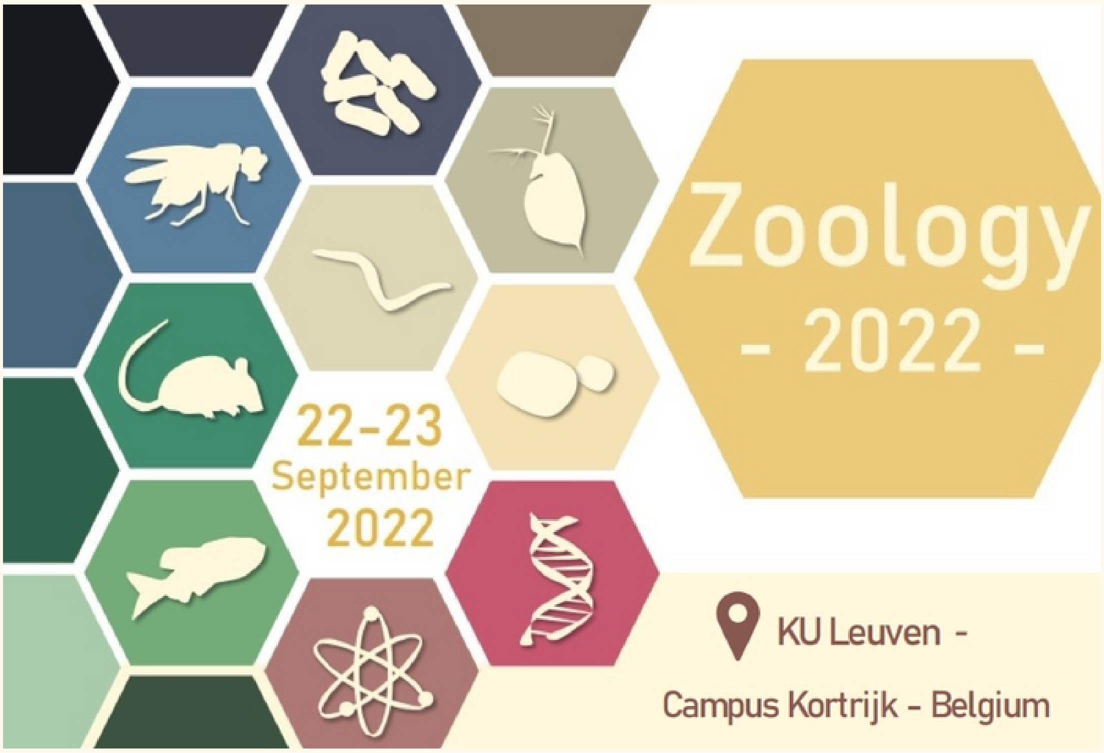
22-23 SEPTEMBER 2022

# BENELUX CONGRESS OF ZOOLOGY 2022

## DIVERSITY OF MODEL ORGANISMS AND MODEL ORGANISMS FROM DIVERSITY

MOLECULAR, PHYSIOLOGICAL AND ECOLOGICAL PERSPECTIVES



BZS
Royal Belgian Zoological Society

KU LEUVEN kulak

Vlaanderen
verbeelding werkt

fwo EVENET

## ZOOLOGY 2022

*SINCE 29 YEARS, THE **ROYAL BELGIAN ZOOLOGICAL SOCIETY (RBZS)** AND THE **ROYAL ZOOLOGICAL SOCIETY OF THE NETHERLANDS (KNDV)** ORGANIZE THIS CONGRESS TOGETHER TO GIVE YOUNG, BUT ALSO SENIOR RESEARCHERS THE FLOOR TO PRESENT THEIR MASTER, PHD AND POSTDOCTORAL WORK. THIS YEAR WE WILL EXPLORE THE **ZOOLOGICAL DIVERSITY** STUDIED AT OUR UNIVERSITIES AND RESEARCH INSTITUTES.*

The aim is to connect researchers in Zoology throughout Belgium and abroad, providing a network for junior and senior members, who benefit through contacts and collaboration.

# Symposia

**Session 1: Ecotoxicology**

**Session 2: Ecophysiology and stress adaptation (inclusive parasitism)**

**Session 3: Biomechanics and -mimetics**

**Session 4: Functional Morphology**

**Session 5: Marine Biology**

**Session 6: Open Symposium**

**Session 7: Evolutionary Genomics**

**Session 8: Eco-Evolutionary interactions/dynamics**

**Session 9: Symbiosis inclusive host-microbiome interactions**

# Thursday 22 September 2022

| | | | | | | |
|---|---|---|---|---|---|---|
| 09h00 | | | | | | |
| 09h15 | Plenary: Emilia Santos +<br>intro and RBZS/Kets prize winner announcement by Ellen Decaestecker<br>KNDV prize winner announcement by Jan Kammenga | | | | | |
| 09h30 | | | | | | |
| 09h45 | | | | | | |
| 10h00 | | | | | | |
| 10h15 | S4. Morphology | Anthony Herrel | S2. Eco-physiology | Wilco Verberk (KNDV prize) | S8. Eco-evo | Dries Bonte |
| 10h30 | | | | | | |
| 10h45 | | Lia Baeteman | | Michiel de Groot | | Karen Bisschop |
| 11h00 | | Yann Delaunois | | Thomas Enriquez | | |
| 11h15 | coffee break (11h15 - 11h45) | | | | | |
| 11h30 | | | | | | |
| 11h45 | S1. Eco-toxicology | Marianna Pinzone | S2. Eco-physiology | Antoine Gekière (Kets public prize) | S7. Evolutionary Genomics | Steven Van Belleghem |
| 12h00 | | | | | | |
| 12h15 | | Anthony Mathiron | | Noelia Valderrama Bhraunxs | | Valentina Burskaya |
| 12h30 | | Sumedha Roy | | Laurie Araspin | | |
| 12h45 | | Johanna Lapere | | | | Sophie Boerman |
| 13h00 | lunch break (13h00 - 14h00) | | | | | |
| 13h15 | | | | | | |
| 13h30 | | | | | | |
| 13h45 | | | | | | |
| 14h00 | S4. Morphology | Mona Goharimanesh | S6. Open Symposium | Lisa Van Linden (Kets prize) | S7. Evolutionary Genomics | Eve Seuntjens |
| 14h15 | | Laurent Mittelheiser | | | | |
| 14h30 | | Michaël Nicolaï | | Jonathan Richir | | Hugo Gante |
| 14h45 | | Priscila Rothier | | | | |
| 15h00 | | Arthur Van Damme | | Victoria Moris | | Alexander Hooft van Huysduynen |
| 15h15 | | Merel Van Gorp | | Heleen Maetens | | Alice Mouton |
| 15h30 | coffee break (15h30 - 16h00) | | | | | |
| 15h45 | | | | | | |
| 16h00 | S5. Marine Biology | Loïc Michel | S6. Open Symposium | Aditi Gurung | S7. Evolutionary Genomics | Els De Keyzer |
| 16h15 | | | | | | |
| 16h30 | | Ulrich Martin | | Youri Nonclercq | | Hannes Svardal |
| 16h45 | | Noé Wambreuse | | Jaysmita Saha | | |
| 17h00 | Poster session with coffee and apero (17h00 - 19h00) | | | | | |
| 17h15 | | | | | | |
| 17h30 | | | | | | |
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| 18h00 | | | | | | |
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| 18h30 | | | | | | |
| 18h45 | | | | | | |
| 19h00 | Pizza dinner<br>& party at Pizzeria Sofia in Kortrijk | | | | | |

| | Friday 23 September 2022 | | | | | |
|---|---|---|---|---|---|---|
| 09h00 | Plenary: Dario Valenzano<br>intro and Pairi Daiza prize winner announcement by Frederic Silvestre | | | | | |
| 09h15 | | | | | | |
| 09h30 | | | | | | |
| 09h45 | | | | | | |
| 10h00 | Plenary: Christian Voolstra intro by Stéphane Roberty | | | | | |
| 10h15 | | | | | | |
| 10h30 | | | | | | |
| 10h45 | | | | | | |
| 11h00 | coffee break (11h00 - 11h30) | | | | | |
| 11h15 | | | | | | |
| 11h30 | S3. Biomechanics and -mimetics | Julian Langowski (KNDV prize) | S9. Symbiosis | Martijn Callens | S8. Eco-evo | Marie Verheye |
| 11h45 | | | | | | |
| 12h00 | | Sam Van Wassenbergh | | Manon Coone | | Pascal Hablützel |
| 12h15 | | | | Naina Goel | | |
| 12h30 | | Loïc Kever | | Mathilde Scheifler | | Benjamin Lejeune |
| 12h45 | lunch break (12h45 - 13h45) | | | | | |
| 13h00 | | | | | | |
| 13h15 | | | | | | |
| 13h30 | | | | | | |
| 13h45 | S6. Open Symposium | Alessandra Whaite | S9. Symbiosis | Guillaume Caulier | S5. Marine Biology | Laurent Duchatelet |
| 14h00 | | | | | | |
| 14h15 | | Luka Vantomme | | Sarah Jorissen | | Jérôme Delroisse |
| 14h30 | | Maarten Van Steenberge | | Alexia Lourtie | | |
| 14h45 | | Xavier Raick | | Ellen Decaestecker | | Caroline Zandecki |
| 15h00 | short break (15h00-15h15) | | | | | |
| 15h15 | Plenary + introduction to PhD workshop: Sofie Claerhout | | | | | |
| 15h30 | PhD workshop by the Floor is Yours (Workshop ‘Pitching your research with impact’) + RBZS/KNDV Board meeting (15h30 - 18h00) | | | | | |
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# SCHEDULE OF TALKS

## Day 1 of congress: 22.09.2022 Thursday

**09u15 - 10u15 Plenary**

- **Emilia Santos**
  On the variation of colour patterning within and between species of cichlid fishes

***Intro and RBZS/Kets prize winner announcement by Ellen Decaestecker***

***KNDV prize winner announcement by Jan Kammenga***

### Session 4: Functional Morphology

location: A301

- **10u15 - 10u45 Anthony Herrel**
  Convergence in axial muscle morphology and locomotor mechanics in relation to habitat use in snakes.

- **10u45 - 11u00 Lia Baeteman**
  Regionalization of the axial skeleton in amphisbaenians (Squamata)

- **11u00 - 11u15 Yann Delaunois**
  The spiky exoskeleton of the spearing mantis shrimp; comparative study of 3 puncturing bio-tools.

### Session 2: Ecophysiology and stress adaptation inclusive parasitism

location: A305

- **10u15 - 10u45 Wilco Verberk**
  An oxygen perspective to explain the thermal biology of ectotherms

- **10u45 - 11u00 Michiel de Groot**
  Parasitized parasites of bats: a tritrophic system

- **11u00 - 11u15 Thomas Enriquez**
  Pupal size as a proxy for fat content in laboratory-reared and field-collected *Drosophila* species

## Session 8: Evolutionary Ecology inclusive Eco-Evolutionary dynamics

location: A307

- **10u15 - 10u45 Dries Bonte**
  Understanding biogeography from experimental populations

- **10u45 - 11u15 Karen Bisschop**
  Insights into favourable conditions for adaptation using experimental evolution with model organisms.

**11u15 - 11u45  Coffee break**

## Session 1: Ecotoxicology

location: A301

- **11u45 Marianna Pinzone**
  Evaluating the role of local mercury sources on spatial and temporal pollution trends in marine predators living in a changing arctic.

- **12u15 Anthony Mathiron**
  Does early life exposure to neurotoxic permethrin affect phenotypic traits in juveniles of the mangrove rivulus *Kryptolebias marmoratus*?

- **12u30 Sumedha Roy**
  Organophosphate induced disruption of female reproductive homeostasis in a non-target model insect *Drosophila melanogaster*.

- **12u45 Johanna Lapere**
  Influence of microfibers on *Daphnia magna* performance, populations and biofilms.

## Session 2: Ecophysiology and stress adaptation inclusive parasitism

location: A305

- **11u45 Antoine Ghekière**
  Poison or Potion: Effects of Sunflower Phenolamides on Bumble Bees and their Gut Parasite.

- **12u15 Noelia Valderrama Bhraunxs**
  Quality control of citizen-collected data in bilharzia snail control: lessons from Lake Albert, Uganda.

- **12u30 Laurie Araspin**
  The impact of thermal environment on locomotor performance in native and invasive populations of *Xenopus laevis*.

## Session 7: Evolutionary Genomics

location: A307

- **11u45 Steven Van Belleghem**
  High level of novelty under the hood of convergent evolution

- **12u15 Valentina Burskaia**
  Does hybridization facilitate explosive speciation of Lake Baikal amphipods?

- **12u45 Sophie Boerman**
  Solving the missing pieces of the gharial puzzle: new phylogenetic framework combining morphological, molecular, and biostratigraphic data to unravel the evolution of long-snouted crocodylians.

**13u00 - 14u00 Lunch break**

## Session 4: Functional Morphology

location: A301

- **14u00 Mona Goharimanes**
  How phylogeny and ecological adaptation describe variation in ophiuroid (Echinodermata: Ophiuroidea) vertebrae

- **14u15 Laurent Mittelheiser**
  Diversity and evolution of color patterns in the goatfishes (Perciforms, Mullidae)

- **14u30 Michaël Nicolaï**
  Evolution of multiple colour mechanisms enhances opportunities for ongoing speciation

- **14u45 Priscila Rothier**
  Ecological and developmental constraints foster the morphological diversity of the mammalian limb

- **15u00 Arthur Van Damme**
  Studying the form diversity of sagittae in teleost fishes by using 3D landmark-based geometric morphometrics

- **15u15 Merel Van Gorp**
  Importance of the keels of boxfish for passive stability during swimming

## Session 6: Open Symposium

location: A305

- **14u00 Lisa Van Linden**
  Learning with Lacertids: comparing cognition across species.

- **14u30 Jonathan Richir**
  The monitoring of recreational hand-fishing in eulittoral boulder fields.

- **15u00 Victoria Moris**
  Finding the receptor of sperm-release pheromone in the marine worm *Platynereis dumerilii* to shed light on the impact of ocean acidification on chemical communication.

- **15u15 Heleen Maetens**
  Introducing *Enteromius* as a new model organism to study speciation in riverine fishes

## Session 7: Evolutionary Genomics

location: A307

- **14u00 Eve Seuntjens**
  CELL TYPE DIVERSITY IN A DEVELOPING OCTOPUS BRAIN

- **14u30 Hugo Gante**
  Improving whole biodiversity monitoring with eDNA metagenomics

- **15u00 Alexander Hooft van Huysduynen**
  Characterising fisheries induced evolution of Malawi cichlids

- **15u15 Alice Mouton**
  The pilot project of the European Reference Genome Atlas (ERGA) initiative

**15u30 - 16u00 Coffee break**

## Session 5: Marine Biology

location: A301

- **16u00 Loïc Michel**
  Food web structure and trophic interactions at the recently discovered deep-sea La Scala hydrothermal vent field (SW Pacific)

- **16u30 Ulrich Martin**
  An insight into the trophic ecology of chimaeras from New-Zealand

- **16u45 Noé Wambreuse**
  The complex immune system of sea cucumbers: a cell story

## Session 6: Open Symposium

location: A305

- **16u00 Aditi Gurung**
  First come first served: Strain dependent priority effects in the gut microbiome assembly of host *Daphnia* and associated fitness

- **16u30 Youri Nonclercq**
  Blind like a sea-cucumber? Opsin-based extraocular photoreception in holothurians (Holothuroidea, Echinodermata)

- **16u45 Jaysmita Saha**
  Investigating the role of structural variants in rapid diversification of Lake Malawi cichlids.

## Session 7: Evolutionary Genomics

location: A307

- **16u00 Els De Keyzer**
  Did hybridisation fuel the adaptive radiation of Silversides in the Malili lakes?

- **16u30 Hannes Svardal**
  Genomic consequences of domestication of the Siamese fighting fish – A promising new model organism.

**17u00 – 19u00 Poster session with coffee and apero**

**19u00 Pizza dinner & party at Pizzeria Sofia in Kortrijk**

## Day 2 of congress: 23.09.2022 Friday

### 09:00h - 10:00h Plenary

- **Dario Valenzano**
  Evolutionary ecology of aging

***Intro and Pairi Daiza prize winner announcement by Frédéric Silvestre***

### 10u00 – 11u00 Plenary

- **Christian Voolstra**
  Coral reefs and climate change - Mitigating the ecological collapse

***Intro by Stéphane Roberty***

**11u00-11u30 coffee break**

### Session 3: Biomechanics/Biomimetics

location: A301

- **11u30 Julian Langowski**
  An integrative study of tree frog attachment: Structures, mechanisms, and biomimetic potential

- **12u00 Sam Van Wassenbergh**
  Vena contracta, central jets, and suction feeding in fish

- **12u30 Loïc Kever**
  Morphological diversity and biomechanical proprieties of lizard osteoderms

### Session 9: Symbiosis inclusive host-microbiome interactions

location: A305

- **11u30 Martijn Callens**
  Environmental dependency of host-microbiota interactions in *Daphnia magna*

- **12u00 Manon Coone**
  Genotype specific and microbiome effects of hypoxia in the model organism *Daphnia magna*.

- **12u15 Naina Goel**
  Choose your diet wisely: the interplay between gut microbiome and host epigenome under cyanobacterial stress in *Daphnia*.

- **12u30 Mathilde Scheifler**
  Investigating the role of external microbiota in the *Sparidae-Lamellodiscus* host-parasite system

## Session 8: Eco-evo

location: A307

- **11u30 Marie Verheye**
  Antarctica as an evolutionary incubator? Phylogenetic comparative study of the amphipod family Iphimediidae on the Antarctic shelf

- **12u00 Pascal Hablützel**
  Simulating adaptive evolution of spatially-distributed populations to climate-driven perturbations: a genomically-explicit modeling approach

- **12u30 Benjamin Lejeune**
  Testing a new hypothesis regarding the advantage of an important developmental process in evolution: Progenesis.

**13u00 – 14u15 Lunch break**

## Session 6: Open Symposium

location: A301

- **13u45 Alessandra Whaite**
  The byssus and byssal-producing glands of the silverlip pearl oyster *Pinctada maxima* (Jameson, 1901)

- **14u15 Luka Vantomme**
  Sea star (Asteroidea) diversity in the Magellanic Region (South-Chile) and their affinities within the Southern Ocean.

- **14u30 Maarten Van Steenberge**
  Revisiting the KEA lakes : A cradle for African ichthyofaunal diversity?

- **14u45 Xavier Raick**
  Diversity of mesophotic coral reefs fish fauna through passive acoustics

## Session 9: Symbiosis inclusive host-microbiome interactions

location: A305

- **13u45 Guillaume Caulier**
  Mutualistic relationship between the amphipod *Stenula normanni* (Stephensen, 1931) and the nephtheid coral *Gersemia rubiformis* (Ehrenberg, 1834)

- **14u15 Sarah Jorissen**
  Does the gut microbiome contribute to the pace-of-life and associated tolerance to a pathogen in damselfly larvae?

- **14u30 Alexia Lourtie**
  Marine symbiotic association: may the host recognition be possible since the early stage of symbiont life?

- **14u45 Ellen Decaestecker**
  The role of the microbiome in eco-evo interactions: *Daphnia* and its microbiome as a model.

## Session 5: Marine Biology

location: A307

- **13u45 Laurent Duchatelet**
  Physiological regulation of bioluminescence through photo-perception: an overview and perspectives.

- **14u15 Jérôme Delroisse**
  Where does your (luciferase) gene come from? Evolution of light-emitting enzymes in animals

**15u - 15u15 short break**

**15u15 - 15u30 Plenary and introduction to PhD workshop**

- **Sofie Claerhout**
  CSY: from Crime Scene to Communicating Science

**15u30 - 18u00 PhD workshop by the Floor is Yours (Workshop 'Pitching your research with impact') + RBZS/KNDV Board meeting**

# Poster Topics

**Justine Dewaele**
ASPI – Wild bees in the city : Urban pollutant effects on the health of insects and plant-pollinator interactions

**Martin Dogniez**
Investigation of the potential of two sea cucumber species, *Holothuria polii* et *Holothuria tubulosa*, as bioindicators in northwestern Mediterranean: the case of trace elements and microplastics

**Gil Gallego**
Delayed effects of early life exposure to the neurotoxic compound permethrin in the mangrove rivulus, *Kryptolebias marmoratus*

**Julia Grinyo-Escuer**
MERCURY AND CIGUATOXINS MEASUREMENTS IN TWO FISH SPECIES FROM DIFFERENT LAGOONS OF FRENCH POLYNESIA WITH EVALUATION FOR HUMAN CONSUMPTION

**Marine Pyl**
Transfer assessment of PCB#153 sorbed onto HDPE microplastics to sea urchins tissues using radiotracers

**Rina Raharinaivo**
Differentiation of petrosourced plastic microfilaments from organic microfilaments by edax in environmental samples

**Simon Van Den Brouck**
Permethrin short and long-term impacts of early-life exposure on the turquoise killifish (*Nothobranchius furzeri*): behavioral and molecular approaches

**Vera Hörger**
THE SEAHORSE SKELETON – MODELLING THE STRENGTH OF THE BONY PROTECTIVE ARMOUR AROUND THE SPINE

**Tim Andries**
CANARIES BECOME MORE SKILLED AT PROCESSING SEEDS WITH AGE AND APPLY DIFFERENT SKILLS FOR DIFFERENT SEEDS

**Mona Goharimanesh**
Investigation into the horizontal arm motion in brittle stars (Echinodermata: Ophiuroidea)

**Guillaume Corbisier**
Morphofunctional analysis and comparision of the stone canal in Holothuroidea

**Gerben Debruyn**
Reconstructing fossil mammal hair coloration

**Ali Murat Elagoz**
Cephalopod approach of evolving a complex brain: morphological and molecular characterization during octopus development

**Bruno Frédérich**
Variation of the trophic ecology in two teleost species associated to seagrass beds at Toliara Reef, Madagascar

**Pablo Martinez-Soarez**
Diversity in mouthpart morphology and trophic niche in Antarctic Iphimediidae (Amphipoda)

**Nathan Puozzo**
MetaMorphos: exploring three-dimensional metazoan body plans through virtual reality

**Hassane Rolland**
Morphological study of the silk glands in two orb web spider species

**Charlotte Nuyt**
ULTRASTRUCTURE AND CYTOLOGICAL CHANGES OF THE KITEFIN SHARK, *DALATIAS LICHA*, PHOTOPHORES DURING LIGHT EMISSION

**Anne Vanhove**
Study of luminescence control and photo-perception in the marine polychaete *Tomopteris helgolandica* (Tomopteridae)

**Ninon Lecoquierre**
Stomach content analysis of two deep-sea shark species: *Etmopterus spinax* and *Galeus melastomus*

**Aschalew Alelign**
SPATIAL AND TEMPORAL DISTRIBUTION OF GREAT WHITE PELICAN (*PELECANUS ONOCROTALUS*) IN AND AROUND LAKE TANA

**Marine Banse**
Comparative study of sound production in Holocentrids

**Mathilde Delacoux**
VARIABILITY IN LEARNING ABILITIES IN RELATION TO PERSONALITY AND EPIGENETIC MECHANISMS IN THE MANGROVE RIVULUS (*Kryptolebias marmoratus*)

**Emilie Duthoo**
MATURATION OF MARINE ADHESIVE PROTEINS: INVOLVEMENT OF TYROSINASES IN MUSSELS AND TUBEWORMS

**Antoine Flandroit**
Ethology in Pycnogonids: the case of the invasive *Ammothea hilgendorfi*

**Michiel Lathouwers**

Rush or relax: migration tactics of a nocturnal insectivore in response to ecological barriers

**Aina Le Don**

SPATIAL OBSERVATION OF THE GREAT REEF OF TOLIARA (MADAGASCAR) FROM 1985 TO 2021

**Sarah Schmidlin**

Friend or foe? – Larvae of the invasive Pacific oyster (*Magallana gigas*) trade off predator and conspecific cues in their decision making for settlement

**Sofie Claerhout**

Opt-in or out? Public opinion on the use of human genetics for forensic familial DNA searching

**Goussanou Appolinaire**

Biodiversity of decapod crustaceans in Benin: Taxonomic assessment and zoogeography

**Karine Lalaina Mahefarisoa**

A One Health approach to protected areas management and governance.

**Lore Van Craenenbroeck**

INTRODUCING THE PROJECT HABITANT – PAST AND FUTURE HABITABILITY IN ANTARCTIC LAKES: SUCCESSION, COLONIZATION, EXTINCTION AND SURVIVAL IN GLACIAL REFUGIA

**Pietro Antolini**

Evolution of genome size in a fast adaptive radiation

**Mondal Niladri**

Variation in genome size and body size across teleosts

**Anissa El Mojahid**

Population genetic of the forest dormouse, *Dryomys nitedula* in Bulgaria

**Ann Vanderheyden**

A Barcoding Facility for Organisms and Tissues of Policy Concern

**Manon Bayat**

Insight into the snow petrel Pagodroma nivea ecology through population genetics and habitat suitability analyses

**Leona Milec**

Long range and long read sequencing enable comparative genomics of two freshwater herring species of Lake Tanganyika

**Justine Bélik**
Role of sexual conformism in learned sexual preferences in a polyphenic butterfly facing alternating wet and dry seasons and male mating partners

**Manon Geerts**
A genomic view of the evolution and biogeography of the ichthyofauna of the Albertine rift: *Clarias gariepinus*

**Shira Houwenhuyse**
Local gut microbiome of *Daphnia* helps to clear toxic cyanobacterial blooms

**Ruben Schols**
Towards a better understanding of the snail-trematode-microbiome interactions driving schistosome transmission in Senegal

**Margaux Jossart**
Facultative endosymbiont, a valuable guest in the multitrophic system "plant-aphid-ant"

**Maud Micha**
What is the RBZS Young Zoologist Group?

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APECS Belgium: an opportunity for early career scientists

# Plenary Speakers

# On the variation of colour patterning within and between species of cichlid fishes

EMÍLIA SANTOS

The evolution of novel morphologies is a key component of organismal diversification, yet the genetic and developmental mechanisms underlying their evolution remain understudied. We address this question in a highly diverse vertebrate model system, cichlid fishes. We specifically focus on variation of a set of brightly pigmented egg-spots on male anal fins that play a key role in the territorial and breeding behaviour of around 1,500 species of cichlids. Using intra and inter-specific genomic comparisons we identified loci associated with egg-spot number variation. Interestingly, the loci associated with variation within species do not overlap with inter-specific mapping approaches, suggesting that in this system variation within populations does not contribute to variation between species. The identified loci are known to be involved in the physiology and development of pigment cells, here we show the progress of the genetic and developmental dissection of candidate gene function and trait ontogeny.

# Coral reefs and climate change - Mitigating the ecological collapse

CHRISTIAN VOOLSTRA

Coral reefs are at the brink of ecological collapse. The primary driver of reef degradation is coral bleaching, the breakdown of the symbiosis of the coral host and its endosymbiotic algae driven by ocean warming. This is now happening almost annually at a global scale, hastening the need to develop strategies that mitigate the devastating effects of climate change on coral reefs. The seminar will outline our efforts to develop a standardized framework to assess thermal tolerance to identify ecological drivers, metaorganism member species, and molecular mechanisms that contribute to increased stress resilience. A particular emphasis is to identify microbes that denote stress tolerance, which can then be screened for using high throughput approaches to better understand their function, prevalence, and the feasibility for microbiome manipulation.

## Evolutionary ecology of aging

DARIO VALENZANO

African killifishes have emerged over the past few years as a powerful model system to answer open questions in biology of aging, developmental and evolutionary biology. Killifish evolved in a range of environments, from rainforest to savannah water holes that desiccate seasonally. Killifish survive periodic desiccation by evolving an annual life cycle, characterized by a specialized embryonic adaptation (embryonic diapause), where embryos suspend development in the dry mud until the external conditions are safe for them to hatch. Annual killifish that evolved in very dry environments often display short natural lifespan and a wide range of age-related changes, including neurodegeneration, inflammation, fibrosis, immune decline and dysbiosis. In my talk, I will share two main research themes pursued by our research group: 1) how studying killifish ecology and evolution has opened new perspectives to understanding that species' lifespan and aging evolve as a function of past demographic constraints and 2) how an ecological perspective to killifish biology, which focuses on host-microbiome functional interactions, opens new insights into biology of aging, as well as offers novel opportunities for anti-aging interventions.

## CSY: from Crime Scene to Communicating Science

SOFIE CLAERHOUT

**PhD cup winner 2021**
Forensic Genetics, KU Leuven
Interdisciplinary Research, KULAK

Sofie Claerhout is fascinated by genetics, in love with genealogy and driven by a strong sense of justice. She is the first in Belgium to obtain a PhD in Forensic Genetics and examines the only piece of DNA that she does not have herself: the male Y-chromosome. WhY? To provide a last resort in forensic cold cases. The male Y-DNA can serve as a powerful tool to identify the unknown perpetrator through large-scale kinship research. With her CSY research she received the 'best oral presentation' prize at the forensic genetics world conference, she won the Flemish PhD cup together with the audience award and became the 'Krak van Kortrijk' in 2021. Currently, she is in close contact with Minister of Justice to implement DNA kinship testing in our Belgian legislation. Next month, she will publish her CSY research into a public book 'Dader onbekend'. Strong science communication is key. All CSY info can be found on the website: www.CSY-Leuven.be

Twitter: twitter.com/SofieClaerhout
Website: www.CSY-Leuven.be
E-mail: sofie.claerhout@kuleuven.be

## Workshop "Floor is yours"

Hans van de Water

# Symposia

# Convergence in axial muscle morphology and locomotor mechanics in relation to habitat use in snakes.

**HERREL ANTHONY**

Herrel Anthony 1,2,3, Adrien Mathou 1, Vincent Stin 1,4, Ramiro Godoy-Diana 4, Xavier Bonnet 5
1 UMR7179, CNRS/MNHN, 75005 Paris, France
2 Department of Biology, Evolutionary Morphology of Vertebrates, Ghent University, Ghent, Belgium
3 Department of Biology, Functional Morphology, University of Antwerp, Antwerp, Belgium
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With nearly 4000 currently described species, snakes are an incredibly successful radiation of limbless squamates. Despite their apparent uniform external body morphology, they have radiated in many different habitats including terrestrial, arboreal, fossorial and aquatic species. Moreover, snakes use at least four different distinct locomotor modes that are used in different contexts. Despite their interest as models for bio-inspired robotics, relatively little is known on the mechanics of locomotion and the underlying variation in muscle architecture. Here we provide novel data on the architecture of the axial musculature in snakes showing that species using similar habitats show similar functional properties of the muscles. Moreover, the pattern of convergence was strongest for the muscles at mid-body. More anterior and posterior muscle segments were similar across ecological groups. Finally, differences were greatest between aquatic and arboreal snakes with terrestrial species showing intermediate morphologies that overlapped those of aquatic and arboreal species. This suggests particular constraints on the musculature in predominantly arboreal or aquatic snakes. Subsequent analysis of the flow around specialised and non-specialised aquatic snakes during swimming using volumetric particle image velocimetry showed similar patterns to those derived from computational fluid dynamics simulations reported in the literature for anguilliform swimmers. This suggests that the differences in anatomy observed in aquatic species may impact the efficiency of force exchanges between the snake and the fluid rather than the pattern thereof. Supported by the ANR project DRAGON2.

**Functional Morphology**

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# Regionalization of the axial skeleton in amphisbaenians (Squamata)

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Amphisbaenians are fossorial squamates that have evolved morphological adaptations to live underground, such as loss of limbs and body elongation. It is commonly thought that limblessness resulted in little regionalization and heterogeneity in the axial skeleton, the so-called deregionalization. The goal of this study is to determine on a morphological level whether the axial skeleton of amphisbaenians shows different regions by comparing the shape of vertebrae along the body using 3D geometric morphometric approaches and addressing the variability of these vertebrae. To address intra- and interspecific differences between vertebrae and reveal possible patterns of vertebral shape variation along the axial skeleton, five vertebrae from five species (Blanus cinereus, Geocalamusacutus, Monopeltis capensis, Trogonophis wiegmanni and Zygaspis quadrifrons) were analysed. This preliminary study revealed two patterns in the axial skeleton of all amphisbaenians included: the gradual elongation and the decrease of the dorsoventral height of the vertebrae along the antero-posterior axis. The principal component analysis and the qualitative differences confirm the hypothesis that there are intraspecific differences between the vertebrae along the axial skeleton of amphisbaenians. As for interspecific differences, the preliminary results suggest that the shape variation along the vertebral column is the same in the five species. The vertebrae studied can be assigned to three different regions from anterior to posterior: cervical, thoracic, and caudal region. However, more research is needed to support regionalization and to verify if these morphologically determined regions also differ functionally.

**Functional Morphology**

# The spiky exoskeleton of the spearing mantis shrimp; comparative study of 3 puncturing bio-tools.

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From the defensives cacti spines to the offensive felid claws and harpooning honeybee stinger, puncturing tools are found in a wide diversity of living organisms. They fulfil various roles and are based on different biological materials. Among those materials, the arthropod cuticle is often pointed out as the most versatile one. It is made of a complex helicoidal arrangement of chitin-protein fibres embedded into an organo-mineral matrix giving rise to an excellent multifunctional material serving for the organism protection and support and for all other secondary tasks as walking, sensing, or hunting. Among arthropods, impressive examples of puncturing tools can be found in the spearing mantis shrimp, an aggressive hunting crustacean known for its fast spiky appendage designed to impale prey within a fraction of second. This animal has the peculiarity to possess three puncturing tools with different roles but derived from the same basic material. Indeed, in addition to the spearing spikes used for hunting, mantis shrimps also possess defensive back spikes (the uropod spikes) to protect against predators, and maxilliped spikes for food treatment. Each of these tools must cope with specific mechanical challenges and therefore shows distinct structural and compositional adaptations. Following a multiscale structural and compositional analysis, we highlight three key adaptive strategies. All three spikes have the endocuticle subdivided into 3 functional regions. Nevertheless, the ultrastructure and the composition of the superior cuticular layers show divergent features, ranging from highly mineralized exocuticle and reduced epicuticle in the raptorial spike, to an organic and prismatic exocuticle surrounded by a bromine enriched epicuticle in the maxilliped spike and an intermediate structure in the uropod spike. This study gave a unique comparison of three different puncturing tools derived from the same structure, highlighting the incredible versatility of the arthropod cuticle.

Functional Morphology

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# An oxygen perspective to explain the thermal biology of ectotherms

**WILCO VERBERK**

Animals are not randomly distributed in nature, but occur in regular, predictable patterns. Elucidating the species-environment relationships that give rise to such patterns requires the integration of different disciplines, notably ecology, evolution and physiology. Given the large number of species this is a daunting task and so an important question is whether it is possible to distil general principles from work on relatively few well-studied species, which can then be extrapolated to species that have not been studied as extensively?
My research focusses on traits that are linked to both temperature and oxygen (e.g.metabolic rate, hypoxia tolerance and thermal tolerance). Oxygen is vital for aerobic energy metabolism and temperature is considered a master variably, especially for ectotherms, directly affecting physiological processes (e.g. development, growth, fecundity), which in turn impact population persistence, species distributions and ecosystem structure and function. I will explore how variation across species in these ecophysiological traits is related to phylogeny, habitat use or morphology.

Ecophysiology and stress adaptation (inclusive parasitism)

# Parasitized parasites of bats: a tritrophic system

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Parasitism is one of the most common and diverse modes of life, and is of great ecological and evolutionary importance. Still, parasitism remains a relatively understudied area of biology. A unique form of parasitism is hyperparasitism: parasites that parasitize other parasites. Bats (Mammalia: Chiroptera) are host to several lineages of parasites, including flies (Diptera: Hippoboscoidea), obligate blood-sucking parasites that live on a bat host for their entire life. Bat flies themselves may be parasitized by fungi of the order Laboulbeniales (Ascomycota: Laboulbeniomycetes). Tritrophic interactions such as these can alter the patterns of energy flow in food webs and have an impact on population dynamics. In this peculiar system, what makes bats such a good host for parasites and their hyperparasites? How host-specific are these parasites? And how do environmental factors and the type of roost the bat uses influence parasitism by bat flies and Laboulbeniales? We answer these questions by analyzing a TriTrophic Traits database of 12,300 bat flies collected in Europe and Central and South America. Mean parasite prevalence of bat flies by Laboulbeniales was 3.8%. Temperature and humidity affected prevalence significantly, but effects were different between Neotropical and European species, likely indicating the importance of local scale data. Bat roosting behavior also had a significant effect on infection rates; roost permanence, as classified from ephemeral (leaf tents) to permanent (caves and tunnels), was positively correlated to Laboulbeniales infection. Bats also have higher levels of bat fly parasitism in more permanent roosts, and our results imply that the Laboulbeniales follow suit in these more stable environments. With our work, following multi-year, standardized data collection and international collaborations, we hope to shed more light on these unique and intriguing associations, and on community ecology patterns of hyperparasitic systems as a whole.

**Ecophysiology and stress adaptation (inclusive parasitism)**

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# Pupal size as a proxy for fat content in laboratory-reared and field-collected *Drosophila* species

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In arthropods, larger individuals tend to have more fat reserves, but data for many taxa are still missing. For the vinegar fly *Drosophila melanogaster*, only few studies have provided experimental data linking body size to fat content. This is rather surprising considering the widespread use of *D. melanogaster* as model system in biology. Here, we hypothesized that fat content in *D. melanogaster* is positively correlated with body size. To test this, we manipulated the developmental environment of *D. melanogaster* by decreasing food availability (through starvation, crowding and reducing nutrient content of the food medium). We then measured pupal size and quantified fat content of both laboratory-reared *D. melanogaster* and field-caught *Drosophila* species. Reduced food availability indeed led to smaller laboratory-reared pupae that contained less fat. Pupal size was indeed positively correlated with fat content. The same results were obtained for pupae of field-caught *Drosophila* species. As fat reserves are often strongly linked to fitness in insects, further knowledge on the relationship between body size and fat content can provide important information for studies on insect ecology and physiology.

**Ecophysiology and stress adaptation (inclusive parasitism)**

# Understanding biogeography from experimental populations

**DRIES BONTE**

Understanding the processes that generate large-scale patterns of biodiversity is uttermost important to forecast the future fate of populations and species under global change. To date our insights are mostly based on correlative approaches that assume environmental matching through static niche-based processes. The distribution of species and populations along environmental gradients is, however, a dynamic process subject to changes in these gradients as well as to changes in species interactions from trait changes within the species. More-over, since our view on species' distribution patterns is usually based on single (series of) observations it remains difficult to infer whether these patterns emerged by chance or by specific interactions between ecology and evolution. The world is difficult to replicate...

I introduce the use of experimental populations of an arthropod model species (spider mites) as a tool to quantify the relative contribution of evolution, ecology and drift as drivers of range sizes, island colonization-extinction dynamics and metapopulation connectivity.

**Ecotoxicology**

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# Insights into favourable conditions for adaptation using experimental evolution with model organisms.

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Many organisms can deal with our incredibly dynamic world, but it is clear that some populations or some species are more capable to adapt to novel conditions than others. This potential to adapt may depend on certain features of the environment, such as the landscape heterogeneity and the possibility for dispersal between populations. However, also more intrinsic factors may influence the outcome, for instance the microbiota living inside the host species can influence the host performance. Using experimental evolution with the two-spotted spider mite, Tetranychus urticae, and the nematode C. elegans, we investigated several ecological factors limiting or enhancing adaptation. Overall, we found that dispersal may be a curse or a blessing, that heterogeneous environments can provide evolutionary stepping stones under harsh conditions, and that communities of microbiota may play a role in host performance in novel environments.

**Ecotoxicology**

# Evaluating the role of local mercury sources on spatial and temporal pollution trends in marine predators living in a changing arctic.

**PINZONE MARIANNA**

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The consequences of a rapidly warming Arctic on environmental mercury (Hg) exposure in marine biota remains largely unknown. Stable carbon (C), nitrogen (N), sulphur (S) and Hg isotope ratios are increasingly used to harmonice and trace Hg sources, pathways and concentrations in marine top predators. Our objective was to identify Hg sources in marine Arctic predators at spatial and temporal scale and evaluate the consequences on Hg exposure over time. We measured THg concentrations, C, N, S, and Hg isotope ratios in muscle tissue of hooded Cystophora cristata and ringed seal Pusa hispida from East Greenland, collected between 1985 and 2019. We created multi-isotopic niches (standard ellipse areas, SEAs), after which we applied linear mixed models to relate temporal variation in Hg exposure and sources to environmental change (e.g. sea-ice, NAO). Hooded seals presented a larger SEA (mode, 95% CI: 0.93, 0.60 – 1.41) than ringed seals (mode, 95% CI: 0.22, 0.14 – 0.37). Ringed seals showed higher THg concentrations (Mean ± SD: 1.10 ± 0.48 µg g-1 dw) than hooded seals (0.88 ± 0.92 µg g-1 dw) on average. THg levels in hooded seal muscle decreased by 1.5% y-1, while no significant change was found for ringed seals. At spatial scale, habitat use (oceanic vs. coastal) was the most important driver of THg variability, with land-fast ice-associated ringed seals being potentially influenced by enhanced coastal MeHg emission and accumulate higher THg levels. Attemporal scale, the shift in local marine biogeochemistry (represented by δ15N values) and prey biomass were the most important drivers of THg in ringed and hooded seals, respectively. The different Hg trends shown by the two species suggested how Hg sources are important drivers of bioaccumulation in Arctic seals, underling the necessity to reevalute their importance for the forecasting of future Hg trends in the Arctic Ocean.

**Ecotoxicology**

# Does early life exposure to neurotoxic permethrin affect phenotypic traits in juveniles of the mangrove *rivulus Kryptolebias* marmoratus?

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Within the animal kingdom, it is well established that the early stages of life are particularly sensitive periods to environmental disturbances. However, in fish, a lack of information remains regarding the impact of environmental stresses experienced during development on the phenotypic traits of individuals. This is surprising given that aquatic organisms are among the first to be exposed to pollution involving neurotoxic compounds that can cause phenotypic changes and potentially affect animal fitness. Here, we explored how early exposure to permethrin, a neurotoxic pyrethroid compound that can be found in insecticide, influences the phenotype in juveniles of the mangrove rivulus, *Kryptolebias marmoratus*. *Kryptolebias marmoratus* has the unique ability among vertebrates to self-fertilize, allowing to naturally produce homozygous individuals within isogenic lineages. It thus provides the opportunity to study how environment shapes organism phenotype while minimizing genetic variability. We designed an experiment to investigate immediate effect of different concentrations of permethrin (0, 5 or 200 µg/L) on life-history traits, behaviours, and hormones levels in 7-days old rivulus larvae. In addition, we studied the relative expression and methylation of potential permethrin target genes, based on their involvement in neurotransmission or their association with individual variation in behaviour. Our first data showed that larvae exposed to 200µg/L permethrin had lower growth, activity, predation success and metabolic rate while they had higher foraging effort and thigmotaxis compared to fish exposed to 0 and 5µg/L permethrin. However, we found no difference in larval cortisol levels between treatments. Overall, our results demonstrate the immediate adverse effects of permethrin during larval development in the mangrove rivulus. Further analyses will determine if epigenetic mechanisms are involved in such effects.

**Ecotoxicology**

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# Organophosphate induced disruption of female reproductive homeostasis in a non-target model insect *Drosophila melanogaster*

SUMEDHA ROY

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All living organisms need to reproduce for the perpetuation of life. To meet the global food demand and to achieve food security for the continually increasing global population, the use of chemical pesticides has been on the rise. Acephate, one such globally used organophosphate pesticide blocks the activity of Acetyl-cholinesterase enzyme in pests, together with various adverse effects in non-target organisms including human beings. In the present study we explored the effect of chronic sub-lethal acephate exposure on female reproductive system of *Drosophila melanogaster*. Different physical (body weight), sub-cellular (Apoptotic and cell viability, comet assays), biochemical (Catalase activity, Lipid Peroxidation, Vitellogenin and Mitoferrin content) and behavioural (Fecundity and egg hatchability) parameters are taken into consideration for this study. Overall health as reflected in the mean body wet weight of treated flies exhibited a reduction. Similar decline in viable germ cell number in females were noted. Acridine orange staining and Comet assay revealed increased apoptotic lesions, structural disorganisation, and genotoxicity in female reproductive system. Increased oxidative stress markers and decreased fecundity, egg hatchability in treated females demonstrated their reproductive insufficiency in comparison to control counterparts. Additionally, protective potentials of vitamin C and E against acephate-induced toxicity is also investigated. Results suggested that co-administration of vitamin C and E together with acephate could reduce the adverse impacts of the organophosphate on female reproduction of *D. melanogaster*. Thus, chronic sub-lethal acephate exposure poses a serious concern on the reproductive health of a non-target model insect, *D. melanogaster*, and vitamin C and E co-administration is found to provide a successful protection against this reproductive toxicity.

**Ecotoxicology**

# Influence of microfibers on *Daphnia magna* performance, populations and biofilms

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Plastic pollution has become a global problem as huge amounts of plastic accumulate in the environment. Plastics are made of chemically synthesized large molecules. These can break down into smaller pieces, often referred to as microplastics. The breakdown into microplastics, however, does not change the polymer structure of the plastic. The accumulation of microplastics in the environment is a major concern because organisms can take up these particles and the possible consequences of plastic ingestion and uptake are still unclear. Biodegradation could lead to the conversion of potentially harmful polymers into smaller molecules that can be used as a food source. There is a lack of studies comparing the effects of biodegradable and common non-biodegradable plastics. This was done in this master's thesis. The freshwater organism *Daphnia magna* was exposed to microfibers for 21 days. Microfibers are a type of microplastic. More specifically, they are fine synthetic polymers with a small diameter and an elongated shape. Polylactic acid (PLA) microfibers were compared with polyethylene terephthalate (PET) microfibers and polyamide (Nylon) microfibers. Unlike the other two fibres, PLA is a biodegradable plastic made from natural materials. The effects were tested by analysing the survival, days to first brood, body size and population density. Water from two different ponds was used as medium for the *Daphnia*. One was a polluted city pond, the other was a natural pond. This had an effect on the analysed characteristics, as the different ponds contained different bacteria. The influence on the gut microbiome is of great importance because the bacterial community inside the organism has an important influence on its health. The experiment showed that a negative effect could be found mainly with a combination of the polluted pond with PLA fibres. Exposure to PET fibers was linked to increased body size. The polluted pond was also linked to an increase in the number of days to first brood, increased body size after 7 and 14 days, and lower population density. A difference between the different *Daphnia* clones used was also shown. Further research is needed to possibly link bacteria and the breakdown of plastics. Organisms such as algae, fungi and bacteria can colonize the surface of plastic particles and form a biofilm. Biofilm formation could possibly lead to biodegradation. A protocol to visualize these biofilms and fibers using a light microscope or scanning electron microscope was therefore tested and optimized.

Ecotoxicology

# Poison or Potion: Effects of Sunflower Phenolamides on Bumble Bees and Their Gut Parasite

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Specific floral resources may help bees to face environmental challenges such as parasite infection, as recently shown for sunflower pollen. Whereas this pollen diet is known to be unsuitable for the larval development of bumble bees, it has been shown to reduce the load of a trypanosomatid parasite (Crithidia bombi) in the bumble bee gut. Recent studies suggested it could be due to phenolamides, a group of compounds commonly found in flowering plants. We, therefore, decided to assess separately the impacts of sunflower pollen and its phenolamides on a bumble bee and its gut parasite. We fed Crithidia-infected and -uninfected microcolonies of Bombus terrestris either with a diet of willow pollen (control), a diet of sunflower pollen (natural diet) or a diet of willow pollen supplemented with sunflower phenolamides (supplemented diet). We measured several parameters at both microcolony (i.e., food collection, parasite load, brood development and stress responses) and individual (i.e., fat body content and phenotypic variation) levels. As expected, the natural diet had detrimental effects on bumble bees but surprisingly, we did not observe any reduction in parasite load, probably because of bee species-specific outcomes. The supplemented diet also induced detrimental effects but by contrast to our a priori hypothesis, it led to an increase in parasite load in infected microcolonies. We hypothesised that it could be due to physiological distress or gut microbiota alteration induced by phenolamide bioactivities. We further challenged the definition of medicinal effects and questioned the way to assess them in controlled conditions, underlining the necessity to clearly define the experimental framework in this research field.

Ecophysiology and stress adaptation (inclusive parasitism)

# Quality control of citizen-collected data in bilharzia snail control: lessons from Lake Albert, Uganda

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Schistosomiasis is caused by parasites of the genus Schistosoma that use freshwater snails as intermediate hosts (IH). Since IH snail distribution determines where snail-borne diseases occur, information on snail population dynamics at fine spatial and temporal scales is highly needed. This information is however hampered by a strong deficit in trained malacologists. Therefore, the ATRAP project implemented a citizen science (CS) approach to monitor the dynamics of IH snail populations (Biomphalaria and Bulinus) in Uganda. We assessed the quality of this data by comparing it to the data collected by an expert malacologist that visited the same sites on a monthly basis.

The binary agreement in presence/absence of Biomphalaria and Bulinus snails for the paired data reports between the expert and the citizens is 76% (N = 907) and 86% (N = 892) with 15.7% and 11.5% false negatives (site wrongly defined as snail-borne disease free/safe), respectively. A generalised logistic mixed-effects regression showed that agreement increased when the abundance of Biomphalaria snails increased ($p < 0.01$), and site type was a significant predictor of binary agreement ($p < 0.01$), lowest at lake sites (55%) and highest at spring site (99%) with variations across snail genera. The citizens and expert data showed similar trends in snail population changes over time, although the expert consistently recorded higher abundances than the citizen scientists.

Our study demonstrates the potential of CS for the detection of the presence and absence of snails IH of schistosomiasis in Lake Albert, Uganda. On the other hand, we recognize the added value of data provided by experts since it gives a more detailed view of snail population dynamics. The pros and cons of involving citizens in mapping putative schistosomiasis transmission sites will be discussed.

Ecophysiology and stress adaptation (inclusive parasitism)

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# The impact of thermal environment on locomotor performance in native and invasive populations of *Xenopus laevis*.

**ARASPIN LAURIE**

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Biological invasions are a major threat for ecosystems. Some invasive species face novel environments, yet often thrive suggesting that they have the potential to rapidly cope with new conditions. The widespread introduction of *Xenopus laevis*, a principally aquatic frog native to southern Africa has led to the establishment of invasive populations on four continents. Ectothermic species as *Xenopus laevis* are dependent on temperature which drives aspects of their physiology including dispersal capacity. An understanding of the temperature dependence of locomotion is a critical trait to predict future dispersal in new environments. Aquatic endurance is a proxy of dispersal and it is determined by the maximum exertion capacity of individuals. We compared the thermal performance curves of populations from their invasive and native ranges to test whether thermal optima of the performance in the invasive population is within the temperature range of native populations. Endurance from a French invasive population and 4 populations from the native range, collected across an altitudinal gradient (0-3000 m above sea level) was estimated at 7 different temperatures (8, 12, 16, 19, 23, 27, 30°C). Results show that populations from cold environments exhibit lower optimal performance temperature than ones from hotter environments. While optimal temperature of performance differs within the native populations, the invasive population performs within this native range of optimal temperatures. Inhabiting such extreme different climatic environments in the native range could allow invasive populations to thrive in various novel environments and increase their invasion potential. Moreover, the understanding of the temperature dependence of locomotor performance in this species may help to better estimate environments of potential invasion.

Ecophysiology and stress adaptation (inclusive parasitism)

# Thermotolerance of five sympatric black coral species differs according to morphology.

**MATHILDE GODEFROID**

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Antipatharians or black corals are colonial Hexacorals that are distributed in all oceans over a wide bathymetric range. Antipatharians are engineer species that can form dense aggregations of one or multiple species, known as marine animal forests or black coral beds (BCBs) which harbour a wide range of associated fauna. Factors shaping the thermal tolerance of antipatharians are uninvestigated despite the ecological importance of this taxon, especially at mesophotic depths. The BCB in the North pass of the Great Reef of Toliara in Madagascar is a good study site to answer this question, as it is one of the most biodiverse mid-depth (10-30m) black coral assemblage described to date, being composed of 20 species belonging to two families (Antipathidae and Myriopathidae). To determine which factors most influence the thermal sensitivity of antipatharians, we tested the thermal stress response of five sympatric antipatharian species (Antipathes grandis, Cuppressopathes abies, Cirrhipathes anguina, Cirrhipathes spiralis and Stichopathes maldivensis), that are representative of the phylogenetic and morphological diversity of this BCB. Based on previous experimentations, we performed acute ramping assays in order to produce thermal performance curves for all species in a rapid and reproducible way. Results revealed that phylogeny alone does not explain differences in thermal sensitivity. On the contrary, morphology appeared as a key factor, with branched species (A. grandis and C. abies) being more sensitive than filiform ones (C. anguina, C. spiralis, S. maldivensis). Several hypothesis could explain these variations in thermal tolerance across morphology, such as the biomass, the surface/volume ratio or the mass-transfer efficiency of the specimens. Altogether, this study suggests that branched antipatharian species are more sensitive to heat stress than sympatric filiform ones. This is a matter of concern as these two morphological groups probably occupy different niches in the BCB.

**Ecophysiology and stress adaptation (inclusive parasitism)**

# High level of novelty under the hood of convergent evolution

**STEVEN VAN BELLEGHEM**

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Many examples exist in nature of species converging in phenotype in response to similar selective pressures. Despite this determinism imposed by the environment, little is known about the extent to which species use the same or non-homologous regulatory architectures to achieve phenotypic convergence. By characterizing the functional portion of the genome, represented by chromatin accessibility and gene expression in developing wing tissues, we aimed to determine to what degree morphological convergence between mimetic butterfly species, Heliconius erato and H. melpomene, was achieved using homologous regulatory architectures. While a handful of color pattern genes are known to be involved in the convergent evolution of these Müllerian mimics, our data suggest that different mutational paths in each species underlie the integration of these genes into the regulation of wing development. We find that (1) a large fraction of accessible chromatin is exclusive to each species, driven in part by non-homologous sequence evolution; (2) the regulatory architecture and expression of wing signaling and transcription factor genes is poorly conserved; and (3) the cis-regulatory architecture of the convergent mimetic red wing pattern is not homologous. These findings may be explained by a high level of developmental drift and evolutionary contingency that must have occurred during the independent evolution of mimicry. Evolution in different genomic backgrounds has thus resulted in the largely non-homologous regulatory integration of color pattern genes and developmental processes to achieve similar outcomes.

**Evolutionary Genomics**

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# Does hybridization facilitate explosive speciation of Lake Baikal amphipods?

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The adaptive radiation of amphipods in Lake Baikal has brought forward more than 340 species (20% of the world's freshwater amphipods), making it one of the largest species flocks after the famous African cichlid radiations, and one of the only large radiations in temperate climates. Despite this iconic status the radiation has not yet been subject to detailed genomic investigation. In this project, I use genomic approaches to test whether the successful adaptive radiation of Lake Baikal Amphipoda could be explained by hybridisation and adaptive introgression. These processes have been shown to occur in other adaptive radiations, but their functional role in rapid diversification is still debated.

My preliminary results, based on transcriptomic analysis of 40 amphipoda species, indicate that hybridization between two independent lineages of Baikalian amphipods emerged before the period when fast speciation started. Furthermore, I found intriguing signals of both negative and positive selection on introgressed loci. These results suggest rich patterns of selection on introgressed genetic material and make the case that the Lake Baikal amphipod adaptive radiation is a promising study system to address the role of hybridisation in adaptive radiation.

**Evolutionary Genomics**

# Solving the missing pieces of the gharial puzzle: new phylogenetic framework combining morphological, molecular, and biostratigraphic data to unravel the evolution of long-snouted crocodylians.

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Among the extant crocodylians are two species with long, narrow snouts: Gavialis gangeticus,the Indian gharial and Tomistoma schlegelii, the "false" gharial. These enigmatic species are considered by the IUCN red list as critically endangered and vulnerable, respectively. However, despite this, knowledge of their evolutionary history is lacking. Extensive debate has surrounded the gharials for over four decades and remains unsolved today: the so-called gharial problem. Whereas molecular studies consistently indicate that these two species are sister taxa, morphological studies of both living and fossil taxa find that they belong to distantly related lineages. Moreover, molecular clock estimates indicate a shallow divergence time of 18-31 million years ago. This entirely contradicts the rich fossil record of gharials: in contrast to the modern gharials, these fossil taxa comprise a huge diversity and suggest that tomistomines and gavialines have diverged from each other at least 70 million years ago, prior to the K/Pg mass extinction.

European museums, and especially the Royal Belgian Institute of Natural Sciences, Brussels, comprise rich collections containing many of the oldest fossil gavialoids, crucial to solving the gharial problem. Nevertheless, few modern morphological studies have been performed on these specimens, and their stratigraphic age is often poorly constrained. Therefore, in a new project we will use a multidisciplinary approach to study these specimens, combining morphological study and biostratigraphic analyses using dinoflagellate cysts. Moreover, we will revise the classical methods used by paleontologists to study fossil crocodylians, devising a new phylogenetic framework that makes use of both morphological, molecular, and biostratigraphic data. Here, we will present some of the first preliminary results of this project.

**Evolutionary Genomics**

# How phylogeny and ecological adaptation describe variation in ophiuroid (Echinodermata: Ophiuroidea) vertebrae

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The arms in brittle stars are supported by a series of articulated vertebrae, allowing a wide range of motion, important for feeding and locomotion. This study provides a 3D geometric morphometric investigation of vertebral shape variation in relation to different functional and ecological aspects of ophiuroid lifestyles. Six segments within one arm from 12 species representing prehensile ophiuroids (with arms that can be wrapped around objects) and non-prehensile behaviors, were CT scanned. The 3D shape variation of the vertebrae was analysed, using 37 landmarks on each vertebra. After a Generalized Procrustes Analysis, a principal component analysis was done on the variance-covariance matrix of the obtained Procrustes coordinates to check the distribution of the species within the morphospace. A PERMANOVA was performed on the PC scores for all vertebrae to test for differences between species, between functional lifestyles (prehensile and non-prehensile species), and between ecological lifestyles (epizoic, endozoic, epiphytic, or free-living). Phylogenetic MANOVA and phylogenetic signal analysis were done to test whether functionality groups significantly differ after controlling for phylogeny and to explore the phylogenetic signal from a set of quantitative traits. The PERMANOVA indicated a significant difference in vertebral morphology between species and between lifestyles. The principal component analysis showed that prehensile species are most distinct from non-prehensile ones in the morphology of their articular structure and vertebral projection. The Phylogenetic MANOVA and phylogenetic signal analysis revealed that characteristics belonging to the aboral and lateral processes on vertebrae are necessary for phylogenetic interpretations, while dorsal and central articular structures probably have limited taxonomic value, as they may show adaptations to functional/ecological lifestyles.

**Functional Morphology**

# Diversity and evolution of color patterns in the goatfishes (Perciforms, Mullidae)

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Goatfishes (Mullidae) are coastal tropical and sub-tropical reef fishes distributed worldwide with some species encountered in temperate waters. Goatfishes belong to the Syngnathiform order and include 98 species grouped in 6 genera: Mullus, Upeneus, Upeneichthys, Mulloidichthys, Pseudupeneus and Parupeneus. Beyond the synapomorphic hyoid barbels, this fish family does not look hyper diverse regarding the diversity of body forms but species differ largely by their colour patterns. Along this study, we aim to test if the diversity (or disparity) of these colour patterns evolved randomly or is explained by different factors. To do so, we compiled data on colour patterns in 80 species by coding the presence/absence of specific marking (e.g. vertical strips, horizontal bars…) on the three main body regions: head, trunk and caudal region (peduncle and fin). The variation of this multivariate dataset was then summarized and visualized using multiple correspondence analysis (MCA). In parallel, we collected on FishBase.org ratios describing head length and body depth, two ecologically relevant morphological traits. First, disparity analyses revealed that genera or species assemblages from different geographical areas do not greatly differ in the disparity levels of colour patterns and trophic morphology. Only the assemblage of goatfishes from Central Pacific shows a higher level of disparity. Second, partial least squares analyses demonstrate strong correlations between body morphology and colour patterns within every genus and geographical area. These preliminary data certainly support that evolution of colour patterns in goatfishes is not random. External factors such as ecology and/or internal factors such as developmental modularity could drive this pattern of disparification, and will be tested in a future phylogenetic framework.

**Functional Morphology**

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# Evolution of multiple colour mechanisms enhances opportunities for ongoing speciation

**NICOLAÏ MICHAËL**

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How and why certain groups become speciose is a key question in evolutionary biology. Novel traits that enable diversification by opening new ecological niches are likely important mechanisms. However, ornamental traits can also promote diversification by opening up novel sensory niches and thereby creating novel inter-specific interactions. More specifically, ornamental colours may enable more precise and/or easier species recognition, and may act as key innovations by increasing the number of species-specific colour patterns and promoting speciation. While the influence of colouration itself on speciation is well-studied, the influence of the mechanisms that produce those colours is less so, even though the ontogeny and evolution of these mechanisms differ. Here we created a novel phylogenetic tree for 121 species of sunbirds and combined colour data with a range of phylogenetic tools to test the hypothesis that the evolution of novel colour mechanisms increases diversification in sunbirds, one of the most colourful bird clades, and had four main results. First, the evolution of novel colour mechanisms open up the visual sensory niche, increasing the number of potential colours. Second, structural colouration moves more readily across the body than pigment-based colouration, enabling an increase in colour complexity. Third, novel colour mechanisms might minimize trade-offs between natural and sexual selection such that colour can function both as camouflage and conspicuous signal. Finally, we found that colour differences between species increase with the number of sympatric species, but that nevertheless, the occupied colour space is nowhere near fully occupied, suggesting that colour-based speciation is ongoing.

**Functional Morphology**

# Ecological and developmental constraints foster the morphological diversity of the mammalian limb

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Variation between traits and between clades emerges from evolutionary patterns of complex and, mostly often, unique interactions, resulting in uneven diversification of morphologies. Developmental constraints and ecological features, such as habitat occupation are important drivers of the evolution of phenotypes. Limbs have been widely studied in mammals due to their remarkable morphological diversity. The patterns structuring the phenotypic variation of mammalian limbs have been interpreted as associated with developmental constraints and with the diversity of the environments used by this group. We explore whether the medium used for locomotion and the temporal sequence of bone condensation predict morphological diversity of the forelimb bones across more than 600 species of mammals. Our findings are consistent with the hypothesis that late developing, distal limb elements should display greater morphological variation than more proximal limb elements, which condense earlier during morphogenesis. Distal limb elements, belonging to the autopod, not only exhibit higher diversity of form, but are also more integrated and, on average, show greater evolutionary versatility than intermediate and upper limb segments. Furthermore, we show that the physical medium used for locomotion impose different constraints on the limb morphology, driving limb form and size. Our findings indicate that the macroevolutionary patterns of within limb segments and between clades are not the same, suggesting that strong functional selection in different media, combined with the higher potential of development to generate variation in more distal limb structures, foster the patterns of morphological evolution of the mammalian limb.

**Functional Morphology**

# Studying the form diversity of sagittae in teleost fishes by using 3D landmark-based geometric morphometrics

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The inner ear of teleost fishes is a complex multifunctional (hearing and balance) organ composed of three semicircular canals and three end organs having each their otoliths. In non-otophysians, the saccular otolith, i.e. the sagitta, is the biggest one and shows the largest morphological diversity. Despite many attempts to relate this disparity to hearing abilities, ecological or life history traits, there is no consensus concerning main drivers of their size and shape diversity. Thanks to the recent advances in 3D data acquisition, the use of 3D geometric morphometric methods offers new perspectives in the study of factors driving otolith shape and size, opening the way to large-scale comparative analyses with ecomorphological perspectives. Here, we aimed both (1) to apply a high-density 3D semi-landmarking technique to cover sagitta surfaces and test the sensitivity of shape quantification by using different densities of semi-landmarks (500, 1000 and 2000), and (2) to have a first glimpse of sagittae disparity in a phylogenetic framework. Therefore, 45 specimens belonging to 29 orders of non-otophysian teleosts with a particular emphasis on Carangaria and Scorpaeniformes were acquired from MorphoSource (https://www.morphosource.org/), a free online repository. Sagittae were 3D reconstructed using Amira software. We then patched points on sagittae models and the coordinates obtained were projected in a morphospace after running a General Procrustes Analysis allowing the visual exploration of their morphological disparity. Then, we increased the density of semi-landmarks on model surfaces. The increasing set of coordinates failed to improve the explained diversity and the accuracy of shape analysis. This preliminary 3D data analysis allows to validate our approach for testing further ecological hypotheses at large and small phylogenetic scales.

**Functional Morphology**

# Importance of the keels of boxfish for passive stability during swimming

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In Boxfish, the keels that are present on their rigid bony carapace were hypothesized to provide them with favourable hydrodynamic properties, such as a low drag coefficient and passive course stabilisation. However, later studies could not reproduce these results, discovering that the carapace shape is inherently unstable. An alternative hypothesis was put forward, namely that the presence of keels increases the body's resistance to roll rotation, which is in better agreement with their ecological needs. Drag coefficients, pitch and yaw moment coefficients, rotational drag moment coefficients for roll rotation, and rotational added mass moment coefficients for roll rotation were examined in five species of Ostraciidae. Modified boxfish models, whose keels were digitally removed, were used to gain insight in the function of the keels by the degree to which the presence of keels determined hydrodynamic properties of the entire carapace. Computational fluid dynamics simulations were made for the modified and control boxfish models, which were placed parallel to the water flow to extract drag forces, and placed under a slight pitch or yaw angle (mimicking deviation of alignment) to extract pitch and yaw moments, respectively. Transient simulations were made of the boxfish undergoing an imposed roll rotation in still water to extract the rotational drag moment and rotational added mass moment. No relationship could be discovered between the presence of keels and drag reduction or passive stability for pitch and yaw; therefore, it seems unlikely that the keels play a prominent role in shaping these characteristics. However, all species showed a strong increase in rotational drag and rotational added mass for roll rotation by the presence of keels, with for some species the rotational drag moment coefficient being doubled. This strongly suggest that keels play a major role in increasing the body's resistance against roll rotation.

**Functional Morphology**

# Learning with Lacertids: comparing cognition across species.

**VAN LINDEN LISA**

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Cognition plays an important role in the life of every individual animal. Essential to foraging, predator avoidance, species recognition, mate selection, and behavioural responses to environmental changes, cognition is a prime determinant of animal survival and reproduction. Different studies have proposed and tested hypotheses on the role of ecological factors on the evolution of cognition but these have yielded inconsistent results, thus the driving forces of cognitive evolution throughout the animal kingdom remain ambiguous. Large-scale comparative studies on multiple species and cognitive traits have been advanced as the best way to facilitate our understanding of cognitive evolution, but such studies are rare and often challenging. In this study, we tested the cognitive skills of 13 species of lacertid lizards (Reptilia: Lacertidae) using a battery of tests measuring inhibitory control, problem-solving, and spatial and reversal learning. We tried to link species' performance to interspecific variation in habitat complexity and habitat variability. We found that species differed markedly in their cognitive abilities, however, such variation was not related to habitat complexity. However, we found that species living in more variable environments exhibited lower behavioural flexibility. The standardised approaches in our study provide opportunities for large-scale collaborative research to increase sample size and replication, essential for advancing the field of comparative cognition. Most importantly, we established lacertid lizards as an appropriate model system to study the evolution of cognition.

**Open Symposium**

# THE MONITORING OF RECREATIONAL HAND-FISHING IN EULITTORAL BOULDER FIELDS

**RICHIR JONATHAN**

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Eulittoral boulder fields are complex rocky habitats of high conservation value. They shelter a high biodiversity of fauna and flora. In France, boulder fields are exposed to important recreational hand-fishing activities; to catch crabs or abalones that hide in the cavities and overhangs during the low-tide periods, fishers overturn boulders and do not replace them in their original position.

The LIFE+ Recreational Hand-Fishing participatory project, started in 2013, aimed to acquire new knowledge on the dynamics and responses of boulder fields under the combined effects of recreational hand-fishing and environmental factors. It remained to assess the relevance of this monitoring, to characterise the spatial variability of the ecological status of boulder fields and to propose indicators of this status that are robust, sensitive and easily transposable geographically.

We adapted a seascape index based on the dominant colour of the upper faces of the mobile boulders (attractive to fishers), indicative of their rate of overturning. We developed an ecological status index based on the dissimilarity between communities of the under and/or upper faces of mobile and fixed (non-returnable) boulders. The join effect of hand-fishing pressure (frequentation, fishing behaviour) and environmental variables (hydrodynamics, boulder size, season ...) on these indicators was studied using generalized linear mixed models.

There was a high variability in the rate of mobile boulder overturning between fields and regions, overturning that affected boulder community structures. The variability of response indicators was explained by hydrodynamics, but also by the frequentation and the inappropriate behaviour of fishers overturning boulders; these effects were modulated by the characteristics of the boulder fields. Using community dissimilarities allowed both the impact of the overturning to be measured and the deviation from ecological reference conditions to be quantified. It had the advantage of being independent of the site community structure, allowing inter-site and inter-regional comparisons.

**Open Symposium**

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# Finding the receptor of sperm-release pheromone in the marine worm Platynereis dumerilii to shed light on the impact of ocean acidification on chemical communication

**VICTORIA CARLA MORIS**

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One important part of climate change is ocean acidification (OA) caused by the increase of atmospheric CO2 since the industrial revolution, lowering the pH from 8.2 to 8.07. By the year 2100, a pH of 7.7 is predicted with increased pH fluctuations during the day. So far, only a few studies have investigated the impact of OA on chemical communication, which is important for the survival of species (detection of prey/predator, mating partner) and whose alteration could lead to dramatic consequences on marine communities. A promising species to investigate this, is the globally distributed annelid worm Platynereis dumerilii (Nereididae) which is experimentally tractable, and for which the sex pheromone, uric acid, has been identified. Uric acid acts as sperm-release pheromone: it is discharged by P. dumerilii females with the release of their eggs and triggers the sperm release in males, synchronizing the spawning. Since a lower pH could affect the production of the pheromone and/or its detection (e.g., changing the signal conformation and charge distribution, or the binding domain of the chemoreceptor), this study first aims to identify the receptor of uric acid. Combining behavioral and electrophysiological assays with comparative transcriptomics, we identified candidate genes for the receptor of uric acid, which code for G-protein-coupled receptors (GPCRs). With gene clustering analysis and deorphanization assays, we narrowed down the list of candidate genes in order to perform later on knock-out experiments to validate the receptor of this pheromone. Once identified, we will be able to determine with computational modelling if such receptor might be impacted by a lower pH and if Platynereis populations living in more acidic environments use different receptors. This study helps to better predict how OA impacts the marine communities by modifying their chemical communication, whether acclimation and adaptation occur and at which costs.

**Open Symposium**

# Introducing *Enteromius* as a new model organism to study speciation in riverine fishes

**HELEEN MAETENS**

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*Enteromius* Cope, 1867 (Cypriniformes: Cyprinidae) is the third largest fish genus in the world, containing 215 valid species and still counting. Identifying these small diploid barbs from Africa is often difficult, because they don't seem to have particular morphological adaptations like reproductive specialisations and most species do not have conspicuous colour patterns. This results in morphological similar species. Furthermore, small-scaled taxonomic revisions showed that a lot of unrecognised species diversity exists. Unrecognised diversity was found in a.o. the Congo basin (23 genetic lineages in four species) and Kenyan rivers (6 genetic lineages in two species). We studied the species of *Enteromius* from the Lake Edward system situated on the border of the Democratic Republic of Congo and Uganda. Initially, five species were recognised for this system: two with a smooth dorsal spine (*E. perince* and *E. stigmatopygus*) and three with a serrated ossified dorsal spine (*E. apleurogramma, E. kerstenii and E. pellegrini*). Based on a combined approach of genetics (COI, mtDNA) and morphometrics, we re-identified the first two species as *E. alberti* and *E. cf. mimus.* These species differed by 8.5% in the COI gene. We discovered that the other three species represent multiple species with genetic distances ranging between 2.4% and 13.4% in the COI gene. The existence of multiple species was also confirmed by nuclear markers. Studying species of *Enteromius* from neighbouring basins revealed the existence of even more species. Based on these recent findings, we can ask ourselves how it is possible that such an inconspicuous genus is so species rich? In order to find answers to this question, we will aim to understand the evolutionary processes involved in the speciation patterns that have led to the species richness in Enteromius and suggest Enteromius as a new model organism to study speciation in tropical riverine systems.

**Open Symposium**

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# CELL TYPE DIVERSITY IN A DEVELOPING OCTOPUS BRAIN

**EVE SEUNTJENS**

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Octopuses are mollusks that have evolved intricate neural systems comparable with vertebrates in terms of cell number, complexity and size. The brain cell types that control their sophisticated behavioral repertoire are still unknown. Here we profiled cell diversity of the paralarval Octopus vulgaris brain to build a cell type atlas that comprised mostly neural cells, but also multiple glial subtypes, endothelial cells and fibroblasts. We spatially mapped cell types to the vertical, subesophageal and optic lobes. Investigation of cell type conservation revealed a shared gene signature between glial cells of mouse, fly and octopus. Genes related to learning and memory were enriched in vertical lobe cells, which showed molecular similarities with Kenyon cells in Drosophila. We constructed a cell type phylogeny revealing transcriptionally related cell types, which tended to appear in the same brain region. Together, our data sheds light on cell type diversity and evolution in the octopus brain.

**Evolutionary Genomics**

# Improving whole biodiversity monitoring with eDNA metagenomics

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Improving whole biodiversity monitoring at large scales requires tools that assess biodiversity in a more holistic and comprehensive manner than is afforded by direct observation alone. The DNA present in the environment (eDNA) is a powerful source of biodiversity information as it is derived from both living microorganisms (endogenous or intracellular eDNA) and remains of macroscopic eukaryotes (exogenous or extracellular eDNA). The implementation of eDNA metabarcoding has quickly become gold standard in biodiversity monitoring. However, metabarcoding relies on PCR amplification of eDNA, which has some limitations, such as priming biases, exclusion of shorter target eDNA fragments, limited taxonomic range, and limited taxonomic information in a single barcode. Alternatively, shotgun sequencing all eDNA present in a sample without enriching for a specific taxonomic group, locus, or fragment length, should overcome these limitations. In this talk I show that eDNA metagenomics is able to describe the whole freshwater biome by detecting taxa across the tree of life. When compared with eDNA metabarcoding, eDNA metagenomics provides a higher detection ability for species represented by low abundant and highly degraded DNA, it differentiates between local and transported eDNA, and it brings light to dark taxa, none of which is possible with eDNA metabarcoding. Combined with efforts to produce genomic resources for all eukaryotes, eDNA metagenomics is a new tool for improved whole biodiversity monitoring.

Evolutionary Genomics

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# Characterising fisheries induced evolution of Malawi cichlids

ALEXANDER HOOFT VAN HUYSDUYNEN

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Anthropogenically driven changes to the environment are (in)directly causing widespread global biodiversity loss. However, some organisms are showing clear signs of rapid evolutionary adaptation to these changes. Commercial fishing is considered a leading cause of human-induced adaptation. In particular, non-selective harvesting is expected to lead to the evolution of life-history traits such as earlier maturation. Such phenotypic changes in growth rate and age at maturity are well documented across the animal kingdom.

One striking example of fisheries induced evolution (FIE) can be observed in Malawi cichlids dispersed throughout Lake Malawi and Lake Malombe. Over the last 40 years, the size distribution of adult individuals of commercially important species has dramatically decreased in Lake Malombe compared to Lake Malawi, which is consistent with the observation that most individuals do not survive to a second breeding year in the heavily fished Lake Malombe. This is in stark contrast to weakly fished Lake Malawi populations, where breeding groups mostly consist of three-year-old or older individuals. This suggests extremely strong selection exerted by fishing in Lake Malombe which is consistent with expectations due FIE.

Extensive genomic resources are available for Malawi cichlids from before and during this period of fishing, thus allow us to investigate the evolutionary history of genes used in recent adaptation. Additionally, we are breeding cichlids in the lab to experimentally quantify genetic and environmental differences in traits implicated in FIE. Promising results in the early stages of this project align with the theoretical hypotheses of long-term genomic effects of fisheries in the ecologically and economically important cichlid fish.
The combination of whole genome sequencing and controlled breeding experiments will greatly advance our understanding of how genomes can rapidly adapt to fishing. Understanding the genomic framework of life-history traits is critical to effective development of sustainable agricultural/harvesting practices.

Evolutionary Genomics

# The pilot project of the European Reference Genome Atlas (ERGA) initiative

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The preservation of biodiversity and restoration of Europe’s ecosystems are included in the six political guidelines and priorities of the European Commission. Europe is the third largest continent and is home to over 200,000 eukaryotic species, many of which are endemic. The IUCN red list for Europe assessed that around 22.7% of the species are threatened with extinction. Therefore, an assessment of pan-European biodiversity that can inform conservation strategies is essential. This can be achieved via genome sequencing and/or DNA barcoding. Particularly important targets include threatened/endangered species, ecologically keystone species and economically important species (e.g. pollinators and their biome, soil, forest, and marine and freshwater communities as well as invasive species and disease vectors). As one of the key steps for cataloging biodiversity across Europe, we established the European Reference Genome Atlas (ERGA) initiative, a pan-European consortium of >500 members with the goal of generating high quality reference genome assemblies of European species. This consortium was built upon growing genomic consortium initiatives in Europe (e.g. Darwin Tree of Life, Endemixit) and globally (e.g. Vertebrate Genome Project, Bat1K) and it is the European hub of the Earth BioGenome Project. To demonstrate the feasibility of such continent-wide collaboration, ERGA has launched a Pilot Project with the goal of generating at least one high-quality reference genome for each European country that can support biological discovery for the broader scientific community. ERGA is committed to diversity, equity and inclusion through synergistic collaborations between ERGA researchers.

Evolutionary Genomics

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# Food web structure and trophic interactions at the recently discovered deep-sea La Scala hydrothermal vent field (SW Pacific)

**LOÏC MICHEL**

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Hydrothermal vents are features of the seafloor where fluids (acidic, geothermally heated water enriched in chemical compounds such as hydrogen sulphide) discharge in the water column. These fluid emissions sustain unusual chemosynthesis-based ecosystems where abundant micro-organisms and animal communities can thrive under extreme conditions. In May 2019, the La Scala vent field was discovered in Woodlark Basin (Papua New Guinea, SW Pacific). Several active "black smokers" harbouring dense fauna were found at depths ranging from 3300 to 3400 m. The main engineer species were symbiont-bearing gastropods *Ifremeria nautilei* and *Alviniconcha* spp. in more active diffuse areas, and stalked barnacles *Vulcanolepas* sp. nov. in mildly active areas. At least 44 taxa were observed in these habitats. Here, we used trophic markers (stable isotope ratios of C, N and S) to identify energy fluxes supporting those communities, and understand how their feeding habits could influence interspecific interactions.

Most sampled animals primarily depended (either directly or indirectly) on endogenous chemosynthetic vent production for their nutrition. This dependence spanned all sampled taxonomic and functional groups. It extended to organisms considered as peripheral fauna, or not strictly found at vents, such as *Vulcanolepas* sp. nov., anemones, or scavenging gastropods. Moreover, other peripheral fauna fed on a mix of both chemosynthesis- and photosynthesis-derived items. This emphasizes the importance of exported vent production for the surrounding deep-sea fauna. Animal communities showed considerable trophic diversity, and depended on several bacterial production mechanisms. Many taxa co-relied on two or more carbon sources, and inter- and intra-taxon differences in feeding habits could lead to a more even segregation of available food resources. While many questions about environmental and biological drivers of food web structure at La Scala vent field remain open, our results constitute a first glimpse at processes shaping those freshly discovered communities.

Marine Biology

# An insight into the trophic ecology of chimaeras from New-Zealand

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Despite the increasing human pressure applied, little is known about the ecology of most of the species found in deep-sea ecosystems. Chimaeras is a taxon of chondrichthyan species found only in the deep sea. They sometimes represent large bycatch biomass in commercial fishing vessels. The role that they play in the deep-sea food web is currently poorly known. The elusiveness, difficulty to access their environment, and inability for chimaeras to survive in aquaria pose main challenges in data collection. The most common method to study trophic ecology is the analysis of stomach contents. However, such analyzes present limitations: (1) only recent preys are satisfactory good conditions, and (2) tissue digestive state restricts often precise identifications. A high number of individuals are thus necessary to determine their diet. Alternative methods such as fatty acid profiling, DNA metabarcoding, or stable isotope analysis (SIA), combined or not with stomach content analysis, are now developed. Thanks to these methods, valuable insights into the trophic ecology of chimaeras, even on a relatively low number of individuals, are gained.

We used stable isotope analysis with stomach content determination to explore the trophic ecology of four chimaera species (Hydrolagus novaezelandiae, Rhinochimaera pacifica, Hydrolagus bemisi, and Harriotta raleighana) obtained on the Chatham Rise in New Zealand onboard the RV Tangaroa. δ13C, δ15N, and δ34S isotope ratios were measured on muscle and liver samples. Isotopic niches were then calculated together with other ecological data. We used mixing models with potential prey collected in the same trophic network to characterize the trophic role of these chimaeras.

**Marine Biology**

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# The complex immune system of sea cucumbers: a cell story

**NOÉ WAMBREUSE**

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Sea cucumbers are curious marine organisms belonging to the echinoderms. Their primitive appearance might suggest that these animals have simple defence mechanisms against pathogens. Instead, sea cucumbers have a complex immune system, capable of neutralising a wide range of invaders. The main actors of this system are circulating cells: the coelomocytes. Several coelomocyte morphotypes are discernible and sea cucumbers appear to have the greatest diversity of cells among the echinoderms. Although their coelomocytes were first described a long time ago, some paradigms concerning them seem incorrect today, and the specific functions of these cells remain poorly understood. This research aims to better understand the diversity and the function of coelomocytes in these particular animals. Initially, a detailed description of coelomocyte morphotypes was performed using different microscopy techniques, including electron microscopy. This allowed to recognise 6 coelomocyte morphotypes, constituting the first description of hemocytes in the Holothuriida clade, and to reconsider the status of vibratile cells – a traditionally recognised coelomocyte type – which are in fact contaminating spermatozoa. Then, to study their immune function, coelomocytes were exposed to lipopolysaccharide (LPS, i.e., molecules characteristic of Gram-negative bacteria). The first investigations consisted of in vivo assays, which allowed us to describe specific cellular behaviours and early events leading to the formation of cellular aggregates. Then, we used a transcriptomic approach to study the differential expression of genes after the LPS challenge. In total, 945 genes were identified as differentially expressed, of which 673 were up-regulated and 272 down-regulated in LPS-treated individuals. Finally, a metabolomic approach was used to identify variations in the abundance of certain metabolites after the LPS challenge. Among the identified metabolites, almost half seemed to be affected by immunostimulation. Overall, the results indicate a multilevel immune response in coelomocytes that illustrates the complexity of the sea cucumber immune system.

**Marine Biology**

# First come first served: Strain dependent priority effects in the gut microbiome assembly of host *Daphnia* and associated fitness

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Historical events such as the order of species arrival and timing are often key in the early assembly of ecological communities. Such events, also known as ecological priority effects have been demonstrated in free living systems but are until now neglected in gut community assembly. With growing interest on the role of priority effects in microbiome assembly, we explored the occurrence of such effects in the gut and their associated effects on host fitness. Specifically, the experiment was designed with three independent combinations of two bacterial strains belonging to the same genus (*Microbacterium*) or two strains belonging to different genera (*Rhizobium* and *Acinetobacter*; *Rhizobium* and *Microbacterium*) introduced into the gut of sterile *Daphnia* at intervals of 48h. The relative abundance of the inoculated strains was examined at two time points namely on Day 8 and Day 12 and in two *Daphnia* genotypes (Genotype LRV4 and O2) to inform us of the transient/permanent nature of priority effects and possible genotype effects. Additionally, life history traits of the inoculated animals were monitored to assess the impact on host fitness. Our results provide clear evidence for classical priority effects in the gut of *Daphnia*, however, not in the direction anticipated. Additionally, strain-specific and genotype specific responses were observed. Host fitness was only affected in 8 instances (11.11%) of the 72 combinations tested, further reinstating the complex nature associated with such effects.

**Open Symposium**

# BLIND LIKE A SEA-CUCUMBER? Opsin-based extraocular photoreception in holothurians (Holothuroidea, Echinodermata)

**YOURI NONCLERQ**

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Vision is a primordial sense in animal evolution, and it has been mainly studied in species that developed complex eyes such as chordates and arthropods. Except for the sea star eyespots, echinoderms do not have complex visual organs but can detect light by extraocular photoreception. In eumetazoan lineages, light detection is mediated by a group of transmembrane proteins named opsins. Eight types of theses opsins have been detected in the Echinoderms and many studies have found their accurate localization in the tissues of sea urchins, brittle stars and starfishes. By contrast, the photoreception of sea cucumbers (Holothuroidea) remains largely unknown. Therefore, we have investigate this photoreception in the holothurian group with three different approaches. (i) We detected, by comparison with the eight reference opsin sequences of the sea urchin (Strongylocentrotus purpuratus) model, at least six opsin classes in the genome of Apostichopus japonicus (the most complete sea cucumber genome, up to now) : one ciliary opsin (Aj-opsin1), two Go-opsins (Aj-opsin3), two melanopsins (Aj-opsin4), one peropsin (Aj-opsin6), one RGR-opsin (Aj-opsin7) and one neuropsin (Aj-opsin8). (ii) We have detected by immunohistochemistry and immunofluorescence one rhabdomeric opsin-4 in the podia and oral tentacles of the Holothuriida species Holothuria forskali. We have also found the expression of one ciliary opsin-1 in particular anatomical structures of two holothurian species belonging to the Apodida (serpentiform sea cucumber without podia). On one hand, ocelli structures in Euapta godeffroyi, on the other hand, sensory cupules in Oestergrenia digitata. These results point to a photoreception role played by theses organs. (iii) We have demonstrated that H. forskali and E. godeffroyi can react to various light stimuli. These species showed a significant negative phototropism when exposed to short wavelengths (blue and green light) which are those which propagate most efficiently and deeply in the marine environment.

**Open Symposium**

# Investigating the role of structural variants in rapid diversification of Lake Malawi cichlids

**SAHA JAYSMITA**

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The cichlid fishes in the African great lakes show a magnificent amount of species diversity. They are well known for their explosive speciation events resulting in a wide range of trophic adaptations and rapidly evolving radiations. This also makes them a system which is an ideal example of evolution in progress. Recent research has identified a hybridisation event in an ancestral species of the Lake Malawi cichlids which has promoted their adaptive radiation. It has been also shown that gene flow between the early diverging species have enabled cross species transfer of the variations assisting in adaptation and aided in the diversification. To understand further about the underlying mechanisms behind the diversification processes we focused on structural variants. They are of particular interest as they are a type of genomic rearrangement which can affect the fitness and phenotype of species by rearranging regulatory regions in the genome. Chromosomal inversions are a type of structural variant which arise when a part of the chromosome breaks and re-joins in a flipped orientation with respect to the original conformation. This kind of rearrangements are thus capable of linking adaptive alleles and making the species more suitable for novel ecological niches. Utilising short and long read sequencing data we have identified several inversions across the lake Malawi radiation. The roles played by these inversion haplotypes differ among the various species, with some being selected for specific ecomorphological clades while others function as sex determining regions in some species and not in others. Hence, analysing the genomic data allows us to identify the fundamental processes governing the evolutionary dynamics of these inversions and their contribution to the rapid diversification in Lake Malawi cichlids.

Open Symposium

# Did hybridisation fuel the adaptive radiation of Silversides in the Malili lakes?

**ELS DE KEYSER**

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Adaptive radiations are bursts of evolution in which many ecologically differentiated species emerge over relatively short evolutionary timescales. Despite the importance of these rapid speciation events, it is still not well understood how they are triggered. One hypothesis that has gained scientific interest is that these radiations may be fuelled by hybridisation events, providing new combinations of genes for natural selection to act upon. In order to shed light on this matter, we will characterise the genomic substrate for rapid ecological adaptation and speciation in the adaptive radiation of sailfin silverside fishes (genus *Thelmaterina*) of the Malili lakes system in Sulawesi. The Malili lakes silverside radiation consists of ~20 species spanning a variety of ecological niches. Besides presumed hybridisation in their early divergence, sailfin silversides also show strong signals of ongoing genetic introgression. This makes silversides radiation ideally suited as a model system to obtain an integrated picture of the effects of hybridisation in adaptive radiation. To unravel the complex evolutionary history of the Malili sailfin silversides, we will use whole genome sequences to detect signals of hybridisation events at the root of the species tree, and to characterise the extent and direction of ongoing hybridisation. It is urgent to conduct this research, because the entire radiation is under imminent threat from human activities such as nickel ore-mining, damming, and deforestation, as well as the introduction of at least 12 invasive fish species. Preliminary results using 16 whole genome sequences are promising, as they show the expected signals of introgression.

Evolutionairy Genomics

# Genomic consequences of domestication of the Siamese fighting fish – A promising new model organism

HANNES SVARDAL

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Siamese fighting fish, commonly known as betta, are among the world’s most popular and morphologically diverse pet fish, but the genetic processes leading to their domestication and phenotypic diversification are largely unknown. We assembled de novo the genome of a wild Betta splendens and whole-genome sequenced 98 individuals across five species within the B. splendens species complex. We find that domesticated ornamental betta individuals have variable contributions from other Betta species. In turn, several wild Betta species have introgression from ornamental betta. We identify dmrt1 as the main sex determination gene in ornamental betta and show that it has lower penetrance in wild B. splendens. Furthermore, we find genes with signatures of recent, strong selection that have large effects on color in specific parts of the body, or on the shape of individual fins, and are almost all unlinked. Our results demonstrate how simple genetic architectures paired with anatomical modularity can lead to vast phenotypic diversity generated during animal domestication, and set the stage for using betta as a powerful new system for evolutionary genetics.

**Evolutionairy Genomics**

# AN INTEGRATIVE STUDY OF TREE FROG ATTACHMENT: STRUCTURES, MECHANISMS, AND BIOMIMETIC POTENTIAL

**JULIAN K.A. LANGOWSKI**

The ‘smooth’ adhesive pads of tree frogs are an important source of inspiration for the design of bioinspired adhesives. Numerous bioinspired adhesives mimic in particular the hierarchical pattern of micro- to nanoscopic pillar-like structures found on the toe pads of tree frogs. Other functionally relevant pad components, however, have barely been considered in the design of tree-frog-inspired adhesives. In this talk, I will present recent research beyond the surface of tree frog’s toe pads, and discuss the functional relevance and biomimetic potential of previously undescribed pad components. Using synchrotron-micro-computer-tomography, we identified an anisotropic network of keratinous and collagenous fibres that connects the adhesive pad surface with the digital skeleton. Finite-element-analysis suggests that such fibre-reinforcement strengthens the toe pad mechanically against high mechanical loads, which arise from rapid manoeuvres such as jumping. Furthermore, tree frog toe pads contain smooth muscle fibre bundles, which to our knowledge is unique among bioadhesive systems. These muscular structures may provide tree frogs with pad-intrinsic control mechanisms to regulate their attachment to the substrate. A comparative analysis of the digital mucus gland morphology and mucus chemistry does not support a specialisation towards attachment. Instead, an analysis of experimental work on bioinspired adhesives indicates that interstitial liquids such as the mucus secreted by tree frogs play a role in detachment. Overall, tree frogs are fascinating models for the design of strong adhesives with fine-tuneable control of attachment strength that function under challenging conditions.

Biomechanics and -mimetics

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# VENA CONTRACTA, CENTRAL JETS, AND SUCTION FEEDING IN FISH

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Despite many decades of research on how fish capture food by generating suction, many questions remain on how food is efficiently transported to the oesophagus. After entering the mouth cavity, water is generally assumed to curve ventro-laterally to flow in between the branchial arches and exit through the opercular slit. This would imply pieces of food to be carried away from the oesophagus and pharyngeal jaw region, and to end up sieved at the branchial basket. Using our stereoscopic high-speed x-ray video system (3D2YMOX) in conjunction with a newly developed protocol of constructing small, neutrally buoyant tracers of water flow with X-rays, we managed to visualise intra-oral water flows in tilapia and carp. Unlike the classical hypothesis, tilapia showed a strong jet in the centre of the mouth cavity, often enabling a direct deposit of the food at the pharyngeal jaw region. At the sides of the mouth cavity, flow tends to recirculate, similar to the vena contracta effect behind a narrow nozzle (the mouth aperture in this case). Such flow pattern also appeared in earlier numerical simulations, but was (apparently wrongly) assumed to be an artefact of modelling inaccuracies. This flow pattern could contribute to improving suction feeding performance and efficiency. The central jet pattern was less pronounced in carps, which could be related to their predominantly bottom-detritus feeding habit relying specifically on branchial sieving and tasting before ingestion.

Biomechanics and -mimetics

# Morphological diversity and biomechanical proprieties of lizard osteoderms

### LOÏC KÉVER

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Many species of lizards are equipped with a dermal armor made of ossified units called osteoderms. Because of their distinct morphological and histological diversity, lizard osteoderms likely evolved under different selective pressures. It has been suggested that heterospecific or conspecific interactions as well as environmental variation may be important drivers of phenotypic variation. This suggests differences in the biomechanical properties of osteoderms between species. We tested this hypothesis by recording tensile and compressive strains in cranial osteoderms subjected to different loading regimes from a diverse sample of lizard species. We instrumented osteoderms with delta rosette strain gauges in 11 lizard species (Tiliqua rugosa, Tiliqua gigas, Corucia zebrata, Pseudopodus apodus, Timon lepidus, Matobosaurus validus, Broadleysaurus major, Tribolonotus gracilis, Tribolonotus novaeguineae, Heloderma horridum, Heloderma suspectum). Next, we applied forces ranging from 1 to 30 N and recorded changes in the magnitude and direction of the principal strains (i.e. maximal tensile strain, maximal compressive strain, shear strain). Our preliminary results show that some species, above all T. rugosa, have very stiff osteoderms. They also suggest that the biomechanical properties of osteoderms are strongly affected by lizard size.

**Biomechanics and -mimetics**

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# Environmental dependency of host-microbiota interactions in *Daphnia magna*

### MARTIJN CALLENS

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Animals live in a symbiotic association with a large diversity of microorganisms: the host-associated microbiota. This host-associated microbiota is known to have the ability to influence various phenotypic characteristics of it's host, either in a positive way (mutualism) or in a negative way (parasitism). The strength and direction of symbiotic interactions is often influenced by environmental factors, which can either affect the composition of the host-associated microbiota or the nature of the interactions themselves. We conducted experiments using the invertebrate ecological model system *Daphnia magna* to investigate the effect of various environmental factors (diet, cyanotoxins, antibiotics and bacterioplankton) and the host genotype on the composition of the *Daphnia*-associated bacterial microbiota. In addition, we measured the effect of these changes in the Daphnia-associated microbiota on the host phenotype by determining effects on growth, reproduction and survival. We found that environmental variation has strong effects on symbiotic interactions between *Daphnia* and its microbiota. These effects were often driven by shifts in the microbiota community composition that alter its functionality. In addition, the host genotype is also a strong determinant of the microbiota composition, resulting in G x E interactions. In conclusion, symbiotic interactions between *Daphnia* and it's associated microbiota have a strong environmental dependency, indicating that the microbiota can be a strong determinant of phenotypic responses of *Daphnia* to environmental change.

**Symbiosis inclusive host-microbiome interactions**

# Genotype specific and microbiome effects of hypoxia in the model organism *Daphnia magna*.

**MANON COONE**

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The depletion of oxygen as a result of increased stratification and decreased oxygen solubility is one of the most significant chemical changes occurring in aquatic ecosystems as a result of global environmental changes. Hence, moreaquatic organisms will be exposed to hypoxic conditions over time. Deciphering the effects of hypoxia on strong ecological interactors in this ecosystem's food web, such as *Daphnia*, is critical for predicting how aquatic communities can respond to such disturbance. Here, I investigated (i) the (sub-)lethal effects of hypoxia and whether these are genotype specific. As studies in *Daphnia* have already described the role of genotype x microbiome interactions in their response to toxic cyanobacterial stressors, I investigated (ii) the effect of hypoxia on the microbiome and (ii) whether the microbiome plays a role in hypoxia tolerance. For this, I performed two experiments: Daphnia were exposed for two weeks to either hypoxia or normoxia and (i) survival, growth and reproduction were monitored together with (ii) the microbial change after this period.
Drivers of hypoxia tolerance were investigated (iii) in a transplant experiment where germ-free recipient Daphnia were inoculated with gut microbiota from Daphnia donors of their own genotype or from the other genotype, that had been either pre-exposed to normoxic or hypoxic conditions. After receiving the gut transplant, (sub-)lethal effects were evaluated for ten days in hypoxia. Gut samples were taken during the transplant experiment to determine shifts in the gut microbiome community composition between normoxic and hypoxic associations.

**Symbiosis inclusive host-microbiome interactions**

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# Choose your diet wisely: the interplay between gut microbiome and host epigenome under cyanobacterial stress in *Daphnia*.

**NAINA GOEL**

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The study aims to investigate the role of the interplay between the gut microbiome and their host, *Daphnia magna*, water flea, with respect to the response of the host to an environmental stress factor for cyanobacteria (Microcystis aeruginosa). More specifically, I am using various molecular targeted techniques in combination with whole genome analyses to disentangle the contribution of the gut microbiome and DNA methylation in the host to the phenotypic stress responses at the organism level (growth, reproduction and survival). Yet, so far, the lack of a combined integrative approach made it impossible to establish causal links between the different levels of regulation. I am using an integrative and innovative approach to unravel the contributions of both the epigenome and gut microbiome and their interaction. Via gut transplants of susceptible and tolerant genotypes, in combination with a whole genome (bisulfite sequencing of Daphnia) and microbiome approach (metagenetics and metagenomics), I aim to unravel whether the microbiome structures the epigenome and vice versa and how this affects the phenoytpic outcome of stress responses up to life history responses and the metabolite level. More in particular, I hypothesise that changes in the composition and gene functions of the gut microbiome drive changes in DNA methylation patterns and gene expression levels, leading to changes in the expression and alternative splicing of digestive proteins (proteases, e.g. trypsins and chymotrypsins) ultimately resulting in increased tolerance to Microcystis stress.

**Symbiosis inclusive host-microbiome interactions**

# Investigating the role of external microbiota in the Sparidae-Lamellodiscus host-parasite system

**MATHILDE SCHEIFLER**

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The link between symbiotic communities, both bacterial and eukaryotic, and their host is currently an emerging question in ecology and evolution. Despite its importance in maintaining homeostasis and preventing infection, little is known about the factors explaining the variability of fish external microbiota, especially in natural populations. Fish are known to be hosts of ectoparasitic monogeneans, often abundant on the skin and gills and generally highly host-specific. Monogeneans seem to be attracted to molecules produced (at least partly) by bacterial communities from the host's surface but this interaction remains unclear.
This study focuses on a teleost-parasite system in the Mediterranean Sea, between Sparidae and their specific monogenean gill ectoparasites from the Lamellodiscus genus, where the pattern of host specificity is well known. We characterized skin and gill's microbiota using 16S rRNA amplicon sequencing, in order to assess the effect of environmental factors, host's ecological traits and evolution (i.e. phylosymbiosis) on microbiota and determine if some bacterial taxa are related to some Lamellodiscus species. We found that the variation in external microbiota is driven by both annual fluctuations of abiotic variables and host-related factors. Bacterial assemblages appeared to be a key element in the relationship between teleosts and their ectoparasites, as suggested by numerous correlations between bacterial genera and Lamellodiscus species, including species-specific associations. Interestingly, the external microbiota of an unparasitized sparid species, Boops boops, harbored significantly more Fusobacteria and three Proteobacteria genera compared to the other sparid species. This work opens new avenues of research, such as understanding the colonization mechanisms of microorganisms and the differences in selection pressures according to fish-associated traits. Novel evidences for a link between parasites and microbiota have been provided, which seems determined by several mechanisms potentially including the protective and attractive role of microorganisms.

**Symbiosis inclusive host-microbiome interactions**

# Antarctica as an evolutionary incubator? Phylogenetic comparative study of the amphipod family Iphimediidae on the Antarctic shelf

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From about 40 Mya, while Antarctica geographically isolated from the rest of the world, the marine shelf fauna faced a dramatic decrease in water temperatures. Many lineages went extinct, while others adapted and flourished. The Antarctic clade of the amphipod family Iphimediidae was among the successful ones. Here, a range of cutting-edge phylogenetic comparative and morphometric methods are used to investigate the evolutionary processes which generated the exceptional diversity of this clade. To this purpose, a novel multigene phylogeny of the family was first reconstructed. Secondly, 3D shape data were obtained by applying 3D-geometric morphometric methods on micro-CT scans of the specimens. As a prerequisite to the study of species diversification, species boundaries were first investigated using a combination of DNA-based delimitation methods and morphological data. The latter showed that species diversity in Antarctic iphimediids is greatly underestimated, as most of the described species appear to be complexes of multiple morphologically similar species. Potential changes in the rate of lineage diversification were explored in parallel to the evolution of morphological traits (mouthparts 3D shape data) along the phylogeny. On one hand, we found no evidence of an early burst of lineage diversification. On the other hand, late bursts (appr. 7-3 Mya) of lineage diversification were detected in two subclades. Such late radiations could result from the invasion of novel ecological niches, as a late partitioning of mouthparts' shape diversity along the phylogeny is also observed. Plio-Pleistocene glacial cycles, which have been hypothesized to act as diversity pumps, might also have promoted late diversification events in Antarctic iphimediids. By applying such an integrative approach for the first time on Antarctic invertebrates, this study improves our general understanding of the evolutionary dynamics shaping the standing Antarctic shelf biodiversity.

**Eco-Evolutionary interactions/dynamics**

# Simulating adaptive evolution of spatially-distributed populations to climate-driven perturbations: a genomically-explicit modeling approach

**PASCAL HABLÜTZEL**

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In natural environments, many species are organized in spatially structured populations with varying degrees of connectivity among them. The patchy organization of a population in a heterogeneous environment presupposes that the evolutionary fate (i.e. persistence or extinction) of subpopulations will be influenced not only by the mutation supply rate (i.e. Ne*μ), but also by the dynamics of dispersal and gene flow. Predicting how these dynamics will influence the future evolutionary trajectory of a spatially distributed population under changing environmental pressures (e.g. sea surface warming) remains a difficult challenge. This problem is not only theoretically appealing, but it is arguably of major concern in conservation genetics, where a great deal of effort is invested in informing the decision making process for the preservation of marine protected areas. In this study, we implemented a simple two-patch population model in the SLiM simulation environment. Based on this flexible, individual-based evolutionary model, we conducted simulations where: 1) locally adapting and age-structured subpopulations must track a patch-specific phenotypic (thermal) optimum over time; 2) dispersal involves the movement between subpopulations of individuals in the reproductive (adult) stage; 3) individuals have the ability to persist across multiple generations depending on their fitness; and 4) the fitness of individuals in each evolving subpopulation is computed using a standard quantitative genetics model, where a trait value results from the additive contribution of a multitude of (linked) genomic loci. We will discuss some preliminary simulation results and emphasize the need of mechanistic modeling inspired on molecular systems biology to adequately study the adaptive responses of populations to climate-driven perturbations under more realistic assumptions about the molecular complexity of the genotype-phenotype map.

**Eco-Evolutionary interactions/dynamics**

# Testing a new hypothesis regarding the advantage of an important developmental process in evolution: Progenesis.

**BENJAMIN LEJEUNE**

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Paedomorphosis, an extreme form of developmental plasticity involving the retention of larval traits at the adult stage, is considered a major evolutionary process in many groups because it can quickly generate phenotypic variation without requiring important genetic modifications. Two main processes underlie paedomorphosis: neoteny, which consists in a slowdown of somatic development, and progenesis, which consists in an acceleration of sexual maturation associated to body size reduction. Because it is essentially a truncation of ontogeny, progenesis has often been deemed an evolutionary dead-end by macroevolutionists, with advantages mainly attributed to a precocious reproduction or small body size required in specific environmental contexts (e.g. parasitism or interstitial life of meiofauna). Yet body size is also recognized as a key factor determining the trophic niche of species. Here, we formalized a new hypothesis regarding the immediate ecological advantage of progenesis which is that via body size reduction, progenesis might intrinsically promote trophic niche differentiation and therefore allow to decrease intraspecific competition for resources. We tested this hypothesis in multiple populations of facultatively progenetic newts where both phenotypes (progenetic and metamorphic) coexist using stable isotope niche modelling and mixing models in relation to morphological and environmental parameters. We show that not only did progenetic individuals occupy a different trophic niche in all populations, but the smaller they were compared to metamorphs due to progenesis, the more different they were in terms of trophic ecology. We argue that beyond generally recognized fitness advantages of progenetic development such as an earlier reproduction, this process may also generally bring immediate trophic advantage via body size reduction.

**Eco-Evolutionary interactions/dynamics**

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# The byssus and byssal-producing glands of the silverlip pearl oyster *Pinctada maxima* (Jameson, 1901)

**ALESSANDRA WHAITE**

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Many bivalve species produce groups of strong proteinaceous byssal threads to rigidly attach to underwater substrates. The model genera for studies in byssus structure and function has historically been the mytilid mussels. However, the macroscopic similarities of byssus across bivalve families often belies their molecular diversity. The byssus and byssal thread producing glands of the silverlip pearl oyster *Pinctada maxima* have not been previously characterised. RNA was isolated from *P. maxima* foot and byssal stem region tissues and sequenced using the Illumina platform. A de novo reference transcriptome comprising 34,281 contiguous sequences was assembled, and tissue replicates were mapped against the reference for quantitative analysis. Tryptic digests of byssal threads were analysed by LC-MS/MS. The resultant peptides were matched to 62 protein sequences derived from our reference transcriptome. Components of the byssus were identified for further characterisation, including a highly expressed perlucin-like foot protein (Pmfp1) and a glycine-rich thread (GRT) protein. Custom polyclonal antibodies were raised against the GRT and Pmfp1 proteins to identify their spatial distribution within the foot tissue of *P. maxima*. The results of the immunodetection, combined with H&E histology, helped to identify the glandular regions of the *P. maxima* foot that contribute to byssal thread production; the byssal gland, the duct gland, and two thread-forming glands of basophilic and acidophilic serous-like cells. This work provides principal knowledge on the molecular components of the non-model *P. maxima* byssus and the foot anatomy involved in the creation of byssal threads. This study advances our knowledge of byssus biosynthesis in non-mytilids, providing a platform for the design of new marine biopolymers.

**Open Symposium**

# SEA STAR (ASTEROIDEA) DIVERSITY IN THE MAGELLANIC REGION (SOUTH-CHILE) AND THEIR AFFINITIES WITHIN THE SOUTHERN OCEAN

**LUKA VANTOMME**

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Sea stars are a diverse and important component of the Southern Ocean benthos. However, only scarce information is available regarding their diversity and evolution, and taxonomic revisions are required. The Magellanic region (south of Chile) remains under-sampled despite its pivotal position for species richness and distribution being at a crossroad between three ocean basins. Therefore we assessed sea star biodiversity in this region and evaluated its geographical position in sea star biogeography. An integrative approach combining morphological identification with DNA barcoding has been implemented to highlight taxonomic discrepancies such as synonymous species and cryptic species. Close to 200 COI sequences were added to the DNA barcode library to aid future genetic identifications. We identified 12 sea star species from the Magellanic region and reported Cycethra frigida there for the first time. Furthermore we proposed to synonymise two species pairs within the Anasterias and Odontaster genera. This project greatly improves the biodiversity baseline for this dominant taxa in a key area for connectivity which is the necessary first step in understanding and monitoring future biodiversity changes. Four geographical patterns were observed covering narrow (endemic to the Magellanic region) to broad (circumpolar to bipolar or possible cosmopolitan) distribution ranges. Although developmental mode has been suggested as important in shaping biogeographical patterns, relying on this alone is insufficient and other life history traits, physiological constraints, competition, bathymetrical range, and the possibility of passively rafting on kelp are suggested to be at least equally important.

**Open Symposium**

# Revisiting the KEA lakes : A cradle for African ichthyofaunal diversity?

MAARTEN VAN STEENBERGE

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Given its high level of endemicity, the Albertine Rift is considered one of the world's major biodiversity hotspots. The Northern Albertine Rift contains three lakes: Kivu, Edward and Albert that differ profoundly in ecological and climatic parameters. The lakes and their basins, hereafter labeled the KEA region, lie on the boundary between three main biogeographical units and the literature contains a lot of confusion concerning their biogeographical assignment, at least with respect to the fish faunas. These stem from the fact that their faunas contain either very wide-spread species, or strict endemics. Neither of these can be used in traditional faunistic approaches. We investigated the biogeography using an integrative approach combining morphology, genetics, genomics and parasitology. For the endemic cichlid species flocks, this revealed that the assemblages from lakes Kivu and Edward formed a single lineage, which radiated separately from that of Lake Albert. This agreed with the pattern in other fish groups. There, a barcoding approach assigned lakes Kivu and Edward to East Africa; but Lake Albert to North and West Africa. The KEA region also contains the wide-spread species Clarias gariepinus, the sharptooth catfish, and Lates niloticus, the Nile perch. These large-bodied fishes and their relatives are of major economic, cultural and ecological importance and support important fisheries. Phylogenetic reconstructions revealed that the KEA region served as the region of origin of these species. The diversification and vicariance events in both C. gariepinus and L. niloticus occurred within a similar time frame and could be linked with changes in climatic conditions and rifting. Finally, the recent spread of both species across Africa is reflected by their parasite faunas as for both fish species, gill parasites were found that infect populations across their native range.

**Open Symposium**

# Diversity of mesophotic coral reefs fish fauna through passive acoustics

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Since it is not an easily accessible environment for humans, few is known on the deeper part of coral reefs (mesophotic coral ecosystems). In this study, fish sounds were used as a proxy to study Polynesian coral reefs. The aim of the study was to determine how the acoustic fish biodiversity varied depending on the depth and the type of island (atoll vs. high island), two features known to impact species richness and diversity. The link between benthic cover and both the acoustic α-diversity and acoustic fish communities was established at –20, –60 and –120 m in three atolls and three high islands. More than 45 different fish sound types were described. The number of some sound types increased with depth while the opposite was observed for other sound types. In most islands, acoustic α-diversity (Shannon index based on sound types) falls between –20 and –60 m but not between –60 and –120 m supporting the existence of a transition zone between two distinct fish communities. The highest similarities between acoustic communities were found between –60 and –120 m, the lowest between –20 and –120 m. Overall, acoustic community composition was mainly driven by the depth due to benthic coral cover differences, and to a lesser extent, by the type of island. These results show fish sounds exhibit a bathymetric stratification. Moreover, differences can reflect different habitat features. It opens new perspectives in the study and monitoring of mesophotic coral ecosystems using passive acoustics.

**Open Symposium**

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# Mutualistic relationship between the amphipod *Stenula normanni* (Stephensen, 1931) and the nephtheid coral *Gersemia rubiformis* (Ehrenberg, 1834)

**CAULIER GUILLAUME**

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*Gersemia rubiformis* is a soft coral belonging to the family Nephtheidae, known to provide habitat for many organisms and to play an essential role in benthic ecosystems. The present study examined the relationship between *G. rubiformis* and the epibiotic amphipod *Stenula nordmanni* in the coastal waters of eastern Canada. The prevalence of the association was 100% with an average burden of 35 amphipods (mostly juveniles) per coral host. The sex ratio in the amphipods was female-biased and there was a distinct sexual dimorphism, males being significantly larger than females. In a single coral colony, about 38% of female amphipods were found to brood propagules at various stages of development up to juveniles. Upon release, juvenile amphipods were transparent and acquired the pink color characteristic of the adult by feeding on the coral tissues, thereby mimicking the coloration of the host. Ingestion of coral tissues was confirmed by the presence of host sclerites in the digestive tract of amphipods. In turn, amphipods were seen to protect their host by repulsing predatory nudibranchs approaching the coral colony. Together, findings suggest that the amphipods display a specific and obligate mutualistic association with their coral host, considering that they benefit from shelter and food, and the host benefits from active protection against potential predators. The apparent trophic relationship does not appear to generate any detriment to the host. In addition, some of the symbiotic amphipods examined were found to be hosts themselves, to chytrid fungi attached to their exoskeleton.

**Symbiosis inclusive host-microbiome interactions**

# Does the gut microbiome contribute to the pace-of-life and associated tolerance to a pathogen in damselfly larvae?

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It has been hypothesized that the gut microbiome may play an important role in shaping differences in the pace-of-life (POL) and associated tolerance to pathogens of their hosts. We tested these ideas by studying whether the gut microbiome can contribute to the POL of damselfly larvae and, associated with this, their tolerance for the pathogen Escherichia coli (E. coli) under global warming conditions. To study the causal role of the microbiome, a reciprocal gut microbiome transplant was performed between fast-paced French and slow-paced Swedish larvae of the damselfly Ischnura elegans. Our results confirmed that French larvae had a faster POL than Swedish larvae and are better adapted to higher temperatures in terms of growth rate. A key finding was that only under warming exposure, E. coli led to an increased mortality and this equally in French and Swedish larvae. We did not find a contribution of the gut microbiome on the POL traits growth rate and mortality of the damselfly larvae. Yet, in line with the slower POL of the Swedish larvae, the Swedish donor microbiome improved the immune function and reduced the E. coli burden compared to the French donor microbiome, thereby mimicking the latitudinal differences at the phenotypic level. By using a space-for-time substitution, our results tentatively suggest that Swedish larvae will have increased growth rates and a lowered immune function if they would be able to evolve by 2100 under future warming but that evolution of the microbiome would not contribute to this. As a general conclusion, we observed POL-differentiation with thermal adaption whereby the microbiome influenced the immune-associated part of the POL of the host.

Symbiosis inclusive host-microbiome interactions

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# Marine symbiotic association: may the host recognition be possible since the early stage of symbiont life?

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Symbioses are intimate and durable associations between at least two heterospecific organisms, commonly named the host and the symbiont. Many symbionts can be highly host dependent, and the chemical communication as, for example, the recognition between symbiotic organisms, is essential for the durability of many symbioses. In marine environments, host selection is considered multimodal but mostly relies on chemical communication. It is made possible by the secretion of secondary metabolites produced by the host, the so-called kairomones or synomones, that are recognized by the symbiont. Several studies already focused on the echinoderm host recognition performed by adult symbiotic crustaceans, but none of them has ever investigated if the crustacean larvae recruitment was mediated by chemical communication. In the lagoon of Moorea (French Polynesia), we decide to investigate Asteroidea - Crustacea association. Indeed, despite their strong chemical defenses, sea stars are known to shelter an important associated fauna, including obligatory ectocommensals crustaceans. We focused on the symbiosis between the sea star Culcita noveaguineae and its symbiotic shrimp Zenopontonia soror. The chemical attractiveness of the adult shrimps was first tested in a Davenport olfactometer and highlights an active attraction of the symbiotic adults to the chemical environment produced by the host. Indeed, 80% of the shrimps could actively swim towards the chemical cue produced by the host. For the first time, we also investigated the host recognition on the shrimp zoea larval stage thanks to a particular Y-tube choice device with a low water flow. Larvae could also recognize the host sea star as they strongly oriented themselves toward the host conditioned water. Therefore, we suggest that the pelagic Z. soror larvae are recruited by a specific chemical cue produced by their host C. noveaguinea in vivo, and, moreover, the host recognition may take place since the early state of the symbiont life.

Symbiosis inclusive host-microbiome interactions

# The role of the microbiome in eco-evo interactions: *Daphnia* and its microbiome as a model.

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In spite of the growing interest in the role of the gut microbiome in host physiology and health, the mechanisms governing its assembly and its effects on the environment are poorly understood. We show that the host genotype and the gut microbiome of *Daphnia* influence the community structure of the surrounding bacterioplankton. When *Daphnia* genotypes were placed in an identical environment, both the gut microbiome and bacterioplankton showed a genotype and diet-dependent taxonomic composition. Overall, the gut microbiome strongly differed from the bacterioplankton in taxonomic composition and was characterized by a lower α-diversity, suggesting a selective rejecting of bacteria from the regional species pool. In microbiome transplant experiments, the assembly of both the gut microbiome and bacterioplankton was strongly affected by the host genotype and the inoculum to which germ-free *Daphnia* were exposed. These results suggests a strong interaction between the host genotype, its gut microbiome and free-living microbial communities. Currently, it is generally assumed that an animal's diet has a strong effect on the animal's gut microbiome, but only a negligible effect on the surrounding environment. However, our results indicate that the diet/microbiome inocula have a small effect on the gut community and a large effect on the community in the surrounding environment. This structuring genotype × microbiome × environment effect affecting host phenotypes is an essential prerequisite that could indicate that microbiomes play an important role in eco-evolutionary processes, especially in the light of stressors and changing climates.

Further read in:

Houwenhuyse S., Stoks R., Mukherjee S., Decaestecker E. 2021. Locally adapted gut microbiomes mediate host stress tolerance. *ISME journal* 15: 2401-2414.
Callens M., De Meester L., Muylaert K., Mukherjee S., Decaestecker E. 2020. The bacterioplankton community composition and a host genotype dependent occurrence of taxa shape the Daphnia magna gut bacterial community. *FEMS Microbial Ecology* 96:8.
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**Symbiosis inclusive host-microbiome interactions**

# Physiological regulation of bioluminescence through photo-perception: an overview and perspectives.

**DUCHATELET LAURENT**
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Bioluminescence is defined as the production of visible light by a living organism. To fulfil its ecological role (i.e. defense, offense, or communication), bioluminescence needs to be finely controlled. Although nervous or hormonal control mechanisms have been demonstrated to occur, another type of local control via extraocular photoreception has been suggested to operate in different marine luminescent taxa. Photoemission and photo-perception association imposed a clear co-evolution between the two light-related processes. Recently, extraocular photo-perception processes were shown or suggested to occur at the level of the bioluminescent production site (i.e. photophore/photocyte) in various marine organisms. Photoreceptor molecular markers, including metazoan prototypical photoreceptor proteins (i.e. opsins), have first been identified in the bioluminescent organ of the cephalopod Euprymna scolopes. In this sepiolid, light produced by symbiotic bacteria is perceived by extraocular opsins located in the tissues of the photophore. The discovery of this extraocular photodetection highlighted the presence of an unsuspected relationship between extraocular perception of light and bioluminescence. Then, studies revealed opsin expression in the photocytes of a ctenophore, Mnemiopsis leydii, reinforcing the idea of a local interconnexion between light emission and reception, even in an organism producing its own luminescence. More recently, opsins were specifically demonstrated (i) to be expressed within the photocytes of the ophiuroid Amphiura filiformis and (ii) to be expressed and functionally active within the photophores of the shrimp Janicella spinicauda. Finally, a deeper characterization of the link between the two processes was made in the lanternshark Etmopterus spinax, where not only opsin characterization and localization within the photophore are depicted, but also the morpho-functional action and intracellular pathways linking light emission and perception. Except for the lanternshark, control mechanisms linking both photobiological processes remain unknown. The functional coupling between photoreception and photoemission is suggested to be an astonishing example of functional convergent evolution in luminescent organisms but needs to be investigated in more details.

**Marine Biology**

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# Where does your (luciferase) gene come from? Evolution of light-emitting enzymes in animals

**DELROISSE JÉRÔME**
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Bioluminescence — the emission of visible light by living organisms — relies on the oxidation of a luciferin substrate catalysed by a luciferase enzyme. This terminology gives a false idea that all luminous organisms are using identical or homologous molecular tools to achieve bioluminescence. Multiple light emission systems co-emerged independently along the tree of life resulting in a plethora of non-homologous luciferases. To investigate the diversity of known luciferase proteins, we analysed a total of 134 sequences coming from 75 species and 11 phyla. We identified 12 distinct groups of luciferases, each comprising homologous proteins but with no homology between groups. It appears that phylogenetically related organisms may sometimes use non-homologous luciferases but also that phylogenetically distant organisms may use homologous luciferases. Genes coding for luciferases may then have emerged as new genes or have been co-opted from ancestral non-luciferase genes. In this latter case, the homologous gene co-options may occur independently in phylogenetically distant organisms as observed in the case of the brittle star/sea pansy luciferases.

Focusing on the bioluminescent brittle star *Amphiura filiformis* (Echinodermata), we used transcriptome and genome analyses to identify a candidate luciferase of the species. Using immunodetection and electron microscopy, we characterised the luciferase expression pattern and the ultrastructure of the light emitting cells. The luciferase localisation is specific to the photocytes and matches with the in vivo bioluminescence detection. Recombinant protein expression allowed to confirm the light-emitting bioactivity of a brittle star luciferase candidate. From an evolutionary point of view, the new luciferase is homologous to the luciferase of the sea pansy *Renilla* (Cnidaria). Our findings indicate that ancestral non-luciferase enzymes have been convergently co-opted into luciferases in cnidarians and echinoderms. In these benthic suspension-feeding organisms, similar ecological pressures would constitute strong selective forces for the functional shift of these enzymes and the emergence of bioluminescence.

**Marine Biology**

# Mapping the progenitor diversity in the fast aging killifish brain

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In recent years, the African turquoise killifish has been successfully established as an innovative aging model with great potential because of its impressive short lifespan, the presence of many mammalian aging hallmarks and an ever-existing stem cell pool. In addition, the killifish displays a significant decrease in neurogenic capacity upon aging. Gaining more knowledge on the key cell types involved in killifish brain regeneration will greatly improve our understanding of the age-related decline in neurogenic potential.

Single cell RNA sequencing of the killifish telencephalon revealed common vertebrate cell types including neurons, microglia, oligodendrocytes, radial glia and vasculature-related cells. Sub-clustering of the progenitor cells identified the non-glial progenitors, four distinct radial glia subpopulations, and two intermediate cell types. Spatial mapping of these different cell (sub)types in this non-model organism can be challenging because of the absence of specific antibodies. We therefore introduced the advanced in situ hybridization tool Hybridization Chain Reaction (HCR) approach allowing multiplexing of mRNA expression. HCR in combination with Light Sheet fluorescence microscopy even makes it possible to study the distribution of specific markers and cell types in three dimensions over the entire telencephalon. Via a selection of marker genes, we were able to chart several regionally distinct cell populations, revealing their spatial setting.

Characterizing the 3D cellular organisation of the neurogenic niche in the young and old killifish telencephalon, and upon repair after injury, creates important knowledge of potential translational value regarding the role of neurogenic stem cells as drivers of successful regeneration upon injury or disease.

**Marine Biology**

# Poster Presentations

# ASPI – Wild bees in the city : Urban pollutant effects on the health of insects and plant-pollinator interactions

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The current "zero-phyto" policies are transforming cities into shelter areas, beneficial for numerous pollinator species. Yet, cities remain environments with severe constraints (fragmented habitats, urban heat islands, air pollutants). Those can be detrimental to natural population development. Notably, chronic exposure to urban pollutants can impair the pollinator health, as well as the plant-pollinator interactions. Some urban pollutants (phthalates, 4-nonylphenol, polyaromatic hydrocarbons [PAH], PBDEs,...) are endocrine disruptors that can cause sub-lethal effects, known to weaken insect populations, or to disrupt hormonal function, e.g. olfaction process and the related behaviors. By combining several different approaches, this project aims to understand the effects of wild pollinator exposure to urban pollutants (especially PAH and phthalates).

**Ecotoxicology**

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# Investigation of the potential of two sea cucumber species, *Holothuria polii* et *Holothuria tubulosa*, as bioindicators in northwestern Mediterranean: the case of trace elements and microplastics

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The Mediterranean is the recipient of numerous anthropic contaminants, such as trace elements (TE) and microplastics (MP), both sharing an affinity for sediments. As detritus feeders living in close proximity to sediments, sea cucumbers make good bioindicator candidates for their monitoring. However, before developing protocols relying on these animals, it is crucial to ensure that they reflect accurately the contamination status of their habitat.

Specimens of *Holothuria tubulosa* and *Holothuria polii* were collected at three periods in three locations of Calvi Bay (fish farm, sewer exit and Punta Revellata) to measure TE concentrations in their organs, in order to study the variability of these concentrations. In the meantime, the MP content of their digestive tract was compared between sites.

The choice of organ for the TE analysis had the biggest influence, with a different sensitivity of every organ to the sources of variability considered (i.e. spatial, temporal and interspecific). The bodywall displayed the lowest TE concentrations, which were homogenous between species at any time and for each site. In contrast, they were the highest in the hæmal system, especially in H. polii, with clear differences between sites. Finally, the muscles and the respiratory trees recorded intermediate concentrations, with respectively weak temporal and interspecific variations. This highlights the inadequacy of bodywalls for TE monitoring, as well as the hæmal system's potential to detect spatial variations of TE in sediments.

Most of the plastics extracted were MP, with a dominance of filaments/fibers. Individuals near the fish farm ingested more items, whereas those living at the sewer exit stood out from the ingestion of rubbers and fragments but also from a higher mean length of the plastics. This ingestion of MP by holothuroids in a way that reflects the anthropization of their habitat confirms their potential as bioindicators of plastic pollution in sediments.

**Ecotoxicology**

# Delayed effects of early life exposure to the neurotoxic compound permethrin in the mangrove rivulus, *Kryptolebias marmoratus*

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It is well known that the everchanging environmental conditions can have major effects on the phenotype of animals and thus their fitness. The early developmental stages are most vulnerable to disturbances of any kind. Here, we studied how early exposure to permethrin, a pyrethroid neurotoxic compound found in numerous insecticides, influences the phenotype in the resulting adults of the mangrove rivulus, Kryptolebias marmoratus.  This species is unique among vertebrates due to its ability to self-fertilize, thus producing natural homozygous individuals within isogenic lineages while maintaining a high degree of phenotypic plasticity. By working with minimal genetic variation, this species can provide valuable insights into how the environment and pollutants can impact both morphological and behavioural phenotypes.

We exposed *K. marmoratus* larvae to different concentrations of permethrin (0, 5 and 200 µg/L) to study the effects on growth, aggressive behaviour, and hormones levels in 148-day old *K. marmoratus* adults. In addition, we studied the differences in gene expression and DNA methylation of different potential permethrin target genes, based on their involvement in neurotransmission or their potential influence on individual behaviour variations.

Size measures from 4 timepoints (Day 1, 7, 70, 149 post-hatch) showed that growth was impacted. In fact, from day 1-70 individuals exposed to 200µg/L of Permethrin grew significantly less than those of the 2 other groups (5µg/L and control), however from day 70-149, individuals exposed to 200µg/L grew significantly more than those of the control group.

Permethrin exposure during development showed effects on behaviour in juveniles however no effect on aggressive behaviour was found in adults during “combats” between two hermaphrodites (number of attacks, probability of initiating or winning the “combat”).

The results of hormone levels, DNA-methylation and gene expression of our target genes are still being collected but will be included on the Poster.

Ecotoxicology

# MERCURY AND CIGUATOXINS MEASUREMENTS IN TWO FISH SPECIES FROM DIFFERENT LAGOONS OF FRENCH POLYNESIA WITH EVALUATION FOR HUMAN CONSUMPTION

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Fish consumption has great nutritional value. However, accumulation of toxic compounds like mercury (Hg) and ciguatoxins (CTXs) in fish is a concern for human health. CTXs are naturally produced by some benthic microalgae typically found in tropical coral reefs. Consumption of seafood contaminated with CTXs can cause Ciguatera Poisoning, a disease that includes gastrointestinal, neurologic, and cardiac complex symptoms. French Polynesia is an endemic ciguatera region with a high fish consumption rate. Since Hg and CTXs data were scarce in lagoon fish from the Society Islands (most populated archipelago of French Polynesia), this work studied both toxic compounds in the herbivore surgeonfish *Ctenochaetus striatus* and the carnivore grouper *Epinephelus merra*, two broadly consumed fish found in all the lagoons of the Society archipelago. Total mercury (THg) was measured in muscle and liver of fish using atomic absorption spectroscopy (AAS). CTXs where extracted from fish flesh and extracts were tested for toxicity using the neuroblastoma cell-based assay (CBA-N2a). Higher THg concentrations were measured in the flesh of the carnivore than that of the herbivore fish. In contrast, higher levels of ciguatoxins were found in herbivores. Flesh of C. striatus and E. merra can be consumed by the average Polynesian adult population without posing potential health problems related to Hg exposure. Lagoon fish consumption from low urbanized places in the Society Islands seems preferable to that of more urbanized sites to minimize the risk of suffering Ciguatera Poisoning. Artificial substrates were deployed to survey the abundance and diversity of CTXs-producing benthic microalgae, but additional studies should be conducted to draw conclusions about the potential risk of ciguatera outbreaks in the Society Islands.

**Ecotoxicology**

# Transfer assessment of PCB#153 sorbed onto HDPE microplastics to sea urchins tissues using radiotracers

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The knowledge of the potential adverse effects of sinking microplastics (MPs) on benthic marine animals, particularly benthic grazers, is still scant. No information is available on the potential "vector" effect of co-contaminants adsorbed onto MPs using adult specimens of the sea urchin *Paracentrotus lividus* as a model, despite being recognised as a species of great ecological and commercial importance in the Mediterranean coastal ecosystem. In this work, three experiments have been conducted to assess whether $^{14}$C-PCB#153 adsorbed onto the surface of MPs is bioavailable for the sea urchin *P.lividus* during 15 days : (1) exposure to a low concentration of $^{14}$C-PCB#153 sorbed onto a high number of virgin MPs (“lowPCB highMP” experiment), (2) exposure to a high concentration of $^{14}$C-PCB#153 sorbed onto a relatively low number of virgin MPs (“highPCB lowMP” experiment) and (3) exposure to a low concentration of $^{14}$C-PCB#153 sorbed onto a relatively low number of “aged” MP (“lowPCB lowMP” experiment). Results showed that the transfer of $^{14}$C-PCB#153 from MPs to sea urchin tissues occurred in each of the three experiments in each body compartment (except in the body wall and Aristotle’s lantern of sea urchins from the “lowPCB lowMP” experiment). Concentrations within the different body compartments of P.lividus were generally ranked in the order : digestive wall ≥ gonads > body wall ≥ Aristotle’s lantern > coelomic fluid. The sea urchins from “lowPCB highMP”, “highPCB lowMP” and “lowPCB lowMP” experiments accumulated on average 10.41 % (± 2.28, n = 9), 2.06% (± 0.59, n = 6) and 0.38% (± 0.08, n = 4) of $^{14}$C-PCB#153 adsorbed on the MPs, respectively. These findings suggest that the $^{14}$C-PCB#153 adsorbed onto the MPs was bioavailable to sea urchins and that these MPs acted as vectors of $^{14}$C-PCB#153 even during short-term exposure periods of only fifteen days.

Ecotoxicology

# DIFFERENTIATION OF PETROSOURCED PLASTIC MICROFILAMENTS FROM ORGANIC MICROFILAMENTS BY EDAX IN ENVIRONMENTAL SAMPLES

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Microplastics (MPs) are extensively studied and received increased attention but their quantification via a stereomicroscope is still a challenge. A visual identification may confuse MPs with small organic filaments, and this is strongly affected by human bias, microscopy quality, efficiency of the sample treatment, sample matrix and size limitation due to microscope resolution. The present study aims to differenciate petrosourced plastic microfilaments from organic microfilaments by using the energy dispersive X-ray analysis (EDAX) in various environmental samples. More than 30 particles resembling MPs (PRMp) were extracted from samples of sediments (from mangroves and from fields for aquaculture) and of organisms (sea cucumbers, bivalve and fishes) from southwestern Madagascar. With them, samples of macroplastic litters as well as macroalgae (found in the same marine environments) were sampled. At first, the atomic surface composition of these marine macroplastics and algae were analyzed. EDAX analyses showed that the ratio C/O was always >1 for macroplastics and <1 for macroalgae. Also, the Si and Al presence was always <1% for macroplastics while macroalgae could have these elements on their surface in a proportion >1%. Then each microplastic sample was photographed with an optic microscope and the photos were given to five observers to be identified as a microplastic or not. We found that there is a difference of observers' perceptions: all observers had same perception for 45% of extracted PRMp and different perceptions for 55% samples. EDAX could be adequate to determine the error on a quantification of MPs already done or to train scientists who have to quantify MPs on samples.

Ecotoxicology

# Permethrin short and long-term impacts of early-life exposure on the turquoise killifish (*Nothobranchius furzeri*): behavioral and molecular approaches.

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It has been proved that neurotoxin exposure during early life stages can impact development and adulthood behaviors. Permethrin is one of the most common neurotoxic insecticide in a wide range of fields from domestic to agricultural uses. Due to its extensive use, this neurotoxin has negative impact on freshwater organisms. The main goal of this study is to determine immediate and delayed impacts of permethrin on the behavior and other phenotypic parameters such as life history and morphological traits following an exposure during early-life stages. The African killifish *Nothobranchius furzeri*, because of its short life span of 4-6 months, is the perfect model to investigate interactions between pesticide exposure and ageing processes. During their first week post hatching, larvae were exposed to 3 concentrations of permethrin (0, 10 and 100µg/L), and then assessed for the effects at 3 different time-points: 1, 5 and 17 weeks post hatching. As *N. furzeri* is highly territorial we conducted a mirror induced aggressivity test (MIA) assessing number of bites as aggressivity proxy. Our results show that high concentration of permethrin significatively decreases the survival probability of fishes during their exposure ($p\text{-value}<0.001$). Even if aggressivity was not significantly affected by permethrin exposure, sex and age of the fish had significant impact on attack occurrences. Indeed, males showed more bites than females ($p\text{-value}=2.25e\text{-}10$) and old males spent more time nearby the mirror with no attack behavior than young males ($p\text{-value}=1.17e\text{-}09$). Interestingly our results also showed that at some point, the anal fin played a significant role in fish's interactions. At 5 weeks post hatching, just after sexual maturity, males showing a longer anal fin also showed greater aggressivity ($p\text{-value}=0.00425$). Further analysis of gene expression and DNA methylation level will permit to link aggressive behavior to candidate genes. At this point we can conclude that age, sex and morphological traits influence aggressivity in *N. furzeri*, while the effects of permethrin are limited.

Ecotoxicology

# THE SEAHORSE SKELETON – MODELLING THE STRENGTH OF THE BONY PROTECTIVE ARMOUR AROUND THE SPINE

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Most organisms have tails with cylindrical profiles. An exception are seahorses that have tails with a square cross-sectional profile, defined by a series of skeletal segments. In these, four elbow-shaped bony plates are distributed around a central axis (the vertebrae), which are overlapping differently at the sides. In this study, we abstracted these geometries on the basis of existing CAD-models from earlier research by Porter et al. (2015). New CAD-models were created using Inventor software, representing a cross-section of such a square tail segment, as well as a cross-section of a hypothetical cylindric profile that represents a non-existing but comparative analogue to the square model. We wanted to test whether the square model has a higher breaking strength than the cylindrical model. It was examined whether less stress occurs in the vertebral body of the square model than in the cylindrical one during a compressive load which could endanger the internal spinal column. Stress analyses were performed on both models, using the FEA-software Marc Mentat. A loading case was realised by compressing the models between two plates, qualitatively mimicking stress induced by a predator, such as when birds exert on the seahorse's tail during holding it between its beak halves and crushing it. The lower plate was fixed to the dorsal edge of the model, the upper plate moved at a speed of 5 m/s dorsally. Stresses were lower in the square model. At the vertebral body's most ventral point a maximum stress was measured in the square profile after 78% of the simulation time, followed by a decrease of stress. In the cylindrical cross-section stresses increased at this point nearly linear. The vertebral body was compressed dorsoventrally by 54.4 % in the cylindrical model and by 13.6 % in the square model at the end of the simulation.

**Biomechanics and -mimetics**

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# CANARIES BECOME MORE SKILLED AT PROCESSING SEEDS WITH AGE AND APPLY DIFFERENT SKILLS FOR DIFFERENT SEEDS

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The dehusking of seeds by granivorous songbirds is a delicate process, involving seed picking, positioning, cracking and swallowing. This likely requires a proper coordination of beak and tongue movements. Still, songbirds complete these actions remarkably fast, presumably to minimize predation risk while feeding. Since executing these precise and complex three-dimensional movements is sensorimotorically challenging, not all individuals will master this equally well. Therefore one can expect there to be considerable variation in feeding performance among individuals of the same species. The extent of this variation is still unknown, let alone how it relates to factors like age, sex or body size, despite the fact that feeding performance can have a strong impact on an individual's survival chances. The goal of this study was to quantify several feeding performance metrics and compare these between different age groups of a lab-bred population of the canary, *Serinus canaria*. We recorded high-speed videos of birds during feeding on two different types of seeds and extracted feeding performance metrics such as the success rate of dehusking seeds and the durations of the phases of the feeding act. We found that adult birds (two years and older) differed in performance from young birds (less than six months old), but in different ways. For large and hard seeds, success rate was significantly higher in adult birds, but they did not process seeds faster in case of successful dehusking attempts. Meanwhile, for smaller and softer seeds, success rate did not differ between both age groups, but adults were significantly faster at cracking seeds. Our results therefore indicate that the seed positioning and cracking steps of the dehusking process are the most difficult steps and that the cranial sensorimotor skills required to do this successfully depend on the type of seed and gradually improve as individuals become more experienced.

**Functional Morphology**

# Investigation into the horizontal arm motion in brittle stars (Echinodermata: Ophiuroidea)

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Brittle stars are among the most active and fastest moving echinoderms. They have the ability to show complex locomotory behaviors and use their flexible arms to produce a coordinated movement. Despite the interest in their movement, little is known about the intra- and interspecies variation in arm flexibility and movement. We performed a two-dimensional (2D) image processing on horizontal movement of three ophiuroid species (Ophiolepis superba, Ophiocoma scolopendrina, Macrophiothrix hirsuta), using two novel parameters, 'sinuosity' and 'slip angle', in a biological context to infer the ophiuroid movement and flexibility. The result illuminated the variability of individual arm use in the studied species. In addition, an investigation on relationship between morphological structure and its function showed that arm length and the extended keel in vertebrae can play a role in angle direction and flexibility of ophiuroid arms.

Functional Morphology

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# Morphofunctional analysis and comparision of the stone canal in Holothuroidea

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Among the least known organ of the echinoderm stand the stone canal. This organ is constituted in two parts with a long peduncle and an embossed madreporite. The stone canal is part of the ambulacral system and is connected with the exterior in most of Echinoderm. Nevertheless, this is not the case for most of Holothuroidea which have a madreporite floating in the main cavity. The morphology and the function of the stone canal of Asteroidea and Echinoidea have been investigated in the past two centuries, but no agreement have been fixed through the function of this organ. Most of the time he is describe as a pressure manager with inflow made by cilia on the surface of the madreporite. An excretory function has been also hypothesized but more recently a bidirectional flow is suspected. All this hypothesis has never been made investigated on sea cucumber. To have a better understanding of the morphology of this organ in Holothuroidea, 6 species of holothuroids have been analyzed through biometrics measures, classical histology, SEM and EDX. The analysis of the function of the organ has been pursued with in vivo experiences by placing fluorescent microbeads near the madreporite and by injection of charcoal directly into the ambulacral system. The structure of the organ is different between order of sea cucumber and actually even between species. Many difference are observable with some species having lacunar madreporite where other species have porous madreporite. The ciliation inside the peduncle show asymmetric canal ciliation which induced a potential bidirectional flow as suspected. This potential function have been strengthen by in vivo analysis where microbeads were found following two way flows.

Functional Morphology

# Reconstructing fossil mammal hair coloration

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Integumentary coloration is ubiquitous among vertebrates and serves many functions including thermoregulation, crypsis, species and individual recognition, sexual display and communication. research on the function and evolution of mammalian coloration lags far behind that of other groups like birds. Until recently, such research has been limited to extant organisms because pigments were thought to be undetectable in fossils. The discovery of both physical and chemical traces of pigments has opened the possibility of direct exploration of colors in the fossil record. The pigment melanin appears to be particularly well-preserved, likely because of its insoluble chemical structure and polymerization inside organelles called melanosomes. In mammals, even more than in birds, melanin is the major contributor to coloration, as carotenoids and other pigments are not known to be deposited in hairs. Moreover, melanosome morphology is broadly associated with human hair color (i.e. elongate eumelanosomes in black hair and spherical pheomelanosomes in red hair), suggesting that it may be used to predict color in fossil pelage. However, this hypothesis has never been tested. Here, we examine the extent to which melanosome morphology and color are related in a diverse group of mammals. We then use these data to, for the first time, reconstruct the color of a fossil mammal.

Functional Morphology

# Cephalopod approach of evolving a complex brain: morphological and molecular characterization during octopus development

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Cephalopods are exceptionally intelligent invertebrates that exhibit a morphological and behavioural complexity similar to vertebrates. The cephalopod nervous system is comparable to the mammalian brain in terms of neuronal number and richness in behavioural output. Nevertheless, the last common ancestor between cephalopods and mammals was a small worm-like marine organism that existed approximately 600 million years ago. Studying cephalopod molluscs presents an opportunity to understand the genetic drivers of neural development that evolved convergently with vertebrates. While the adult anatomy of Octopus vulgaris brain has been substantially described, the morphological, cellular and molecular features of its embryonic brain development remain unclear. Recently, we characterized the developing octopus brain morphologically using conventional histological techniques and gene expression analysis in 2D . We discovered that the neuronal progenitor cells are located in lateral lips, a neurogenic zone surrounding the eyes, and newly born neurons display long-distance migration into the centralized brain, reminiscent of vertebrate neurogenesis. To further elaborate on the morphological characterization of octopus embryonic neurogenesis in 3D, we have carried out multiplexed in situ hybridization chain reaction for specific neuronal and glial markers. Moreover, we have identified differentially expressed transcripts of genes which are part of the evolutionarily conserved growth factor signalling pathways during embryogenesis based on QuantSeq 3' mRNA-Seq. We used multiome data to assess which neurogenic cell types express specific signalling pathway genes at a certain developmental embryonic stage. Finally, we have started to evaluate the role of these signalling pathways in octopus neurogenesis by using small molecule inhibitors and activators.

Functional Morphology

# Variation of the trophic ecology in two teleost species associated to seagrass beds at Toliara Reef, Madagascar

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Small scale fishermen in Toliara (South West of Madagascar) extensively use small mesh seine nets in the seagrass zones and this practice may affect the structure of seagrass-associated fishes by catching small fish, juvenile and even post-larvae. The general objective of the present study is to evaluate the trophic ecology of two dominant teleost species (the rabbitfish *Siganus sutor* and the goby *Oplopomus oplopomus*) from catches of local fishermen using bottom seine nets. More specifically, this study aims to evaluate the temporal and spatial variation of the trophic ecology of those species by using stable isotopes and stomach contents. The sampling was carried out in seagrass beds in front of two villages: Ankilibe on December 2017 and 2018, and in Sarodrano on December 2018. To assess variation in diet, stomach content analyses were performed on 40 specimens/species/village/year. Preys were identified to the level of class and then assigned to different food groups. Stable isotope analyses were performed on muscles to complete information on variation in feeding habits. The combination of these methods revealed that the diet of species varies according to the year and the site of collection. This probably results from plasticity and accommodation to the availability of food sources and changes in environmental factors. In both species, the type of food consumed remains the same but the difference is observed in the frequency and the abundance of prey. Trophic variation is also observed over relatively long period of time as it is confirmed by stable isotope analyses. This study clearly demonstrates the trophic ecology of these two seagrass-associated fishes vary across time and space but additional works are now needed to understand which factors drive this variation.
This work will be communicated as a poster presentation at the congress.

**Functional Morphology**

# Diversity in mouthpart morphology and trophic niche in Antarctic Iphimediidae (Amphipoda)

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The fauna living on the Antarctic shelf has been moulded by millions of years of extreme seasonality, extreme isolation, extreme cold and recurrent glacial periods. With at least 13 genera and 46 species, the family Iphimediidae is one of the predominant amphipod taxon of the Antarctic shelf. Recent molecular studies show the monophyly of these species and the presence of species complexes. The high diversity in mandible morphologies observed in some species as well as their gut content have led to the hypothesis that Iphimediidae are micropredatory browsers with specialist feeding behaviours. Their mandibles are marked by the positioning of the incisor medially enabling it to cut in a frontal plane like scissors, probably one of the major reasons for their local ecological success. Conversely, the basis of their maxillipeds seems to vary less between species with different ecologies.

This study sets out to (i) explore the diversity of mouthpart morphologies and (ii) study the relation between morphology and trophic ecology in Antarctic Iphimediidae. To achieve this, we used a recent time-calibrated phylogeny of the family to control for the effect of relatedness in form-function relationships, isotopic data ($\delta 13C$, $\delta 15N$) as a proxy for the trophic niche, and 3D-geometric-morphometric data from µCT-scans of the mandible and the maxilliped's basis from 50 putative species of Iphimediidae.

Measures of phylogenetic signal and phylomorphospaces show that Iphimediidae present high diversity within subclades while simultaneously high morphological convergence in distant species. Significant results correlating isotopic data to morphology are scarce and while links can be set between both these are not straightforward. Indeed, different adaptations can be found in one functional group and similar adaptations can be found in different functional groups. Morphologies that allow for adaptability and opportunistic behaviour are of interest in such a seasonally variable environment as the Antarctic shelf.

Functional Morphology

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# MetaMorphos: exploring three-dimensional metazoan body plans through virtual reality.

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We are living in a three-dimensional world: we - like all living organisms - have a length, a width, a thickness and all these metrics inform on our body plans. Learning Zoology involves the understanding of all body plans found in animals: it is not possible to understand the function(s) of an organ or an organic system without having a clear idea of its structure and anatomy. If we live in a three-dimensional world, the explanatory means wa have at our disposal still pass most of the time by two-dimensional supports: the blackboard of a professor, a computer screen, the drawings, or the photographs, give us 2D images of objects or structures that we describe and analyze.

MetaMorphos (Metazoan Morphology) is an application that illustrates metazoan structure plans by high-quality 3D reconstructions. It is aimed at people who want to understand animal architecture whether naturalist amateurs, professional zoologists, students or professors in biology.

The organisms presented in MetaMorphos are avatars, 3D reconstructions of typical organisms regrouping the major characteristics of high-ranking taxa in the Linnean hierarchy, usually classes. MetaMorphos allows to explore the external morphology of each avatar as well as its systemic organization

To improve immersion and comprehension of the body plans, we transpose MetaMorphos in VR (virtual reality). With this tool, you can see, for example an arachnid moving around you in a virtual environment. You can also have the animal model alone to focus on its internal structure.

Functional Morphology

# Morphological study of the silk glands in two orb web spider species

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To feed, spiders of the family Araneidae build symmetrical webs. The Araneidae comprises 3000 species. Most of them have 7 pairs of glands, each of which plays a specific role in the building of the web. Silk is the material used to build web. The aggregate glands synthetises a sticky material that covers the web and adheres to preys so that they cannot escape once they are trapped. It was reported that glycoproteins are the main actors of the stickiness. The goal of this thesis is to gather more information about the silk gland complex of araneid spiders with a special emphasis on aggregate glands and their glycoproteins. These glands are not well studied and little is known about them.

To do this, two species were chosen: the walnut orb-weaver spider, *Nuctenea umbratica* (Clerck, 1758), and the red-legged nephila *Trichonephila inaurata madagascariensis* (Vinson, 1863). The former is an European species found all year around and the latter is a Madagascar endemic species.

Different silk glands and a part of their compounds were studied through histology and histochemistry. Aggregate glands are characterized by a large lumen and a thin, simple and cylindrical epithelium. Their associated ducts are embedded within a thick layer of nodules reacting positively to saccharide-specific staining. Lectin staining was therefore used to identify the saccharidic residues present in aggregate glands and associated tissues. Fifteen lectins were used on each species. Overall, the two species were similar in composition of glycoproteins. The comparison between these species and information found in the literature regarding the adhesive systems of other organisms points to the hypothesis of an evolutionary convergence in glue composition. Indeed, mannose, N-acetylgalactosamine, N-acetylglucosamine and sialic acid-derived compounds are found within adhesion-specific organs of spiders and of other phylogenetically distant species (sea cucumbers, velvet worms, starfishes, amphibians ,...).

Functional Morphology

# ULTRASTRUCTURE AND CYTOLOGICAL CHANGES OF THE KITEFIN SHARK, *DALATIAS LICHA*, PHOTOPHORES DURING LIGHT EMISSION

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Bioluminescence is an important ecological trait in the sea as it is produced by a very large number of organisms including three families of sharks, the Etmopteridae, Dalatiidae, and Somniosidae. This study compares the *Dalatias licha* light organ (photophore) with the known ultrastructure and hormonal control of *Etmopterus spinax* ones to give a better understanding of the light emission process and its evolutive conservation within shark families. The kitefin shark, *Dalatias licha* (Bonnaterre, 1788), is a deep-sea shark from the Dalatiidae family recognized as being the biggest luminous vertebrate known to date. In this study, we describe the ultrastructure of its photophores and the morphological changes occurring after hormonal stimulation through melatonin, known to trigger light emission, and α-MSH, a light emission inhibitor. The photophores are composed of a spherical pigmented sheath encompassing a unique regionalized light emitting cell, the photocyte. The photocyte basal area contains a granular area filled with granular inclusions which appear to be the same glowon-type microsources as found in *E. spinax* and would thus be the intracellular site of light emission. An acidophilic secretion is also observed within the granular area and could be involved in photogenesis. The ultrastructure analysis reveals neither lens cells nor reticular layer contrary to the Etmopteridae photophore, further showing the simpler organization of Dalatiidae photophore. Moreover, morphological changes between hormonal treatments have been observed. Melatonin stimulation shows a removal of the pigments of the ILS-associated melanophores at the top of the photophore and an increase in the granular inclusions diameter and coverage in the granular area, further confirming that this last area is the potential site of light emission. Conversely, α-MSH stimulation causes the extension of the melanophores pigments and a decrease in the granular inclusions diameter and coverage. These results support evolutive conservation of photophore organization across luminous sharks.

**Marine Biology**

# Study of luminescence control and photo-perception in the marine polychaete *Tomopteris helgolandica* (Tomopteridae).

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*Tomopteris helgolandica* (Tomopteridae) is a transparent holoplanktonic polychaete found in the North Atlantic mesopelagic zone. This bioluminescent annelid produces a yellow light in specific glands, named rosette glands, located within parapodia. Previous studies demonstrated that its light emission is under a nervous control, via acetylcholine, via nicotinic receptor activation, and a calcium-dependent mechanism involving L-type calcium channels. Recently, the presence of extraocular photoreception associated to luminous sites has been observed in four bioluminescent species - i.e. the ctenophore *Mnemiopsis leidyi*, the brittle star *Amphiura filiformis*, the shrimp *Janicella spinicauda*, and the shark *Etmopterus spinax*. Leading to the hypothesis that extraocular bioluminescence photoreception could regulate the light production directly at the luminous site.

The aims of this study is to highlight a potential link between photoemission and reception in *T. helgolandica* by using a dual approach: transcriptomic data analyses and immunohistology. Transcriptome analyses reveal the presence of sequences for opsins and nicotinic receptors. A specific extraocular opsin 4 is mainly retrieved within the body transcriptome. Transcriptomic data also reveal the expression of transduction cascade actors involved in both photoemission and reception processes Immunohistological analyses demonstrate the presence and localisation of the opsin 4 and nicotinic receptor within the parapodial rosette glands. The transcriptome analyses in addition with the presence and localisation of the opsin 4 strongly suggest that T. helgolandica could be able to perceive its luminescence. Moreover, nicotinic receptor immunodetection with the rosette glands confirm that luminescence is under nervous control. All these results highlight that *T. helgolandica* display the needed proteins to control and perceive its bioluminescence. These first evidences of a coupling between the two photobiological processes in a polychaete add further clue of a potential convergent functional evolution of the bioluminescence regulation via the reception of light at the light emitting cell/organ level in luminous organisms.

Marine Biology

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# Stomach content analysis of two deep-sea shark species: *Etmopterus spinax* and *Galeus melastomus*.

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The deep-sea is a challenging biotope, due to its particular conditions. Deep-sea organisms' ecology is not well known, among which sharks are not the exception. Being mid and upper-level consumers in shallow-water ecosystems, sharks exert top-down regulations and play an important component in marine communities. Yet, in the deep sea, there is a lack of information on the trophic role of sharks. The study of their trophic ecology may help to understand their roles in deep-sea food webs. In the Eastern Atlantic Ocean, and especially in the Gulf of Gascogne, *Galeus melastomus* and *Etmopterus spinax* are two deep-sea sharks commonly found as bycatches in commercial fisheries. Yet deep understanding of their trophic interactions and ecology in this area is still lacking. Stomach content analysis is the most common method to study trophic ecology.

In this study, stomach contents investigations of 266 sharks (112 *Galeus melastomus* and 154 *Etmopterus spinax*) were conducted to determine their food habits in the Gulf of Gascogne. The main prey consumed, trophic levels, and niches breadth were determined. Comparison of food habits of the two species showed that despite the consommation of the same main preys,  The niche breadth of *Galeus melastomus*  is more extensive (35% for 23%) and the estimation of the trophic niche overlaps reveals 85% of niche overlap between them. Moreover, both species present a ontogenic shift.
These data allow a better understanding of their trophic interactions within the Gulf of Gascogne.

Marine Biology

# Comparative study of sound production in Holocentrids

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Fishes use sounds to communicate in different behavioural contexts such as courtship, reproduction, defence and aggressive behaviours. This ability is found in several unrelated taxa highlighting its significance in life. Among them, Holocentridae are vocal reef fishes found worldwide and in abundance. Since they are nocturnal, being able to produce sounds to communicate is essential. However, sounds of only few species of this family have been studied so far. Similarly, the morphology of their sound-producing apparatus has been investigated. Because morphological differences have been found between genera, differences in terms of sound features are expected too. The aim of this study is dual. We first want to compare sounds of different species recorded in the same behavioural context to determine if sounds are species-specific. Second, we also want to seek whether sounds of species from the same genus show more common acoustical features in comparison with species from other genera. Different temporal (sound duration, pulse period, number of pulses, etc.) and frequential features were used for comparisons between species and genera. Results strongly support that sounds are species-specific since Discriminant Analysis allowed to relocate their sounds to the different species. It also appears that sounds can testify the belonging to a given genus.

Open Symposium

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# VARIABILITY IN LEARNING ABILITIES IN RELATION TO PERSONALITY AND EPIGENETIC MECHANISMS IN THE MANGROVE RIVULUS (*Kryptolebias marmoratus*)

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After the emergence of the concepts of animal personalities and behavioral syndromes, it has recently been noticed that personality traits can also be correlated with individuals' learning abilities. In addition, there are several cognitive types, which could sometimes be correlated with each other and/or affected differently by personality. These correlations are called “cognitive syndromes” and are mainly unexplored, while they can have an important impact in ecology. In this study, personality and cognitive traits, their variability and potential syndromes, as well as epigenetic regulation of some cognition-related genes were investigated in a fish species, the mangrove rivulus (*Kryptolebias marmoratus*). This species is the only self-fertilizing vertebrate known, allowing the creation of isogenic linages and making it a good model for epigenetic studies. Each individual has been tested with a novel object and a spatial learning task. Multiple positive correlations have been found between personality traits related to exploration, activity and boldness. However, none has been observed between learning and personality. As behavior influences an individual's adaptation to its environment, syndromes may correlate traits that have opposite adaptive values. The absence of cognitive syndrome can then be related to the rivulus's environment, mangroves, a highly changing environment where individuals must cope with wide variations in environmental conditions. As epigenetic measure, variability in the rate of CpG methylation has been investigated in some sequences of bdnf, egr1, grin1b and mecp2. No correlation has been found between methylation rate of the studied sequences and learning abilities, but a very large inter-individual variation in CpG methylation is observed for the studied sequence of mecp2 (methyl CpG binding protein 2; methylation level from 2% up to 22% on multiple CpG). As epigenetic mis-regulation of this gene is linked to neurological disorders in humans, understanding its role in the rivulus could have important human health implications.

Open Symposium

# MATURATION OF MARINE ADHESIVE PROTEINS: INVOLVEMENT OF TYROSINASES IN MUSSELS AND TUBEWORMS

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Many benthic invertebrate organisms have developed attachment strategies to cope with the dynamic ocean environment. Permanent adhesion through the secretion of an underwater glue is one of these strategies and it allows sessile organisms such as mussels, tubeworms, and barnacles to remain attached at the same place throughout their lifetime and not being dislodged by waves. The blue mussel (*Mytilus edulis*) and the honeycomb worm (*Sabellaria alveolata*) have long been studied for their adhesion mechanisms known for their superior strength and durability compared to man-made materials. Mussels attach to surfaces by producing a proteinaceous holdfast called byssus, which consists of many load-bearing threads each terminated by a plaque that mediates adhesion. Honeycomb worms are tube-dwelling and build their tube by collecting particles with their tentacles and then applying dots of cement on these particles to bind them together. Both organisms have developed an underwater adhesive system based on numerous adhesive proteins rich in post-translationally modified amino acids, notably DOPA (3,4-dihydroxyphenylalanine) which plays important interfacial adhesive as well as bulk cohesive roles. DOPA is produced by the post-translational hydroxylation of tyrosine residues via a tyrosinase enzyme. However, the variability and specificity of the tyrosinases involved in the modification of adhesive proteins in both species are poorly understood.

By performing a BLAST search in the transcriptomes of *S. alveolata* and *M. edulis* with tyrosinase sequences known to be involved in the maturation of adhesive proteins in related species, several tyrosinases candidates were retrieved. These candidates were then analyzed in silico and localized by in situ hybridization in mussel and tubeworm tissues to confirm their expression in the adhesive glands of the two studied species. These findings provide new insights into the specificity and diversity of tyrosinases in these organisms with relevance for understanding the materials performance of this biological adhesion role model.

Open Symposium

# Ethology in Pycnogonids: the case of the invasive *Ammothea hilgendorfi*

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Pycnogonids, or sea spiders, are a class of marine arthropods scarcely studied due to populations of low densities. They display peculiar morphological and behavioural features such as a very long proboscis but a tiny abdomen, and ovigerous legs with an egg-bearing role carried out by males only. During monthly collections on wave brakers in Knokke (Belgium), the pycnogonid population was compared to a study realised 50 years ago. It has varied a lot: *Ammothea hilgendorfi* accounted for 95% of the specimens. Yet, it was absent from former records. In fact, *A. hilgendorfi* originates from the North-Pacific Ocean (Japan, California...) and has become more and more widespread in Europe since the early 1980s: Italy, United Kingdom, the Netherlands, then Belgium from 2018. To evaluate if European and oversea specimens were equally sized, collected organisms were measured (trunk length and width) and compared to measurements from American and Japanese studies. On average, they were as long and as wide as each other.

Such a species outside of its native range is called an alien species. When the alien can reproduce, adapt, and locally spread in its new environment, it is called an invasive. Invasive species are of great concern nowadays as they may severely impact ecosystems in which they settle (via direct predation, niche displacement, competition for resources...). In several places in Europe, *A. hilgendorfi* has reached records in pycnogonid densities. Therefore, it can be considered as the first ever described invasive pycnogonid. *A. hilgendorfi* behaviour was studied to evaluate its impact on marine ecosystems. First, phototaxis experiments showed that it was photonegative, meaning that it may steal the ecological niche of other photonegative species. Second, olfaction experiments pointed out that it was attracted by the smell of relatives, sea cucumbers, and was able to chemo-detect crabs, implying interactions with them.

**Open Symposium**

# Rush or relax: migration tactics of a nocturnal insectivore in response to ecological barriers

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In order to balance travel with refuelling opportunities, flight tactics of avian migrants can be determined by local habitat conditions. We hypothesise that European Nightjars spend less time on migratory flight in global biomes which may provide daily foraging opportunities. Conversely, we expect the probability of migratory flight to be higher in global biomes without such foraging opportunities. We tracked the autumn migration of 24 European Nightjars from breeding populations in Mongolia, Belgium and UK, using GPS-loggers and multi-sensor data loggers to quantify crepuscular and nocturnal migration and foraging probabilities, as well as daily travel speed and flight altitude in response to global biomes.

Nightjars were observed to employ a “rushed” migration strategy, reflected in a high daily travel speed and high nocturnal and crepuscular migration probabilities, while crossing ecological barriers. Hospitable biomes were traversed with a “relaxed” migration strategy, characterised by high foraging probability at dusk, lower travel speed and lower nocturnal and crepuscular migration probabilities, suggesting that nightjars may alternate between feeding and short migratory flight bouts within the same night.

The rushed migration tactic adopted when traversing ecological barrier seems to indicate that nightjars attempt to minimize the time spent in these unfavourable areas, while nightjars seem to opportunistically feed during the crepuscular hours when they encounter hospitable biomes. How this may truly affect individuals’ fuel stores and whether different biomes actually provide refueling opportunities en route remains to be investigated, in particular to understand how future land-use change may affect migration patterns and survival probabilities.

Open Symposium

# SPATIAL OBSERVATION OF THE GREAT REEF OF TOLIARA (MADAGASCAR) FROM 1985 TO 2021

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Coral reefs are calcareous structures made up mainly of reef-building corals. They can extend over tens of kilometres, which makes it possible to follow their evolution from space. The Great Reef of Toliara (GRT) in Madagascar has been exposed to several pressures between 1985 and 2021. This analysis was performed using a change detection process on satellite images (Landsat5, Landsat7, Landsat8) covering the years 1985 and 1990, 2000 and 2021. This process was performed on each image in several steps including atmospheric correction, water column correction, segmentation and image classification. For the latter, a nearest neighbour machine learning algorithm was used to separate corals from seagrass, mud, intertidal and subtidal sand. Preliminary results show a significant increase in the coral, seagrass, and subtidal sand classes (90, 72, and 34%, respectively) compared to the 1985 and 1990 classified scenes. However, major decreases of 40 and 36% are noted in the intertidal sand and mud classes, respectively. In addition, the 2000 and 2021 classified scenes revealed increases in the mud, subtidal and, intertidal sand classes of 24, 30, and 13%, respectively, while major decreases of 53%, 41% are observed in the coral, and seagrass classes, respectively. Combined in a geographic information system (GIS), the mapping results of this project can help stakeholders to rapidly assess the coverage of benthic habitats (corals, seagrasses, algae, etc.), define management and conservation objectives, and identify potential conservation areas and vulnerable ecosystems.

**Open Symposium**

# Friend or foe? – Larvae of the invasive Pacific oyster (*Magallana gigas*) trade off predator and conspecific cues in their decision making for settlement

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Many factors contribute to the successful colonization of new substrates by bivalves. One key factor is settlement preference at the final larval stage. Understanding how ecological cues influence larvae settlement is critical to inform habitat restoration projects, aquaculture, and antifouling efforts.
It is well known that larvae of the Pacific oyster are attracted to cues from conspecific adults, which have been shown to originate from shells of dead or living individuals, and waterborne cues released from living individuals. We further know from other benthic organisms, that predator cues reduce settlement propensity. However, in bivalves, these cues have rarely been studied in combination. Here, we investigated the settlement preferences of the Pacific oyster (*Magallana gigas*) when exposed to conspecific and predator cues separately or in combination in an experimental setup. We used a positive cue associated with conspecific shells, a positive cue from water conditioned by live adults and a negative (non-consumptive) cue from kairomones of a main predator, the European green crab (*Carcinus maenas*).
We found that predator cues from *C. maenas* significantly decreased settlement propensity, even in the presence of a positive waterborne conspecific cue. Our results suggest that the effects of both types of cues interact in a mainly additive manner. This is first study (to the best of our knowledge) that shows decreased settlement from non-consumptive predator cues for *M. gigas*. Furthermore, we demonstrated that surface bound cues from conspecific shells increased the probability of settlement more strongly than waterborne conspecific cues.
In parallel to manual assessment of settlement success trials, we are developing a scalable and low-cost video analysis setup. Specifically, we use Raspberry pi HQ cameras and computers, and particle tracking software. This is an experimental attempt to improve traditional manual observation of larvae settlement as well as complement settlement studies with analysis of larvae behaviors prior to settlement.

**Open Symposium**

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# Opt-in or out? Public opinion on the use of human genetics for forensic familial DNA searching

**Sofie Claerhout, Hanna Noppe**

Forensic familial DNA searching is a powerful tool to provide a last resort opportunity to solve criminal (cold) cases. Although the benefits are strong, strict regulations are required to address the doubts expressed by opponents concerning privacy and ethical issues. Therefore, we aimed to investigate the public opinion. Through an online survey distributed through social media, population information of 578 participants living in the Low Countries was analyzed. The survey was divided into three parts: (1) personal information to check data reliability (2) general DNA knowledge questions and (3) personal opinions on ‘forensic DNA analysis’. Our population graduated cum laude with an average score of 71%. A significantly higher score was observed for highly educated participants. Surprisingly, 95% of the participants is willing to cooperate in a forensic familial search. Important factors for participation are painless sampling and privacy security. Moreover, we saw that people with a failed DNA score were significantly more afraid to cooperate in forensic DNA analysis. Nevertheless, almost all participants (96%) agreed to use online DNA databases to resolve crimes with violence, but half of them stated that member informed consents should be obtained prior to the search. To conclude, the ‘fear of the unknown’ combined with strong feelings towards privacy are two major influencing factors to not cooperate in a forensic familial DNA search. Yet, the highly positive attitude towards forensic DNA analysis was a pleasant surprise and point towards people’s high empathy and willingness to help justice.

**Open Symposium**

# Biodiversity of decapod crustaceans in Benin: Taxonomic assessment and zoogeography

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Decapod crustaceans constitute a fairly diverse faunal group that includes several species of commercial interest such as lobsters and some crabs and shrimps. In Benin, the inventory of decapod biodiversity is still poor and systematic revisions are necessary for several taxa. The aim of the work we present in this poster is to draw up an illustrated and commented catalogue of the marine, lagoon and freshwater decapods of Benin in order to one day have a real faunistic guide with determination keys and illustrations for most of the species. To do this, documentary summaries will be carried out and sampling campaigns will be organised in the freshwater, brackish and lagoon environments of Benin. The species listed will be identified, described and inventoried. This inventory work will be aimed at scientists and schoolchildren, to raise awareness about biodiversity, and at managers for better recognition, management and sharing of the benefits derived from the biological diversity of species. At the end of this project, species of interest to aquaculture will be inventoried for the development of aquaculture. This will contribute to food security, employment and income generation and poverty reduction.

Open symposium

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# A One Health approach to protected areas management and governance.

**Karine Lalaina Mahefarisoa – PhD student**
**Supervisors: Prof. Ellen Decaestecker, Prof. Raf Aerts**

Our research is framed on "The One Health concept", which is a collaborative and multi-sectorial approach integrating the human, animal, and environmental interface. Considering that the human – animal – environmental health are interconnected, our study will focus on lemurs related diseases and protected areas (PA) —lemurs' sanctuaries— governance in Madagascar. Lemurs are endemic species in danger of extinction due to anthropogenic pressures. Lemur's natural habitats are reduced due to human activities (deforestation, over exploitation of natural resources, etc.) which increase their proximity. This could lead to pathogens transmission from vertebrate animals to humans and/or vice versa. In this project, we want to screen zoonotic diseases that could circulate among lemurs and domestic animals in their vicinity. This is to provide an early recognition of threat(s) regarding (re)emerging zoonotic disease(s). Our focus is on two different lemur species which are in the red list of IUCN : Propithecus diadema which is considered as critically endangered, and Eulemur fulvus which is a vulnerable species. The first part of our project consist of the captures of wild lemurs for sample collection. Sampling on lemurs is described step by step. Samples are used for a genetic analysis using NGS approach to detect zoonotic pathogens, and microbiome analysis to characterize lemur microbiome in three different sites in Madagascar. We expect to detect zoonotic virus, bacteria and parasites. The second part of our research identify the key stakeholders involved in protected area management, and assess their structural interactions. Furthermore, we want to understand the challenges that they are currently facing in PA governance in order to provide a mitigation approach in improving the current situation in conservation and environmental governance and prevent the spread of an eventual (re) emerging zoonotic diseases.

Open symposium

# INTRODUCING THE PROJECT HABITANT – PAST AND FUTURE HABITABILITY IN ANTARCTIC LAKES: SUCCESSION, COLONIZATION, EXTINCTION AND SURVIVAL IN GLACIAL REFUGIA

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Climate change is predicted to increase temperatures and alter precipitation patterns in certain regions of Maritime and coastal Continental Antarctica, leading to expansion of ice-free areas, increased habitat connectivity and changes in hydrology. This could have a significant impact on Antarctic biota, which has a high degree of endemism due to long-term isolation and diversification of taxa in glacial refugia. Increased connectivity between regions could result in spread of invasive species, biotic homogenization and loss of endemic species.

In the framework of the HabitAnt project, we will study the past, present and future habitability of lakes in three ice-free regions of coastal East Antarctica with a focus on ostracods, copepods and rotifers. We will perform high-throughput sequencing of ancient DNA (aDNA) and microfossil analysis from dated lake sediment cores to acquire information on past diversity and on how biological communities changed over time. Using a paleotemperature proxy, this data can be linked to reconstructions of past air surface temperature. The sequenced aDNA will also be used to construct molecular phylogenies. In addition, recent lake samples will be analysed to assess the present-day biodiversity. With these datasets, we can obtain a better understanding of the processes that shaped the current community structure, such as isolation in glacial refugia, colonization, extinction, diversification and biological succession in response to past climatic changes, and help predict how communities might respond to future environmental change.

**Open Symposium**

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# Evolution of genome size in a fast adaptive radiation

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The size of the genome is a highly variable trait in eukaryotes that shows remarkably different values even between closely-related species. The origin of this variation is complex but, among other things, related with the activity of families of transposable elements present in the genome. We are studying the evolution of this trait within the group of African cichlids that inhabits lakes Kivu, Edward and Albert (KEA region), to examine how genome size can vary in the framework of a fast adaptive radiation.

Through an especially designed pipeline that combines different bioinformatics tools, we estimated the genome size of these species using a k-mer approach, which uses only raw Illumina reads of the genome and consumes less time and resource than genome assembly methods.

With these estimations we are tracking the evolution of the trait on a new phylogeny based on our data, to understand how and where genome size changed within our group, with a particular attention to variation between close-related species. In the end we aim at surveying genomes for families of transposable elements that can explain the observed size variation.

**Evolutionary Genomics**

# Variation in genome size and body size across teleosts

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Genome size is one of the main factors shaping organismal traits by impacting metabolism and cell size. Smaller or larger, body size can affect the overall morphology and development of a species. While it is expected that body size varies depending on the number of cells and cell size, and that cell size is dependent on genome size, how body size and genome size covary has been rarely investigated. Fishes are the largest group of vertebrates and possess a wide range of genome size and body size across the phylogeny. Those conditions make them suitable to investigate a possible correlation between genome size and body size. We collected genome size and body size data for 1169 ray-finned species (including Cichliformes) and looked for a correlation between them using both phylogeny-dependent and phylogeny-independent regression analyses. Both positive and negative correlations were found at subclade levels (e.g., order). We also examined trends in genome size and body size along the phylogeny to determine, for example, how many times reduction or increase occurred. We argue that biological size – calculated by factoring both genome size and body size – is a more sensible metric when discussing size of an organism.

Evolutionary Genomics

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# Population genetic of the forest dormouse, *Dryomys nitedula* in Bulgaria

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The forest dormouse (*Dryomys nitedula*) is one of the most widespread species of the Gliridae family occurring in Eastern Mediterranean, Central Asia, Caucasus and the Arabian plateau. The populations are mostly threatened by the destruction of their habitats, the forests. Despite being considered as Least Concern by the IUCN, the general population trend is unknown and the species is listed in the Annex IV of the Habitat Directive in Europe and the Annex III of the Bern convention. Our goal was to determine the population structure of the species in Bulgaria where the species is well studied. We generated reduced representation genomic libraries using the 3RAD method on 62 samples collected from April 2020 to June 2021 in several study sites. Preliminary results based on clustering analyses seem to evidence the presence of several geographically well-structured populations. With this study, we hope to bring new insights into the population genetics and trends of this overlooked species.

Evolutionary Genomics

# A Barcoding Facility for Organisms and Tissues of Policy Concern

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The Barcoding Facility for Organisms and Tissues of Policy Concern (BopCo) acts as a focal point for identifying biological materials upon request, by providing access to the expertise and infrastructure necessary to identify organisms of policy concern and their derived products. BopCo's identification service is available to all stakeholders who deal with such material and who need accurate identifications. These can rely on traditional morphology based approaches employing the taxonomic expertise and specimen collections at the Royal Belgian Institute of Natural Sciences (RBINS) and the Royal Museum for Central Africa (RMCA) and/or on DNA-based techniques like DNA barcoding, qPCR, RFLP, RADP, µsatellites or MinION sequencing technology for which BopCo has access to fully equipped DNA laboratories at both RBINS and RMCA. A prerequisite to use DNA-based techniques, however, is the availability of comprehensive and reliable reference barcode libraries. Therefore, BopCo also contributes to populating DNA barcode databases of taxa of policy concern by producing new DNA barcodes, which are made publicly available, and evaluates existing DNA barcodes for their utility. Examples displaying the taxonomic diversity, stakeholder range, policy concern issues and utilised techniques will be presented.

Evolutionary Genomics

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# Insight into the snow petrel *Pagodroma nivea* ecology through population genetics and habitat suitability analyses

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Climate change is severely affecting the Southern Ocean, where a strong increase in air temperature as well as a decrease in sea-ice extent are happening at fast pace. The resulting biological and ecological responses of such changes influence the structure and dynamics of ecosystems, which impacts on species are still largely under-studied.

The endemic snow petrel *Pagodroma nivea* is expected to be impacted by these changes, mainly due to its close relation to the Southern Ocean ecosystem. Using this species as eco-indicator of ecosystem changes is therefore suggested, but its ecology is still largely unknown.

This study aimed at investigating the fundamental ecology of the snow petrel through population connectivity and breeding sites habitat suitability.

First, the connectivity among two colonies in Adelaide Island and Signy Island, and five colonies in Sør Rondane mountain, was studied using microsatellites. Then, the environmental variables playing a role in the suitability of the habitat were assessed and compared between regions.

Results revealed that a high connectivity would occur between Signy and Adelaide Island colonies ($F_{ST} = 0.000$), as well as among Sør Rondane colonies ($F_{ST} = 0.000$ or $0.001$). A low differentiation is observed between colonies in Sør Rondane and the colonies in Adelaide and Signy Island ($F_{ST} = 0.055$). The main hypothesis explaining this connectivity between colonies is based on the overlapping of non-breeding areas. Regarding the breeding sites habitat, the resolution of environmental variables was not high enough to infer their respective importance, but different environments at the colonies were found between regions.

Further improvements of data quality, meaning higher environmental variables resolution and higher population sample size, are of a major importance to obtain significant results. Advanced knowledge of these ecological traits is essential for the bioindicator role of the snow petrel, in particular in a rapidly changing environment.

Evolutionary Genomics

# Long range and long read sequencing enable comparative genomics of two freshwater herring species of Lake Tanganyika

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Small pelagic fishes not only support productive fisheries in the ocean, but also in large inland water bodies. These fishes are typically characterized as r-selected, with large population sizes and low levels of genetic differentiation. However, selection acting on large genomic regions ('islands of selection') can still lead to rapid differentiation between well connected populations and species. The freshwater clupeids *Stolothrissa tanganicae* and *Limnothrissa miodon* are two important pelagic fisheries targets of Lake Tanganyika, in Central Africa. Despite their recent divergence from each other, and generally shallow population structure, previous research showed that their genomes have evolved rapidly. Interspecifically, the two species have completely different sex chromosome organisation. Intraspecifically, a large putative inversion is segregating in *L. miodon*. Using a combined approach of three long-linkage and one long read sequencing technology, 10X Chromium libraries, Chicago, Hi-C, and PacBio IsoSeq, we present the first nearly chromosome-level, annotated reference genomes of S. *tanganicae* and *L. miodon*. We align the genomes of the two species and compare their architecture to each other and to the well characterized genomes of two other clupeiforms (the marine *Clupea harengus* and the African riverine *Denticeps clupeoides*). We perform synteny analysis and establish conserved regions between the four clupeids. In addition, we use lake-wide spatio-temporal RAD-seq SNP data of the Tanganyika clupeids mapped to the new reference genomes to define regions involved in sex determination of the two species, and a putative inversion in L. miodon. Finally, we identify the genes falling in or close to the sex determining regions and inversion polymorphism, highlighting pathways that may mark the difference in lifestyle between the fully pelagic, planktivorous *S. tanganicae* and the more generalist, partly littoral *L. miodon*. The sequences will serve as a gene catalogue for the pellonuline herring of Africa, many of which are important fisheries targets. This will accelerate future genetic work and aid the development of sustainable fisheries practices in hitherto data-poor systems.

Evolutionary Genomics

# Role of sexual conformism in learned sexual preferences in a polyphenic butterfly facing alternating wet and dry seasons and male mating partners

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The role of learning in the adaptation and evolution of species as become a central topic of research in non-social insects. Learning is known to modify the sexual preferences of mating partners, notably through conformism in the fly *Drosophila melanogaster*. Here we quantify the extent of sexual conformism through imprinting in the development of sexual preferences for females of the tropical butterly *Bicyclus anynana*. *B. anynana* is an African butterfly with marked seasonal polyphenism, whose adaptation to wet and dry seasons will be climate warming (Holveck et al, in revision). Indeed, temperature increase leads to the emergence of wet season individuals during the dry season, a form of maladaptation.
In short, we exposed naïve, recently emerged, virgin females to different proportions of "wet" and "dry" seasonal male phenotypes for an imprinting phase: 100 % wet males, 80% wet and 20% dry males, 60% wet and 40% dry males, 40% wet and 60% dry males, 20% wet and 80% dry males and 100% dry males. Two days later, these experienced females could choose to mate among groups of wet and dry seasonal males available in equal proportions. Learned sexual preferences were found on the basis that mating numbers with wet and dry seasonal males differed according to the proportions of wet and dry males that naive females experienced during imprinting. Our analyses include the effects of male and female ages and male courtship effort, known to affect mating success. Specifically, a sigmoidal model is likely the best model to apply to our data, suggesting a significant effect of imprinting and conformism on learned female sexual preferences, where the female displays a sexual preference for the most abundant male type at a higher proportion than the frequency of the male type in the population.

Eco-Evolutionary interactions/dynamics

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# A genomic view of the evolution and biogeography of the ichthyofauna of the Albertine rift: *Clarias gariepinus*

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*Clarias gariepinus*, also known as the African sharptooth catfish, has the widest distribution of all African freshwater fishes and occurs in almost all types of aquatic habitats. In spite of its large and almost continuous distribution and its high ecological tolerance, *C. gariepinus* contains geographically structured populations. It has therefore been shown to be a well-suited model to study landscape and climate evolution. A recent population genetics study of C. gariepinus and its daughter species - based on mitochondrial DNA and microsatellites - suggested the possible role of the Great lakes, and particularly Lake Kivu, as the centre of diversification from where the species spread over Africa. Using short paired-end sequencing, we compare mitochondrial and nuclear genomes of 108 samples stemming from 17 countries sampled between 1996 and 2018 to conduct phylogenomic and population genomic analyses. This dataset will allow us to investigate the diversity of the lineage that includes C. gariepinus and its daughter species, *C. anguillaris* and *Bathyclarias ssp.*, all still understudied today. Studying their evolution and biogeography based on whole genomes, will give us the opportunity to further investigate the role of the Great lakes as the cradle of widespread fish species that are currently found throughout Africa.

Eco-Evolutionary interactions/dynamics

# Local gut microbiome of *Daphnia* helps to clear toxic cyanobacterial blooms

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While evidence for the role of the microbiome in shaping host stress tolerance is becoming well-established, to what extent this depends on the interaction between the host and its local microbiome is less clear. Therefore, we investigated whether locally adapted gut microbiomes affect host stress tolerance. In the water flea *Daphnia magna*, we studied if the host performs better when receiving a microbiome from their source region than from another region when facing a stressful condition, more in particular exposure to the toxic cyanobacteria *Microcystis aeruginosa*. Therefore, a reciprocal transplant experiment was performed in which recipient, germ-free *D. magna*, isolated from different ponds, received a donor microbiome from sympatric or allopatric D. magna that were pre-exposed to toxic cyanobacteria or not. We tested for effects on host life history traits and gut microbiome composition. Our data indicate that Daphnia interact with particular microbial strains mediating local adaptation in host stress tolerance. Most recipient *D. magna* individuals performed better when inoculated with sympatric than with allopatric microbiomes. This effect was most pronounced when the donors were pre-exposed to the toxic cyanobacteria, but this effect was also pond and genotype dependent. We discuss how this host fitness benefit is associated with microbiome diversity patterns.

Symbiosis inclusive host-microbiome interactions

# Towards a better understanding of the snail-trematode-microbiome interactions driving schistosome transmission in Senegal

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## Background and aims

Trematode parasites generally use freshwater snails as obligate intermediate hosts in their lifecycle. A single snail species often serves as an intermediate host for several co-occurring trematode species. This can lead to within-host interactions that can impact infection outcome and subsequent transmission to the final host. Additionally, recent research has emphasized the importance of the snail microbiome in susceptibility to trematode infections. Therefore, it is paramount to document microbiome and trematode communities within individual snail species from natural settings. We focus on a highly endemic setting for schistosomiasis in the Senegal River Basin (SRB). Following the embankment of the Senegal River in the 1980s, a major outbreak of intestinal schistosomiasis occurred. Yet, nowadays, the urinary form is highly prevalent, a shift that remains hitherto unexplained. This study aims to characterize the microbiome and trematode communities of *Biomphalaria* and *Bulinus* snail species sampled along the SRB to assess their role in the susceptibility towards schistosome infection.

## Methods

Snails collected from five localities across the SRB in 2012, 2014 and 2021 are studied. First, a rapid diagnostic PCR is applied to detect infected snails. Second, an amplicon sequencing workflow is used to genotype 10 infected snails per species per site and their infecting trematodes. Finally, 16S metabarcoding is applied to map the microbiome of five non-, five single- and five co-infected snails per species per site.

## Results

Patterns of genetic diversity, microbiome, and trematode communities of snail hosts in the SRB will be presented and discussed.

## Conclusions

This will provide greater insight into the processes that influence disease dynamics.

Symbiosis inclusive host-microbiome interactions

# Facultative endosymbiont, a valuable guest in the multitrophic system "plant-aphid-ant"

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Multitrophic systems are characterized by cascading effects which may be mutualistic, neutral or antagonistic depending on the cost/benefit balance gained by actors at each trophic level. In these networks, symbiotic microorganisms, which have a variable degree of dependence with their host, can have evolutionary consequences and exert selection pressures on host organisms.

The plant-aphid-ant network allows to understand how symbiotic bacteria may condition relationships between the different protagonists. From this multitrophic system, we have a particular interest in the mutualist relationships between aphids and honeydew-feeding ants. The story does not end there since bacterial symbionts of aphids such as *Serratia symbiotica* can induce a fitness cost to their homopteran host but also confer a protection against parasitoids. Recently, research showed that facultative strains of *S. symbiotica* were found in natural populations of aphids but also in their host plant and their mutualistic ants. Concerning the impact of bacteria on ant-aphid mutualism, in a binary choice experiment, ants did not show any significant attraction towards a *Serratia*-infected sugar solution. This solution was first chosen by only 35% of foragers which did not drink for longer duration. Thus, the bacteria alone did not seem to release volatiles or phagostimulants appealing for the ants. Possible indirect effects of the bacteria may however arise from induced changes in volatiles and/or sugar content of honeydew, thereby altering honeydew attractiveness to ants. Further studies on the whole system should now assess how this bacteria influences the tending and trail-laying behaviour of foragers, which both are central to the ant-aphid mutualism.

Facultative bacterial symbionts can thus influence the whole ecological community by changing the way the aphids interact with their mutualistic partners. These discoveries open entirely new perspectives on the importance of free-living symbiotic bacteria in multitrophic systems including ants.

Symbiosis inclusive host-microbiome interactions

# APECS Belgium: an opportunity for early career scientists

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The Association of Polar Early Career Scientists (APECS) is an international and interdisciplinary organization for undergraduate and graduate students, postdoctoral researchers, early faculty members, educators and other people with interests in Polar Regions and the wider cryosphere. APECS serves to facilitate networking, collaboration, and gaining leadership skills for early career scientists as well as communication, education and outreach towards the outer public. APECS is an important legacy of the International Polar Year (IPY 2007-2008) Youth Steering Committee and became a strong global organisation. Its leadership team is comprised of early career researchers that are interested in and committed to furthering the activities and the future directions of the organization. Project initiation and management, web-based or in-person events, are carried out by a number of member-initiated (thematic) working groups and (national) committees made up of both members and mentors. APECS Belgium was among the first national committees to be founded in 2006 as part of the global IPY-YSC, and was transformed into a formal NGO in 2011. Throughout the years, APECS Belgium organized and participated in many events and activities, such as Conference Symposia, Science fairs, school visits, workshops, documentary screenings, outreach events and many more. The group supports polar research at the national level by promoting research projects and institutes in Belgium and sharing the fascination for the Poles with other researchers and the general public.

Any early career scientist based in Belgium with an interest in the Polar Regions is highly encouraged to join APECS Belgium! The group also strongly welcomes other people with links to polar education and research. For more information, visit our website: www.apecsbelgium.wordpress.com.

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# What is the RBZS Young Zoologist Group?

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Royal Belgian Zoological Society (RBZS) is a non-profit organization aiming at promoting zoology and connecting junior and senior researchers from Belgium and abroad. The Society organizes zoology-related events, such as the Benelux Congress of Zoology, the Jacques Kets Award for Zoology which rewards a master thesis and gives a €1000 grant for conference and workshops, the Masters day which offers an overview of the Biology courses available in Belgium, and proposes three annual grants for laboratory internship, field trip and conference. RBZS also comprises the Young Zoologist Group (YZG) which currently gathers PhD students and young doctors that are pleased to organize workshops to help PhD candidates improving their academic skill-set. For example, last workshops were about how to present your research online and how to display your data in an attractive manner. For this 2021 event in Leuven, we invited experts in data property, open access publications and ethical protocols. Our group also shares PhD, job, funding and awards opportunities, as well as attractive courses on social media and always welcomes MSc and PhD students working on a subject related to zoology that would be interested in joining us.

Thanks to all attendes

# Organizing committee

**Ellen Decaestecker, Gilles Lepoint, Stéphane Roberty, Isabel Vanoverberghe, Sofie Claerhout, Naina Goel, Manon Coone, Ruben Schols, Shira Houwenhuyse, Lore Bulteel, Karine Mahefarisoa, Karen Bisschop, Aditi Gurung, Arne Sinnesael, Emma Gouwy, Broos Van de Moortel, Johanna Lapere and Thomas Pluym**

# Scientific committee

**Ellen Decaestecker, Gilles Lepoint, Frédéric Silvestre, Stéphane Roberty, Isabelle Schon, Liesbet Temmerman, Sam Van Wassenbergh, Joost Andre M Raeymaekers, Bram Vanschoenwinkel, Caroline Nieberding, Bruno Frédérich, Jérôme Delroisse, Dominique Adriaens, Maarten Vanhove, Dries Bonte, Robby Stoks, Astrid Groot, Jan Kammenga, Jean-François Flot, Patrick Mardulyn, Lien Reyserhove, Evie Vereecke, Hannes Svardal, Hugo Gante, Tom Pinceel, Thomas Luypaert, Philippe Helsen, Sofie Claerhout, Karen Bisschop and Marianna Pinzone.**