological differences that supported their recognition as distinct. The present study redescribed *P. ngamensis* s.s., confined to the Okavango and upper Zambezi systems, and also described six new species, two from the Kwanza Basin and four from the Kasai sub-basin. Two additional new species without molecular data were described from the Luenda and Chiumbe rivers (Kasai) based on distinctive colouration pattern and morphology. The fact that some of the species occur allopatrically, whereas others are sympatric and even syntopic indicates the complex palaeogeographic history of the region that promoted species diversification and shaped contemporary biogeographic distribution patterns of freshwater fishes. Accurate delimitation of species boundaries and mapping their distribution ranges is important to inform conservation status assessments and guide management options to enhance biodiversity protection.

The contribution of fish data to the last decade of conservation planning in South Africa

Smit, Kaylee[1,2]; Bernard, Anthony[2]; Green, Andrew[3]; Harris, Jean[4]; Kerwath, Sven[5]; Lombard, Mandy[1]; Palmer, Ryan[2]; Sink, Kerry[1,6]

[1]*Institute for Coastal and Marine Science (CMR), Nelson Mandela University*

[2]*South African Institute for Aquatic Biodiversity (SAIAB)*

[3]*University of KwaZulu-Natal (UKZN)*

[4]*WILDOCEANS Program, WILDLANDS Conservation Trust*

[5]*Department of Environment, Forestry and Fisheries (DFFE)*

[6]*South African National Biodiversity Institute (SANBI)*

Biodiversity observation data are collected at a variety of scales and used in several different processes that aim to inform management and conservation planning. However, data and information often don't feed through the right channels in a way that meets end-user needs. In South Africa, we can learn from a number of success stories linked to national and sub-national conservation processes, including marine protected area design and identification of ecologically and biologically significant areas. Through these processes, challenges, gaps and opportunities have been identified including the need to improve science-to-policy pathways. Here, we provide results from a synthesis of some of the key multidisciplinary research projects that have been conducted over the last decade under the African Coelacanth Ecosystem Programme. Demersal fish data, among other things, were collected from the continental shelf with the aims of improving spatial biodiversity assessment for planning, marine protected area expansion and effective long-term management. We provide an overview of spatial prioritization and planning processes at a national scale from a semi-developed country perspective including the design of a new national MPA network, and the role of fish and fisheries data in these processes. Furthermore, we discuss two case study examples of more fine-scale planning processes in two MPAs on the east coast of South Africa where we also reflect on challenges and research gaps. We will end by paving a way forward by discussing potential ways of optimising the value chain of fish data to inform management processes, in a South African context.

Utilization of non-invasive environmental DNA (eDNA) sample collection for shark species identification and mitochondrial haplotyping in Hawai'i.

Call, Jenna[1]; Andrus, Kai[1]; Buxton, Alyvia[1]; Lader, AnnElise[1]; Smith, Brad[1]

[1]*Brigham Young University - Hawaii*

Environmental DNA (eDNA) describes portions of genetic material from sources such as skin, saliva, sperm, mucous, urine, and blood observed in environmental samples and is a novel non-invasive methodology for marine ecosystem monitoring. In Hawai'i it is vital for shark conservation and management that population genetic studies rely on collecting accurate data. Dugal et al. (2021) reported that eDNA in water samples collected surrounding whale shark individuals could be used for mitochondrial haplotyping in population genetic surveys. Similarly, we examine the utility of eDNA water collections as a noninvasive method for studying smaller reef shark species populations in Hawaii as well as sought to develop species identification assays. Tissue biopsies and 1 L seawater collections were collected from individual Galapagos sharks (*Carcharhinus galapagensis*). Following collection seawater was filtered and eDNA was isolated from filters and tissue using Qiagen DNeasy kits and regions of the mitochondrial control region were amplified. While the study is ongoing, preliminary results suggest that eDNA is a viable non-invasive methodology.

How can we motivate citizen scientists to help uncover the secrets of billfish?

Smith, Laura[1]; Holmes, Bonnie[2]; Martin, Victoria[1]; Pepperell, Julian[3]; Tibbetts, Ian[1]; Williams, Samuel[4]

[1]*The University of Queensland*

[2]*University of the Sunshine Coast*

[3]*Pepperell Research and Consulting Pty Ltd*

[4]*Fisheries Queensland, Department of Agriculture and Fisheries*

Billfishes are both difficult to study and to manage because they are highly migratory and have very broad, patchy distributions that span international jurisdictions. Marlins and the sailfish are valued by recreational catch-and-release fishers, however, often the fisheries data that are required to accurately assess stocks are lacking, which has led to uncertainty about their stock statuses and the validity of current management controls. Engaging recreational anglers in data collection is a cost-effective tool to gather information on billfish that would otherwise be logistically difficult to survey independently by fisheries agencies. Game fishers have contributed to billfish research as citizen scientists for many decades. A great opportunity exists for researchers, fisheries managers, and game fishing organisations to collaborate to strategically improve our knowledge of billfish stocks and biology using citizen science. However, an important challenge is recruiting and maintaining the interest of citizen scientists.

I used an Australia-wide online survey of game fishers to examine the drivers and barriers to game fisher participation in citizen science programs that have contributed to billfish research. Many of the respondents had been involved in past research activities, predominantly catch-tag-recapture programs. Eighty-eight percent of 153 respondents indicated that they were willing to participate in research activities in the next two years. They listed several factors that impact their future participation including project logistics, their personal situation, altruistic motivations, and fisheries management. Communications about project opportunities, expectations, data use and access, and research outcomes were identified as being important to overcome barriers to participation.

Nearshore habitat utilization and movement of Hawaiian bonefish (*Albula glossodonta*) on the reef flats of Moloka'i

Smith, Brad[1]; Dance, Michael[2]; Rooker, Jay[3]; Tinhan, Thomas[4]

[1]*Brigham Young University - Hawaii*

[2]*Louisiana State University*

[3]*Texas A&M University at Galveston*

[4]*University of Hawai'i at Mānoa*

Bonefishes (*Albula* spp.) have a circumtropical distribution and in Hawai'i two species of bonefish are recognized, *A. glossodonta* or "round jaw" and *A. virgata* or "sharp jaw". Both species are important culturally and recreationally, particularly on the island of Moloka'i. Moloka'i's south shore is comprised of a 50 km long fringing reef that provides ideal reef flats for *A. glossodonta*. While Moloka'i is not heavily populated, subsistence fishing is extremely high, and the island has become a destination for sport fly fishing. These targeted pressures necessitate a better understanding of habitat utilization and bonefish movement to ensure better population assessment and management. While there have been many tagging studies in the Caribbean and Indo-Pacific to investigate bonefish movement and habitat utilization this is less understood within Hawaiian bonefish populations. In a preliminary acoustic telemetry study in 2019 an acoustic array of 10 Vemco acoustic receivers was established on a reef flat bounded by two deep channels on the southeast of Molokai. *A. glossodonta* (n = 10) were caught, surgically implanted with Vemco V13 acoustic transmitters, and released in August of 2019. Analysis of 95% kernel utilization densities indicated differences in area use patterns and strong site fidelity among individuals. Unlike similar studies in the Pacific or Indian oceans significant tidal and diel cycles were not found in our small sample study.

A new species of eight-gilled hagfish (Agnatha, Myxinidae) based on imported fish specimens

Young-Sun, Song[1]; Jin-Koo, Kim[2]

[1] *Dokdo Fisheries Research Center, National Institute of Fisheries Science, Pohang 37709, Republic of Korea*

[2] *Department of Marine Biology, Pukyong National University, Busan, 48513, Republic of Korea*

Hagfishes (Family Myxinidae) are currently classified into 6 genera and 88 species, of which 55 species belong to the genus *Eptatretus* worldwide. Recent molecule-based research has resolved many taxonomic problems, suggested new classification, and revealed new species. Here, we describe a new species of hagfish from off western Nagasaki by analysing multiple information of morphological characters, mitochondrial and nuclear gene sequences. The new species was well distinguished from all congeners by a combination of the following morphologic characters: eyespots conspicuous, no nostril-sinus papillae, eight pairs of gill pouches and gill apertures, 3/2 multicusps, total cusps 46-50, 4–5 gill pouches at the end of dental muscle, total slime pores 85-90 (prebranchial 13-17, branchial 7-8, truck 54-58, tail 11-15), branchial length 7.5%-8.3% of total length, pharyngocutaneous duct confluent with last gill aperture, ventral aorta bifurcating at about the 5th to 6th gill pouches, ventral fin-fold small or vestigial, and dark brown to blackish body color. In addition, the new species was separated from the congeneric species with high genetic differences (1.5%-14.3% in COI, 0.7%-5.0% in 16S rRNA, 0.2%-1.3% in 18S rRNA+28S rRNA). Also, we herein suggested a key to 23 species of genus *Eptatretus* in Indo-Pacific Ocean.

How active is the brain in elevated temperature? Brain imaging of larval fishes responding to olfactory cues

Sourisse, Jade M. [1]; and Schunter, Celia[1]

[1] *The Swire Institute of Marine Science, School of Biological Sciences, The University of Hong Kong, Pok Fu Lam Road, Hong Kong SAR*

Olfaction is one main way fish gather information about their environment. Various behaviours are influenced by olfactory stimuli detection. However, olfactory-mediated responses are sensitive to external factors such as water temperature, and especially considering rapid climate change it is important to understand how warming modulates olfactory-mediated behaviours that fish need for survival. In our study, we investigate the effects of elevated developmental temperature on the brain activity to an alarming olfactory cue first in the model organism zebrafish, *Danio rerio* to then apply this technique to non-model *Amphiprion* larvae. We exposed zebrafish and anemonefish embryos to control and future-predicted temperatures (+2°C) from embryonic stage until 7 days post fertilization. By injecting larvae with a fluorescent calcium dye, we assess brain activity in the forebrain, notably the olfactory epithelium and bulb, using a confocal microscope. Larvae are semi-immobilized in agarose with tail free moving, given a conspecific alarm cue (CAC) then their brain activity is recorded. While this is the first time brain activity is assessed in response to CAC with different temperature regimes in zebrafish, the technique is common in neurological models. However, brain activity has never been assessed in marine fish experimental research and we therefore expand brain calcium imaging to non-model, yet ecologically relevant fishes by investigating the effects of temperature on the brain activity. Understanding the effects of environmental factors on sensory-mediated neural activity can provide important new insights into the influence of global changes on aquatic life at high resolution, from model to non-model species.

3.3C Themed Session B: Ecology of Indo-Pacific Fishes, 260-115, November 22, 2023, 4:00 PM - 6:00 PM

Herbivores in the hot-seat: resilience of *Acanthurus triostegus* functions to ocean warming

Souza, Taylor K.[1]; Brijs, Jeroen[2]; Crowder, Larry B.[1]; Johansen, Jacob L.[2]; Tran, Leon[2]

[1]*Hopkins Marine Station, Stanford Oceans, Stanford Doerr School of Sustainability, Pacific Grove, CA 93950, USA*

[2]*Hawai'i Institute of Marine Biology, University of Hawai'i at Mānoa, Kāne'ohe, HI, USA*

The protection of herbivorous fishes is seen as essential for the preservation of coral reefs threatened by thermal stress (*e.g.*, marine heatwaves [MHWs] and long-term ocean warming), as these fishes help maintain reefs in a coral-dominated state via the removal of algae. However, as thermally sensitive ectotherms, rising thermal stress may also pose a serious threat to these fishes and the critical ecosystem functions they deliver. Thus, here we evaluate the consequences of thermal stress on a herbivorous coral reef fish (*Acanthurus triostegus*) by characterizing changes in metabolic demands, diurnal foraging rates, swimming activity and individual fitness within their current thermal window (*i.e.*, during winter and summer, 24.0±0.1°C and 27.5±0.1°C, respectively) and beyond (*i.e.*, at the peak of a simulated MHW, 31.0±0.1°C). Rising temperatures cause significant increases in standard metabolic rate and activity, but not foraging rate. As a result, fishes were able to increase or maintained body mass during summer and winter, but a mismatch between energy demand and intake at the peak of the MHW resulted in a significant decrease in body mass. Given MHWs can last for many weeks these results indicate that while herbivorous coral reef fishes may continue to remove algae during periods of thermal stress, they may only be able to do so for a limited period due to the rapid reductions in individual fitness. Therefore, considerations of thermal sensitivity and tolerance in herbivorous reef fishes will need to be considered for the successful implementation of coral reef management strategies in a warmer world.

Novel use of environmental DNA metabarcoding to assess impacts from a large-scale seismic survey on tropical fish communities

Speed, Conrad[1]; Dugal, Laurence[1,2], Meekan, Mark[2], Birt, Matthew[1], Parsons, Miles[1,2,3], McLean, Dianne[1,2], Taylor, Brett[1], McCauley, Robert[3], Semmens, Jayson[4], Newman, Stephen[5], and Thomas, Luke[1]

[1]*Australian Institute of Marine Science, Perth, Western Australia, 6009.*

[2]*UWA Oceans Institute, University of Western Australia, 6009.*

[3]*Centre for Marine Science and Technology, Curtin University, Bentley, Western Australia, 6109.*

[4]*Institute for Marine and Antarctic Studies, University of Tasmania, Battery Point, Tasmania, 7004.*

[5]*Western Australian Fisheries and Marine Research Laboratories, Department of Primary Industries and Regional Development, Government of Western Australia, P.O. Box 20, North Beach 6920, Western Australia, Australia.*

Environmental DNA (eDNA) metabarcoding has become a widespread tool used by ecologists to monitor wildlife diversity, although to date there has been little application of the method for impact assessments. Here we use eDNA collected in a before after control impact (BACI) design to determine if a seismic survey impacts a tropical fish shelf community. Furthermore, we compare a number of indices such as eDNA counts and an eDNA index of abundance to that derived from estimates of fish relative abundance using baited remote underwater video stations (BRUVS). We found no evidence of significant changes in fish community structure at the high impact zone compared to control zones. This result was also confirmed using all metrics across all fish groupings within the BACI framework, suggesting no evidence of material impacts to richness or abundance due to the seismic survey. However, the overall power to detect change in the fish community structure was low for all metrics, with the highest power observed using the eDNA index. In total, we detected 109 different genera using the BRUVS and eDNA datasets, although there were more genera observed using BRUVS (n=52) than with eDNA metabarcoding (n= 23). There was also a positive relationship between the estimates of relative abundance observed using BRUVS compared to eDNA counts when combining data from all genera together, although the relationship was weak. This study highlights the utility and applicability of using eDNA to assess point-source impacts on fish communities.

5.4A Themed Session G: Long Term Monitoring of Indo-Pacific Fishes, 260-092, November 24, 2023, 10:30 AM - 12:30 PM

Informing management with bioregional maps of benthic and fish assemblages from standardised stereo-video data

Spencer, Claude[1]; Gibbons, Brooke[1]; Langlois, Tim[1], Mastrantonis, Stanley[1]; Monk, Jacquomo[2]; Navarro, Matt[1]

[1]*The University of Western Australia*

[2]*University of Tasmania*

The Australian Marine Parks represent a national and continental scale system of protected areas with an objective to achieve biodiversity conservation. They are made up of biogeographic networks with constituent parks and zones with varying levels of protection, at regional and local scales across Australia’s Commonwealth waters. Here we propose and demonstrate a set of benthic and fish assemblage metrics and generate spatial distribution maps at the scale of the South-west Network of the Australian Marine Parks. These metrics have been informed using previous syntheses of stereo-video fish and habitat annotation data and incorporate decades of fisheries science that have been used to select representative indicator species that are likely to respond within no-take zones. We synthesised fish and habitat assemblage annotation data from 3,283 stereo-video deployments across the spatial extent of the South-west Network and adjacent State waters along 1,800 km of coastline. We used generalised additive models, with a full-subset model selection, to determine correlations between habitat and fish metrics and physical, environmental, and anthropogenic predictors. Benthic habitat distributions were correlated with geomorphological features that were captured in the model as bathymetry-derived metrics. For the fish metrics considered, depth, primary productivity and recreational fishing pressure were highly influential predictors. This synthesis demonstrates how stereo-video data can be used in conjunction with freely available bathymetry, environmental and human-use data to create benchmarks and spatial distribution maps of benthic and fish assemblage metrics at the large biogeographic scale of a national marine park network.

Long term monitoring of fish and benthic communities on inshore island fringing reefs in the Great Barrier Reef Marine Park

Srinivasan, Maya[1]; Ceccarelli, Daniela[2]; Cresswell, Benjamin[1]; Galbraith, Gemma[1]; McClure, Eva[1]; Williamson David[3]

[1]*James Cook University*

[2]*Australian Institute of Marine Science*

[3]*Great Barrier Reef Marine Park Authority*

Fringing coral reefs around inshore islands of the Great Barrier Reef Marine Park have high biodiversity and support high levels of recreational use. Systematic long-term monitoring of these reefs is fundamental to tracking the temporal dynamics of fish communities, detecting impacts and recovery from disturbance events, assessing the effects no-take marine reserves, triggering management actions and improving awareness. Significant reductions in coral cover, habitat complexity, and fish abundance and diversity have been documented at four inshore island locations between 1998 and 2019 by the Inshore Reef Zoning Monitoring Program. A new monitoring project is continuing to monitor the four locations and 4 new locations, from the Turtle Group in the far north to the Keppel Islands in the southern GBR. The first year of monitoring has reinforced what we know from the previous monitoring project, that fish abundances, species richness and assemblage composition varied among island locations and were generally related to the cover of structurally complex corals and turf algae. At each island location, coral cover was related to the history of disturbance and recovery, with considerable variation among sites. For example, at the Whitsunday Islands, a severe cyclone in 2017 caused a significant decline in branching coral cover and fish abundance, and in 2022, branching coral cover and the abundance and species richness of corallivores remained much lower than at other island groups. With predictions of increased frequency and intensity of disturbances such as cyclones and warming events, spatially replicated long term monitoring projects are crucial.

Genomic and epigenomic signatures of thermal adaptation in fish

Stajic, Dragan[1]; Berezenko, Anastasiia[1]; Adrian-Kalchhauser, Irene[1]

[1]Institute for Fish and Wildlife Health, 3012 Bern, Switzerland

Climate change associated temperature fluctuations pose significant selective pressure on natural populations. Aquatic ectotherms, such as fish, are especially vulnerable to the temperature effects as their body temperature closely resembles that of the environment. Populations deal with environmental change through two distinct processes, acclimation (i.e. transient environment dependent physiological response) and evolutionary adaptation (i.e. pertinent allele frequency changes in the population).

To understand the molecular basis and relative contribution of acclimation vs adaptation to thermal tolerance evolution in fish, we intend to perform experimental evolution using wild-caught populations of zebrafish. We will expose populations of zebrafish to three selection regimes: constant cold temperature, constant hot temperature and transient heat-shock regime.

To understand genetic components of adaptation, we will perform pooled whole population sequencing of both ancestral and evolved populations. The alleles that increase in frequency between ancestral and evolved populations will be further validated to determine their effect on thermal tolerance.

To understand non-genetic components of adaptation, we will transfer the evolved populations to the non-selective environment and determine the relative change in thermal tolerance upon the transfer. To unravel the gene regulatory changes associated with acclimation, we will perform ATAC-seq (chromatin accessibility assay) and RNA-seq (changes in transcriptome) of evolved individuals before and after the transfer to the non-selective environment.

The synergistic analysis of both epigenomic/transcriptomic and genomic data will not only enable us to reconstruct a more holistic picture of thermal adaptation in fish, but also help us predict the effect of thermal stress on natural populations.

1.2B Special Session 4: The evolution and ecology of fishes: assessing traits and functions in a changing world, 260-073, November 20, 2023, 2:00 PM - 4:15 PM

Functional traits to predict fish futures – Pandora’s Box or Rosetta Stone?

Streit, Robert[1]; Bellwood, David[1]

[1]Research Hub for Coral Reef Ecosystem Functions, College of Science and Engineering, James Cook University, Townsville, Australia

Fish ecologists have embraced functional traits. Functional traits are a powerful tool to move beyond taxonomic perspectives of fish communities and to add an extra layer of ecological information. Functional traits are quantifiable, species names are not. Therefore, traits open abundant new analytical perspectives on community- and macroecology. At their best, they promise the dawn of a predictive ecology - ecological forecasts by measuring which species are present.

We challenge the current consensus on the sweeping, general promises of functional traits. Indeed, traits are powerful because they provide extra information. But we need to be clear which inferences we can and cannot make from a given trait. The term ‘functional’ may be the underlying problem, a vague linguistic ornament clouding clarity and causing confusion. The broad allure of the term is an incentive to retrofit ‘functionality’, i.e. purported ecological relevance, to any easily accessible traits. To harness the power of traits for fish ecology, and abandon the preoccupation with ‘functional’ traits, we propose a three-step ‘taxonomy of traits’ – a conceptual compass to navigate the diverse applications of traits in ecology. The first step is to recognise a foundational distinction in what we may want to achieve with traits: to either identify patterns in biodiversity or to predict ecological processes arising from communities. Both goals are valuable. Yet they require different data and potentially different traits. Only once our intentions are clear, can we invest in new traits that are fit-for-purpose.

New records of fishes from Rangitāhua/Kermadec Region

Struthers, Carl[1]; Stewart, Andrew[1]; Trnski, Thomas[2]; Duffy, Clinton[2,3]; Barker, Jeremy[1]; McMillian, Peter[1]; Roberts, Clive[1]; Clark, Malcolm[4]; Liggins, Libby[5]; Middleton, Crispin[4]; Middleton, Irene [4]

[1]*Museum of New Zealand Te Papa Tongarewa, PO Box 467, Wellington, New Zealand*

[2]*Auckland War Memorial Museum, Private Bag 92018, Auckland 1142, New Zealand*

[3]*Department of Conservation, Private Bag 68908 Newton, Auckland 1145, New Zealand*

[4]*National Institute of Water and Atmospheric, Research Limited, Private Bag 14 901 Wellington, New Zealand*

[5]*School of Natural Sciences, Massey University, Auckland, New Zealand*

The Kermadec/Rangitāhua region is an extensive area of subtropical ocean 370 km northeast of the New Zealand mainland between the latitudes 25.9 S to 34.7 S, with a total area of 620,000 km2 (~15 % of the NZ EEZ). The region is delimited by the New Zealand 200 nautical mile EEZ boundary around the Kermadec/Rangitāhua Islands. This area has a diverse array of habitats, including trench (~10,000 m), abyssal plain (2000 m), hydrothermal vents, shallow reef systems, intertidal rocky reefs.

Traditionally the fish fauna of this area has been poorly sampled with limited research focusing on either, the shallow water around the islands, or the hadal depths within the trench. More recently, to add to this knowledge, targeted research expeditions have been undertaken in the region focused on sampling the biodiversity in a wider range of habitats and depths. From these surveys over 90 new records have been documented and will soon to be added to the faunal list of the region.

This talk will provide an update on the current knowledge of the fish fauna and will illustrate some of these new records. The relationships with the New Zealand fauna and notable species absences will also be discussed.

Why have Mesopelagic Boundary Communities only been documented off Hawaii? Likely cosmopolitanism of mesopelagic associations with landmasses and their importance

Sutton, Tracey[1]; Boswell, Kevin[2]; Bracken-Grissom, Heather[2]; Cook, April[1]; Frank, Tamara[1]; Milligan, Rosanna[1]; Moore, Jon[3]

[1]*Guy Harvey Oceanographic Research Center, Halmos College of Arts and Sciences, Nova Southeastern University, Dania Beach, FL, USA*

[2]*Department of Biology, Florida International University, North Miami, FL, USA*

[3]*Wilkes Honors College, Florida Atlantic University, Jupiter, FL, USA*

Mesopelagic biogeographic boundaries in the open ocean are generally diffuse and coincide with meso-to-basin-scale physical oceanography. A notable exception occurs in certain topographic boundary regions, where spatially compressed midwater areas are constrained by 200-m and 700-m isobaths that may harbor ‘indicator’ mesopelagic species that are rare offshore and that exhibit behaviors influenced by the bottom. The presence of indicator species differentiates these ‘mesopelagic boundary communities’ (MBCs) from areas where oceanic deep-scattering layers impinge upon the continental slopes, but where the species composition is similar to that found offshore (although sometimes in high densities). MBCs have been well-documented over the upper slope of the Hawaiian Islands but have rarely been reported elsewhere. The possible reasons for the lack of MBC ubiquity are many, ranging from environmental to ecological to methodological. The last reason may be particularly important; for an MBC to be detected, a well-established offshore faunal inventory and/or behavioral catalog is necessary, against which uniqueness of a potential MBC fauna can be determined. Such inventories are lacking for much of the World Ocean. Here we will take a deep dive into the MBC phenomenon, comparing MBCs to other forms of topographic association (e.g., canyons, ridges), discussing requirements for maintenance of MBCs in a high dispersal environment, and presenting preliminary evidence of a possible MBC over a large deep-water coral complex in the Gulf of Mexico. We will finish by discussing the importance of MBCs for managed and/or protected marine species and for planning protected areas.

Clubbing stomatopods dominate cryptobenthic fish predation in coral-depauperate habitats

Swan, Sam[1]; Yan, Helen F.[1]; Bellwood, David R.[1]

[1]*Research Hub for Coral Reef Ecosystem Functions, College of Science and Engineering, James Cook University, Townsville, QLD 4811, Australia*

Cryptobenthic reef fishes contribute disproportionally to the consumed biomass on coral reefs; yet, the majority of studies of piscivores focus on large-bodied, fish predators. Here, we quantified the consumption rates of the cryptobenthic clubbing stomatopod, *Haptosquilla trispinosa*, and combined their consumption rates with stomatopod abundances across a range of reef habitats. Given that an individual stomatopod is able to consume, on average, 25 gobies per year, we found that the highest estimated goby consumption rates occurred in macroalgae or turf-dominated systems with low levels of rugosity. Indeed, stomatopods can potentially contribute to the consumption of 690 gobies per square meter per year in low-lying habitats, compared to an average of fewer than three individuals per square meter per year in coral-dominated systems. Given that the annual mortality rate of gobies is roughly 342 individuals per square meter per year, our findings highlight that stomatopods are likely the dominant cryptic predators in coral-depauperate habitats, characterised by low structural complexity. Although the stomatopods *H. trispinosa* do not have the raptorial appendages typically associated with piscivory, they are still effective cryptobenthic fish predators. As coral reefs of the Anthropocene become increasingly dynamic, stomatopods may benefit from the loss of complexity and become the dominant predators of highly-productive cryptobenthic fishes.

Updates on *Encheloclarias* (Siluriformes: Clariidae), an uncommon acid-water catfish

Tan, Heok Hui[1]

[1]*Lee Kong Chian Natural History Museum, National University of Singapore, 2 Conservatory Drive, Singapore 117377. E-mail: heokhui@nus.edu.sg*

The genus *Encheloclarias* is one of the most poorly known siluriform fish to date, with less than 20 specimens belonging to 7 species. It was first described from Bangka Island by Pieter Bleeker in 1853 based on a single specimen – *E. tapeinopterus*. For 140 years, this genus was thought to be monotypic until Ng & Lim revised the genus and added 4 more species in 1993 (viz. *E. baculum*, *E. prolatus*, *E. kelioides*, *E. curtisoma*). Subsequently, Ng & Tan and Ng added two more species – *E. velatus* in 2000 and *E. medialis* in 2012 respectively. This genus has always been thought to be stenotopic to peat swamp forest habitats with highly acidic waters. In 2023, range extension and discoveries of 2 species - *E. kelioides* in Singapore and *E. baculum* in Brunei, provided fresh insights. This talk will update new ecological information, new distributional ranges and discuss synonymy of existing species. This will have implications on future conservation strategies for *Encheloclarias* in their respective distributional ranges and IUCN Red Listing.

4.3A Themed Session B: Ecology of Indo-Pacific Fishes, 260-115, November 23, 2023, 10:30 AM - 12:30 PM

Understanding thermal preferences and movement patterns of trawl whiting (*Sillago* sp.) using otolith oxygen isotopes

Tan, Melissa[1]; Hall, Karina[2]; Kelaher, Brendan[1]

[1]*National Marine Science Centre, Southern Cross University, Coffs Harbour, NSW Australia*

[2]*NSW Department of Primary Industries (Fisheries), National Marine Science Centre, Coffs Harbour, NSW Australia*

Ocean warming poses a significant threat to marine species, ecosystems and fisheries sustainability. Trawl whiting, including eastern school whiting (*Sillago flindersi*) and stout whiting (*Sillago robusta*), play a crucial role in commercial fisheries along the east coast of Australia, with an annual catch of approximately 3000 tonnes. However, comprehensive knowledge regarding the early life history and seasonal movements of these fish remains limited, impacting effective stock management strategies. To address this gap, we employed otolith oxygen isotope ratios ($\delta^{18}O_{otolith}$) as a proxy for thermal preferences, enabling an assessment of fish movement and habitat use. Thin-sectioned otoliths were sampled using a micromill to obtain calcium carbonate powder from both core and edge portions, and powdered samples were analysed for $\delta^{18}O_{otolith}$ using a Kiel IV carbonate device coupled with a ThermoMAT253 isotope ratio mass spectrometer. The results derived from core samples represented the water temperature experienced during the fish's juvenile stage, while the edge samples reflected the water temperature averaged over 1-2 years prior to capture as an adult. A latitudinal trend was observed in $\delta^{18}O_{otolith}$ values obtained from the otolith edge, with substantial variations among fish from different locations, but a narrower range of values within each location. In contrast, core values showed relatively uniform patterns among fish across all locations but exhibited greater variations within each location. These findings have crucial implications for the utilisation of $\delta^{18}O_{otolith}$ values as a proxy for water temperature and the interpretation of such data concerning thermal preferences and spatial distributions under projected climate change.

Systematics of the Indo-West Pacific anthiadids, with emphasis on the genus *Plectranthias* Bleeker, 1873 and their relatives (Perciformes: Anthiadidae)

Tang, Chi Ngai[1]; Chen, Wei-Jen[1]

[1]*Institute of Oceanography, National Taiwan University, Taipei, Taiwan*

The Anthiadidae comprises a group of small-sized reef-associated fishes found from tropical to temperate seas worldwide and includes 248 valid species. In spite of its wide distribution and species richness, our knowledge about their phylogenetic relationships, species diversity, and the taxonomy is still limited due to sampling difficulties. Therefore, the classification, especially at generic level, is still in debate. The *Plectranthias* is the most speciose genus of the Anthiadidae and was suspected to be non-monophyletic. Here, based on the samples collected during several oceanographic expeditions in the Indo-West Pacific (IWP) over the last decade under the program “Tropical Deep-Sea Benthos” and joint efforts between Taiwan and France teams, the present study aims to (1) reconstruct the phylogeny of the IWP anthiadids to evaluate the monophyly of the anthiadid genera, especially the *Plectranthias*; (2) establish a new classification for *Plectranthias* species. To reconstruct the phylogeny, a multi-gene dataset with one mitochondrial and four nuclear gene sequences obtained from 80 morphospecies representing 17 genera was compiled and used. Our results revealed non-monophyly of *Odontanthias*, *Pseudanthias*, and *Plectranthias*. In “*Plectranthias*”, seven distinct clades (A to G) were resolved. Tentatively, we suggest the following changes for the classification: (1) resurrection of the junior synonym of *Plectranthias*, *Sayonara* Jordon & Seale, 1906, for clade B; (2) establishment of a new genus for clade F; (3) restriction of *Plectranthias* species only to clade D. Further morphological evaluations are still required for the remaining four clades before assigning suitable genus names to them.

3.1A Themed session A: Evolution, Taxonomy and Biogeography of Indo-Pacific Fishes, 260-098, November 22, 2023, 10:30 AM - 12:30 PM

Fish using tools: Uncovering factors driving tool use evolution

Tariel-Adam, Juliette[1]; Brown, Culum[1]

[1]*School of Natural Sciences, Macquarie University, North Ryde, NSW, Australia*

The use of tools by fish has been understudied for a long time mainly because of the challenges of observing fish underwater and because fish has been considered to have low cognitive abilities. Studying fish using tools will provide an understanding of the ecological significance of tool use and the physical and cognitive abilities required which remain largely unknown. We focused on anvil use where a fish uses a rock as a tool to crack open a prey item by quickly and repeatedly smacking the prey item onto a hard surface while holding the prey in its mouth. Anvil use is presumed to allow the fish to access prey that are harder to crush or damage using the mouth alone, thus broadening its foraging niche. This amazing behaviour has been observed in some wrasses (Labridae), but the observations for each species are restricted to one or few individuals at a single location. We have started a community science project to determine what species, where and how fish use rocks as cracking tools. So far, people's observations have identified 9 new wrasse species in addition to the 20 species in the literature, and very likely more to come. Most of these species occur in the Indo-Pacific region. Besides providing scientific evidence of this tool-use behaviour, the list of tool-using fish will be powerful to determine the factors (cognitive, physical and ecological) that drive the evolution of tool use by comparing tool-using fish to their closely related non-tool-using species.

Biological responses to climate change will reduce yields in tropical fisheries

Taylor, Brett[1]; Roff, George[2]; DeMartini, Edward[3]; DiBattista, Joseph[4]; Hamilton, Richard[5]; Lindfield, Steven[6]; Marshell, Alyssa[7]; Meekan, Mark[8]; Newman, Stephen[9]; Pardee, Cassandra[10]; Pears, Rachel[11]; Priest, Mark[7]; Rhodes, Kevin[12]; Sinclair-Taylor, Tane[8]; Swords, John[6]; Wakefield, Corey[9]; Waldie, Peter[5]; Choat, J. Howard[13]

[1]*University of Guam Marine Laboratory, Mangilao, Guam*

[2]*CSIRO Oceans and Atmosphere, Brisbane, Australia*

[3]*University of Hawaii, Hawaii, USA*

[4]*Australia Museum, Sydney, Australia*

[5]*The Nature Conservancy, Brisbane, Australia*

[6]*Coral Reef Research Foundation, Palau*

[7]*University of Tasmania, Hobart, Australia*

[8]*Australian Institute of Marine Science, Australia*

[9]*Department of Primary Industries & Regional Development, Hillarys, Australia*

[10]*Poseidon Fisheries Research, Hawaii, USA*

[11]*Great Barrier Reef Marine Park Authority, Townsville, Australia*

[12]*Pacific Marine Science and Conservation, California, USA*

[13]*James Cook University, Townsville, Australia*

Climate change is among the greatest current threats to fisheries production, especially in the tropical regions of the globe. The nature of thermally-induced changes to the biology of harvested species is expected to decrease the potential fisheries yield across the tropics, yet our understanding of the magnitude of changes in growth and life span is limited. Here, using over 35,000 individual years of growth quantified across nine fish species, we integrate biogeographical and biochronological relationships among otolith size, fish body size, and ocean temperature to predict thermal responses of growth and life span across the Indo-Pacific region. We use this model to predict biological responses to climate change scenarios and examine the impact on fisheries yield across the Indo-Pacific. We find significant changes in growth rate, asymptotic body size, and life span from contemporary estimates to the end of the century, and the differences increase with the severity of climate change scenarios. These changes facilitate substantial reductions in fisheries yield, although patterns of change were unique across taxonomic groups. Equatorial areas were among the most heavily impacted, meaning that many countries with the greatest climate change threat have the highest dependency on coastal fisheries and the lowest capacity for agricultural production.

The genome of the spotted parrotfish provides evolutionary insight into the ecological adaptation of a keystone dietary specialist

Tea, Yi-Kai[1,2]; Zhou, Yulu[3], Ewart, Kyle M.[1], Cheng, Guo[3], Jaya, Frederick R.[4], Kawasaki, Kazuhiko[5], DiBattista, Joseph D.[2,6], Ho, Simon Y.W.[1], Lo, Nathan[1], and Fan, Shao Hua[3].

[1]*School of Life and Environmental Sciences, University of Sydney, Sydney, New South Wales, Australia*
[2]*Australian Museum Research Institute, Australian Museum, 1 William Street, Sydney, New South Wales 2010, Australia*
[3]*State Key Laboratory of Genetic Engineering, Lab for Evolutionary Synthesis, Human Phenome Institute, Zhangjiang Fudan International Innovation Center, School of Life Science, Fudan University, Shanghai, 200438, China*
[4]*Ecology and Evolution, Research School of Biology, Australian National University, Acton, Australian Capital Territory, Australia*
[5]*Department of Anthropology, Pennsylvania State University, University Park, PA 16802, USA*

[6]*School of Molecular and Life Sciences, Curtin University, Perth, Western Australia 6102, Australia*

Adaptive radiation as a result of ecological opportunity can have profound effects on the evolutionary outcome of species. On coral reefs, parrotfishes have been considered as one of the most dramatic examples of adaptive radiation unique in their extreme dietary specialisation. Using abrasion-resistant biomineralized teeth, parrotfishes are able to mechanically extract microphotoautotrophs such as filamentous cyanobacteria growing in and amongst reef carbonate material. Several reef inhabiting cyanobacterial taxa are thought to contain toxins that deter feeding in herbivorous fishes, including parrotfish species. The extent of secondary metabolite content in cyanobacteria is however unclear, as are its post-ingestive effects. Whether parrotfishes are able to detoxify secondary metabolites is similarly unclear. Nonetheless, this ability to exploit a previously untapped trophic resource is thought to have led to the early diversification of the parrotfishes. In order to better understand the key evolutionary innovations leading to the success of these dietary specialists, we sequenced and analysed the genome of the Spotted Parrotfish (*Cetoscarus ocellatus*). Our findings reveal significant expansion, selection, and duplication within several gene families responsible for detoxification, including the cytochrome p450 gene family and non-cyp450 carboxylesterases. We find preliminary evidence that the structural mechanism responsible for the extreme hardness and biomineralization of parrotfish teeth may be a result of poly-glutamine expansion in the enamel protein ameloblastin. We also detect expansion and selection for several genes related to pigmentation and sequential hermaphroditism. Together, these results highlight a potentially complex interplay of adaptive radiation and sexual selection operating on coral reef ecosystems.

Quantifying patterns versus processes in herbivorous fishes on Anthropocene coral reefs

Tebbett, Sterling[1]; Bellwood, David[1]; Bennett, Scott[2]

[1]*Research Hub for Coral Reef Ecosystem Functions, and College of Science and Engineering, James Cook University, Townsville, Queensland 4811, Australia*

[2]*Institute for Marine and Antarctic Studies, University of Tasmania, Hobart, Tasmania, Australia*

Globally, coral reef ecosystems have been transformed. In these altered reef ecosystems herbivorous fishes are expected to play an important role, with a vast body of research reflecting this perceived importance. Yet, while there has been substantial progress in this research field, major challenges still exist, especially when it comes to quantifying patterns versus processes. Indeed, in this talk we explore how the very definition of ‘herbivorous reef fishes’ (i.e., a fish in which the diet is predominantly based on plant material) precludes an easy translation between patterns of herbivore abundance and the process of herbivory. This is because, such a definition encompasses a diverse suite of fishes which all remove and target different primary producers to varying extents and, therefore, have markedly different impacts on reef functioning. Given this situation, we then examine how approaches to directly quantifying herbivory on reefs have progressed, and highlight lessons learnt from macroalgal assays. However, we will also highlight how a focus on macroalgae herbivory means that this research field has fallen out of alignment with the relative prevalence of macroalgae-based versus turf-based herbivory on reefs. Given the abundance of turfs (both algal and cyanobacterial) on reefs, and their relative importance in herbivore dynamics, widespread assessment of turf-based herbivory represents the key avenue for future research. Recognising the difficulty of translating patterns in herbivorous fish abundance to the process of herbivory, and an enhanced focus on turf-based herbivory, will be necessary to comprehensively understand the process of herbivory on Anthropocene coral reefs.

Novel molecular methods to investigate vision in coral reef fishes

Tettamanti, Valerio[1]; Cortesi, Fabio[1, 2]

[1]*Queensland Brain Institute, University of Queensland, Brisbane, Australia,*

[2]*School of the Environment, University of Queensland, Brisbane, Australia*

The visual system of fish plays a vital role in their daily life when undertaking tasks such as foraging, predator avoidance, and communication. Damselfish (Pomacentridae) vision has been studied extensively in the last decade, both at a molecular and behavioural level. Damselfishes have been found to have visual adaptations to the light environment, their feeding ecology and intra and interspecific signalling. However, the exact processes behind colour perception and the function of the different photoreceptors types are still poorly understood. To investigate the visual pathway in coral reef fish, we used a multidisciplinary approach that tackled the visual system of the false percula anemonefish (*Amphiprion ocellaris*) from a genetic to a behaviour standpoint. Here, I will present the first insights we gained from developing novel molecular methodologies, including genetic engineering and single-nuclei RNA sequencing (snRNAseq) in coral reef fish. The CRISPR/Cas9 technology was used to knock out the blue-green sensitive photoreceptor (*rh2b* expressing). Then we used a behavioural experiment to compare brightness vision in 'colour-blind' anemonefish with wild-type fish. We found that colour-blind fish had decreased ability to detect brightness differences in green but not for other colours within their visual space. snRNAseq analysis allowed us to identify the different retinal cell types in wild-type and knockout clownfish and create a reference for future research in marine fishes. This work showcases modern molecular techniques applied to non-model species while advancing our understanding of coral reef fish vision.

Assessing a novel ingredient as part of a sustainable diet to support growth in captive Yellowbelly flounder

Thomson, Caitlin[1]; Fletcher, Katrina[2]; Moran, Damian[2]; Muncaster, Simon[1]

[1]*School of Science, University of Waikato*

[2] *Seafood Technologies, Plant and Food Research*

Aquaculture is becoming an increasingly important food production sector to meet the demands of global population growth. It is even more relevant due to a decline in wild fisheries, as a result of overfishing. In order for the aquaculture industry to grow successfully, it needs to address sustainability issues such as the development of feeds based on wild sourced fishmeal (FM). Many carnivorous marine fish require protein-rich diets with essential amino acids that are often lacking in terrestrial crop proteins such as soy, pea and corn. Consequently, there is great interest in sourcing alternative feed ingredients. One of the key challenges here is that the amount of FM that can be replaced by alternative ingredients is species dependent.

Pātiki, or yellowbelly flounder (*Rhombosolea leporina*), are an endemic tāonga flatfish which is currently in decline around NZ. It is also a high value species that naturally feed at a lower trophic level, eating small crustaceans and worms. This suggests that they may adapt well to non-fishmeal-based feeds such as insect meals. This study compares the effect of dietary replacement of FM with sustainably produced black soldier fly (BSF) meal in juvenile pātiki. This will be achieved by measuring specific growth rate and gut morphology of fish fed one of three diets in which the main protein source is based on FM, BSF or a wild-type diet. Developing new aquaculture species that can be fed on sustainably sourced diets will enhance the profile and marketability of the NZ aquaculture industry.

Spatiophylogenetic modelling of freshwater fish invasion potential

Tims, Amy[1]; McGee, Matthew[1]

[1]School of Biological Sciences, Monash University, Melbourne, Victoria, Australia 3800

Invasive species pose a significant threat to global ecosystems, contributing to native biodiversity loss, habitat degradation and ecosystem disruption. However, the specific risk posed by an invasive species can vary depending on the characteristics of the invader, the ecosystem they invade, and the interactions with native species and environmental conditions. It can therefore be hard to predict which species may pose the highest invasion risk to any given ecoregion. Here, we develop spatiophylogenetic models to model the invasion risk posed by different species using a global dataset of freshwater fish invasion records. We apply climate filters to identify species that may be an invasion risk to Australia based on successful invasions of other places with similar climate parameters. We find that invasion risks vary significantly with phylogeny, and are correlated more strongly with sport fish than with aquarium fish. However, some clades of aquarium fish do pose significant invasion risks. Our results will help to identify species that are likely to cause significant disruption to Australian ecoregions should they become established, and to develop blacklists to prevent such species from being imported.

Introducing the Pacific Islands Region Acoustic Telemetry (PIRAT) Network

TinHan, Thomas[1,2]; Hutchinson, Melanie[2]; Scott, Molly[2], Iwamoto, Melissa[1]

[1]*Pacific Island Ocean Observing System (PacIOOS) – University of Hawai'i*

[2] *Hawai'i Institute of Marine Biology (HIMB)*

Electronic tagging is a powerful tool for the study of fish behavior, particularly as it relates to movement. In recent years, acoustic telemetry has become more widespread and user-friendly, and technological improvements (e.g. improved battery life of tags) have expanded the temporal and spatial scale of this technique. Furthermore, equipment compatibility among studies provides an opportunity to address questions beyond the scale and scope of individual studies. Since 2010, nearly 200 telemetry studies have been conducted across the eastern and western Central Pacific. With the exception of a small number of telemetry networks in the southwest (IMOS) and eastern Pacific (MIGRAMAR), formalized means of data sharing are scarce, despite the potential for connectivity among Pacific insular systems. In May of 2022, the Pacific Islands Region Acoustic Telemetry (PIRAT) Network was established with the intent of providing a system of organizing and archiving acoustic telemetry data, as well as a framework for the fair exchange of those data that fosters collaboration among telemetry studies in the Pacific Ocean. Here we present the PIRAT Network, outlining the advantages of collaborative telemetry networks for long-term monitoring, and giving an overview of the varied telemetry projects it currently supports.

Towards adaptive management for the reintroduction of a wetland specialist fish

Todd, Charles[1]; Wootton, Henry[1]; Koehn, John[1,2]; Rose, Peter[3]; Honybun, Will[3].

[1]*Applied Aquatic Ecology, Arthur Rylah Institute for Environmental Research, Department of Energy, Environment and Climate Action, P.O. Box 137 Heidelberg, VIC 3084, Australia*

[2]*Institution Gulbali Institute for Agriculture, Water and Environment, Charles Sturt University, P.O. Box 789, Albury, NSW, 2640, Australia*

[3]*North Central Catchment Management Authority, PO Box 18, Huntly Vic 3551, Australia*

With limited funding for natural resource management, population modelling is being used to provide the decision-making support and justification of the allocation of resources assigned to conservation actions. To achieve this population modelling must be undertaken in a cycle of setting management actions; monitoring responses; reassessing assumptions; updating the model; and then set new management actions/goals if warranted. Most researchers would recognize this cycle as a form of adaptive management, frequently cited and rarely achieved.

Southern pygmy perch, a small wetland species, were once found in the system of wetlands of Gunbower Island, on the Murray River in SE Australia. With the aim of reintroducing the species to this system of wetlands, management wanted to use a population model to help to prioritise the options and assess the likelihood of success. A metapopulation model of southern pygmy perch was developed using the latest available ecological information for the species, together with management objectives and options to identify optimal reintroduction strategies. The model was developed as part of an adaptive management cycle where monitoring of populations after reintroduction will provide important information for updating our knowledge and understanding of the species as well as updating the model to refine ongoing management of the wetland specialist. We outline the metapopulation model, reintroduction strategies, and the monitoring required to assist the reintroduction efforts of southern pygmy perch in the wetlands of Gunbower Island over the next decade and where this fits within an adaptive management cycle.

Multiple gene phylogeny challenges the current classification of the Indo-West Pacific sinistral flounders (Pleuronectiformes: Bothidae)

Tongboonkua, Pakorn[1]; Chen, Wei-Jen[1]

[1]*Institute of Oceanography, National Taiwan University, Taipei, Taiwan*

The sinistral flounders of the pleuronectiform family Bothidae include 172 recognized species in 20 genera. They are widely distributed in tropical and temperate seas, with the highest species diversity found in the Indo-West Pacific (IWP) (114 species). Although the previous molecular and morphological studies have supported the monophyly of the family, the intra-familiar relationships remain largely unexplored. As a result, the monophyly of the 20 existing genera has never been tested throughout. With a comprehensive sampling, primarily through the recent collaboration between Taiwan and France under the *Tropical Deep-Sea Benthos* (TDSB) program surveying IWP benthic fauna, this study aims to resolve the taxonomic issue at the generic level and further infer the evolutionary relationships of the IWP bothid species using a multiple gene approach. The dataset for phylogenetic inference was compiled from the DNA sequences obtained from two mitochondrial and three nuclear genes from 87 taxa (68 morphospecies in 16 genera). Our results revealed that *Grammatobothus* was the sister group of the rest of the bothids and four of the genera were found non-monophyletic: *Arnoglossus* (4 clades), *Laeops* (2 clades), *Parabothus* (4 clades), and *Psettina* (2 clades). Accordingly, a combination of evidence (phylogeny, morphology, biogeography, etc.) was utilized to solve this taxonomic issue, especially in the “wastebasket taxon” - *Arnoglossus*. Here, we confine the genus solely to clade D (Atlantic-Mediterranean *Arnoglossus* [AM *Arnoglossus*]) and propose new genera for the IWP *Arnoglossus* (Clade A to C). Lastly, detailed taxonomic works are in progress for revising the other polyphyletic genera.

Using eDNA to assess how estuarine fish communities respond to consecutive extreme events of drought, bushfire, and flood.

Tout-Lyon, Jessica[1,2]; Ajani, Penelope[3]; Baumgartner, Lee[2]; Duncan, Meaghan[4]; Furlan, Elise[2]; Humphries, Paul[2,5]; Jeffries, Peta[2,6]; Knott, Nathan[4]; Leck, Jessica[1,2], Lungu, Ryan[7]; McCasker, N[2]; Morris, Stephen[4]; Murray, Shauna[3]; Price, Amina[2,5]; Rees, Matt[4]; Roe, Sebatian[1] and Stat, Michael[8]

[1] *School of Agricultural, Environmental and Veterinary Sciences, Charles Sturt University, Birpai Country, Port Macquarie, NSW, Australia*

[2] *Gulbali Institute, Wiradjuri Country, Albury, NSW, Australia*

[3] *School of Life Sciences, University of Technology Sydney, Gadigal Country, Sydney, NSW, Australia*

[4] *NSW DPI Fisheries, Department of Regional NSW, Australia*

[5] *School of Agricultural, Environmental and Veterinary Sciences, Charles Sturt University, Wiradjuri Country, Albury, NSW, Australia*

[6] *School of Indigenous Australian Studies, Charles Sturt University, Wiradjuri Country, Dubbo, NSW, Australia*

[7] *OzFish, Yuin Country, NSW, Australia*

[8] *School of Environmental and Life Sciences, Awabakal Country, Newcastle, NSW, Australia.*

In the face of climate change, it is vital to gather baseline data to improve our limited understanding of the diversity and distribution of fish community composition in estuaries and how native Australian fishes respond to extreme weather events such as drought, fire, and flood. This project combines the expertise of an interdisciplinary research team, recreational and First Nations fishers to conduct a pilot study of the largest fish survey in NSW estuaries using environmental DNA (eDNA). Historical eDNA samples were collected weekly by NSW Oyster Farmers over a 24-month period. This project will assess how the diversity and distribution of fish assemblages in three estuaries in NSW were impacted by consecutive extreme weather events of 2018-2020, including the hottest and driest drought on record, the black summer megafires and the first flood pulse of 2020. It will allow us to explore the impact of climate change, where warmer sea surface temperatures extend further south, resulting in the tropicalisation and latitudinal range-shifts of fishes. Furthermore, recreational and First Nation fishers will conduct present-day follow-up eDNA sampling of fish communities in the three estuaries, and to reflect on observations during these consecutive extreme weather events. This will highlight the importance of involving citizen scientists in collecting samples, integrating their diverse knowledges to create a wholistic understanding, and to inform the expansion and design of long-term biomonitoring programs in estuaries. Findings will shape on ground conservation and management practises for estuarine fish communities in preparation for future extreme weather events.

Larval competency and seascape context determines the influence offshore structure have on marine metapopulation dynamics

Treml, Eric[1,2,3]; Galaiduk, R[1,2]; McLean, D[1]; Pastor, A[3]; Sobol, J[3]

[1]Australian Institute of Marine Science

[2]University of Western Australia, Oceans Institute

[3]Deakin University

Offshore energy infrastructure is becoming increasingly abundant in our coastal oceans globally, yet our understanding of their ecological impact is poorly understood. Some evidence exists that offshore infrastructure may facilitate population connectivity for a variety of marine taxa, including non-native species. Yet, the degree to which these structures influence metapopulation dynamics remains largely unclear and likely varies within and between regions. Here, we present a synthesis of several studies aimed at understanding the role offshore energy infrastructure has on multi-species population connectivity and marine metapopulation dynamics. Across this work, we have used biophysical modelling, network analysis and metapopulation theory to quantify the ecological impact of offshore structures and determine the influence of life histories, seascape context and oceanography on these dynamics. We demonstrate how this approach can efficiently identify the individual structures and habitat patches that have the most significant impact on connectivity and metapopulation dynamics.

Collectively, our results suggest that for many species, offshore structures have the potential to contribute significantly to population dynamics, yet this influence is not distributed equally across the seascape. In addition, structures can often facilitate stepping-stone movement between natural habitat, but this is highly dependent on life histories. Finally, we show evidence that in some contexts, artificial structures may be acting as ecological traps – effectively stealing larvae from higher quality natural habitat patches. Quantifying the influence of ocean infrastructure through this metapopulation lens offers unique insights for the decommissioning debates, as well as for informing the future placement and prioritisation of renewable energy infrastructure.

Macroevolutionary patterns of diversity imbalance and persistence of depauperate lineages across fishes

Isaac Trindade-Santos[1], Michael Alfaro[2], Jonathan Chang[2], Lauren Sallan[1]

[1]Macroevolution Unit, Okinawa Institute of Science and Technology Graduate University, Okinawa, Japan

[2]Department of Ecology and Evolutionary Biology, University of California, Los Angeles, CA, USA

The diversification of fishes is primarily studied in terms of speciose, and often nested, radiations, such as teleosts, acanthomorphs, and wrasses. Highly diversified clades are considered the predictable result of new opportunities, inherent evolvability and key innovations. All things being equal, there is expectation that lineage diversification will also be equal. However, fishes also contain lineages which seem to have persisted at low diversity with little phenotypic change, such as monotypic families or “living fossils”. These depauperate lineages are usually considered to be exceptions, as extinction risk does not decrease with age. However, it is unclear how widespread such lineages are across fish phylogeny, and whether their frequency is as expected by chance or from current models. Here, we combine megaphylogenies and trait databases to calculate the true incidence of unexpected persistence at low diversity, as measured by imbalance between sister taxa across ray-finned fishes (31,516 species; 320 million years) and sharks (610 sp.; 208 Ma) relative to simulated trees. Our results show that while recent (0-15 Ma) clades are as balanced as expected from chance and in models, there is significantly higher diversity imbalance in lineages over 15 million years old. Over 42% of all sister clades older than 20 million years in the actinopterygian tree have species ratios worse than 10-1 despite shared ancestral states. Similar patterns are also found across other vertebrates megaphylogenies. We suggest that while lineages undergo equal diversification early on, persistence and radiation emerge as alternative pathways on macroevolutionary scales.

Three-dimensional morphometric data reveals patterns of integration and disparity in fossil and extant tetraodontiform fishes

Troyer, Emily[1]; Evans, Kory[2]; Goatley, Christopher[3]; Arcila, Dahiana[4]

[1]*University of Oklahoma, Norman, OK, USA*

[2]*Rice University, Houston, TX, USA*

[3]*University of Southampton, Southampton, Hampshire, UK*

[4]*Scripps Institute of Oceanography, San Diego, CA, USA*

Phenotypic integration, which describes the intricate interplay of traits during the course of morphological evolution, has been hypothesized as the driving force behind the emergence of strikingly extraordinary morphologies, such as the dorsal-ventrally compressed skulls of flatfishes or the elongated snouts of gymnotiform fishes. Among vertebrates, tetraodontiform fishes exhibit a wide array of extreme shapes and sizes, ranging from squared-shaped boxfishes to spheroidal pufferfishes. Moreover, one of the most speciose families, Tetraodontidae has evolved a remarkable adaptation, a parrot-like beak formed by fused teeth, which is thought to facilitate the predation of hard-shelled prey. Here, we use three-dimensional geometric morphometric data for 176 fossil and extant tetraodontiform species to uncover patterns of cranial integration and morphological disparity. We find that beaked species have undergone a remarkable expansion into novel trait space with PC1 (representing ~50% of the variation) being largely explained by the presence or absence of a beak. Furthermore, our study reveals that beaked species exhibit higher levels of cranial integration and greater morphological disparity compared to their non-beaked counterparts. This suggests that the evolution of a beak may be a pivotal innovation that has enabled Tetraodontiformes to occupy novel adaptive zones and expand into new ecological and dietary niches.

Using deep learning to automate the detection of seabird bycatch and bird scaring lines on fishing vessels

Tuck, Geoff[1]; Acharya, Debaditya[2]; Devine, Carlie[1]; Little, L. Richard[1]; Saqib, Muhammad[3]; Untiedt, Candice[1]; Wang, Dadong[3]

[1] *CSIRO Environment, Hobart Tasmania, Australia*

[2] *RMIT University, Melbourne Victoria, Australia*

[3] *CSIRO Data 61, Marsfield NSW, Australia*

Fatal interactions with fishing vessels can occur when seabirds dive on the baited hooks of longlines, become entangled in gillnets, or strike the warp cables of trawl vessels. Albatrosses and petrels are most imperilled, with significant declines in populations worldwide being directly attributed to high levels of bycatch in industrial fisheries. To understand and mitigate these interactions, it is important to quantify the numbers of interactions, by species if possible, and ensure mandated mitigation devices are deployed. Human observers on board vessels have been the primary source of independent at-sea fisheries data, but the need to increase coverage, coupled with the increasing cost and risk of using observers, has catalysed the global use of Electronic Monitoring (EM) cameras. Bird-scaring lines (BSLs) are an essential on-vessel bycatch mitigation device to reduce seabird incidental mortality. Confirmation of seabirds caught and the deployments of BSLs, also known as tori lines, can be facilitated by EM cameras installed on fishing vessels to monitor commercial fishing activities. We conducted a comprehensive analysis using an Artificial Intelligence and Machine Learning framework for detecting bycatch and BSLs under varying weather and light conditions. The results demonstrate the accuracy and efficiency of the proposed approach, making it a valuable AIML tool that can be used to reduce the time and costs of human EM footage review, increase coverage, and automatically flag events for compliance checking and endangered species monitoring.

Elusive and Vulnerable: Evaluating the distribution of the Reef Manta (*Mobula alfredi*) around Oahu using Environmental DNA

Tuthill-Christensen, Grace[1]; Crow, Karen[1]

[1]San Francisco State University, California, United States

There are three well characterized, stable aggregations of manta rays off Kauai, Maui, and the big island of Hawai'i. However, it is unknown whether any stable populations occur around Oahu. This study uses Environmental DNA (eDNA) sampling and quantitative PCR (qPCR) to address the challenging yet compelling question of Mobulid habitat usage in a locale that is highly disturbed by human populations, particularly given that the reef manta is listed as vulnerable to extinction (IUCN red list). eDNA is genetic material that is sloughed off living organisms that is detectable using this molecular technique, in the absence of direct observation. This is particularly effective for studying cartilaginous fishes because they do not breath at the surface, therefore visual surveys are challenging and can be biased. Plankton tows are used to filter and collect eDNA, and is synergistic for this study because the same collection method used to collect cellular debris for detection via eDNA is used to characterize the reef manta prey abundance/assemblage. We found variation in spatial and temporal patterns of reef manta distribution around Oahu. Plankton tows represent a novel application of eDNA because conventional sampling schemes filter small volumes (1L seawater) compared to DNA extraction from plankton tows that filter much larger volumes (4,000L seawater), greatly increasing the detectability of reef manta DNA in the environment.

A century of shark fisheries and trade in India

Tyabji, Zoya[1]; Jabado, Rima W.[2,3]; Martins, Ana P.B.[1,3]; Mull, Christopher[1]; MacNeil, M. Aaron[1,4]

[1]*Department of Biology, Dalhousie University, Halifax, Nova Scotia, Canada*

[2]*Elasmo Project, P.O. Box 29588, Dubai, United Arab Emirates*

[3]*James Cook University, Australia*

[4]*Ocean Frontier Institute, Dalhousie University, Halifax, Nova Scotia, Canada*

India is a key global player in shark, ray, and chimaera (hereafter ‘shark’) fisheries and is considered one of the top shark harvesting nations. Fishing and trade of shark resources contribute to food security, and generate employment and revenue to a diverse range of stakeholders. However, understanding the trade of sharks is challenging given the uncertainty surrounding fisheries reporting and traceability. This is particularly difficult due to the complex nature of trade routes, diversity of products, widespread markets, as well as costs and benefits of being involved in the fishery. The increase in the demand for shark products, coupled with the lack of data, is concerning since these species are highly threatened globally due to overexploitation, with India highlighted as a priority region for their conservation. Although studies on sharks in India date back to the 18th century, there has been no consolidated, nation-wide assessment of the fisheries they interact with, their impact on shark populations, and the livelihoods of stakeholders involved. By reviewing the literature, we characterise shark fisheries across India, the stakeholders involved, value chain, and utilisation of shark products. Although sharks are mostly caught as bycatch, targeted fisheries for pelagic and deep-sea species exist across India’s maritime states, and their fishing pressure is exacerbated by the growing demand for their products. Both, utilisation and trade destined for national and international markets vary considerably across sites and states, demonstrating that a suite of management actions are required to curb overfishing and ensure the sustainability of shark fisheries.

Linking environmental knowledge and values on conservation actions

Vaishampayan, Alexander[1]; Lyon, Jarod[2]; Morrongiello, John[1]; van Eeden, Lily[2]; West, Matt[1]

[1]University of Melbourne

[2]Arthur Rylah Institute

Freshwater ecosystems are threatened by a range of factors such as rising temperatures, pollution and development. To counter these impacts, management agencies undertake proactive and remedial actions such as designating protected areas, riparian restoration and monitoring stream flow rates. Recreational fishers are a key stakeholder group in the management of freshwater areas and understanding the views of the angler community is essential to developing and implementing effective management actions that result in sustainable and well-supported ecological outcomes.

Value Orientations are one way to examine a person's ideals about how humans should view and interact with the environment. Examining an individual's values and their amount of environmental knowledge with level of support for different conservation actions could help managers improve community support and engagement for necessary conservation work.

This project has two goals: 1) develop a quantitative understanding of the values of freshwater recreational fishers in Victoria and their willingness to support different conservation and management activities and 2) examine if there are opportunities to better engage with anglers to continue supporting the care of freshwater ecosystems with projects they are likely to support. Over 300 Victorian anglers participated in an online survey in 2023. Initial results include no relationship between general education level and riparian environmental knowledge and varying levels of support for different management actions based on participants value orientation. Anglers may be more willing to support stronger conservation action even if the action does not result in increased catch.

Insight into the diet of early stages of mesopelagic fishes in the Indian Ocean using DNA metabarcoding

van der Reis, Aimee[1]; Beckley, Lynnath[2]; Jeffs, Andrew[1]; O'Rorke, Richard[1]; Olivar, Pilar[3]

[1] *School of Biological Sciences, University of Auckland, New Zealand*

[2] *Environmental and Conservation Sciences, Murdoch University, Australia*

[3]*Institut de Ciències del Mar, CSIC, Passeig Marítim de la Barceloneta, Barcelona, Spain*

Despite playing a critical role in oligotrophic ocean food webs, relatively little is known about the diet of mesopelagic fishes in the Indian Ocean. These fishes are an abundant component of the micronekton assemblages and are themselves a major energy- and nutrient-rich food source, linking the plankton which they feed on to higher marine predators. DNA metabarcoding, a molecular method to identify species from mixed assemblages, has not been commonly used in studies of mesopelagic fish diet. This method can greatly improve the understanding of mesopelagic fish feeding ecology. We leveraged DNA metabarcoding (18S rRNA V4 and COI gene regions) to identify the gut contents from Indian Ocean Stomiiformes and Myctophiformes species. In total 174 fish specimens from 13 genera were used. Differences in the gut content among fish families, geographic areas and fish stages were identified. Specimens within the family Myctophidae had the most diverse diet, and Gonostomatidae had the least diverse diet. The most frequently identified prey items were calanoid copepods and halocyprid ostracods. Halocyprids were also identified to be significantly different among Myctophidae larvae and juveniles; which is a potential ontogenic shift in diet towards a higher ostracod contribution in the diet in juvenile stages. In comparison with other zooplankton abundance data, Copepoda were the most abundant plankton throughout the latitudinal gradient allowing them to be a potential food resource through the region, while other zooplankton components like Ostracoda and Malacostraca, despite being less abundant prove to be preferentially targeted by some mesopelagic fish families.

Methodological concerns with the use of DNA metabarcoding to investigate parrotfish diets

van der Reis, Aimee L.[1]; Clements, Kendall D.[1]

[1]*School of Biological Sciences, University of Auckland, New Zealand*

Recent advances in DNA sequencing have resulted in an unprecedented decrease in DNA sequencing costs, thus enabling the relatively fast uptake and utilization of new sequencing technologies. The advent of next-generation sequencing technologies has provided an effective and efficient means of improving taxonomic resolution in community ecology studies and predator-prey interactions in dietary studies. However, biases are present in these molecular methods which, if not taken into consideration and/or mitigated, can skew results and lead to erroneous conclusions. Here we will discuss important methodological aspects to consider in dietary DNA metabarcoding studies with a focus on parrotfish diets. Parrotfish are central to bioerosion and sediment dynamics in coral reef ecosystems, but the exact predator-prey dynamics between these herbivorous fish and their dietary targets remain unresolved. Using pharyngeal content from *Scarus rivulatus* as an exemplar, this preliminary research focuses on the use of 16S V3-V4 and 18S V4 rRNA sequences to assess diet. Specifically, this work highlighted 1) the value of *in silico* and *in vitro* investigation of 18S primers prior to sequencing, 2) the subsequent impacts that different primers can have on determining the relative importance of different elements in the diet, 3) the need to use up-to-date DNA reference databases, and 4) the constraints of different databases for taxonomic assignment of food items. Our results indicate that DNA metabarcoding provided better taxonomic resolution than traditional methods, but understanding the relative contributions of different dietary targets of grazing fishes such as *S. rivulatus* is complex and will require multiple methods.

Utilising natural tags to identify seafood provenance

Van Eck, Rhiannon[1]; Gillanders, Bronwyn[1], Reis-Santos, Patrick[1]

[1]*School of Biological Sciences, The University of Adelaide, SA, 5005, Australia.*

Fraud in the seafood industry is often a hidden issue but it affects the seafood industry globally. Complex supply chains allow ample opportunity for seafood to be mislabelled through intentional or unintentional practices, concealing the true provenance of seafood products. Seafood provenance fraud occurs when the geographical origin of seafood is incorrectly disclosed, allowing for instance, products from illegal or unsustainable fisheries to enter the market, which can cause cascading effects across the industry to consumers and the marine environment. Whilst many natural tags have been used to track movement and origin, there is still a lack of translation and application to combatting seafood provenance fraud. We investigated the capacity to use chemical and isotopic fingerprints in the hard calcified tissues of otoliths and shells for three key commercial species (southern garfish, pacific oysters and greenlip abalone) to determine the collection and production origin in Southern Australia. The combination of both elemental and isotope markers allowed overall classification accuracies of up to 88% across sites in South Australia, Victoria and New South Wales. Markers worked well at a local scale, and showed an enhanced signal at regional and interstate scales (with classification accuracies of up to 100%). Overall, these tools show promise to support the seafood industry and the certification of local produce, as well as underpin management, regulation and compliance to support sustainable seafood.

Investigating methods to mitigate shark depredation in line-based fisheries in Queensland, Australia

Vardon, Jaeden[1]; Williams, Samuel[2]; Morgan, Jessica[3] ; Dudgeon, Christine[4]; Holmes, Bonnie[5]; Barnett, Adam[6].

[1]*University of the Sunshine Coast*

[2]*Queensland Department of Agriculture and Fisheries*

[3]*Queensland Department of Agriculture and Fisheries*

[4]*University of the Sunshine Coast*

[5]*University of the Sunshine Coast*

[6]*Biopixel Oceans Foundation*

Depredation around the world is a growing issue, with fishers reporting frequently losing their fish catches to depredation. While several different species have been found to be causing depredation, sharks are frequently reported by fishers to be responsible for the greatest loss of catch in Queensland, Australia. Although shark repellents are available, research has found varying levels of success in existing shark deterrents on their ability to reduce shark interactions. There is a need for further applied research in real world settings of the use of existing shark deterrents (that have been identified as most effective) in standard fishery operations and their ability to reduce shark depredation. My research contributed to the emerging evidence base by testing a range of repellents available on the market to assess their effectiveness onboard an operating charter fishing vessel to gauge the feasibility of industry uptake of shark repellents. I will share my research findings which identified that using some shark repellents did result in successfully landing more fish however were not successful at stopping depredation altogether. Also I discovered through my research that there were several physical and social limitations impacting the ability of shark repellents to be used effectively in a commercial setting. In order for shark repellents to be adopted by the fishing industry it will be necessary for the identified limitations to be overcome. It is clear that shark depredation cannot be mitigated by repellents alone and requires a multistrategic effort which includes repellents along with other proven and emerging methods.

Life history traits of the honeycomb leatherjacket *Cantherhines pardalis* and the broom leatherjacket *Amanses scopas* (Monacanthidae) from Solomon Islands

Visconti, Valerio[1]; Woodgate, Ian[1]; Laman-Trip, Elizabeth[2] ; Sabetian, Armagan[3]; Clements, Kendall D.[4]

[1] *Centre for Environment, Fisheries and Aquaculture Science (Cefas), Lowestoft, United Kingdom*

[2] *HalieuMer, Arzon, France*

[3] *School of Science, Auckland University of Technology, Auckland, New Zealand*

[4] *School of Biological Sciences, University of Auckland, Auckland, New Zealand*

Species of the family Monacanthidae are found in both temperate and tropical waters, and support growing fisheries in both the Indo-Pacific and Atlantic Oceans. In general, monacanthids are characterised by a relatively short lifespan and indeterminate growth patterns, but the life history parameters of most species are poorly understood. Additional interest in studying monacanthid life history traits arises from two aspects of their biology: a) they represent a major geographically constrained diversification in southern Australia, with over 20 species occurring in temperate reef and seagrass habitats, while over 32 genera occur in Australian waters as a whole, and b) monacanthids feed selectively on benthic reef biota, and some species have profound effects on this assemblage by removing significant biomass of sponges, ascidians and bryozoans from reef surfaces. Here we present the life history traits of two common Indo-Pacific monacanthids, the honeycomb leatherjacket *Cantherhines pardalis* and the broom leatherjacket *Amanses scopas*. Age-based information was derived from sagittal otolith analysis of 259 individuals collected between January 2016 and February 2017 in the Western Province of the Solomon Islands. Both species showed rapid growth in the first-year of life, attaining a maximum age of 9 and 12 years for *C. pardalis* and *A. scopas*, respectively. Growth curves (VBGF) revealed significant differences between the species with *C. pardalis* growing faster but reaching smaller asymptotic length than *A. scopas*. A noticeable growth difference was found between sexes in *C. pardalis*. The histological analysis of ovaries revealed no signs of hermaphrodism in either species.

Blue Belt Programme – Preliminary results on age-based life-history traits of three targeted species from the Pitcairn Islands.

Visconti, Valerio[1]; Archer-Rand, Simeon[1]; Woodgate, Ian[1]; Christian, Torika[2]; Evans, Melva[2]; Christian, Michele[2]

[1] *Centre for Environment, Fisheries and Aquaculture Science (Cefas), Lowestoft (UK)*

[2] *Environmental, Conservation & Natural Resources Division, Government of Pitcairn, Adamstown, Pitcairn Island.*

The Blue Belt Programme (BBP) is the UK Government’s flagship international marine conservation initiative supporting in a collaborative manner several UK Overseas Territories (UKOTs) in creating and maintaining healthy and productive ecosystems. Pitcairn Islands are the only islands located in the Pacific Ocean being considered some of the most remote of all the UKOTs, part of the BBP. The fishing activity at the Pitcairn Islands represents the typical small-scale fishery of small sub-tropical islands; reduced numbers of local fishermen, small boats, handline and spearfishing gears, and it generates a considerable source of food for local consumption with low monetary income for Pitcairn islanders. With the legal designation of the Pitcairn Islands Marine Reserve in 2016, fisheries activities are regulated by a fishery management plan aiming to preserve the inshore and coastal marine resources sustainably. However, little is known about the three main species targeted by the local community, the blacktip grouper (*Epinephelus fasciatus*), yellow edge-lyretail (*Variola louti*) and a drummer (*Kyphosus spp.*), therefore a biological sampling plan has been recently developed and put in place. Over a 16 days survey across the Pitcairn archipelago (February 2023), a biological sampling training and monitoring plan was delivered to two local volunteers. This work included the collection of morphometric measurements, otoliths and gonad tissue extraction and preservation. Here we present the preliminary results of the age-based life-history traits highlighting the distinctive characteristics of local populations. The collected data will inform the local fishery management, conservation plans and dedicated training activities across the MPA.

Current status of the type specimens of extant fishes registered in The University Museum, The University of Tokyo

Hidetoshi, Wada[1]; Masahiro, Aizawa[1.], Kazuo Sakamoto[1, 2.], Keita Koeda[1, 3.], Harutaka Hata[1, 4.], Rei Ueshima[5.], Mari Kuroki[6.]

[1]*The University Museum, The University of Tokyo*

[2]*Fish Information Center and Museum*

[3]*Faculty of Science, University of the Ryukyus*

[4]*National Museum of Natural History, Smithsonian Institution*

[5]*Department of Biological Sciences, Graduate School of Science, The University of Tokyo*

[6]*Graduate School of Agricultural and Life Sciences, The University of Tokyo*

The University Museum, The University of Tokyo holds two different collections of specimens of extant fish species, the Department of Zoology (ZUMT) and the Department of Fisheries (FUMT), belonging to the faculties of Science and Agriculture, respectively. ZUMT is one of the oldest fish collections in Japan, comprising specimens collected mainly by the late Shigeho Tanaka since 1904. Currently, 933 and 83 type specimen lots are recorded in ZUMT and FUMT, respectively, most having been used in the original descriptions of species from Japanese waters. The results of investigations mainly by the second and third authors, together with the late Yoshiaki Tominaga, since 1984, as well as recent exhaustive work by the first, fourth, and fifth authors, has clarified the current taxonomic status and whereabouts of these specimens, with detailed information on some of them now being available in catalogues published by the museum, and a public database on the museum's website. This investigation has also revealed detailed information on specimens whose registration numbers had previously been considered unknown, such as the holotype of *Synaphobranchus taketae* Tanaka, 1916 (Synaphobranchidae) and syntypes of *Chlorophthalmus acutifrons* Hiyama, 1940 (Chlorophthalmidae). On the other hand, several type specimens were missing from the collections, with no loan records. This presentation will present as much information as possible for such specimens and make a broad appeal for information helpful for their rediscovery.

Phylogeography of the sabretooth blenny genus *Plagiotremus* with special consideration of Hawaiian endemics

Walsh, Cameron A.J.[1]; Hoban, Mykle L.[1]; Kosaki, Randall K.[2]; Bowen, Brian W.[1]

[1]*Hawai‘i Institute of Marine Biology, Hawai‘i*

[2]*Papahānaumokuākea Marine National Monument, Hawai‘i*

The genus *Plagiotremus* contains at least ten species distributed across both the Indian and Pacific Oceans, many of which may have evolved to mimic cleaner fishes or those that produce toxic venom. The evolutionary history of *Plagiotremus* is not well resolved, as molecular phylogenies have typically included only a few species. To shed light on the evolution of *Plagiotremus* species, we combined mitochondrial DNA sequence data from hundreds of new samples with sequences from a public database to create a molecular phylogeny and carry out population genetic analyses. With data from nine putative *Plagiotremus* species, we present the most comprehensive molecular phylogeny of *Plagiotremus* to date. We use this molecular phylogeny in conjunction with the morphology-based taxonomy of the genus to reconsider hypothesized relationships between species. We also found that *Plagiotremus tapeinosoma* (a widespread Indo-Pacific species) and its putative sister species *Plagiotremus goslinei* (endemic to Hawai‘i), shared multiple haplotypes, indicating that *P. goslinei* may not warrant species-level status. On the other hand, *P. tapeinosoma* from the Marquesas Islands was more diverged than *P. goslinei* and all other *P. tapeinosoma* across the Indo-Pacific, indicating that the Marquesan group may warrant further investigation. A reassessment of the taxonomic status of Hawaiian and Marquesan specimens should be considered. Further genetic studies of *Plagiotremus* species could resolve their interrelationships and geographic origins, as well as the evolutionary history of the genus as a whole.

3.2A Themed Session C: Fisheries and Aquaculture in the Indo-Pacific, 260-073, November 22, 2023, 10:30 AM - 12:30 PM

El Niño–Southern Oscillation causes shifts in the vertical distribution of Pacific pelagic fishes

Wang, Juan[1]; Swearer, Stephen[1]; Macdonald, Jed[2]; Morrongiello, John[1]

[1]*School of BioSciences, The University of Melbourne, Australia*

[2]*The Pacific Community, Nouméa, New Caledonia*

El Niño–Southern Oscillation (ENSO) is a major climatic phenomenon in the Pacific Ocean and has been suggested to be a major driver of the longitudinal distribution of pelagic fishes. Despite this, we currently lack a detailed understanding of how ENSO affects species' vertical distribution, and whether commercial fishers adequately adapt their fishing effort in accordance with any distributional shifts. Understanding how ENSO affects the depth at which pelagic fish forage is fundamentally important as these fishes play a vital role in the economic and food security of Pacific island countries and territories. We sourced longline fishing records in New Caledonia over 25 years and reconstructed the depth and catch history of more than 3.6 million individual hooks. Our study focussed on two diving species, albacore tuna and yellowfin tuna, and one surface-associated species, dolphinfish, and explored how their catch per unit effort varied with depth and ENSO. We then compared each species' actual catch to its expected catch to see whether fishers were dynamically adjusting hook depth to track ENSO-related fish redistributions. We found that albacore and yellowfin tuna shallowed their distribution under El Niño and deepened their distribution under La Niña. Despite the vertical distribution of pelagic fishes shifting with ENSO, evidence suggests that commercial fishers do not adapt their practices to optimise catches. Our results are important because they indicate that large scale climate phenomena affect fish but that human systems are slow to respond, which in turn poses challenges to regional food and economic security.

4.4B Themed Session I Novel Methods and Techniques Advancing our Understanding of Fish Biology, 260-092, November 23, 2023, 1:30 PM - 3:00 PM

Interspecific and intraspecific difference in egg size of two mackerel species *Scomber* spp. in the western North Pacific

Mikio Watai[1], Tohya Yasuda[1], Junji Kinoshita[1], Mitsuo Nyuji[2], Satoshi Nagai[2], Akinori Takasuka[3], Michio Yoneda[2]

[1]Fisheries Resources Institute, Japan Fisheries Research and Education Agency, Japan.
[2]Fisheries Technology Institute, Japan Fisheries Research and Education Agency, Japan.
[3]Graduate School of Agricultural and Life Sciences, The University of Tokyo, Japan.

Spawning of two fisheries important species of mackerel, chub mackerel *Scomber japonicus* and blue mackerel *S. australasicus*, occurs in the same season in the western North Pacific. Although estimating total egg production is important to evaluate spawning stock biomass of each species, it is difficult to distinguish their eggs in formalin-preserved specimens collected by ichthyoplankton surveys. The objective of the present study proposed a new identification criteria based on egg size in relation to temperature. We then investigated recent annual changes in total production and mean size in eggs for the two species. We measured the diameter of 37,304 mackerel eggs collected over 16 years (2006–2021) and described frequency distributions of egg diameter across 1 °C intervals of sea surface temperature (SST) ranges. Using a Gaussian mixture model, the frequency distributions were classified into two groups. There were negative linear relationships between the SST in the sampling station and the mean egg diameter for both groups. DNA analysis suggested that the small group was chub mackerel and the large group was blue mackerel. We found that the mean egg diameter and the total egg production of chub mackerel increased with year, whereas those of blue mackerel decreased. These trends were analogous to their biomass trends. The quantitative discrimination criterion in this study could assist us to promote understanding reproductive potential for the two mackerel species.

Density effects on growth rates and fecundity of *Galaxias maculatus* in whitebait refuges

Watson, Andrew,[1] Hickford, Mike,[1] Schiel, David,[2]
[1]*National Institute of Water & Atmospheric Research, Christchurch, New Zealand*
[2]*Marine Ecology Research Group, School of Biological Sciences, University of Canterbury, Christchurch, New Zealand*

New Zealand's iconic whitebait fishery (mostly *Galaxias maculatus*, or īnanga) is unique, and its complexities for management are numerous. As a precautionary conservation measure, several areas on the West Coast were closed to fishing to prevent overexploitation. Some of these protected populations (whitebait refuges) involve areas completely protected from the whitebait fishery (closed), whereas others protect tributaries but allow fishing downstream (partially closed). After populations recover from fishing pressure, abundances and densities of formerly-fished species usually increase, and we should therefore expect changes in life-history traits compared to those in exploited populations. To test this, we examined the additive and interactive effects of individual size, population density, and stream temperature on īnanga growth rates and fecundity across a density gradient mediated by levels of fishery closure (closed, partially closed, and no protection). Specifically, increased abundance but reduced growth rates were found in high-density (closed) sites. However, there was no evidence of a trade-off between egg size and fecundity, or of negative density-dependent effects on egg size or fecundity within the whitebait refuges. Īnanga fecundity increased with body size, highlighting the importance of available forage to maintain individual growth in dense populations. This study emphasises the importance of understanding how the life-history traits of exploited populations respond to fishery closure. For the whitebait refuges to be more effective as a management tool, efforts should focus on the remediation of in-stream and requisite riparian spawning habitats, the degradation of which has caused population bottlenecks for this culturally and economically important amphidromous species.

The influence of macroalgal biomass and thallus density on the recruitment of coral reef fishes

Webber, Kelsey[1]; Fabricius, Katharina[2]; Hoey, Andrew[1]; Wilson, Shaun[3]

[1]*College of Science and Engineering, James Cook University, Townsville Qld 4810, Australia*

[2]*Australian Institute of Marine Science, Townsville, Qld 4810, Australia*

[3]*Australian Institute of Marine Science, Perth, WA 6009, Australia*

Structural complexity of a habitat often shapes the composition of inhabiting organisms. On tropical reefs, a large body of work has demonstrated coral structural complexity to be an important determinant of associated fish assemblages, yet the importance of structural complexity of macroalgal assemblages is largely unknown. An emerging body of work is highlighting the importance of macroalgal habitats to juvenile reef fishes, however, few studies have directly investigated the influence of the structural complexity of tropical macroalgal habitats on the recruitment of coral reef fish. Here, we used experimental patches of the canopy-forming macroalga *Sargassum* to test the effect of structural characteristics of macroalgae on the settlement of coral reef fishes. Twenty-five patches (75 x 75cm) were established on areas of rubble on the reef flat of Orpheus Island, Great Barrier Reef, with five patches randomly assigned to each of five treatments that differed in the density and/or biomass of *Sargassum*. Over eighteen austral summer days, juvenile fishes representing thirty species were quantified daily on patches. *Sargassum* biomass, and less so density, were positively related to the abundance and species richness of associated fish assemblages. These relationships were primarily driven by the abundance of recently-settled *Siganus doliatus* and *Pomacentrus tripunctatus*, and may reflect greater availability of shelter from predators or food (i.e., abundant and richer epibiota) in higher biomass patches. Our findings highlight that fine scales of complexity within tropical macroalgal beds may influence the value of these often underappreciated areas as recruitment habitats for reef fishes.

Facing invasion, how to save the marine fisheries ecosystem from a persistently escaping alien competitor *Sciaenops ocellatus*?

Yongshuang Xiao[1], Jing Liu[1], Jiehong Wei[1]

[1] *Institute of Oceanology, Chinese Academy of Sciences, Qingdao 266071, China*

The red drum, *Sciaenops ocellatus*, an estuarine fish, native to the western Atlantic Ocean from Massachusetts in the USA to northern Mexico, is one of the most important farmed fish worldwide. In recent decades, an unprecedented frequency of red drum (*S. ocellatus*) escapes from seawater nets (*i.e.*, million tail level) has generated an enormous pressure on local marine biodiversity and ecosystems. The aim of this study was to assess the distribution and shifts of hotspot fitness zones for *S. ocellatus* under global climate change and to identify the trophic levels in the coastal waters of China. Stress responses and adaptation potential, under different salinities, were also determined to provide valuable insights into the invasion potential and ecological impacts of alien species. In the present study, we first identified four hotspot fitness zones for *S. ocellatus* at the global scale located in the Atlantic Ocean along the Gulf of Mexico and Uruguayan coasts, and in the Pacific Ocean along the Chinese and Australian coasts based on the species distribution model analyses. Under the global warming and climate change, the most suitable habitat for *S. ocellatus* would be expanded (448,178.6 km^2) and the centre of mass would shift northwards. Stable isotope $\delta^{15}N$ and $\delta^{13}C$ ratios showed that *S. ocellatus* has a very high ecological competition with wide feeding range and high ecological position in the escape zone off the coast of China.

Mapping of global mitochondrial data brings new insights into taxonomy and species distribution of genus *Pampus* (Pelagiaria: Stromateidae)

Jiehong Wei[1]; Jing Liu[1]; Yongshuang Xiao[1]

[1]*Institute of Oceanology, Chinese Academy of Sciences, Qingdao 266071, China*

The highly similar external morphology and resultant misidentifications of the *Pampus* species have been an important issue hindering the understanding of the taxonomy and species distributions of the genus. We analysed 1497 mitochondrial sequences from our collection and the public databases to study the species diversity and distributions of the genus *Pampus*. Most phylogenetic analyses and species delimitations congruently concluded seven valid species within the genus *Pampus*, which based on type materials are: *P. argenteus*, *P. candidus*, *P. chinensis*, *P. cinereus*, *P. liuorum*, *P. minor*, and *P. punctatissimus*. Sequences of *P. argenteus* are reported through the northern South China Sea to the Japan Archipelago, which covered the type locality of *P. echinogaster*, the Bohai Sea. Sequences denoted as "*P. echinogaster*" in the public databases are all identified as *P. argenteus*, suggesting that the species should be synonymized with *P. argenteus*. Similarly, sequences of *P. griseus* were identical to our *P. cinereus* data and, therefore, should be a junior synonym of the latter. Moreover, paratypes of *P. liuorum* showed clear genetic differentiation with its congener, suggesting that the species should be treated as a valid species. Inference on divergence time and ancestral distribution implied that the genus *Pampus* originated in the central Indo-Pacific region around 8.35–11.33 million years ago (the late Miocene), associated with the rise of the Indonesian-Australian Archipelago biodiversity hotspot. The divergence between *P. cinereus* and *P. liuorum* dated back to 1.20–1.72 million years ago, which might be related to glacial isolation during the Mid-Pleistocene transition.

Pacific-wide distribution of reef fish contamination

Wejieme, Noreen[1]; Bustamante, Paco[4]; Parravicini, Valeriano[3]; Sellanes, Javier[6]; Vigliola, Laurent[2]; Wafo, Emmanuel[5]; Zapata-Hernandez, German[6]; Letourneur, Yves[1]

[1]*UMR ENTROPIE (UR-IRD-CNRS-IFREMER-UNC), LabEx « Corail », Université de la Nouvelle-Calédonie, BP R4, 98851 Nouméa Cedex, New Caledonia.*
[2] *UMR ENTROPIE (UR-IRD-CNRS-IFREMER-UNC), LabEx « Corail », Centre IRD, BP A5, 101 Promenade Roger Laroque, 98848 Nouméa, New-Caledonia.*
[3]*CRIOBE, PSL Research University, USR 3278 EPHE-CNRS-UPVD, LabEx « Corail », Université de Perpignan, Avenue Paul Alduy, 66860 Perpignan Cedex, France.*
[4]*UMR LIENSs, Université de La Rochelle, 2 rue Olympe de Gouges, 17000 La Rochelle, France.*
[5]*Laboratoire chimie analytique, Faculté de Pharmacie, Aix-Marseille Université, 27 boulevard Jean Moulin, 13385 Marseille cedex 05, France.*
[6]*Departamento de Biología Marina, Facultad de Ciencias del Mar, Universidad Católica del Norte (UCN), Coquimbo, Chile.*

Many Pacific islands nations are mostly geographically remote, have limited industrial production and relatively small populations. The presence and amount of anthropogenic pollution in these locations was, overall, poorly studied and has often been considered limited. However, in recent decades, coral reefs are increasingly threatened by a wide range of natural and anthropogenic disturbances, including chemical pollution. Three major classes of contaminants are of particular concern: polychlorinated biphenyls (PCBs), pesticides and metallic trace elements (MTE). These ubiquitous contaminants can be toxic, even at low concentrations, because they are resistant to degradation, transported over long distances, and can bioaccumulate in marine organisms and/or biomagnify along food webs. Marine pollution therefore poses a serious threat to coral reef fish, as well as potentially to human consumers, as many Pacific communities rely heavily on marine resources for food and livelihoods. This study aims to (i) describe contaminants' distribution and (ii) determine the drivers of the contamination, through ecological modeling, the impacts of several environmental and human-related parameters at the Pacific scale. These results therefore provide essential baseline information to better interpret the impact of contaminants on coral reef fish, and also highlight the urgent need for long-term monitoring of various contaminants over large spatial and temporal scales.

Epigenomic responses to temperature in snapper (*Chrysophrys auratus*)

Maren Wellenreuther[1,2], Dafni Anastasiadi[1], and Louis Bernatchez[3]

[1]The New Zealand Institute for Plant and Food Research Limited, Nelson, New Zealand

[2]The School of Biological Sciences, University of Auckland, Auckland, New Zealand

[3] Institut de Biologie Intégrative et des Systèmes (IBIS), Université Laval, Québec, Canada

The effects of environmental control on phenotypes and fitness, via epigenetic mechanisms, is essential for understanding the ability of organisms to rapidly adapt to environmental change. We investigated the role of methylation changes in temperature adaptation in wild populations of snapper (*Chrysophrys auratus*) by surveying replicate populations along New Zealand's East and West Coast. The mean surface temperature explained a significant amount of the observed DNA methylation divergence of natural populations. Additionally, we exposed cultured adult snapper to cold and warm temperatures during their sexual maturation and measured how this influences the methylation of offspring, and their fitness. We detected DNA methylation changes and gene expression changes associated with metabolic processes in juveniles of parents that were subjected to different temperatures. This shows that epigenetic modifications induced by different thermal environments are transmitted through generations and have functional implications. We further submitted offspring to a temperature challenge, and we found a higher growth gain for some combinations. Our work is one of the first to show in a commercially important marine species that methylation patterns can change rapidly in response to environmental factors, namely temperature. Further, our results are also in line with the idea that epigenetic changes in parents can be passed to progeny and impact offspring fitness. While causal links between epigenetic modifications and fitness needs to be investigated further, our study highlights the need to go beyond genetic variation as measure of environmental adaptation.

2.3B Themed Session B: Ecology of Indo-Pacific Fishes, 260-115, November 21, 2023, 1:30 PM - 3:00 PM

Beyond the shell: dissecting the underwhelming habitat function of giant clam for reef fishes

Wen, Colin Kuo-Chang[1,2,4], Chang, Wen-Yuan[1], Meng, Yan-Zhen[1], Price, Nathan[1,2,3]

[1]Department of Life Science, Tunghai University, Taichung, Taiwan
[2]International Graduate Degree Program for Biodiversity, Tunghai University, Taichung, Taiwan
[3]Biodiversity Program, Taiwan International Graduate Program, Academia Sinica, Taipei, Taiwan
[4]Center for Ecology and Environment, Tunghai University, Taichung, Taiwan

Giant clams (Tridacna spp.) are facing severe threats from overexploitation, resulting in global declines of most species. Despite claims of their ecological significance, the role of giant clams in supporting reef fishes remains uncertain due to conflicting results from restocking studies. This study aims to investigate the relationship between giant clams and reef fishes using a combination of field surveys and in situ and tank manipulations. Our findings suggest that fish abundance and species richness are jointly influenced by the density of giant clams and benthic composition. However, restocking efforts did not yield noticeable short-term changes in fish abundance, species richness, or species composition. Surprisingly, the sixline wrasse (Pseudocheilinus hexataenia) exhibited clear avoidance rather than preference for the giant clams. Conversely, the black damselfish (Neoglyphidodon melas) demonstrated equal utilization of all habitats, indicating no specific preference. Based on our results, we conclude that while giant clams may serve as indicators of reef health through certain interactions, they are unlikely to play a critical habitat role for reef fishes in the studied region. Further research, employing a combination of field and experimental manipulation designs, is necessary to ascertain the ecological role of giant clams for different reef fish species in various regions.

Whitebait: multiple species, fishing methods, values, measurements, and challenges

West, Dave[1]; Comrie, Joy[1]; Ough Dealy, Helen[1]; Park, Eriora[1]; Watson, Andrew[1,2]

[1]*Department of Conservation (DOC).* [2]*National Institute of Water and Atmospheric Research (NIWA)*

In Aotearoa (New Zealand), the juveniles of six species of native fish “whitebait” form an iconic fishery. Most of the whitebait catch is inanga (*Galaxias maculatus*). In some rivers, smelt (*Retropinna retropinna*) is a larger part of the catch and in more intact catchments banded, giant, shortjaw kōkopu, and kōaro (*Galaxias fasciatus, G. argenteus, G. postvectis* and *G. brevipinnis* respectively) are caught. The values of whitebaiting and whitebait are many including, cultural, endemic biodiversity, recreational, social and economic. Kiwi ingenuity has resulted in clever methods to access the best fishing spots, a variety of nets and innovative fishing structures. New methods and more extensive information about whitebaiting are needed. We present results of our trials of novel methods and approaches collecting data on species caught, whitebaiters and social dimensions of the fishery. The identification of which of the six species are caught and at what time of the season was studied in three Bay of Plenty rivers using kaitiaki and DOC staff sampling, visual ID and environmental eDNA samples. Hi-resolution aerial images captured during fixed wing flights recorded whitebaiting data. Fishing methods observed in images were quite river specific and combinations of net type (scoop versus set nets) and stand use were recorded between and within rivers. Informed by public submissions on whitebait management, two social surveys were undertaken to gain a better understanding of who whitebaits and why. The variety of information gathered provide new insights that will aid management of this diverse and important whitebait fishery.

Movements of tiger sharks at a remote Northwestern Hawaiian Island are strongly influenced by prey availability

Wetherbee, Bradley[1]; Kresge, Colby[1]; Hughes, Emma[1]; Lowe, Christopher G[2]

[1]*University of Rhode Island*

[2]*California State University Long Beach*

Obtaining adequate food is critical for survival of animals and prey availability is often a fundamental driver of the movement patterns of mobile species. At the French Frigate Shoals atoll, Northwestern Hawaiian Islands, tiger sharks (*Galeocerdo cuvier*) demonstrate remarkably consistent diel and seasonal movement patterns in relation to the availability of fledgling black footed albatross (*Phoebastria nigripes*). These sharks exhibit high site fidelity within a relatively small area, near a small island, where the albatross hatch and from which they often make short flights and land on the water and represent easy prey for tiger sharks. Tiger sharks are present at the atoll year-round, but concentrate their activities repeatedly on a daily basis near the fledging site during the month of June and during the first few hours following sunrise. Our findings illustrate how reliably consistent and available prey may influence the location and timing of movements of predators.

The influence of MPAs, reef habitat, and human population on changes in fish diversity in the center of marine diversity

Whalen, John[1]; Bucol, Abner[2]; Ruiz, Rebecca[3]; Bird, Chris[3]; Carpenter, Kent[1]

[1]*Old Dominion University, Department of Biological Sciences, Norfolk, Virginia, USA*

[2]*Silliman University – Angelo King Center for Research & Environmental Management, Dumaguete, Philippines*

[3]*Texas A&M University – Corpus Christi, Department of Life Sciences, Corpus Christi, Texas, USA*

The Central Visayas of the Philippines is a global epicenter of marine fish biodiversity. Hypotheses attribute this peak of species richness within the Coral Triangle to processes that occur at geological time scales. However, changes in biodiversity may occur on shorter ecological time scales, allowing for the assessment of the potential impact of anthropogenic activities. Recent declines in species richness of the Central Visayas have previously been associated with stressors such as habitat degradation and overfishing. Many marine protected areas (MPAs) have been established throughout the Philippines to mitigate the cumulative negative effect of these stressors. While most of the country's MPAs lie within the Central Visayas, this region has been termed the "epicenter of conservation adversity" within the Philippines. This study examines the effect of MPAs, reef habitat, and human population on changes in fish diversity in the Central Visayas between surveys conducted in the 1970s, 2010s, and 2020s. Individual- and sample-based species accumulation and rarefaction curves were used to create snapshots of species diversity from these distinct periods. Site-specific species richness and MPA indices (distance, size, age) were compared to determine the effect of MPAs on fish diversity. Preliminary results indicate a significant relationship between MPAs and species richness. However, there is a counterintuitive effect where MPAs are associated with lower diversity in the 1970s. This highlights the importance of incorporating other potential covariates like the choice of MPA sites, and their rules, as well as reef habitat and human population to better understand this complex dynamic.

Reconstructing long-term growth of deep-water snappers throughout the Indo-Pacific using otolith chronologies

Widdrington, Joseph[1]; Reis-Santos, Patrick[1]; Morrongiello, John[2]; Macdonald, Jed[3]; Nicol, Simon[3]; Gillanders, Bronwyn[1]

[1]Southern Seas Ecology Laboratories, School of Biological Sciences, The University of Adelaide, SA, Australia
[2] School of BioSciences, University of Melbourne, Melbourne, Victoria, Australia;
[3]Oceanic Fisheries Programme, The Pacific Community, Noumea, New Caledonia

Tropical deep-water snappers have significant commercial, ecological and cultural importance throughout the Indo-Pacific region. However, little is known about their life-history, and the lack of historical data limits our ability to predict the current and future effects of global change on population dynamics and productivity. This is of particular concern as environmental processes such as the El Nino Southern Oscillation (ENSO), which have widespread impacts throughout the Indo-Pacific region, are influenced by climate change. Here, we provide the first investigation into long-term growth trends of commercially important deep-water snappers across various Indian and Pacific Ocean exclusive economic zones (EEZs). We used the information stored in fish otoliths to reconstruct 50-year growth histories for three deep-water snapper species; *Etelis carbunculus*, *E. boweni* and *E. coruscans*. We developed a series of increasingly complex linear mixed-effects models to partition the variation in otolith growth among intrinsic (e.g. individual, cohort, age effects) and extrinsic factors such as ENSO, Pacific Decadal Oscillation (PDO) and boundary current strength. Results explore variation in growth among species and areas, and are discussed in the context of how large-scale and regional climate or environmental factors influence synchronous or nonsynchronous responses across the Indo-Pacific. Overall, understanding how deep-water snappers respond to environmental variability is central to developing sustainable fisheries and management strategies under climate change.

Application of an Electronic Monitoring system and Artificial Intelligence data analysis in a small-scale tuna fishery

Widyatmoko, Ahmad Catur [1, 2]; Hardesty, Britta Denise [2, 4]; Tracey, Sean[1, 3]; Semmens, Jayson[1, 3]; Wilcox, Chris[2,4].

[1]*CSIRO-UTAS Quantitative Marine Sciences PhD Program, Institute for Marine and Antarctic Studies, University of Tasmania, Hobart, Tasmania, Australia*

[2]*Commonwealth Scientific and Industrial Research Organisation (CSIRO) Environment, Hobart, 7000, TAS, Australia*

[3]*Marine Research Laboratories, Tasmanian Aquaculture and Fisheries Institute, University of Tasmania, Private Bag 49, Hobart, Tasmania 7001, Australia*

[4]*Center for Marine Socioecology, University of Tasmania, Hobart, Tas 7000 Australia.*

The use of Electronic Monitoring (EM) on fishing vessels is increasingly being adopted in the fisheries management. However, to date these efforts have primarily focused on industrial vessels, with little application to smaller vessel operations. Combine with the use of Artificial Intelligence (AI) and other data analysis, EM data can be analysed quickly to produce comprehensive fisheries information as opposed to compliance tools. To demonstrate application of this method, we attached low-cost cameras and GPS tracking devices to small vessels conducting 103 handline fishing trips. Trained to identify Yellowfin and Skipjack tuna, the AI model performed accurate identification for the big Yellowfin >10 kg from the EM video, while misclassification occurred for both small Yellowfin and Skipjack tuna <10kg. With the average catch per trip is four fishes, the AI model overestimate the individual calculation with 165 and 143 individuals from two cameras. We were able to estimate the weight of the fish by using length weight relationship and assign a geographic location for the capture of each individual catch by matching the time with vessel tracking data. This study provides a new perspective of fully documenting small-scale fishing operation in affordable and scalable manner yet producing unbiased data.

Improving downstream fish passage at flood infrastructure with New Zealand's first Encased Archimedes Screw Pump north Waikato, New Zealand

Williams, Alicia[1]; Bartels, Brenda[2]; Lake, Mike[3]

[1] *Waikato Regional Council, Hamilton, New Zealand*

[2] *2 Awa Ecology, Cambridge, New Zealand*

[3] *Tonkin & Taylor Limited, Hamilton, New Zealand*

Waikato Regional Council (WRC) is responsible for the maintenance and operation of flood control schemes installed over 50 years ago to maximise the rate of floodwater clearance and with little consideration to aquatic life. There is growing awareness of the impacts of this infrastructure on native freshwater fish. Critically, tuna (freshwater eels, *Anguilla spp.*) are known to have low survival rates if they pass through pumps (as are other fish) the population impacts of which are amplified during the downstream migration season which coincides with rainfall events.

To begin addressing this WRC installed an Encased Archimedes Screw Pump (EASP) from FishFlow Innovations in the Mangawhero catchment, the first pump of its type installed in New Zealand. EASPs have been reported to have very little impact on fish that pass through, but this has not been tested for New Zealand eels, which can grow larger than anguillids elsewhere. Our objectives were to assess the EASP for i) mortality and injury rates of eels passing through, ii) the size range of eels that safely pass through, and iii) potential pump avoidance by eels. 255 eels ranging from 328 to 956mm passed through the EASP, with a 100% survival rate. Overall, 99.2% of fish had no, or only minor injuries, likely from netting and handling. Results from this study are extremely positive, and will contribute to a regional strategy to guide future decision making regarding the management and upgrading of new or existing infrastructure to minimise the effects on native fish populations.

Spatial ecology of silky sharks at a provisioning site in the Red Sea.

Williams, Collin[1]**;** Berumen, Michael[1]; Clarke, Chris[2]; Cochran**,** Jesse[1]; Lea, James[3]; McIvor, Ashlie[4]; Ormond, Rupert[5]; Richardson, Eloise[1]

[1]*Red Sea Research Center, Division of Biological and Environmental Science and Engineering, King Abdullah University of Science and Technology, Thuwal, Kingdom of Saudi Arabia*

[2]*Danah Divers Marine Research Facility, Beach Palace, Jeddah, Kingdom of Saudi Arabia*

[3]*Save Our Seas Foundation, South Queensferry, Edinburgh, Scotland, UK*

[4]*MARE - Marine and Environmental Sciences Centre/ ARNET-Aquatic Research Network, Regional Agency for the Development of Research, Technology and Innovation (ARDITI), Funchal, Madeira, Portugal*

[5]*Marine Conservation International, South Queensferry, Edinburgh, Scotland, UK*

In the eastern Red Sea, a population of silky sharks (*Carcharhinus falciformis*) has been regularly provisioned for the last forty years, presenting a unique context to examine this species' behavior. Silky sharks are a pelagic predator capable of long-distance migrations (>10,000km), but at this site, individuals can exhibit year-round residency. Here, we utilize satellite telemetry to explore broader space and habitat use of silky sharks in the Red Sea as well as the potential influence of provisioning on this population's movements. Ten individuals (~2-2.5m TL) were equipped with a combination of Smart Position and Temperature (SPOT) tags and Pop-up Satellite Archival Tags (PSAT). Only one individual left the east-central Red Sea, making a trans-basin migration to Sudan (west-central Red Sea). All other sharks remained within ~100km of the provisioning site, making periodic forays away from the site before returning again. Tagged sharks spent most of their time between 0-100m depth, but were more surface oriented around the provisioning site itself. Our results indicate that silky sharks present at the Saudi provisioning site exhibit limited space use and a greater utilization of coastal reef habitats relative to individuals tagged in other oceanic basins. While it was not possible to disentangle the influence of provisioning on observed horizontal movements, we demonstrate an association between surface-oriented behavior and presence at the provisioning site. These findings provide novel insights into the spatial ecology of pelagic sharks exposed to provisioning activities and potential management strategies that may benefit silky shark populations in the Red Sea.

Fine-scale bathymetry data explains variability fish assemblage structure of temperate mesophotic reefs in the Hunter Marine Park

Williams, Joel[1]; Ingleton, Tim[2]; Harasti, David[3]; Jordan, Alan[1]; Hill, Nicole[1]; Barrett Neville[1]

[1]*Institute for Marine and Antarctic Studies, University of Tasmania*

[2]*New South Wales Department of Planning and Environment*

[3]*Fisheries Research - New South Wales Department of Primary Industries*

Understanding the distribution and diversity of fishes is important for ecosystem-based fisheries management and marine park planning and monitoring. Temperate mesophotic ecosystems are a relatively newly described systems that is generally associated with the transition from an algal dominated habitat to a sessile invertebrate dominated habitats at depths between 30 m and 150 m. There is a large knowledge gap on the distribution and structure of fish assemblages at mesophotic depths. It is important to improve this understanding as several of the newly established Australian Marine Parks recognised these mesophotic reefs as key ecological features. In this study, we collected data on fish prevalence and abundance using stereo baited remote underwater video. Data on reef structure and complexity was obtained from multibeam echo sounder data. Using contemporary joint species distribution models, we were able to investigate fish assemblage structure and distribution of individual species in relation to reef structure and complexity, and season. Reef structure and complexity alone explained 17-83% of variance in species prevalence. This was mainly driven by mean depth, standard deviation of depth, and kurtosis. There were also notable seasonal patterns for many species. Using these joint species distribution models, we could make predictions and create three-dimensional species distribution models to illustrate the fine-scale distribution of fish across reef structure. These results highlight the need for monitoring programs to stratify sampling across depths, reef structure, habitats, and season if trends in biodiversity through time are the core metrics of interest to marine park managers.

Modernising large-scale surveys of sea cucumbers and other benthic species using towed Remote Operated Vehicles (ROVs) and Aerial Drones

Williamson, Jane[1]; Joyce, Karen[2,6]; Gaston, Troy[3]; Duce, Stephanie[4]; Knuckey, Ian[5]; Koopman, Matthew[5]; Li, Joan[6]; McSpadden, Kristen[3]; Garner, Natasha[1]; Cornet, Valerie[4]; Raoult, Vincent[1]

[1]*School of Natural Sciences, Wallumattagal Campus, Macquarie University, NSW 2109, Australia*

[2]*College of Science and Engineering, James Cook University, Nguma-bada Campus, Cairns, QLD 4878, Australia*

[3]*School of Environmental and Life Sciences, University of Newcastle, Ourimbah, New South Wales, Australia* [4]*Institution*

[4]*College of Science and Engineering, James Cook University, Bebegu Yumba Campus, Townsville, QLD 4811, Australia*

[5]*Fishwell Consulting, Queenscliff, VIC 3225, Australia*

[6] *GeoNadir, Trinity Beach, Cairns, QLD 4879, Australia*

Due to the global commercial harvesting of sea cucumber populations, there is an urgent need to develop enhanced monitoring approaches that can rapidly assess the status of populations at ecologically relevant scales to inform effective management strategies. Traditional surveys rely on in-water visual counts of sea cucumbers using snorkel, manta tows, or SCUBA. Sea cucumbers are found across a wide range of depths, however, encompassing depths greater than those reachable by occupational SCUBA diving (> 30 m), as well as extremely shallow areas that cannot be accessed by boats or manta tows (< 2 m).

In this study, the effectiveness of towed ROVs and aerial drones was examined for assessing sea cucumber populations, and their performance was compared to more conventional snorkel and SCUBA-based assessments. While video and ROV methods generally counted fewer sea cucumbers across transects than by snorkel or SCUBA, counts by towed ROVs and aerial drones did not differ remarkably from those done on SCUBA or snorkel. Given that the towed ROV can cover a greater range of depths at a rapid rate relative to SCUBA or snorkel, and that aerial drones can efficiently survey vast areas of habitat, we propose that the combined use of towed ROV systems and aerial drones should become standard for thorough sea cucumber assessments. Our approach can be extended to other survey targets such as benthic organisms or fishes, and offers the advantage of being capable of assessing multiple types of data from a single source.

How do temperature impacts on growth and mortality shape fish size distributions and why does it matter?

Willington, Sarah[1]; Audzijonyte, Asta[1]; Krueck, Nils[1]; Trebilco, Rowan[2]

[1] *Institute for Marine and Antarctic Studies, University of Tasmania, Hobart, TAS, Australia*

[2] *CSIRO Environment, Hobart, TAS, Australia*

Increasing ocean temperatures change growth and mortality of fishes. These changes in growth and mortality are likely to affect fish population size distributions, i.e., relative abundances of small, medium size and large individuals in a population. Changes in species size distributions have implications for size-based fisheries assessment, stock productivity, and fisheries management. Size structure also plays an important ecological role, governing species interactions and population resilience. Yet, although temperature effects on individual body size are well studied, we have limited knowledge of how these changes in growth (and changes in mortality) might impact population size distributions. For example, while it is predicted that temperature should lead to declining maximum sizes in fish, a large-scale empirical study of 335 coastal fish species from around Australia showed that population mean sizes can either decrease or increase with warming. Here we use size-based population models to explore how realistic and empirically observed temperature impacts on growth and mortality change fish population size structure and their mean and maximum sizes. We explore conditions under which mean and maximum sizes change in different directions and show implications of warming driven size structure changes on size-based population model predictions.

How well does recruitment predict abundance of adult lethrinids?

Wilson, Shaun[1,2], Depczynski, Martial[1,2], Fulton, Christopher[1,2], Holmes, Thomas[2,3], Goetze, Jordan[3,4], Birt, Matthew[1], Radford, Ben[1,2], Tinkler, Paul[5]

[1] *Australian Institute of Marine Science, Indian Ocean Marine Research Centre, Crawley, Western Australia*

[2] *Oceans Institute, Indian Ocean Marine Research Centre, The University of Western Australia, Crawley, Western Australia*

[3] *Marine Science Programs, Department of Biodiversity, Conservation and Attractions, Kensington, Western Australia*

[4] *School of Molecular and Life Sciences, Curtin University, Perth, Western Australia, Australia*

[5] *Deakin Marine, School of Life and Environmental Sciences, Deakin University Warrnambool Campus, Warrnambool, Victoria, Australia*

Recruitment of larvae into settlement habitats underpins the replenishment of fish populations. Recruitment rates, however, are inherently variable, which may shape adult populations both spatially and temporally. To assess the influence of recruitment on adult fish stocks we modelled 13 years of lethrinid recruitment (fish <5cm) against abundance estimates of fish approximately 1-2, 2-3 and >3 years old. Annual surveys were conducted across 18 sites, spanning 150km of the Ningaloo coast, where lethrinids are a primary fishery target. Recruitment pulses were positively linked to the Southern Oscillation Index (SOI), with more recruits observed during La Niña years. Pulses in recruitment were also associated with increased abundance of 1-2 year old *Lethrinus nebulosus* and *Lethrinus atkinsoni* the following year, with recruitment explaining >66% of variations in fish abundance at 1-2 years old. The relationship was spatially variable, with the northern abundance of 1-2 year old *L. atkinsoni* associated with fewer recruits the preceding year than on southern reefs, inferring greater survival of young fish in the warmer northern waters. Post-settlement mortality likely plays an increasing role in determining abundance of lethrinids older than 2 years, as local sea temperature and climate metrics (SOI) become better predictors of adult abundance than recruitment. Density estimates of *L. nebulosus* 1-2 years did however reliably predict abundance of fish 2-3 and >3 years of age. Our results demonstrate that recruitment and juvenile abundance clearly affect fluctuations in the size distribution of lethrinids and provides a basis for predicting perspective abundance of adults.

Environmental DNA primer selection for reef-associated and pelagic Indo-Pacific and Hawaiian fish species

Wishingrad, Van[1]; Bowen, Brian W.[1]; Timmers, Molly A.[2]; Toonen, Robert J.[1]; Whitney, Jonathan L.[3]

[1]*Hawai'i Institute of Marine Biology, 46-007 Lilipuna Road, Kāneʻohe, HI 96744*

[2]*Smithsonian Institution, PO Box 3701, SI Building Room 153, MRC 010, Washington, D.C. 2001*

[3]*NOAA Pacific Islands Fisheries Science Center 1845 Wasp Boulevard, Building 176, Honolulu HI 96818*

The Indo-Pacific is a region of exceptional fish species diversity. In the Hawaiian Islands, more than 400 species of inshore and reef fishes inhabit a chain of islands and atolls over an area of approximately 16,000 km^2. A great deal of research has contributed to our understanding of fish diversity in the Hawaiian Islands and the processes which established past and present biogeographic patterns including approximately 25% endemism. Environmental DNA (eDNA) has emerged as a powerful tool to contribute to our understanding of diverse communities of species. However, much remains to be known about how well eDNA primers, designed for fish species generally or in other regions, recover the unique fish communities around Hawaiʻi. This information is critical to evaluate the utility of distinct eDNA primers for robust biodiversity monitoring in the Hawaiian Island region. Here we leverage a dataset of 43 reef-associated and 25 pelagic fish species sampled in the Hawaiian region to evaluate the performance of eDNA primers designed for the detection of fish species. We find eDNA primers published to date vary with respect to recovering a known fish community, and show differences in their ability to recover either reef-associated or pelagic fish communities in terms of both detection rates and taxonomic precision. Other aspects of the eDNA workflow can alter the outcome, including sampling methodology, wet lab protocols, and bioinformatic processing. Environmental primer choices therefore are a foundational aspect of eDNA studies and of utmost importance to consider for the success of an eDNA project in terms of adequate sampling of target species or communities.

Movement behaviour of swordfish provisions connectivity between the temperate and tropical southwest Pacific Ocean

Wolfe, Barrett[1]; Hartmann, Klaas[1]; Pepperell, Julian[2]; Tracey, Sean[1]; Williams, Sam[3]

[1]*Institute for Marine and Antarctic Studies, University of Tasmania, Private Bag 49, Hobart, Tasmania 7001, Australia.*

[2]*Pepperell Research and Consulting Pty Ltd, P.O. Box 1475, Noosaville DC, Queensland 4566, Australia.*

[3]*School of Biomedical Sciences, The University of Queensland, St Lucia, Queensland 4072, Australia.*

Swordfish (*Xiphias gladius*) are a large-bodied, widely distributed (45°N–45°S) pelagic predator targeted by fisheries worldwide. Swordfish occurring at high latitudes tend to be larger adults, so their movements have implications for population dynamics. In the southwest Pacific the cool-temperate subset of swordfish is largely undescribed but existing evidence suggests limited movement here from the subtropics.

We capitalized on the recent emergence of a recreational swordfish fishery off temperate southeast Australia to characterize movements of swordfish with pop-up satellite archival tags. Data were recovered from tags deployed in the western Tasman Sea (38–43°S) on 11 swordfish (50–350 kg) for 56–250 days. Five swordfish entered the Coral Sea (<30°S), up to 3275 km away from capture. Behavior modelling suggests partial seasonal migration: four swordfish rapidly transited north to 23–27 °C water (potential spawning habitat), where they lingered for several months. One migrating swordfish still carrying a tag post-spawning season returned to ~120 km of its release location, suggesting site fidelity. Swordfish predominantly demonstrated diel vertical migration, descending into the mesopelagic zone at dawn to 495 m (95% CI 460–530 m). At night, swordfish were deeper during full moons, 46 m (38–55 m) versus 18 m (15–22 m) during new moons, and we demonstrate the effect of moon phase varies dynamically across time of night with implications for fisheries interactions. Tagging highly migratory fishes near range limits enables characterization of the breadth of movement phenotypes present, a key consideration for fish stocks in changing oceans.

Stable isotope analysis reveals differential niche plasticity in co-occurring temperate estuarine fishes

Wong, James[1]; Gaston, Troy[1]; Platell, Margaret[1]; Raoult, Vincent[1,2]; Smith, Tim[3]

[1] *School of Environmental and Life Sciences, University of Newcastle*

[2] *School of Natural Sciences, Macquarie University*

[3] *Centre for Tropical Water & Aquatic Ecosystem Research, James Cook University*

Estuaries throughout history have been the loci of commercial and recreational pursuits. In the advent of anthropogenic temperature shifts, an understanding of responses by estuarine ecosystems and trophic connectivity of their commercially and recreationally important fish species remains relatively unknown. Lake Macquarie, a wave-dominated barrier estuary on Australia’s eastern coast, has two coal-fired power plants that use the adjacent lake for cooling water. This has resulted in artificially elevated water temperatures adjacent to discharge points. In the present study, samples of three fish species (Yellowfin Bream, Tarwhine (Sparidae) and Sand Whiting (Sillaginidae)) were obtained from thermally affected and control sites in Lake Macquarie between October 2020 and February 2021. Dietary analysis, via stable isotope mixing models, was conducted to determine basal dietary sources of those species, and isotopic niche analyses used to determine whether species’ diets and trophic levels differed by site. Stable isotope mixing models identified that epiphytic algae typically made the greatest basal dietary contribution for the three fish species at all sites. Stable isotope niche analysis showed that, for sites with artificially increased ambient temperature (ie., thermally affected sites), Sand Whiting, which have a more specialized diet and feeding method, had a greater probability of feeding within the dietary niche of the two more generalist species of sparid. The results indicate an emergent pattern for fishes with specialist feeding strategies and diets, which may be driven to feeding outside of their functional niche when ambient water temperatures increase, resulting in more direct competition with co-occurring generalists.

Fisheries ecology of rock flathead (*Platycephalus laevigatus*) in south-eastern Australia

Wong, Darren[1]

[1]*School of Life and Environmental Sciences; Faculty of Science, Engineering and Built Environment; Deakin University; Queenscliff, VIC, Australia*

Rock flathead (*Platycephalus laevigatus*) forms part of a commercially significant fishery in Corner Inlet, Victoria, Australia. However, stock structure of the species is largely unknown. This presents uncertainty for stakeholders when assessing its status and in ensuring its long-term sustainability. A key uncertainty is whether the Corner Inlet rock flathead population is a localised and self-replenishing stock. This is pertinent as it determines whether monitoring, assessment and management could be confidently focused within just Corner Inlet. However, anecdotal observations from commercial fishers suggest that rock flathead move in and out of the inlet, particularly during spawning. This may influence catch rate dynamics, as it renders other sources of replenishment, such as immigration of fish from outside the inlet, or larval dispersal into the inlet from distant spawning populations. Approaches required to assess the fishery may need to be modified because key performance indicators, such as catch rates, may be influenced by movement patterns, which in turn can have implications for targeting practices and economic performance.

This project aims to investigate the stock structure and ecological niche of rock flathead in south-eastern Australia, using an integrated approach involving a combination of acoustic telemetry, population genetics and otolith microchemistry. Preliminary findings indicate that there is limited mixing between populations, and that the Corner Inlet population remains a largely isolated stock. The knowledge gained from this study will greatly improve our understanding of the population structure and fishery, leading to better informed assessments and sustainable management of the fishery.

Exploring the phylogeny and depth evolution of the Indo-West Pacific cusk eels and their relatives (Ophidiiformes: Ophidioidei)

Wong, Man Kwan[1]; CHEN, Wei-Jen[1]

[1]*Institute of Oceanography, National Taiwan University, Taipei, Taiwan*

The family Ophidiidae (51 genera and 280 species) is placed together with Carapidae under the ophidiiform suborder Ophidioidei. Ophidiids mainly inhabit the deep sea (>200m). Due to sampling difficulties, their phylogenetic relationships and depth evolution remain unexplored. The present study aims to (1) reconstruct a comprehensive phylogeny of the Ophidiidae and their allies based on a new multi-gene dataset; (2) investigate their evolution in different depths with the reconstructed time tree and ancestral state. Most specimens (n = 639) examined were collected through several oceanographic expeditions under the program “Tropical Deep-Sea Benthos” and joint efforts between Taiwan and France teams from the localities across the Indo-West Pacific in the past 15 years. Our results found that the Ophidiidae forms a paraphyletic group with respect to Carapidae. Five main clades resolved are the clade comprising subfamily Brotulinae; the clade including the genera *Acanthonus* and *Xyelacyba*; the clade grouping *Hypopleuron caninum* and carapids; the clade containing *Hoplobrotula* of the subfamily Neobythitinae and the subfamily Ophidiinae; and the clade with at least 21 genera from the subfamily Neobythitinae. We suggest the following taxonomic revisions based on the inferred phylogeny and new diagnostic characters. The subfamily Brotulinae should be elevated to the family level; the genera *Acanthonus* and *Xyelacyba* together form a new family Acanthonidae. The newly defined families Carapidae and Ophidiidae are also proposed. As to the depth evolution, mesopelagic to shallow and mesopelagic to bathypelagic transitions were observed within the newly defined Ophidiidae, which may relate to the Paleocene-Eocene Thermal Maximum event.

Goby social mixers: mixed-species group formation in a model marine system (genus *Gobiodon*) and the potential impacts of habitat degradation

Wong, Marian[1]; Froehlich, Catheline[2]; Hildebrandt, Courtney[1]; Hing, Martin[3]; Klanten, Selma[4]

[1]*School of Earth, Atmospheric & Life Sciences, University of Wollongong, Wollongong, NSW, Australia*

[2] *Department of Biology, University of Alabama, Tuscaloosa, AL, USA*

[3]*NSW Department of Primary Industries, Sanctuary Point, NSW, Australia*

[4] *School of Life Sciences, University of Technology Sydney, Sydney, NSW, Australia*

Understanding how animal societies are maintained despite conflict between group members is an enduring topic in evolutionary ecology, owing to the important fitness consequences of group-living. For marine fishes, current hypotheses focus on explaining single-species groups and postulate that ecological and social constraints play a key role. However, many fishes also form stable groups with other species i.e. mixed-species societies, and whether they are governed by the same ‘rules’ as single-species groups is an unexplored area of research. For example, we do not know whether the types of conflicts that arise between individuals within a species also arise between individuals of different species. To address this knowledge gap, I will describe the phenomenon of mixed-species group formation in a model marine system, coral-dwelling gobies (genus *Gobiodon*). These fishes live in corals and vary not only in intraspecific social structure (i.e. pair- or group-forming), but also whether they form single- or mixed-species groups. Based on long-term field data spanning 3 locations, I describe the relative occurrence of single and mixed species groups in this genus, correlate the occurrence of mixed species groups with ecological and social variables, and relate the occurrence of mixed species grouping to the species sociality index and environmental disturbances. I then utilise this long-term data to generate hypotheses for mixed species societies and predictions regarding the maintenance of these societies considering ongoing habitat degradation. In so doing, I highlight the need to incorporate the mechanisms surrounding interspecific conflict and its resolution into current theories of social evolution.

Reproductive biology of the Melbourne skate to inform fisheries management and conservation

Woolley, Bailee[1]; Awruch, Cynthia[1] ; McAllister, Jaime[1]; Moreno, David[1]; Semmens, Jayson[1]

[1]*University of Tasmania, Institute for Marine and Antarctic Studies, Hobart, Tasmania, Australia*

The Melbourne skate (*Spiniraja whitleyi*), a large oviparous skate endemic to the continental shelf of Australia, has experienced localised depletion, a trend attributed to sustained catches in the Commonwealth trawl fishery over recent years. Given that large skate species are more prone to local extinction compared to smaller species, coupled with the already observed population declines and its high susceptibility to fishing pressure, the Melbourne skate may be particularly vulnerable to local extinction. However, there is still a lack of essential biological information for this species. This has led to its listing as vulnerable on the International Union for Conservation of Nature red list, while the Action Plan for Australian Sharks and Rays (2021) has also recommended the assessment of Melbourne skate reproduction as high priority. In this context, this study is providing reproductive information on Melbourne skate inhabiting protected shark refuge areas in southeast Tasmania by using non-invasive techniques. Sexual maturity and reproductive cycle was obtained by examining seasonal plasma and mucous concentrations of sex hormones (testosterone, progesterone, estrogen) using radioimmunoassay. Ultrasonography was used to confirm female skate maturity and determine maximum follicle diameter. Based on the results, mature female Melbourne skate displayed asynchronous, discontinuous reproductive cycles. Slightly elevated levels of sex hormones in Spring/Summer were also found, suggesting females may be ovulating/producing follicles in this period. This reproductive data will be inputted into demographic models needed for wider population analyses to assess current and future risks to this vulnerable species.

2.4A Themed Session F: Conservation of Indo-Pacific Fishes, 260-092, November 21, 2023, 10:30 AM - 12:30 PM

The implications of plastic pollution on seafood species

Nina Wootton[1], Patrick Reis-Santos[1], Bronwyn M Gillanders[1]

[1]*School of Biological Sciences, The University of Adelaide, SA, 5005, Australia.*

Plastic pollution has increased significantly in the past decades, creating a plethora of environmental issues, particularly in marine ecosystems. Plastic debris enters the ocean and is broken down into smaller pieces, with wastewater and coastal runoff also contributing to the accumulation of microplastic (plastic <5mm). Here, microplastic can be ingested by a suite of marine life, including seafood species, which are important both commercially for fisheries, and environmentally for healthy oceans. It is well documented that microplastics are being consumed by a number of seafood species, however, we still do not understand what effects this may have on individual species health, or how extensive these effects are at a population level.

To understand the implications of microplastic exposure to seafood species, we systematically reviewed the published literature that tested the effects of microplastic on fish, bivalve and crustacean species. We discovered that of the ~900 papers identified, more than 90% found that plastic polymers negatively affected the health of the organisms. A variety of different toxicological endpoints and biomarkers were tested, with varying levels of impact depending on the type and dosage level of the polymer. Studies commonly reported effects to the digestive and endocrine systems, and changes in reproductive function, behaviour, and growth. Providing information on how marine pollution may affect the seafood industry and seafood species fished will guide the urgency of future research and allow management and mitigation strategies that support the seafood sector to be developed.

5.1B Themed Session: K. General Session, 260-098, November 24, 2023, 1:30 PM - 3:00 PM

Using empirical data to validate and update population models: a case study using a model for Golden Perch

Wootton, Henry[1]; Tonkin, Zeb[1]; Fanson, Ben[1]; Yen Jian[1], Todd, Charles[1]

[1]*Applied Aquatic Ecology, Arthur Rylah Institute for Environmental Research, Department of Energy, Environment and Climate Action, P.O. Box 137 Heidelberg, VIC 3084, Australia*

Population modelling is a crucial tool to manage ecosystems and can be used to predict long-term responses to management interventions at a population level. Population models include explicit characterisations of ecological processes, and it is common to use theory or expert opinion to address gaps in our knowledge of these processes. Less common, but no less important, is to revisit these knowledge gaps as new data become available.

We used newly available data on movement to validate and update a stochastic metapopulation model for Golden Perch across the Murray Darling Basin. Movement information was sourced from large-scale acoustic telemetry and otolith microchemistry studies which provided new insights into Golden Perch (*Macquaria ambigua*) movement among reaches. Comparing this empirical movement information with the theory- and expert-derived characterisations of movement in the current model allowed us to identify where the model was reliable and where modifications were required.

Comparisons with empirical data indicated that theory- and expert-derived characterisations of movements were reliable in some locations but under- and over-predicted in others. We used the empirical patterns to update the movement rules in the metapopulation model and assessed the effects of these changes on model outputs.

Our approach demonstrates an important part of model development, often not reported on, where population models are updated as ecological understanding is improved through time. Repeatedly updating and applying models is a crucial step towards true adaptive management.

2.5B Themed Session E: Biology and Conservation of Sharks and Top-predators, 260-051, November 21, 2023, 1:30 PM - 3:00 PM

Importance of the Mitchell River (Queensland, Australia) as habitat for freshwater sawfish *Pristis pristis*

Wueringer, Barbara E.[1, 2]; Biskis, Veronika[1, 3]; Cooper, Madalyn[4]; Frank, Anzac[5]; Lawrence, Fitzroy[5]

[1] *Sharks And Rays Australia, Bungalow, Queensland 4870, Australia*
[2] *School of Natural Sciences, Macquarie University, NSW 2109, Australia*
[3] *School of Science, Technology and Engineering, University of the Sunshine Coast, Hervey Bay, QLD 4655, Australia*
[4] *Centre for Sustainable Tropical Fisheries and Aquaculture, James Cook University, Townsville QLD 4811, Australia*
[5] *Kowanyama Land and Sea Rangers, Kowanyama Council, Kowanyama, Queensland 4892, Australia*

Globally, the decline of sawfishes is attributed to trophy hunting, high catchability in commercial fisheries, the high value of sawfish fins in the shark fin trade, as well as habitat destruction. As a result, the remote regions of Northern Australia are now considered to be the last remaining global hotspot for four out of five species of sawfish. Here, we assessed the occurrence of freshwater sawfish *Pristis pristis* in the Mitchell River and its tributaries, in Far North Queensland, Australia, over a period of 8 years. A variety of methods were incorporated to identify the species' distribution within the system. Environmental DNA was collected from 7 sites over 5 years. Sawfish eDNA was detected in all locations, and in three locations over multiple years. Through an ongoing citizen science campaign, n=44 sawfish sightings and historic accounts were collected from the region, with 31.8% from within the last five years. Since 2016, research gill nets and lines were set for a total of 227.8 hrs and 646.3 hrs respectively, resulting in the capture and release of 6 freshwater sawfish. The Mitchell River continues to be a significant habitat for *P. pristis*, but the population is under threat, as evidenced by the capture of a saw-less sawfish, and the illegal take of rostra by commercial fishers. Moreover, even though the Mitchell River is considered to be one of the last wild places globally, it has recently been assessed for the potential of water extractions for irrigated agriculture.

Optimal recommendations for field and laboratory protocols of eDNA and applications in fish diversity in lake ecosystem of China

Xing, Yingchun[1*]; Zhao, Yahui[2*]

[1]*Resource and Environmental Research Center, Chinese Academy of Fishery Sciences, Beijing, China*
[2]*Key Laboratory of the Zoological Systematics and Evolution, Institute of Zoology, Chinese Academy of Sciences, Beijing, China*

Environmental DNA (eDNA) could offer a new opportunity to improve fish detection. How to choose optimal laboratory protocols is the first question to be considered. Based on our research experiences and previous published articles, we recommend a set of optimal protocols for regular eDNA-based fish detection and presented the suggestions for water sample volume collected and subsequent sample filtered and storage, and experiment protocols including optimal choices for DNA extraction kits, PCR primer sets and reaction condition, high-throughput sequencing platforms and software packages used for eDNA sequences analysis and taxon annotation. A study case was presented to prove this set of optimal eDNA field and laboratory protocols could be used for fish species detection and revealed taxonomical diversity (TD) and functional diversity (FD) of fish in the lake ecosystem of China. The Poyang Lake, the largest freshwater lake in China, provides habitats for abundant aquatic animals and plants, especially some Chinese rare and endangered aquatic animals such as *Lipotes vexillifer*, *Acipenser sinensis* and *Grus leucogeranus*. We used above eDNA protocols to detect fish species composition in the Poyang Lake, and the results indicated 74 fish species were detected, which was near 70% of historical records. One rare species *Ochetobius elongates* was detected through eDNA, and it is difficult to be found based on fishing nets. Alpha and Beta TD and FD of fish were analyzed, and Pearson correlation coefficient indicated B_{sor} for TD and FD positive correlation.

Survival strategies reveal rarity of Naru eagle ray, *Aetobatus narutobiei*: Exploring new ecosystem conservation measures through top-down control of elasmobranchs

Yamaguchi, Atsuko[1]; Furumitsu, Keisuke[1]

[1]Institute of Integrated Science and Technology, Nagasaki University

The Naru eagle ray, *Aetobatus narutobiei*, is a mid-sized endemic species distributed predominantly around Japan, East Asia. This species was suspected of having increased along the southwestern coast of Japan due to global warming, causing feeding damage to important bivalve fisheries. Therefore, a predator control program was started in 2001 and the ray populations have declined; however, bivalve catches have not yet increased. This ray is a specialist bivalve feeder. Their optimal feeding and nursery area is in shallow estuarine waters in the inner bay during the warmer season. However, when water temperatures drop in winter, they need to migrate to deeper waters outside the bay. Habitats with suitable environmental conditions for this ray, such as Ariake Bay, are limited. Although the fecundity of *A. narutobiei* averages approximately three pups, the embryos in the uterus have a prolonged period of embryonic diapause (9.5 months during the twelve-month gestation period). Embryonic diapause allows the females to concentrate on reproduction during the summer and the males to complete mating before overwintering when the risk of natural mortality increases. The newborn pups can delay parturition until the optimal season for survival. Still, the ray population is declining and is at risk of extinction due to continued fishing pressures, reduction of estuaries, and environmental changes. We have researched *A. narutobiei* biology and have monitored it since 2001. Here, we show the current status of *A. narutobiei* and our research project to propose new ecosystem conservation measures through top-down control of elasmobranch predators, including sharks.

Long-term changes in the growth of the Japanese rockfish *Sebastes cheni* in a macroalgal bed in relation to seaweed abundances

Yamamoto, Keito[1]; Ohnishi, Rumina[1]; Iwasaki, Sadaharu[1]; Kamimura, Yasuhiro[2]; Nishijima, Wataru[3]; Matsunaga, Hisahiro[4]; Miyata, Yasuhito[4]; Tomiyama, Takeshi[1]

[1]*Graduate School of Integrated Sciences, Hiroshima University*

[2]*Fisheries Resources Institute, Japan Fisheries Research and Education Agency*

[3]*Environmental Research and Management Center, Hiroshima University*

[4]*JFE Steel Corporation*

Seagrass and seaweed beds are important habitats for juveniles of many fish species. In the central Seto Inland Sea of Japan, the Japanese rockfish *Sebastes cheni* juveniles are dominant from early spring to summer in seagrass (*Zostera marina*) and macroalgal (*Sargassum* spp.) beds, and *S. cheni* are highly dependent on the growth of macroalgal beds for their survival. Lately, however, macroalgal beds have been deteriorated in the Seto Inland Sea, possibly related to global warming. The purpose of this study was to compare the growth and survival of *S. cheni* in recent years and those in 2007, when the macroalgal beds were well developed. In the spring of 2022 and 2023, *S. cheni* juveniles were collected monthly using a small seine net (2-m high and 5-mm mesh) in a macroalgal bed at the coast of Aba Island in the central Seto Inland Sea. The density of juveniles peaked around April and it varied greatly from year to year, ranging from approximately 3% of the 2007 level in 2022 to 240% of the 2007 level in 2023. Growth rates evaluated from the length-frequency distribution showed no difference between 2022 and 2007. To test the hypothesis that habitat deterioration causes negative impacts on growth of juveniles, we will assess growth rates of juveniles by otolith microstructure analyses.

Over a century of global decline in the growth performance of marine fishes

Yan, Helen F.[1]; Watkins, Hannah V.[2], Bellwood, David R.[1]

[1]*Research Hub for Coral Reef Ecosystem Functions, College of Science and Engineering, James Cook University, Townsville, QLD 4811, Australia*

[2]*Earth to Ocean Group, Department of Biological Sciences, Simon Fraser University, Burnaby, BC, V5A 1S6, Canada*

Growth is a fundamental life history trait, shaping the ecology and functioning of marine fishes. By standardising growth rates at the species level, we can infer changes in fishes' life histories in response to natural and anthropogenic pressures across macroevolutionary and macroecological scales. Here, we used the composite life history trait, growth performance, to assess the global impacts of climate change on the life histories of marine teleost fishes over the last century. Growth performance is a standardised metric of growth, whereby higher growth performance values denote species growing to larger body sizes relatively quickly. By combining more than 7,500 growth curves across 1,480 species with a Bayesian state-space framework, we found a global pattern of decline in the growth performance of marine fishes from 1908 onwards. This global decline was mainly driven by a strong decline in growth performance occurring in temperate regions, which experienced nearly one degree of heating over the last century. These declines in growth performance values are likely indicative of fishes growing to relatively smaller body sizes, which can threaten critical ecosystem functions and services, such as biomass production and fisheries yields.

Using recreational squid jigging techniques to determine the distribution and abundance of southern calamari *Sepioteuthis australis*

Yeoh, Daniel[1], Mitchell, Peter[1], West, Lisa[1]

[1]*Department of Primary Industries and Regional Development Western Australia*

Southern calamari *Sepioteuthis australis* (Loliginidae) are a popular recreational fishery species throughout the southern waters of Australia and New Zealand where they are typically targeted by squid jigging, *i.e*., line fishing using purpose-designed artificial baits with barbless prongs. We utilised this technique as a cost effective and species selective sampling method to determine the distribution and abundance of *S. australis* throughout Cockburn Sound, a temperate embayment in south-western Australia. We also aimed to quantify environmental and gear effects on catch rates and catchability. To robust and quantifiable data sampling followed set protocols (*e.g*., specific gear, site boundaries and fishing periods) over two years of monthly surveys. Fine-scale catch and effort information was recorded (GPS coordinates and depths of individual captures) along with a range of environmental and habitat variables to determine drivers of catch-per-unit-effort (CPUE; squid hr^{-1}) at various spatial scales. Marked temporal trends occurred throughout the year, with highest CPUE during autumn and early-winter (7–17 squid hr^{-1}) and lowest CPUE during late-spring and summer (2–5 squid hr^{-1}). Spatially, sites with seagrass coverage and high depth relief typically had higher CPUE than vegetated areas with low depth gradients and unvegetated areas. Environmental conditions (temperature, wind speed and water clarity), squid jig colour and research fisher technique also significantly affected CPUE. This knowledge of fine-scale habitat associations and environmental responses can form the basis of distribution models for *S. australis* and improve the robustness of squid jigging CPUE standardisations for fisheries stock assessments.

The eradication of common carp from Tasmania

Yick, Jonah[1]; Diggle, John[1]; Wisniewski, Chris[1]

[1]*Inland Fisheries Service, New Norfolk, TAS, Australia*

Common carp (*Cyprinus carpio*) were first discovered in Lakes Crescent (23 km^2) and Sorell (53km^2) in January 1995. As a result, the Carp Management Program (CMP) was established to contain, control, and ultimately eradicate carp from the lakes. Through the development of various techniques over 12 years (1995-2007), a complete eradication of carp from Lake Crescent was achieved using an integrated approach. Efforts were then focused on the much larger Lake Sorell. Using the proven strategies implemented in Lake Crescent, improvements were made to increase catch and inhibit spawning more effectively. The techniques included intensive gill netting, biotelemetry, electro-fishing, spawning habitat barriers, and traps. After 28 years, and the removal of 41,504 carp from Lake Sorell, and 7,797 carp from Lake Crescent, functional eradication of carp from Tasmania was declared. Eradication efforts have been supported by the prevalence of the jelly gonad condition (JGC) in male carp, which causes sterility in the advanced stages. Any remaining carp in Lake Sorell are likely to be either female or sterile JGC males, with the last fertile male caught in December 2018. Annual juvenile carp surveys in Lake Sorell indicates that there has not been a significant spawning event since 2009, leading to the conclusion that the remaining carp are unable to breed. Both lakes are now open to the public, with the aim to restore Lake Sorell back to its previous form as a popular recreational fishery, and to allow the endemic golden galaxias to flourish.

Taxonomic review of the pipefish genus *Corythoichthys* Kaup, 1853 (Syngnathiformes: Syngnathidae) in the Pacific Ocean

Yuki, Daijiro[1]; Endo, Hiromitsu[2]; Motomura, Hiroyuki[3]

[1] *The United Graduate School of Agricultural Sciences, Kagoshima University, Japan*

[2] *Laboratory of Marine Biology, Faculty of Science and Technology, Kochi University, Japan*

[3] *The Kagoshima University Museum, Japan*

The pipefish genus *Corythoichthys* (Syngnathiformes: Syngnathidae), including 19 nominal species, is reviewed taxonomically based on 512 specimens from the Pacific Ocean. The present study recognized 12 valid and two undescribed species in the genus: *C. amplexus* Dawson and Randall, 1975, *C. benedetto* Allen and Erdmann, 2008, *C. conspicillatus* (Jenyns, 1842), *C. flavofasciatus* (Rüppell, 1838), *C. haematopterus* (Bleeker, 1851), *C. insularis* Dawson, 1977, *C. intestinalis* (Ramsay, 1881), *C. nigripectus* Herald, 1953, *C. ocellatus* Herald, 1953, *C. paxtoni* Dawson, 1977, *C. polynotatus* Dawson, 1977, *C. schultzi* Herald, 1953, and *Corythoichthys* sp. 1 and sp. 2. Our study revealed that 200 specimens previously identified as "*C. haematopterus*" from Japan included *C. haematopterus*, *C. intestinalis*, and *C.* sp.1: *C.* sp. 1 can be distinguished from the former two species by distance between the posterior margin of the orbit and tip of pectoral-fin base (DPP) (100.4–124.6% of snout length in *C.* sp. 1 vs. 79.1–100% in *C. haematopterus* and 81.8–99.7% in *C. intestinalis*), modal trunk ring count (17 vs. 17 and 16), and tail ring count [35–39 (usually 37 or 38) vs. 31–36 (34–36) and 33–35 (34 or 35)]. *Corythoichthys* sp. 2 is similar to *C. intestinalis* but differs from the latter by DPP (100.2–119.6% of snout length in *C.* sp. 2 vs. 81.8–99.7% in *C. intestinalis*).

4.3A Themed Session B: Ecology of Indo-Pacific Fishes, 260-115, November 23, 2023, 10:30 AM - 12:30 PM

Submarine groundwater discharge drives changes in reef fish community structure and function

Zeff, Maya[1]; Barnas, Danielle[2]; Lee, Renee[3]; Silbiger, Nyssa J.[4]

[1]*Department of Ecology and Evolutionary Biology, University of California, Santa Cruz, USA*

[2]*Hawaiʻi Institute of Marine Biology, University of Hawaiʻi at Mānoa, Kāneʻohe, Hawaiʻi , USA*

[3]*Cornell University, New York, USA*

[4]*Department of Biology, California State University, Northridge, USA*

Submarine groundwater discharge (SGD) is a widespread phenomenon of nearshore coral reefs and a key driver of environmental change in these ecosystems. SGD is associated with unique shifts in temperature, salinity, and carbonate chemistry, yet there is little information on its role in reef dynamics and ecosystem functioning. This study characterized reef fish community composition and herbivory across a gradient of SGD in tropical coral reef lagoons in Mo'orea, French Polynesia using paired camera surveys and herbivory assays. Proximity to SGD significantly altered community structure, where high SGD habitats were characterized by high diversity and distinct fish communities. Tide-driven diel changes in groundwater significantly increased feeding frequency and shifted feeding regimes from benthic herbivory-dominated to planktivory-dominated, due to species turnover and the utilization of dietary plasticity in relevant species. Fishes consistently preferred algae from near groundwater seeps compared to algae grown in ambient conditions during herbivory assays. Algal nutrient composition was also affected by SGD exposure; nitrogen concentrations and isotopic ratios ($\delta^{15}N$) increased with proximity to groundwater, likely improving algal palatability and driving observed differences in herbivory. Our results demonstrate that SGD plays a key role in the structure and function of reef fish communities, highlighting the effects of groundwater springs on coral reef processes.

Poster Function, OGGB Level 0 Foyer, November 21, 2023, 4:15 PM - 6:30 PM

A chromosome-level genome assembly of the Antarctic lanternfish *Electrona antarctica*: a resource for adaptation and conservation studies on polar fish

Zhang, Jie[1*]; Li, Xuanzhao [1, 2]; Qi, Jiwei[1]
[1] *Institute of Zoology, Chinese Academy of Sciences, Beijing, China*
[2] *School of Life Sciences, Hebei University, Baoding, China*

Mesopelagic fishes—the small fishes inhabiting in the ocean's twilight zone, comprising an enormous biomass and playing an important role in the open-ocean ecosystem, with major gaps in our knowledge of their ecology and adaptations. Antarctic lanternfish *Electrona antarctica* belongs to the group known as Mesopelagic fishes and is the most abundant, resourceful, and schooling species of Myctophidae living in the Antarctic ocean. In this study, we produced a high-quality chromosome-level genome of *E. antarctica* by using PacBio CCS (circular consensus sequencing) and Hi-C (high-throughput chromosome conformation capture) technology. The final assembly genome size is 1.38Gb, and 1.27Gb (91.81%) of the assembly was placed on 24 chromosome groups, with contig N50 and scaffold N50 values of 917Kb and 56Mb respectively and containing 50.93% repetitive sequences. A total of 44975 protein-coding genes were predicted and annotated. A variety of methods have shown that the assembled genome of the *E. antarctica* has high integrity and accuracy, and the genome is also the first chromosome-level genome in the family Myctophidae as well as in the order Myctophiformes. A phylogeney with related species, demographic history as well as gene family expansion, contraction and the convergence of evolutionary genes in *E. antarctica* were also detected. Our assembled genome provides a valuable tool for future species and clade specific research in additional to comparative studies addressing the ecological adaptation and conservation genetics in polar fish.

Chasing the Unknown: Cavefishes

Zhao, Yahui

Insititute of Zoology, Chinese Academy of Sciences, Beijing, China

Cavefishes, or hypogean fishes, are a distinctive group of fishes restricted to subterranean environments for at least for part of their lives. Based on their troglomorphism, which includes morphological adaptations to the cave environment such as the reduction or loss of eyes and pigmentation, cavefishes can be divided to two types: stygobites (troglomorphic) and stygophiles (non-troglomorphic). China is home to the highest number of cavefish species in the world, with more than 80 stygobitic species out of about 170 cavefish species. As our fieldwork continues, more species are being found and described. All of these cavefish species are endemic to China. With the exception of *Onychostoma macrolepis* in north China, all species are found in southwest China, mostly in the karst environment of the Yunnan-Guizhou Plateau. *Sinocyclocheilus*, the largest cavefish genus, has experienced rapid evolution and diversification. Species from this genus possess horns and humpbacks (i.e. horn-like structures and hyperdevelopment of a dorsal protuberance similar to a humpback), probably resulting from parallel evolution. Sympatric distribution of Chinese cavefishes is common, and sometimes several species are found in the same cave or subterranean river. Caves and karsts are very fragile, balanced habitats, and cavefish species are extremely sensitive to environmental change. Threats from rapid economic growth have increased the need for conservation efforts for cave-dwelling communities in recent decades. Conservation of Chinese cavefishes is an urgent issue.

4.4B Themed Session I Novel Methods and Techniques Advancing our Understanding of Fish Biology, 260-092, November 23, 2023, 1:30 PM - 3:00 PM

Anatomy of adaptation: exploring the internal structure of locomotor fins in the terrestrial mudskipper, *Periophthalmus argentilineatus*, using contrast enhanced micro-CT

Ziadi-Künzli, **Fabienne**[1]; Maeda, Ken[2]; Puchenkov, Pavel[3]; Venkadesan, Madhusudhan[4]; Bandi, Mahesh[1]

[1]*Nonlinear and Non-equilibrium Physics Unit, Okinawa Institute of Science and Technology Graduate University, Okinawa, 904-0495, Japan.*
[2]*Marine Eco-Evo-Devo Unit, Okinawa Institute of Science and Technology Graduate University, Okinawa, 904-0495, Japan.*
[3]*Scientific Computing & Data Analysis Section, Okinawa Institute of Science and Technology Graduate University, Okinawa, 904-0495, Japan.*
[4]*Department of Mechanical Engineering and Materials Science, Yale University, New Haven, CT 06520, USA.*

Mudskippers represent an extant group of ray-finned fishes with an amphibious lifestyle, serving as exemplars for the evolution of amphibious capability in teleosts. Comprehensive anatomical mapping, detailing both soft and hard tissues within their propulsive fins, is essential for enhancing our understanding of terrestrial locomotor adaptations in fish. However, data on such musculoskeletal anatomy remains limited. In this study, we utilized high-resolution contrast enhanced X-ray computed tomography to investigate the barred mudskipper, *Periophthalmus argentilineatus*. This technique allowed to structurally reconstruct and compare the pectoral, pelvic, and caudal fins of this species with those of other aquatic gobies, with a spatial resolution of 2.4 – 24.1 µm.

Our anatomical investigations unveiled a distinct increase in the complexity of the pectoral and pelvic fin structures in *P. argentilineatus* compared to other gobies. This complexity is characterized by a marked differentiation of fin muscle anatomy, an expansion of muscle volume, and the presence of aponeuroses adhering to pectoral fin rays. Along with these muscular enhancements, we observed substantial skeletal modifications, such as a shoulder-pelvic joint, enlarged proximal radials in the pectoral fin and thickened fin rays, which contribute to the structural integrity necessary for terrestrial movement.

The adaptations in the paired fins, and to a lesser extent, the caudal fin, are particularly striking, demonstrating an accommodation for gravitational forces during substrate-based locomotion. This suggests strong selective pressure for these enhancements in terrestrial environments. These adaptive traits, evident in extant fishes, may have been pivotal during the early evolution of tetrapodomorph fishes.

Phenotypic plasticity in Clark's Anemonefish *Amphiprion clarkii* pigmentation in response to host anemones

Zwahlen, Jann[1]; Mercader, Manon[1], Herrera Sarrias, Marcela[1], Laudet, Vincent[1,2]

[1]*Okinawa Institute of Science and Technology, Onna-son, Okinawa, Japan*

[2]*Institute of Cellular and Organismic Biology (ICOB), Academia Sinica, Jiaoxi, Yilan, Taiwan*

Acclimation – the process of an individual organism adapting to novel environmental conditions – is limited by the scope of the organism's capacity of phenotypic plasticity. Especially in times of the current global change it is crucial for an organism to be able to acclimate to survive and thrive. However, if a plastic phenotype gets incorporated genetically, for instance via genetic assimilation, this plasticity will be lost.

The anemonefish *Amphiprion clarkii* presents an exciting opportunity to study phenotypic plasticity, since it is the anemonefish with the widest distribution globally, and the only fish that can live symbiotically in all giant sea anemone species. *A. clarkii* in *Stichodactyla* anemones are completely black apart from their white bars and tail, while fish living in *Heteractis* and *Entacmaea* are orange anterior-ventrally. Interestingly, *A. clarkii* from the isolated Ogasawara islands (Japan) are also black, even though their associated host (*Entacmaea*) would suggest the prevalence of the orange morph.

We demonstrate that the colour polymorphism is a phenotypic plasticity that is retained in adult fish. When transferring orange fish from *Heteractis* to *Stichodactyla*, they change their colour to black rapidly within 2 months. In the other direction, the colour change is slower, but they steadily turn more orange within several months.

Using the transcriptome of plastic *A. clarkii* from different host anemones, and a whole-genome sequencing from plastic and Ogasawara *A. clarkii*, we describe genes involved in the phenotypic plasticity and verify whether they experienced genome-level modifications in the Ogasawara population.