

## Contents

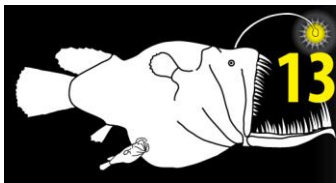
• Welcome	Page 2
• International Steering & Local Organising Committee	Page 2
• Sponsors	Page 3
• Sponsors Ads	Page 4
• General Information	Page 10
• Health & Safety	Page 11
• Conference Programme	Page 13
• Additional Side Meetings	Page 21
• Social Events & Exhibition	Page 22
• Excursion Suggestions	Page 23
• Oral Abstracts (alpha order by author surname)	Page 25
• Poster Listing	Page 171
• Poster Abstracts (alpha order by author surname)	Page 185
• List of Participants	Page 251
• Maps of Te Papa	Page 256
• Map of Wellington	Page 258

### Conference Secretariat

Conferences & Events Ltd  
PO Box 24078  
Manners Street, Wellington

conferences  
& events PT LTD





International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

## Welcome

Welcome to Wellington, New Zealand and the 13<sup>th</sup> International Deep-Sea Biology Symposium. This is the first time that the symposium has been held in the Southern Hemisphere and it is encouraging, in these difficult financial times, that so many of you have made the long journey to take part in the meeting.

The hope is that this meeting will maintain the success of the previous gatherings of deep-sea scientists, and representatives of government, non-government organisations, and industry — where the results of the latest research are exchanged and discussed, particularly with a view as to how this information can be used to effectively manage the increasing pressure placed on deep-sea ecosystems by human activities. On offer at this symposium is a wide array of oral and poster presentations, which I'm sure, will contribute to this goal.

As well as engaging fully with the presentations and resulting discussions I hope that you will also enjoy the food and drink that is provided to fuel these activities, as well as take time in the evenings and Wednesday afternoon to explore the “coolest little capital in the world” and its surrounds.

Finally, I wish to thank members of the International Steering Committee and the Local Organising Committee for all their enthusiastic and valuable advice, input and labours. Louise Watson, the symposium manager from Conference & Events Ltd, deserves particular recognition for making things happen. My original co-convener, Mireille Consalvey, provided a mass of good ideas and energy at the outset of the symposium organisation — without her contribution this symposium would not have gotten off the ground. Special thanks are also owed to all the symposium sponsors — for without their financial contribution this symposium would not have been possible at all.

Here's to a productive and fun symposium.

Ashley Rowden

Symposium Convener

### **International Steering Committee**

Maria Baker, University of Southampton, UK  
Antje Boetius, AWI, Germany  
Hiroshi Kitazato, JAMSTEC, Japan  
Lenaick Menot, IFREMER, France  
Ashley Rowden, NIWA, New Zealand  
Thomas Schlacher, University of Sunshine Coast, Australia  
Javier Sellanes, University Catolica Norte/ COPAS - University Concepcion, Chile  
Craig Smith, University of Hawaii, USA  
Andrew Thurber, Oregon State University, USA

### **Local Organising Committee**

Jennifer Beaumont, Rachel Boschen, David Bowden, Malcolm Clark, Matthew Dunn, Dennis Gordon, Daniel Leduc, Anne-Nina Loerz, Erika Mackay, Els Maas, Scott Nodder, Peter "Chazz" Marriott, Matt Pinkerton, Ashley Rowden, Kareen Schnabel, Di Tracey, NIWA  
Mark Costello, University of Auckland  
Simon Davy, Victoria University of Wellington  
Conrad Pilditch, University of Waikato  
Keith Probert, University of Otago  
Andrew Stewart, Rick Webber, Museum of New Zealand Te Papa Tongarewa



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**Sponsors**

The 13<sup>th</sup> Deep-Sea Biology Symposium Organising Committee wishes to acknowledge the generous support of our sponsors:



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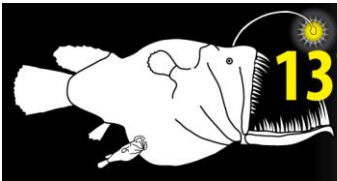
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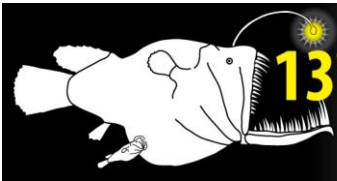
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# 13<sup>th</sup> Deep-Sea Biology Symposium

Wellington, New Zealand  3 – 7 December 2012

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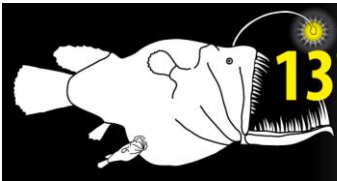
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Wellington, New Zealand  3 – 7 December 2012

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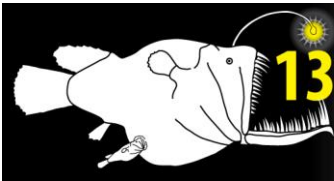
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Wellington, New Zealand  3 – 7 December 2012

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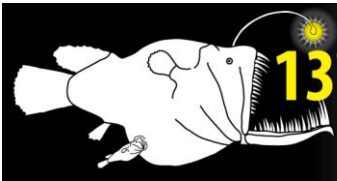


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**13<sup>th</sup> Deep-Sea Biology Symposium**

Wellington, New Zealand  3 – 7 December 2012

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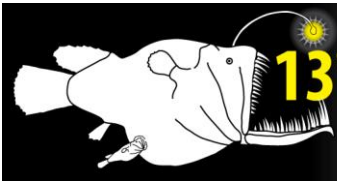
# 13<sup>th</sup> Deep-Sea Biology Symposium

Wellington, New Zealand  3 – 7 December 2012

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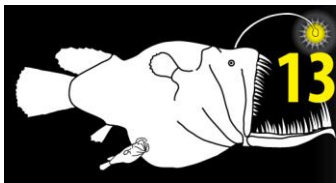
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# 13<sup>th</sup> Deep-Sea Biology Symposium

Wellington, New Zealand  3 – 7 December 2012

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**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

## General Information

### Registration and Information Desk

Registration desk phone: 021 225 0337

The registration and information desk will be located in Oceania on level 3 of Te Papa from Sunday 2<sup>nd</sup> December at 15.00hrs until 17.00hrs on Friday 7<sup>th</sup> December, during the conference between the hours listed below:

- Sunday 2<sup>nd</sup> December 15.00 – 17.00
- Monday 3<sup>rd</sup> December 08.00 – 17.00
- Tuesday 4<sup>th</sup> December 08.00 – 17.00
- Wednesday 5<sup>th</sup> December 08.00 – 17.00
- Thursday 6<sup>th</sup> December 08.00 – 17.00
- Friday 7<sup>th</sup> December 08.00 – 17.00

The following information is offered to make your attendance at the conference as pleasant and trouble-free as possible. If you require help, please call at the registration desk and we will do everything we can to assist you.

### Accommodation

For those registrants who have reserved accommodation through Conference & Events, please ensure accounts are settled in full on departure, including all meals, telephone calls and mini bar charges. No accounts can be charged to the 13<sup>th</sup> Deep-Sea Biology Symposium

### Doctors and Pharmacies

- **City Medical Centre**  
Level 1, 10 Brandon Street, phone 471 2161  
8am – 6pm weekdays
- **After Hours Medical Centre**  
17 Adelaide Road, Newtown, phone 384 4944  
8am – 11pm every day (no appointment necessary)

### Health and Safety

#### Emergency Procedures

- **General Emergency**  
For fire, ambulance or police, **dial 1 for an outside line, then 111.**
- **Fire**  
If you discover a fire or hear continuous ringing of the fire alarm, leave the building immediately and assemble outside the building as instructed by Te Papa Hosts.
- **Earthquake**  
In the event of an earthquake, please remain in the building. Move away from any windows or equipment that may fall and take immediate shelter under, or close to, solid furniture such as tables or desks. If no furniture is available, drop to your knees, with your back to windows, clasp both hands firmly behind your head and bury your head in your hands. Most importantly, keep calm.



- **Evacuation**

The continuous sounding of an alarm will indicate that the building is to be evacuated. When the alarm is activated, all magnetically locked doors will be released, making emergency escape routes available for use. Leave the building immediately, using the nearest stairway or exit.

### **Messages**

The message board will be located by the registration desk in *Oceania* on Level 3 of Te Papa.

### **Mobile Phones and Pagers**

Mobile phones and pagers must be turned off (or set to vibrate) while sessions are in progress.

### **Name Badges**

As a security requirement, we request that participants wear their conference name badges to all sessions and refreshment breaks. Please return these for recycling, along with your lanyard to the registration desk at the conclusion of the conference.

### **Oral Presentations**

If you are using PowerPoint you have been requested to email your presentation prior to the conference. If you were unable to do this, please hand in your presentation on a USB stick to the AV technician at the information desk as soon as possible.

Chairpersons of sessions are asked to be present at least five minutes before the session starts so that speakers can introduce themselves. All speakers are requested to remain within their allocated time (including time for questions from the audience if wanted).

### **Parking**

Te Papa's car park is open 24 hours, 7 days a week.

A special discounted conference rate of **\$9 per day** is available for delegates. After you park your car, please ask for the discounted ticket before departing from the registration desk staff in Oceania.

Car parking charges (if you don't need to stay for the day)

- 15 min–1 hour \$3.5
- 1–2 hours \$7

Anything over 2 hours is charged at \$10 so it would be in your interest to request a discounted parking ticket from registration desk staff in Oceania.

### **Posters / Poster Session**

All posters are located in Oceania on level 3 of Te Papa. Please hang your poster (using the Velcro provided) by your poster number (which was communicated to you via email prior to the conference). Poster numbers are also in the poster section of this handbook. Please ensure your poster is hung up when you first arrive at the conference.

The Poster Session will take place on Monday 3<sup>rd</sup> December from 17.00 hrs – 19.00 hrs; we ask that you stand by your board at this time to answer questions. Drinks and canapés will be served during this time.

### **Public Transport**

The Airport Flyer is an express bus service that runs into central Wellington every 20 minutes during the day and every 30 minutes in the evenings. It costs \$6.50 each way.



The Airport Flyer departs from the southern end of the airport terminal, Level 0 (exit from baggage claim doors on Level 0 and turn right) past the Airport Flyer waiting area.

The timetable for the Airport Flyer is available at [www.metlink.org.nz](http://www.metlink.org.nz) (select the timetable for Route 91 – Airport Flyer).

### **Smoking**

Te Papa is a smoke-free venue (including outdoor areas, such as balconies). Smokers are requested to smoke outside the premises of Te Papa.

### **Storage of Luggage**

Storage of luggage on departure date can be arranged through the hotel concierge for those staying at the conference hotels. For all other delegates, luggage can be stored with the Conference Secretariat staff at the registration desk.

### **Taxis/Shuttles**

- Wellington Combined Taxis (ph 0800 38 44 44)
- Corporate Cabs (ph 04 387 4600)
- Cooperative Shuttles (ph 04 387 8787)

When booking a taxi or shuttle, the street address for the conference venue is: **Te Papa, Wakefield Street**

### **Teas and Lunches**

Teas and lunches will be served in *Oceania* on level 3 of Te Papa. If you have specified a dietary requirement when completing the online registration, this will have been passed on to the venue and will be available for you. Please make yourself known to catering staff.

### **Wireless Internet**

Wireless internet is available within *Oceania*. Access is free and does not require a username or password.



**Programme**

**Room Key**

*(Te Papa maps are at the back of this handbook)*

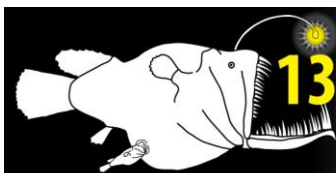
Oceania	Level 3, Te Papa
Soundings Theatre	Level 2, Te Papa
Rangimarie 1	Level 3, Telstra Clear Ctr, Te Papa

**Sunday 2nd December**

15.00 - 17.00	Registration	Oceania
17.00 - 19.00	Icebreaker	Macs Brewbar

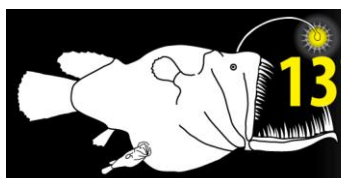
**Monday 3rd December**

08.00 - 17.00	Registration		Oceania
08.50 - 10.20	<b>Mihi Whakatau</b> Welcome Addresses from dignitaries		Soundings Theatre
10.20 - 10.50	Tea/Coffee break		Oceania
10.50 - 11.30	<b>NZ Context Plenary</b> <b>Pawson</b> ; Deep-sea research in the New Zealand region, 1865–1965		Soundings Theatre
<b>Concurrent Session</b>	<b>SOUNDINGS THEATRE</b> <b>Biodiversity Pattern – Large-Scale 1</b>	<b>RANGIMARIE ROOM 1</b> <b>Dispersal and Connectivity 1</b>	
11.30 - 11.50	<b>Vanreusel</b> ; Free-living nematodes associated with chemosynthetic habitats: a large-scale integrated analysis of distribution and diversity patterns	<b>Miller</b> ; Connectivity and conservation of seamount communities: a seascape genetic approach	
11.50 - 12.10	<b>George</b> ; Abyssal species are everywhere – geographical distribution of benthic Copepoda in the deep sea	<b>Howell</b> ; Investigating potential larval dispersal from a NE Atlantic seamount (Anton Dohrn) using a Lagrangian particle tracing model.	
12.10 - 12.30	<b>Yasuhara</b> ; Patterns and controlling factors of species diversity in the Arctic Ocean	<b>Teixeira</b> ; High connectivity of shrimp across large spatial scales and distinct chemosynthetic habitats	
12.30 - 13.30	Lunch		Oceania



International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
 Wellington, New Zealand 3 – 7 December 2012

Concurrent Session	SOUNDINGS THEATRE <i>Biodiversity Pattern – Large-Scale 2</i>	RANGIMARIE ROOM 1 <i>Dispersal and Connectivity 2</i>	
13.30 - 13.50	<b>Ross</b> ; Global biogeography of abyssal sea-cucumbers; species distributions, population genetics and the importance of ecological and historical factors.	<b>O'Hara</b> ; The 'L' superhighway: bathyal connectivity across Atlantic, Indian and South Pacific Oceans	
13.50 - 14.10	<b>Woolley</b> ; Beta diversity in the deep-sea – patterns of community composition turnover for bathyal species around Australia and New Zealand	<b>Shank</b> ; Coral ecosystem diversity in the deep Gulf of Mexico: host coral-invertebrate symbiont relationships and the genetic connectivity of deep-sea coral ecosystems	
14.10 - 14.30	<b>Buhl-Mortensen (Lene)</b> ; Classification of deep-sea habitats and biotopes off Norway	<b>Young</b> ; Dispersal trajectories of cold-seep tubeworm larvae ( <i>Lamellibrachia luymesii</i> ) predicted by ocean models and empirical data on larval development	
14.30 - 14.50	<b>Kaiser</b> ; New Zealand's deep-sea isopod crustaceans: spatial patterns of diversity, abundance and composition	<b>Plouviez</b> ; High-throughput population genetics in a deep-sea hydrothermal-vent limpet	
14.50 - 15.10	<b>Lindsay</b> ; Biodiversity, community structure and vertical distribution of planktonic cnidarians in the Celebes and Sulu Seas	<b>Beedessee</b> ; Dispersal abilities of hydrothermal vent animals in the Indian Ocean inferred from mitochondrial DNA sequencing	
15.10 - 15.40	<b>Tea/Coffee break</b>		<b>Oceania</b>
Concurrent Session	SOUNDINGS THEATRE <i>Biodiversity Pattern – Large-Scale 3</i>	RANGIMARIE ROOM 1 <i>Evolution 1</i>	
15.40 - 16.00	<b>Woodall</b> ; Meiofaunal community assessment of seamounts on the Southwest Indian Ocean Ridge	<b>Herrera</b> ; Evolutionary history and biogeographical patterns of barnacles from hydrothermal vents	
16.00 - 16.20	<b>Sutton</b> ; The deep-pelagic Biome of the Atlantic Ocean: character and ecological discreteness of the meso- and bathypelagic fish faunas	<b>Johnson</b> ; Sympatric speciation in the sea: The many faces of <i>Alviniconcha</i>	
16.20 - 16.40	<b>Parker</b> ; Distribution and life history of shovelnose dogfish <i>Deania calcea</i> in New Zealand waters	<b>Krylova</b> ; Small vesicomys (Bivalvia: Vesicomysidae, Vesicomysinae) vs large-size symbiotrophic confamilial relatives	
16.40 - 17.00	<b>Buhl-Mortensen (Pål)</b> ; Cold-water coral habitats in Norway	<b>Voight</b> ; The enigma of high species diversity in wood-boring bivalves	
17.00 - 17.20	TBC	<b>Riehl</b> ; On the phylogeny of Macrostylidae (Isopoda) and their position amongst the Janiroidea	
17.20 - 19.00	<b>Poster session</b>		<b>Oceania</b>

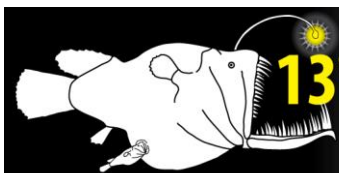


International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
 Wellington, New Zealand 3 – 7 December 2012

Tuesday 4<sup>th</sup> December

15.00 - 17.00	Registration		Oceania
08.15 - 09.00	Plenary Presentation Cameron; Deepsea Challenge: Science Platforms for Research at Hadal Depths		Soundings Theatre
Concurrent Session	SOUNDINGS THEATRE <i>Biodiversity Pattern – Large-Scale 4</i>	RANGIMARIE ROOM 1 <i>Evolution 2</i>	
09.00 - 09.20	Thistle; Minimum range sizes of sediment-dwelling species in the deep sea: insights from harpacticoid copepods	Kim (See-Joo); Diversity of hydrothermal-vent decapods at Tofua Arc in the Southwest Pacific using the CO1 barcoding	
09.20 - 09.40	Schnabel; Squat lobster depth distribution in the Southwest Pacific	Ardila; Phylogenetic systematics of Coralliidae (Octocorallia): a time-calibrated molecular phylogeny and species delimitation of the precious corals	
09.40 - 10.00	Cook (April); Pelagic fish distribution over a mid-ocean ridge system, with evidence of diel vertical migration by the bathypelagic fauna	Lins; Distribution and habitat selectivity of deep-sea canyon nematodes	
10.00 - 10.20	Schnurr; Distribution of selected Munnopsidae (Crustacea, Isopoda, Asellota) species around Iceland linked to long-term oceanographic data	de Busserolles; Spectral tuning in the eye of lanternfishes (Myctophidae).	
10.20 - 10.50	Tea/Coffee break		Oceania
Concurrent Session	SOUNDINGS THEATRE	RANGIMARIE ROOM 1 <i>Autoecology 1</i>	
10.50 - 11.10	Sponsor Announcements	Rodrigues; A bacterium's eye view of chemosynthetic symbioses in bivalves from the East Atlantic cold seeps	
	Cook (Adam); The International Seabed Authority and marine scientific research	Laming; Dispersal capacity and symbiont acquisition in <i>Idas</i> sp., a small chemosymbiotic mytilid from deep-sea environments	
11.10 - 11.30	Baker; INDEEP NOW!		
11.30 - 11.50	<i>Biodiversity Pattern – Intermediate 1</i>	Nunes-Jorge; Symbiotic diversity in deep-sea wood boring Xylophaginae clams	
	Ross; Significant deep-sea coral and hardbottom habitats on the West Florida Slope, Eastern Gulf of Mexico	Cambon-Bonavita; Rimicaris exoculata: all you want to know about a complex symbiosis	
11.50 - 12.10	Chivers; The Biodiversity and Ecology of Senghor Seamount (North Atlantic)		
	Wagstaff; Beta diversity in echinoderms is structured by spatial turnover along a bathymetric gradient in the Porcupine Seabight and Abyssal Plain	Forget; Symbiont diversity in the tubeworm <i>Ridgeia piscesae</i> : Who's in, who's out?	
12.30 - 13.30	Lunch		Oceania

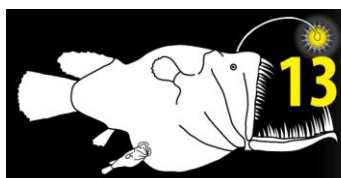




International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
 Wellington, New Zealand 3 – 7 December 2012

Concurrent Session	SOUNDINGS THEATRE <i>Biodiversity Pattern – Intermediate 2</i>	RANGIMARIE ROOM 1 <i>Autoecology 2</i>	
13.30 - 13.50	<b>Demopoulos;</b> Biodiversity and community composition of macrofauna associated with multiple deep-sea coral habitats in the Gulf of Mexico	<b>Judge;</b> A 3D investigation of the morphology of lepetellid limpets ( <i>Lepetella sierrai</i> ): hypotheses on feeding ecology and symbiosis	
13.50 - 14.10	<b>Brooke;</b> A deep-sea reef community at unusually shallow depths off northeastern Florida	<b>Kuhar;</b> The limits of vision: specialisations in the small eyes of the deep-sea bristlemouth <i>Cyclothone microdon</i> (Teleostei)	
14.10 - 14.30	<b>Kamenskaya;</b> Giant protists (xenophyophores and komokiaceans) from the ferromanganese nodule fields of the Pacific and Atlantic Oceans	<b>Miyamoto;</b> Development and reproductive strategy of the bone-eating worm <i>Osedax japonicus</i>	
14.30 - 14.50	<b>Haddock;</b> Metazoan biodiversity patterns of the deep-sea water column	<b>Seike;</b> In situ burrow casting reveals new clues to the deep-sea biology	
14.50 - 15.10	<b>Maclsaac;</b> The larger pelagic crustacea of the Gully Submarine Canyon	<b>Trench 1</b> <b>Kitazato;</b> Trench Biology: Exemplified from the Japan-Bonin-Mariana Trenches cruises	
15.10 - 15.40	<b>Tea/Coffee break</b>		<b>Oceania</b>
Concurrent Session	SOUNDINGS THEATRE <i>Biodiversity Pattern – Intermediate 3</i>	RANGIMARIE ROOM 1 <i>Trench 2</i>	
15.40 - 16.00	<b>Knox;</b> Diversity and evolution of New Zealand deep-sea Amphipoda examined using molecular methods	<b>Gebruk;</b> Evolutionary relationships in trench species of the genus <i>Elpidia</i> (Holothuroidea, Elaspodida, Elpidiidae).	
16.00 - 16.20	<b>Durden;</b> Spatial variation in the megabenthos at the Porcupine Abyssal Plain	<b>Gerringer;</b> High trimethylamine oxide contents in hadal snailfish (Liparidae) indicate a depth limit for teleost fishes	
16.20 - 16.40	<b>Watanabe;</b> Biodiversity of deep-sea hydrothermal vent fauna and its relationships to environments in Okinawa Trough	<b>Kupriyanova;</b> Hadal serpulid polychaetes: calcareous tubeworms beyond the abyss	
16.40 - 17.00	<b>Grupe;</b> Hard-substrate colonization experiments provide insight into macrofaunal community patterns at East Pacific methane seeps	<b>Lecroq;</b> Ultra-deep sequencing of ultra-deep sediment	
17.00 - 17.20	<b>Barry;</b> Biology of bathyal benthic communities in the Gulf of California: comparison of cold, hypoxic waters in the Guaymas Basin with warm, oxygenated basins in the northern gulf	<b>Jamieson;</b> Abyssal and hadal bait-attending communities of the Kermadec Trench (SW Pacific)	

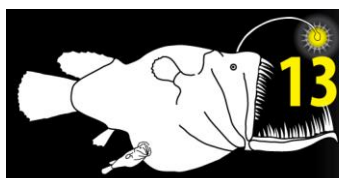




International  
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 Wellington, New Zealand 🌊 3 – 7 December 2012

Wednesday 5<sup>th</sup> December

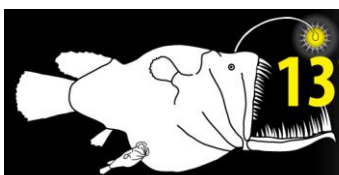
08.00 - 17.00	<b>Registration</b>		<b>Oceania</b>
08.15 - 09.00	<b>Plenary Presentation</b> Tittensor, The deep sea as a testbed for ecological theory		<b>Soundings Theatre</b>
<b>Concurrent Session</b>	<b>SOUNDINGS THEATRE</b> <i>Biodiversity Pattern – Small 1</i>	<b>RANGIMARIE ROOM 1</b> <i>Discovery 1</i>	
09.00 - 09.20	<b>Sarrazin</b> ; Small-scale variations of hydrothermal faunal assemblages on the Tour Eiffel edifice (Mid-Atlantic Ridge) in relation to abiotic conditions	<b>Brandt</b> ; SoJaBio (Sea of Japan Biodiversity) and KuramBio (Kurile Kamchatka Deep-Sea Biodiversity) studies – joint German-Russian deep-sea investigations in the western Pacific	
09.20 - 09.40	<b>Olu</b> ; Distribution of vesicomid bivalve species associated to cold seeps in the Congo basin: spatial or dynamic control?	<b>Narayanaswamy</b> ; Discoveries made on seamounts along the Southwest Indian Ocean Ridge	
09.40 - 10.00	<b>Paterson</b> ; Characterising habitat complexity – using microCT scanners to study coral frameworks	<b>Baco</b> ; DNA barcoding reveals high diversity of Hawaiian deep-sea octocorals	
10.00 - 10.20	<b>Pasulka</b> ; The distribution and diversity of heterotrophic protists in a methane seep ecosystem off the coast of Oregon	<b>Menot</b> ; Discovery of a tube-worm dominated hydrothermal vent community in the South-West Pacific: species composition, spatial distribution and biogeography	
10.20 - 10.50	<b>Tea/Coffee break</b>		<b>Oceania</b>
<b>Concurrent Session</b>	<b>SOUNDINGS THEATRE</b> <i>New Methods and Novel Techniques 1</i>	<b>RANGIMARIE ROOM 1</b> <i>Discovery 2</i>	
10.50 - 11.10	<b>Sherman</b> ; Capturing episodic events in the deep-sea community using a continuously monitoring instrument suite	<b>Cunha</b> ; Biological assemblages of three new mud volcanoes along deep-reaching transform faults in the Horseshoe Abyssal Plain (NE Atlantic)	
11.10 - 11.30	<b>Wagner</b> ; Innovations in seep exploration: remote AUV operations from a shore-based center	<b>Nagano</b> ; Fungal diversity in deep-sea environments	
11.30 - 11.50	<b>Bett</b> ; Autonomous Ecological Surveying of the Abyss (AESAs): Towards a landscape-scale perspective in deep-sea ecology	<b>New Methods and Novel Techniques 2</b> <b>Glover</b> ; What do deep-sea animals do? A new functional trait classification for deep-sea fauna	
11.50 - 12.10	<b>Robert</b> ; Combining landscape ecology and species-environment relationships for improved high-resolution habitat mapping in the deep sea	<b>Reisenbichler</b> ; Taking the laboratory into the deep: In situ midwater oxygen-consumption measurements as tools to address the changing vertical distribution of the sergestid shrimp, <i>Sergestes similis</i> , in Monterey Bay, California	
FREE AFTERNOON	<b>Optional Excursions / Explore Wellington</b>		
19.00 - Late	<b>Symposium Dinner</b>		<b>The Boatshed</b>



International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
 Wellington, New Zealand 3 – 7 December 2012

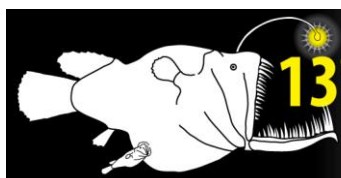
Thursday 6<sup>th</sup> December

08.00 - 17.00	Registration		Oceania
08.15 - 09.00	Plenary Presentation Fisher; Impact to deepwater coral gardens from the <i>Deep Water Horizon</i> disaster		Soundings Theatre
Concurrent Session	<b>SOUNDINGS THEATRE</b> <i>Temporal Patterns 1</i>	<b>RANGIMARIE ROOM 1</b> <i>Reproduction and Population 1</i>	
09.00 - 09.20	Fujiwara; Early succession of whale-fall ecosystems in Japanese waters	Hoving; Life-history strategies in oceanic squid	
09.20 - 09.40	Morrongiello; Parallel decadal variability in juvenile growth rates for Northern and Southern Hemisphere Orange Roughy populations	Nye; Reproductive biology and population structure of the alvinocaridid shrimp <i>Rimicaris hybisae</i> at hydrothermal vents on the Mid-Cayman Spreading Centre	
09.40 - 10.00	Thresher; Millennial-scale variability in Southern Hemisphere Intermediate Water Mass temperatures from analysis of deep-sea coral proxies	Boschen; Distribution, population structure, reproduction, and diet of <i>Ophiolimna antarctica</i> (Lyman, 1879) from Kemp Caldera in the Southern Ocean	
10.00 - 10.20	Matabos; Influence of seasonal and episodic events on deep-sea communities in a submarine canyon: First results from the NEPTUNE Canada cabled network	Baillon; Seasonal reproduction of deep-sea pennatulacean corals in the Northwest Atlantic	
10.20 - 10.50	Tea/Coffee break		Oceania
Concurrent Session	<b>SOUNDINGS THEATRE</b> <i>Temporal Patterns 2</i>	<b>RANGIMARIE ROOM 1</b> <i>Reproduction and Population 2</i>	
10.50 - 11.10	Cuvelier; A comparison of the day-to-day of deep-sea hydrothermal faunal assemblages in the Atlantic and the North-East Pacific – a multidisciplinary observatory approach	Ramirez-Llodra; Reproductive biology and recruitment in the deep-sea fish community of the north-western Mediterranean continental margin	
11.10 - 11.30	Munro; Temporal and spatial patterns of in situ community structure using time-lapse camera systems at a vent field on the East Pacific Rise	Catarino; Postglacial isolation of the Mediterranean <i>Centroscymnus coelolepis</i> reveals the importance of the Pillars of Hercules as geographical barrier for deep sea sharks.	
11.30 - 11.50	Atkinson; Monitoring South Africa's offshore invertebrate biodiversity	Nakamura; Gametogenesis and population structure of a hydrothermal vent gastropod <i>Lepetodrilus nux</i> at different vent sites in Okinawa Trough	
11.50 - 12.10	Laguionie-Marchais; Inter-annual change in the abyssal plain – the macrofaunal response to climatic changes	Duffy; Scavenging amphipods of the Iberian submarine canyons; a comparative analysis at the community and population level	
12.10 - 12.30	<b>Human Impacts 1</b> Meyer; Increase of litter at the Arctic deep-sea observatory HAUSGARTEN – indirect effect of global warming?	Nedoncelle; Combined sclerochronological and in situ staining approach to study the growth rate of deep-sea hydrothermal vent mussel shells	
12.30 - 13.30	Lunch		Oceania



International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
 Wellington, New Zealand 3 – 7 December 2012

Concurrent Session	SOUNDINGS THEATRE <i>Human Impacts 2</i>	RANGIMARIE ROOM 1 <i>Trophic &amp; Process 1</i>	
13.30 - 13.50	<b>Jones</b> ; Future reductions in global-ocean benthic biomass predicted as a result of climate change	<b>Mayor</b> ; Is the deep-sea different? A cross-ecosystem study investigating how the quantity and quality of organic matter influence benthic carbon cycling	
13.50 - 14.10	<b>Robison</b> ; The consequences of expanding oxygen minimum zones for mesopelagic animals	<b>Nodder</b> ; Depth variability of particle fluxes and implications for the energy requirements of deep-ocean benthic communities	
14.10 - 14.30	<b>Cordes</b> ; Roberts' Reef: An enigmatic cold-water coral mound in the deep-, low-aragonite-saturation-state Gulf of Mexico.	<b>Smith</b> ; Massive krill falls and high macrofaunal abundance in deep-sea fjords along the West Antarctic Peninsula (WAP)	
14.30 - 14.50	<b>Becheler</b> ; Genetic diversity of the coldwater coral <i>Lophelia pertusa</i> in reefs exhibiting different levels of environmental impacts	<b>Drazen</b> ; The role of carrion supply in the abundance of deep-water fish off California	
14.50 - 15.10	<b>Taylor</b> ; Don't rock the boat: Impacts of a lost shipping container on the deep-sea benthos of the Monterey Bay National Marine Sanctuary, CA	<b>Amaro</b> ; The response of deep-sea benthic megafauna to sediment gravity flows in main channel of the Whittard Canyon	
15.10 - 15.40	Tea/Coffee break		Oceania
Concurrent Session	SOUNDINGS THEATRE <i>Human Impacts 3</i>	RANGIMARIE ROOM 1 <i>Trophic and Process 2</i>	
15.40 - 16.00	<b>Priede</b> ; Changes in biomass and population size structure of demersal deep-sea fishes of the Porcupine Seabight and Abyssal Plain (ICES Sub-area VII), North East Atlantic Ocean; impacts of a deep-water fishery?	<b>Sweetman</b> ; Scavenger diversity and scavenging rates at jellyfish-falls and fish-falls at the deep-sea floor	
16.00 - 16.20	<b>Milligan</b> ; The effects of oil production on deep-water fish communities in West Africa: Early results from the DELOS project	<b>Van Oevelen</b> ; Insights in faunal feeding strategies in the benthic food webs: a compilation of isotope tracer data	
16.20 - 16.40	<b>Main</b> ; Investigating the effects of deep-sea oil spills on sediment community oxygen consumption	<b>Jeffreys</b> ; Differences in benthic food-web structure under two contrasting productivity regimes: NE Atlantic vs W. Mediterranean.	
16.40 - 17.00	<b>Gates</b> ; The SERPENT Project: Exploring deep-sea life, anthropogenic disturbance and recovery at hydrocarbon exploration sites	<b>Thurber</b> ; Warm mud at the Chile Triple Junction: A methane ladder between stepping stones?	
17.00 - 17.20	<b>Currie</b> ; Benthic fauna of the Namibian shelf under threat	<b>Gale</b> ; Trophic ecology of deep-sea asteroids from the continental slope of eastern Canada	
18.00 - 20.30	Kermadec Voices Art Exhibition Sponsored by PEW Environment Group		City Gallery



International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
 Wellington, New Zealand 3 – 7 December 2012

Friday 7<sup>th</sup> December

08.00 - 17.00	Registration		Oceania
08.15 - 09.00	Plenary Presentation <b>Hilário</b> ; How far do larvae go? Dispersal and MPA design in the deep sea		Soundings Theatre
<b>Concurrent Session</b>	<b>SOUNDINGS THEATRE</b> <i>Conservation and Management 1</i>	<b>RANGIMARIE ROOM 1</b> <i>Trophic and Process 3</i>	
09.00 - 09.20	<b>Mazurek</b> ; Conserving the deep-sea at very large spatial scales: Pew's Global Ocean Legacy Project	<b>McClain</b> ; The energetics of life on the deep seafloor	
09.20 - 09.40	<b>Ross</b> ; Use of predictive habitat modelling to assess the distribution and extent of the current protection of 'listed' deep-sea habitats	<b>Wolff</b> ; Natural iron fertilisation is reflected in the stable-isotopic composition of carbon in deep-sea holothurians	
09.40 - 10.00	<b>Bowden</b> ; Evaluation of the New Zealand Marine Environment Classifications using independent data from the Chatham Rise and Challenger Plateau.	<b>Nomaki</b> ; In situ experimental measurements of carbon fixation on the deep seafloor	
10.00 - 10.20	<b>Morato</b> ; Setting global conservation priorities for seamounts: coupling deep-sea with pelagic conservation	<b>Flynn</b> ; Cross-basin heterogeneity in lanternfish (family Myctophidae) assemblages and isotopic niches (d13C and d15N) in the southern Tasman Sea abyssal basin	
10.20 - 10.50	Tea/Coffee break		Oceania
<b>Concurrent Session</b>	<b>SOUNDINGS THEATRE</b> <i>Conservation and Management 2</i>	<b>RANGIMARIE ROOM 1</b> <i>Trophic and Process 4</i>	
10.50 - 11.10	<b>Dunstan</b> ; Conservation on the High Seas – Defining Ecologically and Biologically Significant Areas (EBSAs) in the South Pacific	<b>Bernardino</b> ; Comparative composition, diversity and trophic ecology of sediment macrofauna at vents, seeps and organic falls	
11.10 - 11.30	<b>Bors</b> ; Implications of deep-sea genetic connectivity patterns for the management of benthic ecosystems in the New Zealand Region: Recent work and future directions	<b>Wigham</b> ; Spatial differences in Southern Ocean hydrothermal vent food webs: influences of chemistry, microbiology and predation on trophodynamics.	
11.30 - 11.50	<b>Serpetti</b> ; Ecological adaptations of macro-epifauna on deep-sea corals in the Southwest Indian Ocean	<b>Stevenson</b> ; Investigation of deep-sea echinoid feeding ecology in the NE Atlantic: Implications for deep-sea coral ecosystems	
11.50 - 12.10	<b>Dunn</b> ; Could an orange roughy fishery achieve Marine Stewardship Certification?	<b>Choy</b> ; Insights into the trophic ecology of large mesopelagic fishes from the central North Pacific using stomach content and fatty-acid biomarker analyses	
12.10 - 12.30	<b>Clark</b> ; Closed areas for deep-sea habitat recovery: a case of shutting the door after the horse has bolted?	<b>Lacey</b> ; Lipid and fatty-acid composition of <i>Hirondellea dubia</i> (Amphipoda: Lyssianasidae) from hadal depths within the Kermadec Trench, SW Pacific	
12:30 - 13:30	Lunch		Oceania



Concurrent Session	SOUNDINGS THEATRE <i>New Methods and Novel Techniques 3</i>	RANGIMARIE ROOM 1 <i>New Methods and Novel Techniques 4</i>	
13.30 - 13.50	<b>Schoening</b> ; The impact of experts' inter- and intra-observer agreements on computational object classification in images from the deep seafloor of the HAUSGARTEN observatory	<b>Lejzerowicz</b> ; Identifying active foraminiferans in the Sea of Japan using DNA and RNA-based metagenetics	
13.50 - 14.10	<b>Knudby</b> ; Evaluation of geospatial tools for delineating concentrations of deep-sea sponges	<b>Sinniger</b> ; Uncovering abyssal communities using high-throughput sequencing: Wwhere are we and what to expect?	
14.10 - 14.30	<b>Easton</b> ; Deep-sea harpacticoids: are cryptic species a problem?	<b>Colaço</b> ; Colonization experiments in the Azores deep sea	
14.30 - 14.50	<b>Voting for venue of next DSBS in 2015</b>		
14.50 - 15.10	<b>Student Prizes and Closing Ceremony</b>		<b>Soundings Theatre</b>

## Additional Side Meetings

### Introducing the HADES trench programme

**Where:** Rangimarie 1 Room

**When:** Tuesday 4<sup>th</sup> December, 2012 @ 17:20

**Leader of the presentation:** Dr. Tim Shank

### Discussion on "High-throughput sequencing approaches in the deep Sea"

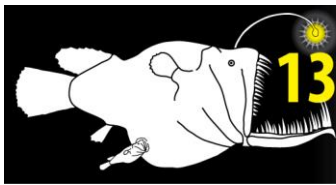
**Where:** Rangimarie 1 Room

**When:** Thursday 6<sup>th</sup> December, 2012 @ 17.20

**Leaders of the discussion:** Dr Sophie Plouviez, Dr Andrew Thaler

**Funding support:** This discussion is supported by INDEEP





International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

## Social Events

### Icebreaker

Sunday 2<sup>nd</sup> December from 17.00 – 19.00

Cable Room, Mac's Brewbar

Taranaki St Wharf, Wellington

Join us for the welcome reception prior to the conference opening in the Cable Room at the famous Mac's Brewbar on Wellington's popular waterfront.

This function is included with your registration (full and student) but must have been selected when completing the registration process to guarantee attendance.

### Conference Dinner

Wednesday 5 December from 19.00 – late

The Boatshed

Taranaki St Wharf, Wellington

We look forward to welcoming you to the iconic Boatshed which is our venue for the Conference Dinner. Surrounded by spectacular views of the inner harbour, the Boatshed is the perfect setting for the highlight of the social programme.

Enjoy entertainment and a sumptuous three course dinner using locally sourced fresh produce accompanied by fine New Zealand wines.

This function is at an additional cost and places are limited. Please see the registration desk staff if you wish to purchase a ticket and they will advise if this is possible.

## Exhibition

### Deep New Zealand: Our underwater wilderness

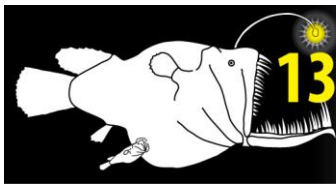
Level 3, Te Papa (outside Oceania)

Free entry

Travel deep down into New Zealand's ocean and you'll discover a wilderness of underwater mountains, great canyons, and vast plains of rubble and mud. Contrary to what you might expect – and to what scientists once thought – this deep, dark world is teeming with life.

The deep sea ranges from 200 metres to more than 10,000 metres. Light fades as you descend, becoming too dim for plants to survive, and below 1,000 metres darkness prevails. The water is generally bitterly cold, but in some areas, volcanic vents release super-heated water. Animals have adapted to these extreme conditions in amazing ways.

Showcased in this exhibition are research findings from Te Papa, NIWA, and GNS Science. Research is vital – to learn more about this mysterious underwater world and ensure its sustainable management. The sea in New Zealand's Exclusive Economic Zone covers more than 4 million square kilometres, yet less than 1 percent has been closely studied – a mere drop in the ocean.



International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

### Suggested Excursions – Afternoon of Wednesday 5 December

There will be no official conference excursions for the free afternoon on Wednesday 5 of December. However, you may wish to consider some of the attractions on offer.

- Advance booking is advisable for many tours at this time of year
- Check individual websites for up-to-date information on costs and timings

#### **Zealandia**

Just 10 minutes from central Wellington, Zealandia is a must-see eco-attraction and groundbreaking restoration project: a nature-lover's paradise and a sanctuary by the city!

See some of New Zealand's rarest birds, reptiles and insects living wild in their natural environment, including hihi, tuatara, saddleback, kākā and (at night) little spotted kiwi. Indoors, NZ's incredible natural history and world-renowned conservation movement are brought to life in a state-of-the-art exhibition.

#### **Entry Fees:**

**Exhibition Only - \$18.50**

**Sanctuary Only - \$18.50**

**Exhibition & Sanctuary - \$28.50**

<http://www.visitzealandia.com/>

#### **Matiu/Somes Island**

Travel by ferry to this fascinating Island, only recently opened to the public. A reserve administered by the Department of Conservation, it is steeped in local history, from early Maori settlement to more recent times as a prisoner of war camp, and quarantine station. Now it is being allowed to revert back to its native flora and fauna. Being rodent free, the birdlife is amazing and you may even be lucky enough to see the native tuatara that have recently been reintroduced to the island. The views from all over the easy walking tracks on the island are unsurpassed and not to be missed!

**Return Ferry - \$23.00**

**If you wish to do a guided tour of Matiu/Somes Island, we recommend Flat Earth at**

<http://www.flatearth.co.nz/tours/matiu-somes-island-tour>

#### **Lord of the Rings - Middle Earth Tour**

A wonderful half day film locations experience with your own expert guide in a small group. The tour runs for half a day and takes you to the filming locations for Rivendell where Frodo recovered from his knife attack; the Anduin River where the Fellowship voyaged to Amon Hen; the river where Aragorn was washed ashore after the attack of the Wargs; the Gardens of Isengard, the site of the Orcs Felling the Trees and where Gandalf rode to see Saruman; go to the Mount Victoria lookout and Buckland Forest where you can race to the Buckleberry Ferry and "Get off the Road", where the Hobbits hid from the Nazgul/Black Riders and where they found the mushrooms on the Road; Dunharrow Rohirrim encampment; visit the quarry used for the filming of Helms Deep in Rohan and Minas Tirith in Gondor.

**Adult - \$159.00**

<http://www.flatearth.co.nz/tours/middle-earth-film-locations>



### Seal Coast Safari

Would you visit Egypt and not see the Pyramids? Well you can't visit Wellington without seeing our seals! Get up-close and personal with wild New Zealand fur seals as you explore Wellington's spectacular coastline with Seal Coast Safari. Leaving from Downtown Wellington, you'll be in four wheel drive mode 15 minutes later! Our Safaris depart from the [Wellington i-SITE Visitor Centre](http://www.wellingtonnz.com/sights_activities) at 10.00am and 1.30pm daily. Seals guaranteed 364 days of the year!

**Adult - \$115.00**

<http://www.sealcoast.co.nz/>

**For more tour ideas, we recommend you visit the Wellington iSite:**

[http://www.wellingtonnz.com/sights\\_activities](http://www.wellingtonnz.com/sights_activities)

**They are located in Civic Square on the corner Victoria and Wakefield Streets.**

**Opening hours:**

Monday to Sunday 8.30am - 5.00pm

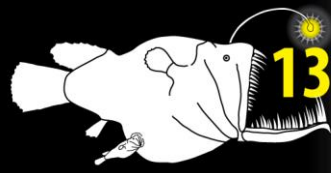
Public Holidays 11.00am - 4.00pm

We are open everyday except Christmas Day.

**Phone: +64 4 802 4860**

**[bookings@WellingtonNZ.com](mailto:bookings@WellingtonNZ.com)**





International

**13<sup>th</sup> Deep-Sea Biology Symposium**

Wellington, New Zealand  3 – 7 December 2012

# Oral Abstracts

**Alphabetical  
by Presenting Author  
Surname**



*Thursday 6<sup>th</sup> December*

*Trophic and Process 1*

## **THE RESPONSE OF DEEP-SEA BENTHIC MEGAFUNA TO SEDIMENT GRAVITY FLOWS IN THE MAIN CHANNEL OF THE WHITTARD CANYON**

**Amaro T**<sup>1</sup>, de Stigter H<sup>2</sup>, Duineveld G<sup>3</sup>, Niewland G<sup>4</sup>, Cunha M<sup>5</sup>

<sup>1</sup> NIVA, <sup>2</sup> NIOZ, <sup>3</sup> NIOZ, <sup>4</sup> NIOZ, <sup>5</sup> UA & CESAM

Six video transects were used to evaluate the role of the Whittard Canyon, as a hot-spot of diversity and abundance for megafauna. High densities of the holothurian *Peniagone azorica* were observed in one of the transects along the Whittard channel, at 4300 m depth. In the other transects, this deep-sea holothurian was scarce, when not absent. At the same transects, sediment samples were collected by a multicorer and phytopigments (chlorophylls and carotenoids) were extracted in the lab by means of HPLC.

Concentrations of chlorophylls were significantly higher in the area where *P. azorica* was abundant than from those where these deep-sea organism was absent. We also present evidence from a long-term lander deployment of the existence of two major sediment gravity flows events (one during spring and another one during the summer). Concentrations of chlorophylls were significantly higher on those months than for the rest of the year.

Our results demonstrate that the Whittard Canyon act as a sink for OM burial and is active. Sediments and fresh OM are transported from the continental shelf down the canyon and into the deep sea. Enrichment of fresh OM in Whittard channel sediments leads to enhanced *P. azorica* abundance and biomass. These deep-sea holothurians appear to react quickly to fresh OM and are ideally suited to reworking fresh OM in unstable canyon sediments.



Tuesday 4<sup>th</sup> December

Evolution 2

## PHYLOGENETIC SYSTEMATICS OF CORALLIIDAE (OCTOCORALLIA): A TIME-CALIBRATED MOLECULAR PHYLOGENY AND SPECIES DELIMITATION OF THE PRECIOUS CORALS

Ardila NE<sup>1,2</sup>, Sanchez JA<sup>1</sup>

<sup>1</sup> Universidad de los Andes, Departamento de Ciencias Biológicas-Facultad de Ciencias, Laboratorio de Biología Molecular Marina (BIOMMAR), Carrera 1E No 18A-10, P.O.Box 4976, Bogotá, COLOMBIA, <sup>2</sup> Universidad de la Salle, Programa de Biología, Departamento de Ciencias Básicas, Carrera 2 No. 10-70, Bogotá, COLOMBIA

Species delimitation and phylogenetic studies in deep-sea organisms remain scarce and sometimes controversial. The phylogenetic relationships within the precious coral family Coralliidae remain largely unexplored and the monophyly of its two constituent genera, *Corallium* Cuvier and *Paracorallium* Bayer & Cairns, has not been resolved. We thus used mitochondrial sequence data to evaluate the monophyly of *Corallium* and *Paracorallium* and the species boundaries for nearly all named taxa in the family. Species from across the coralliid range, including material from Antarctica, Hawaii, New Zealand, Taiwan, Tasmania, Japan, the eastern Pacific and the western Atlantic were examined. The concatenated analysis of five mitochondrial regions (COI, 16S rRNA, ND2, and ND3-ND6) recovered two major coralliid clades. One clade is composed of two subgroups, the first including *Corallium rubrum*, the type species of the genus, together with a small group of *Paracorallium* species (*P. japonicum* and *P. tortuosum*) and *C. medea* (clade I-A); the other subgroup includes a poorly-resolved assemblage of six *Corallium* species. The second major clade is well resolved and includes species of *Corallium* and *Paracorallium*. A traditional taxonomic study of this clade delineated 11 morphospecies that were congruent with the general mixed Yule-coalescent (GMYC) model. A multilocus species-tree approach also identified the same two well-supported clades. However, clade I-B is more recent in the species tree (~5 My) than in the gene tree (~35 My) approach. No differences in the diversification times for clade-II (~44 My) were found between approaches. Our results provide no support for the taxonomic status of the two currently recognized genera in the family Coralliidae. Our study is the first to reconstruct a dated phylogeny in an octocoral group. Some species have wide distributions, recent diversification times and low mtDNA divergence whereas other species exhibit narrower allopatric distributions, older diversification times and greater levels of mtDNA resolution.



*Thursday 6<sup>th</sup> December*

*Temporal Patterns 1*

## **MONITORING SOUTH AFRICA'S OFFSHORE INVERTEBRATE BIODIVERSITY**

**Atkinson L**<sup>1</sup>, **Leslie R**<sup>2</sup>, **Maduray S**<sup>3</sup>, **Sink K**<sup>4</sup>

<sup>1</sup> South African Environmental Observation Network, <sup>2</sup> Department of Agriculture, Forestry and Fisheries, <sup>3</sup> Department of Environmental Affairs, <sup>4</sup> South African National Biodiversity Institute

With the acknowledged increasing importance of biodiversity in regulating effects of global change and a focus on ecosystem based management, South Africa is committed to strengthening long-term marine observations by increasing the opportunities and scope of monitoring the environment. Relevant South African government departments have undertaken dedicated annual demersal fisheries research surveys since 1986 spanning South Africa's south and west coasts up to a maximum depth of 900 m. Approximately 100 benthic trawls are conducted during each survey, using a research trawl net with a 60–75 m otter trawl door spread, mouth opening 3–4 m vertical and 20–29 m horizontal, rubber-roller footrope and a 110 mm net mesh size with 35 mm mesh size cod-end liner. Over time, an increasing number of fish species have begun to be accurately identified and recorded during these surveys, however, major commercial fish or species relating to specific projects, formed the main focus of these surveys. Since 2007 however, invertebrate species landed in the net have begun to be identified and included in the monitoring programme. This provided an ideal platform from which to develop a long-term invertebrate monitoring program in South Africa's offshore regions. This project aims to develop a South African offshore invertebrate field identification guide, build local taxonomic capacity and develop international collaborations to support a long term benthic invertebrate monitoring program. This project has substantially increased taxonomic knowledge of offshore benthic invertebrates and has successfully developed capacity for long-term monitoring thereof. To date a total of 151 invertebrate species have been collected and will be accurately identified for incorporation into the field guide for ongoing monitoring. Such invertebrate biodiversity information will be integrated in future ecosystem assessments and can provide increased biodiversity knowledge for spatial management decisions.



*Wednesday 5<sup>th</sup> December*

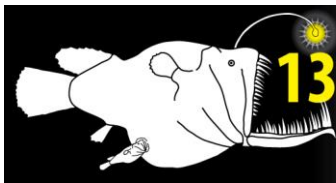
*Discovery 1*

## **DNA BARCODING REVEALS HIGH DIVERSITY OF HAWAIIAN DEEP-SEA OCTOCORALS**

**Baco A<sup>1</sup>, LaBelle B<sup>1</sup>, Morgan N<sup>1</sup>, Figueroa D<sup>1</sup>, Cairns S<sup>2</sup>, Ormos A<sup>2</sup>, Driskell A<sup>2</sup>**

<sup>1</sup> Florida State University, <sup>2</sup> Smithsonian Institution

Globally, studies of deep-sea octocoral distribution and diversity have been hampered by a lack of keys and a plethora of unidentified specimens. Even in areas where intensive morphological work has been done, as many as half of the specimens remain unidentified to species or even genus. Recently, a suite of genetic markers have been identified as barcoding proxies for octocorals. Here, we make one of the first attempts at broad-scale application of three of these markers, to recent and museum collections of octocorals of approximately 1000 specimens from the Hawaiian Archipelago, to gain a better understanding of the diversity and distribution of deep-sea octocorals there. Sequence results for all three markers show a greater number of haplotypes than morphological species. Each of these markers as taken alone has been shown to underestimate species richness. Extrapolating from this we show that morphological work to date on these specimens underestimates species richness by 30–40%, suggesting the diversity of octocorals in the Hawaiian Archipelago is substantially greater than previously thought. The large percentage of haplotypes represented by single individuals suggests that the full diversity of deep-sea octocorals in Hawaii remains drastically undersampled. This work also shows that species ranges based on current species designations are overestimated, with multiple smaller-range haplotypes for given morphological operational taxonomic units. We evaluate these results to assess the usefulness of application of these markers to understanding deep-sea coral distributions in the broader Pacific and beyond. We will also summarize attempts to develop better markers using next-generation sequencing.



International

# 13<sup>th</sup> Deep-Sea Biology Symposium

Wellington, New Zealand 3 – 7 December 2012

Thursday 6<sup>th</sup> December

Reproduction and Population 1

## SEASONAL REPRODUCTION OF DEEP-SEA PENNATULACEAN CORALS IN THE NORTHWEST ATLANTIC

Baillon S<sup>1</sup>, Hamel JF<sup>2</sup>, Mercier A<sup>1</sup>

<sup>1</sup> Ocean Sciences Centre (OSC), Memorial University, St John's, A1C 5S7, Canada, Newfoundland and Labrador, <sup>2</sup> Society for the Exploration and Valuing of the Environment (SEVE), 21 Phils Hill Road, Portugal Cove-St. Philips, A1M 2B7, Canada, Newfoundland and Labrador

*Halipteris finmarchica* and *Anthoptilum grandiflorum* are two of the most common species of sea pens (Octocorallia: Pennatulacea) in the Northwest Atlantic. Their reproductive cycle was investigated in colonies sampled over two years. Both species exhibited large lecithotrophic oocytes (maximum diameter of 1000 and 1100  $\mu\text{m}$ , respectively). Size at first maturity for both sexes was estimated at 40 cm (whole colony length) for *H. finmarchica* and 25 cm for *A. grandiflorum*. Polyps of *H. finmarchica* showed the presence of two cohorts of oocytes, with only one cohort implicated in each annual spawning (April-August). In contrast, *A. grandiflorum* presented a single cohort of oocytes which was completely released between April and July. Males of both species presented only one cohort of spermatocysts which were emptied simultaneously with oocyte release. A latitudinal shift in the spawning period occurred in both species, from South (April, Laurentian Channel) to North (May, Grand Bank and July-August, Labrador), following the development of the spring phytoplankton bloom. The general reproductive season of *A. grandiflorum* was confirmed by the observation of a spawning event in the laboratory in April 2011. This is the first account of seasonal reproduction in deep-sea pennatulaceans, contrasting with the few previous studies that suggested 'continuous' reproduction with no seasonal pattern in three bathyal species (Gulf of Maine, Southwest and Northeast Atlantic). From the present and previous studies, it is becoming clear that most bathyal corals in the Northwest Atlantic display breeding seasonalities very similar to shallow-water macro-invertebrates in the same region.



*Tuesday 4<sup>th</sup> December*

*Sponsor Announcements*

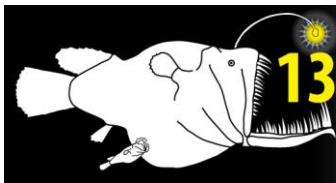
## **INDEEP NOW!**

**Baker M**<sup>1</sup>, **Consalvey M**<sup>2</sup>, **Ramirez-Llodra E**<sup>3</sup>, **Glover A**<sup>4</sup>, **Menot L**<sup>5</sup>, **O'Hara T**<sup>6</sup>, **Metaxas A**<sup>7</sup>, **Thurber A**<sup>8</sup>, **Sweetman A**<sup>9</sup>, **Narayanaswamy B**<sup>10</sup>

<sup>1</sup> University of Southampton, UK, <sup>2</sup> NIWA, NZ, <sup>3</sup> Institut de Ciències del Mar, CSIC, Spain, <sup>4</sup> Natural History Museum, London, UK, <sup>5</sup> IFREMER, France, <sup>6</sup> Museum Victoria, Australia, <sup>7</sup> Dalhousie University, Canada

The International Network for Scientific Investigations of Deep-Sea Ecosystems (INDEEP) programme (currently funded by the Total Foundation until Dec 2013) follows in the footsteps of the Census of Marine Life programme (2000-2010). It is the intention of INDEEP to capture the momentum of collaboration generated during the Census decade to ensure it continues and grows in the long-term and includes future generations of deep-sea scientists. INDEEP is focusing on determining the global biodiversity and functioning of deep-sea ecosystems in order to achieve a synthesis of sound knowledge that can be used in the formation of sustainable management strategies, bridging the gap between science and policy. INDEEP is already leading to the development of new large-scale scientific proposals involving teams and infrastructure from different nations. INDEEP now has over 350 members from 32 countries and communication between these experts is progressing well. This presentation will outline the excellent progress and current activities of each of the 5 INDEEP working groups.





International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

**Tuesday 4<sup>th</sup> December**

**Biodiversity Pattern – Intermediate 3**

**BIOLOGY OF BATHYAL BENTHIC COMMUNITIES IN THE GULF OF CALIFORNIA: COMPARISON OF COLD, HYPOXIC WATERS IN THE GUAYMAS BASIN WITH WARM, OXYGENATED BASINS IN THE NORTHERN GULF**

Barry J<sup>1</sup>, Buck K<sup>1</sup>, Taylor J<sup>1</sup>, Lovera C<sup>1</sup>, Herlien R<sup>1</sup>, Whaling P<sup>1</sup>, Johnson K<sup>1</sup>, Gayton-Caballero A<sup>2</sup>, Tapia de la O Y<sup>2</sup>

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Unlike the Oxygen Minimum Zone (OMZ) across much of the N.E. Pacific where waters are cold (3–4° C) and hypoxic (< 10  $\mu\text{M O}_2$ ), hydrographic conditions in the deep (~900 m) basins of the northern Gulf of California are warm (11–12° C) and well-oxygenated (15–80  $\mu\text{M O}_2$ ). We compared faunal communities and metabolic rates of animals inhabiting the anomalous conditions in the Salsipuedes and Delfin basins (~900 m) in the northern Gulf of California, with communities in the OMZ of the Guaymas Basin, just 200 km away. In addition to warmer waters, the northern basins are far more turbid, owing to sediment suspended by rapid tidal currents. Benthic faunal communities in the north were depauperate compared to those in the Guaymas Basin, particularly in highly turbid areas. Measurements of oxygen respiration rates using an in situ respiration system were completed in the Guaymas Basin (batfish: Ogcocephalidae, *Dibranchus* sp.), Delfin Basin (sea star: Goniasteridae, *Mediaster* sp.), and Salsipuedes Basin (heart urchin: Spatangidae, *Spatangus californicus*). Metabolic rates the batfish were half to a third of similar sized sea stars, perhaps largely due to temperature. Even when standardized to 4 degrees C, sea star respiration rates were still 50% higher than the batfish. Lower metabolism in batfish was related to environmental hypoxia, with respiration rates correlated significantly to oxygen concentrations over an ambient range of 3–5  $\mu\text{M O}_2$ . These results suggest that hypoxic waters in the eastern Pacific constrain metabolism in batfish and other metazoans, likely leading to reduced growth, reproduction, or survival.





*Thursday 6<sup>th</sup> December*

*Human Impacts 2*

**GENETIC DIVERSITY OF THE COLD WATER CORAL *LOPHELIA PERTUSA* IN REEFS EXHIBITING DIFFERENT LEVELS OF ENVIRONMENTAL IMPACTS**

**Becheler R<sup>1</sup>**, Mouchel O<sup>1</sup>, Van Den Belt I<sup>1</sup>, Dahl MI<sup>2</sup>, Bourillet JF<sup>3</sup>, Arnaud-Haond S<sup>1</sup>

<sup>1</sup> EEP-LEP Ifremer, France, <sup>2</sup> Dept Marine Ecology, University of Gothenburg; Sweden, <sup>3</sup> GM-LES Ifremer, France

Cold-water corals are distributed worldwide. Some species, e.g. the scleractinian *Lophelia pertusa*, form reefs and structuring ecosystems that support a high biodiversity. Yet cold-water coral reefs are impacted by human activities, particularly bottom trawling, and threatened by climate change. The main goals of the present study are 1) the assessment of the level of genetic connectivity, to infer the degree of genetic and demographic interdependence and 2) the survey of genetic and clonal composition under a range of impact levels, to assess the influence of impact on genetic diversity, theoretically reflecting the evolutionary potential of the species to future environmental fluctuations. Samples were collected following a standardized procedure across geographic locations in the North Atlantic (30 sampling units for each site, a rectangle sampling area of 100\*200 m<sup>2</sup> and random coordinates; all the sampling units are geo-referenced), and genotyped using 9 microsatellite markers. Genetic and clonal diversity was estimated from the clonal discrimination based on microsatellites multi-locus genotypes. Results will be discussed on the light of the cross-cutting of those genetic data with the level of impact estimated through video analysis.



Monday 3<sup>rd</sup> December

Dispersal and Connectivity 2

## DISPERSAL ABILITIES OF HYDROTHERMAL VENT ANIMALS IN INDIAN OCEAN INFERRED FROM MITOCHONDRIAL DNA SEQUENCE

Beedessee G<sup>1</sup>, Watanabe H<sup>2</sup>, Ogura T<sup>2,3</sup>, Nakagawa S<sup>4</sup>, Nakamura K<sup>5</sup>, Takai K<sup>2,5</sup>, Koonjul M<sup>6</sup>, Daniel EPM<sup>1</sup>, Tamaki K

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\* Dedicated to Late Prof. Kensaku Tamaki

Dispersal ability is one of the main factors to maintain the species in spatially and temporally discrete environment of deep-sea hydrothermal vent fields. Dispersals of most animals in the mid-oceanic ridge systems are thought to be limited by geographical barriers such as trench, transform faults and microplates based on the population genetic analyses in the eastern Pacific vent fields. In the mid-oceanic ridge system in Indian ocean, the four hydrothermal vent fields, Kairei and Edmond fields near the triple junction, and Dodo and Solitaire fields in the Central Indian Ridge) have been discovered to date, and the phylogeographic analyses based on partial mitochondrial COI sequence was carried out for the four representative vent animals, *Alviniconcha* and scaly-foot gastropods, bythograeid crab *Austinograea rodriguezensis*, and alvinocaridid shrimp *Rimicaris kairei*, in these areas. Potentially high dispersal abilities, i.e. no genetic difference between several thousands of kilometers departed vent fields, were estimated for all the four analyzed species. The genetic diversities were relatively high in gastropods compared to the crustaceans, even in the swarmed *Rimicaris* shrimps. The dispersal strategies seemed to be different among the species, the present results on connectivity between the triple junction and the Central Indian Ridge vent fields may suggest strong physico-chemical factors independent to the ecological characteristics of the animals.



*Friday 7<sup>th</sup> December*

*Trophic and Process 4*

## **COMPARATIVE COMPOSITION, DIVERSITY AND TROPHIC ECOLOGY OF SEDIMENT MACROFAUNA AT VENTS, SEEPS AND ORGANIC FALLS**

**Bernardino A**<sup>1</sup>, Levin L<sup>2</sup>, Thurber A<sup>3</sup>, Smith C<sup>4</sup>

<sup>1</sup> Universidade Federal Do Espirito Santo, <sup>2</sup> Scripps Institution Of Oceanography, <sup>3</sup> Oregon State University, <sup>4</sup> University Of Hawaii

Sediments associated with hydrothermal venting, methane seepage and large organic falls such as whale, wood and plant detritus create deep-sea networks of soft-sediment habitats fueled, at least in part, by the oxidation of reduced chemicals. Biological studies at deep-sea vents, seeps and organic falls have looked at macrofaunal taxa, but there has yet to be a systematic comparison of the community-level attributes of sediment macrobenthos in various reducing ecosystems. Here we review key similarities and differences in the sediment-dwelling assemblages of each system with the goals of (1) generating a predictive framework for the exploration and study of newly identified reducing habitats, and (2) identifying taxa and communities that overlap across ecosystems. We show that deep-sea seep, vent and organic-fall sediments are highly heterogeneous. They sustain different geochemical and microbial processes that are reflected in a complex mosaic of habitats inhabited by a mixture of specialist (heterotrophic and symbiont-associated) and background fauna. Community-level comparisons reveal that vent, seep and organic-fall macrofauna are very distinct in terms of composition at the family-level, although they share many dominant taxa among these highly sulphidic habitats. Stress gradients are good predictors of macrofaunal diversity at some sites, but habitat heterogeneity and facilitation often modify community structure. The biogeochemical differences across ecosystems and within habitats result in wide differences in organic utilization (i.e., food sources) and in the prevalence of chemosynthesis-derived nutrition. In the Pacific, vents, seeps and organic-falls exhibit distinct macrofaunal assemblages at broad-scales contributing to  $\beta$  diversity. This has important implications for the conservation of reducing ecosystems, which face growing threats from human activities.



Friday 7<sup>th</sup> December

Conservation and Management 2

## IMPLICATIONS OF DEEP-SEA GENETIC CONNECTIVITY PATTERNS FOR THE MANAGEMENT OF BENTHIC ECOSYSTEMS IN THE NEW ZEALAND REGION: RECENT WORK AND FUTURE DIRECTIONS

Bors E<sup>1</sup>, Rowden A<sup>2</sup>, Maas E<sup>2</sup>, Clark M<sup>2</sup>, Shank T<sup>1</sup>

<sup>1</sup> Woods Hole Oceanographic Institution, Woods Hole MA, USA, <sup>2</sup> NIWA Greta Point, Wellington, New Zealand

Patterns of genetic connectivity are increasingly considered in the design of marine protected areas (MPAs) in both shallow and deep water. The methods used in connectivity research influence the spatial and temporal resolution of the results, raising questions about the relevance of such research to management decision-making.

We report results from recent genetic connectivity studies and analyses of plausible next steps for connectivity research in New Zealand's deep sea in the light of MPA design principles. In the New Zealand Exclusive Economic Zone, deep-sea communities at upper bathyal depths (<2000 m) are vulnerable to anthropogenic disturbance from fishing and potential mining operations. In our studies, mitochondrial cytochrome oxidase I and 16S rRNA genetic markers revealed patterns of genetic connectivity among populations of the squat lobster *Munida gracilis* and the polychaete *Hyalinoecia longibranchiata* from continental slopes, seamounts, and offshore rise habitats on the Chatham Rise, Hikurangi Margin, and Challenger Plateau. Contrasting patterns of genetic structure were observed for the two study species with significant population structure found among distinct populations of the polychaete worm on the Chatham Rise, the Hikurangi Margin, and the Challenger Plateau, and no significant structure among the sampled squat lobster populations. Results from this study will be discussed in the context of existing conservation areas in the New Zealand region. Possible next steps towards understanding management-relevant connectivity patterns will be highlighted.



Thursday 6<sup>th</sup> December

Reproduction and Population 1

**DISTRIBUTION, POPULATION STRUCTURE, REPRODUCTION, AND DIET OF *OPHIOLIMNA ANTARCTICA* (LYMAN, 1879) FROM KEMP CALDERA IN THE SOUTHERN OCEAN**

Boschen R, Tyler P, Copley J

University of Southampton, England, United Kingdom

A large population of *Ophiolimna antarctica* (Lyman, 1879) was discovered at 1546 m in Kemp Caldera, a topographic feature with active hydrothermal venting at the southern end of the South Sandwich Islands, Southern Ocean. The distribution, population structure, reproduction, and diet of *Ophiolimna antarctica* were investigated. *O. antarctica* were found predominantly on basalt with an over-dispersed distribution. The mean density was 17 individuals m<sup>-2</sup> with a range of 9–24 individuals m<sup>-2</sup>. There was a bimodal population structure, with separate juvenile and adult peaks. Sexes were separate and the sex ratio was not significantly different from equality. The maximum oocyte diameter was 520 µm, suggesting direct or lecithotrophic development, whilst individual females reproduced asynchronously. Stomach contents revealed a varied diet indicative of omnivory, including crustacean fragments, flocculate material, diatoms, forams, fish scales and ophiuroid tissue and spines. There was no influence of the nearby hydrothermal vents on the diet of *O. antarctica*. The ecology of *O. antarctica* is consistent with what is known for other Antarctic and deep-sea ophiuroid species.



*Friday 7<sup>th</sup> December*

*Conservation and Management 1*

**EVALUATION OF THE NEW ZEALAND MARINE ENVIRONMENT CLASSIFICATIONS USING INDEPENDENT DATA FROM CHATHAM RISE AND CHALLENGER PLATEAU.**

**Bowden D**<sup>1</sup>, Compton T<sup>2</sup>, Snelder T<sup>3</sup>, Hewitt J<sup>2</sup>

<sup>1</sup> NIWA, Wellington, <sup>2</sup> NIWA, Hamilton, <sup>3</sup> NIWA, Christchurch

Environmental classifications are potentially useful for summarising broad-scale patterns in faunal distributions when sample data are limited. Such classifications can be tuned with respect to specific faunal groups but they depend on the assumption that biological distributions are correlated with environmental gradients. Two marine environment classifications have been developed for New Zealand: the Marine Environment Classification (MEC) and the Benthic Optimised Marine Environment Classification (BOMECE). We used benthic invertebrate data from video and epibenthic sled samples collected during recent surveys to assess whether the MEC and BOMECE provide a reliable means of predicting benthic habitats and variations in community composition. First, we compared the environmental classifications with a set of 12 “biotic habitat” classes derived by clustering of the survey faunal data alone. Comparisons were made both visually and using chi-squared tests of goodness-of-fit. Second, using the full multivariate detail of the survey faunal data, we used ANOSIM R and homogeneity statistics to assess how well each classification grouped the survey sites at all classification levels up to 60 classes. Third, we compared how well each of the environmental classifications grouped the survey sites in relation to a suite of biodiversity metrics calculated from the survey data at each site. None of the classifications provided reliable information at the spatial scale of individual sample sites. At larger spatial scales, however (ca.100s km), they were broadly consistent with sampled benthic distributions, suggesting applications in regional-scale assessment of benthic habitats. For such environmental classifications to be useful in management applications, however, we conclude that objective criteria for determining appropriate, ecologically relevant, classification levels and spatial scales are needed.



Wednesday 5<sup>th</sup> December

Discovery 1

**SOJABIO (SEA OF JAPAN BIODIVERSITY) AND KURAMBIO (KURILE KAMCHATKA DEEP-SEA BIODIVERSITY) STUDIES – JOINT GERMAN-RUSSIAN DEEP-SEA INVESTIGATIONS IN THE WESTERN PACIFIC**

**Brandt A**<sup>1</sup>, Malyutina M<sup>2</sup>

<sup>1</sup> Zoological Museum of Hamburg, <sup>2</sup> Institute of Marine Biology, Vladivostok

Faunistic data from a newly designed camera-epibenthic sledge (C-EBS) are presented from two recent expeditions to the western Pacific. These were collected during the joint Russian-German expedition SoJaBio (Sea of Japan Biodiversity Studies) on board the RV Akademik Lavrentyev in summer of 2010 between 460 and 3,660 m depth. In total, 244,531 macro- and megafaunal individuals were sampled with the classes Malacostraca (36 %), Polychaeta (15 %) and Ophiuroidea (14 %) being most abundant. Within the Malacostraca, Peracarida (75,716 ind.) were most abundant and within these the Isopoda were the dominant taxon (27,931 ind.), however, only one isopod species was sampled at abyssal depths in the Sea of Japan but at very high abundance: *Eurycope spinifrons* Gurjanova, 1933 (Asellota: Munnopsidae). A German-Russian expedition with RV Sonne takes place in summer of 2012 in the Kurile-Kamchatka Trench (KKT) and adjacent abyssal plain. Aims of the expedition to the KKT region are to investigate the biodiversity and community patterns and compare the results with those from previous expeditions to the KKT and the deep semi-enclosed and younger Sea of Japan. In 1971 after few Russian expeditions to the KKT and Japanese Trench 103 species of Asellota were known deeper 1000 m including 76 new species from 29 stations of the 39<sup>th</sup> Vitjaz expedition in the KKT. These were 25% of the species known of the world fauna of Asellota deeper 1000 m at that time. Preliminary results of the Sonne cruise and a general comparison to the Sea of Japan will be presented.





Tuesday 4<sup>th</sup> December

Biodiversity Pattern – Intermediate 2

## A DEEP-SEA REEF COMMUNITY AT UNUSUALLY SHALLOW DEPTHS OFF NORTHEASTERN FLORIDA

Brooke S<sup>1</sup>, Ross S<sup>2</sup>, Quattrini A<sup>3</sup>, Watterson JC<sup>4</sup>

<sup>1</sup> Marine Conservation Institute, Bellevue, WA, <sup>2</sup> University of North Carolina at Wilmington, Wilmington, NC, <sup>3</sup> Temple University, Philadelphia, PA, <sup>4</sup> U.S. Dept. of the Navy, Norfolk, VA

During remotely operated vehicle (ROV) and multibeam sonar bottom surveys of the shelf edge and upper slope off north-eastern Florida, living colonies of the deep-sea scleractinian coral *Lophelia pertusa* and other typically deep-water organisms were observed in unusually shallow depths of 180–220 m. There was evidence of bioherm formation and abundant *L. pertusa* rubble in this area, which indicates relatively long term colonization. Hard substrata were also colonized by several species of octocorals, antipatharians and cup corals. The most common mobile invertebrates included sea urchins (*Echinus* sp., *Cidaris* sp.) and golden crabs (*Chaceon fenneri*). The most common hard-bottom fishes in this area were blackbelly rosefish (*Helicolenus dactylopterus*), the cutthroat eel *Dysommia rugosa*, shortbeard codling (*Laemonema barbatulum*), and deep-water reef fish in the genus *Anthias*. These species appear to be much more abundant and larger than observed in deeper waters, and could potentially be targeted by commercial fishing fleets. Bottom temperatures at this site were colder than expected at these depths (8–10° C) and were similar to those normally encountered at 400–600 m. The well-developed cold-water sessile community and the abundance of associated fauna suggest this site is a long-term feature, rather than short-term opportunistic colonization. The site occurs near or at the western wall of the Gulf Stream in an area known for frequent upwelling of deep, cold, nutrient rich water. Also, a long-term primary productivity envelope was documented in the area associated with the nutrient rich upwelling. These oceanographic features could explain the unusual occurrence of a deep-sea community at this site. Considering the unusual depth, long-term colonization by the corals, and the apparent productivity of benthic fauna, this site has been proposed as an expansion of the Stetson-Miami Terrace Coral Habitat Area of Particular Concern by the South Atlantic Fishery Management Council.





Monday 3<sup>rd</sup> December

Biodiversity Pattern – Large Scale 3

## COLD-WATER CORAL HABITATS IN NORWAY

Buhl-Mortensen P<sup>1</sup>, Buhl-Mortensen L<sup>2</sup>

<sup>1</sup> Institute of Marine Research, Bergen, Norway, <sup>2</sup> Institute of Marine Research, Bergen, Norway

Around 40 species of Norwegian anthozoans water are defined as corals. Only 12 of these can be regarded as habitat-forming. Here we present a new classification for coral habitats, together with a description of the environment and associated fauna. The main groups of corals: sea pens, gorgonians and scleractinians form a variety of habitats depending on species. *Lophelia pertusa* is the only scleractinian in Norway that forms cold-water coral reefs. These may occur as two different morphologies: elongated with an up-current living part, and semi-circular with multidirectional growth. In this presentation we discuss implications of reef morphology to the community ecology. Off Norway the mapping programme MAREANO has documented that different sea pen communities occur on different substrate types. In deep water (> ca 700m) the sea pen *Umbellula encrinus* may form habitats similar to sea pen habitats in troughs on the shelf and in fjords. Gorgonian corals form habitats with a rich associated fauna on different substrates. On hard bottom *Paragorgia arborea*, *Paramuricea placomus*, and *Primnoa resedaeformis* form hard-bottom coral gardens from relatively shallow depths (ca 30 m) in some fjords, down to the upper part of the continental slope (ca 700 m). Two types of soft bottom coral gardens can be found in Norwegian water, with *Isidella lofotensis* in the fjords and *Radicipes* sp. in deep slope areas between the Norwegian main land and Bear Island. Destructive effects of fishing have been documented in all of the coral habitats, but only cold-water coral reefs have yet been protected.



*Monday 3<sup>rd</sup> December*

*Biodiversity Pattern – Large Scale 2*

## **CLASSIFICATION OF DEEP-SEA HABITATS AND BIOTOPES OFF NORWAY**

**Buhl-Mortensen L<sup>1</sup>, Buhl-Mortensen P<sup>2</sup>**

<sup>1</sup> Institute of Marine Research, Bergen, Norway, <sup>2</sup> Institute of Marine Research, Bergen, Norway

Recognition of habitats and biotopes in deep water has traditionally been based on collected fauna from dredges, trawls and sleds. Due to large areas with little variation in topography and sediments, together with traditional sampling techniques, the deep sea has been perceived to have a homogeneous fauna. Visual inspections on rugged parts of the deep sea (e.g. mid oceanic ridges and canyons) however, show that this is not a general feature. Off the Norwegian coast the MAREANO programme has video-surveyed 945 locations in areas previously mapped with multibeam echosounder. Classification of the seabed habitats and biotopes was based on the composition of fauna and substrates documented by video. The main classes identified in the dataset show that the contrasting water bodies occurring off Norway explains the division of the fauna into a deep (> 700 m), cold (< 0.5°C), and a shallow, warm class. Subdivisions of these classes reflect different environmental settings in marine landscapes. Banks and troughs on the shelf are the major features comprising habitats with different substrates. Prominent examples are sea pens stands in troughs with soft substrates, and encrusting fauna on gravelly moraines and shallow banks. Certain sponge communities are prevailing in areas with higher sedimentation. Characteristic communities in deeper waters were: 1) filter-feeders (basket stars and cauliflower corals) along the shelf break, 2) upper slope, 3) lower slope, 4) canyon communities, and 5) the abyssal plain. We present subdivisions of these communities reflecting biotopes occurring at various spatial scales relating to substrates and habitat-forming species.



Tuesday 4<sup>th</sup> December

Autoecology 1

### **RIMICARIS EXOCULATA: ALL YOU WANT TO KNOW ABOUT A COMPLEX SYMBIOSIS**

**Cambon-Bonavita MA**<sup>1</sup>, Durand L<sup>1</sup>, Guri M<sup>2</sup>, Ponsard J<sup>3</sup>, Jan C<sup>4</sup>, Cueff-Gauchard V<sup>1</sup>, Jebbar M<sup>4</sup>, Compère P<sup>3</sup>, Shillito B<sup>5</sup>, Zbinden M<sup>5</sup>

<sup>1</sup> Ifremer DEEP/LMEE Ifremer centre de Brest BP70 29280 Plouzané France, <sup>2</sup> CNRS, LMEE, Technopôle Pointe du diable, Plouzané, France, <sup>3</sup> Université de Liège, Laboratoire de Morphologie fonctionnelle et évolutive, Liège, Belgium, <sup>4</sup> Université de Bretagne Occidentale, Plouzané, France, <sup>5</sup> UMR CNRS 7138, Systématique, Adaptations et Evolution, UPMC, Paris, France

*Rimicaris exoculata*, a hydrothermal shrimp, dominates the megafauna of some Mid Atlantic ridge sites. This species harbors a complex and rich community of bacterial epibionts inside its gill chamber and its digestive tract. To describe these two microbial communities, several approaches have been used, microscopy (SEM, TEM, FISH), molecular biology (16S diversity, functional genes research, metagenomic), as well as in vivo experiments.

Our data indicated wider gill chamber diversity than previously assumed with Epsilonproteobacteria lineages but also occurrence of Gammaproteobacteria (two lineages) and Zetaproteobacteria. We observed bacterial intracellular sulfur- and iron-enriched granules and some methanotrophic-like bacteria cells for the first time (1, 2). A shift is observed between the egg microbial population and the adult one (2). Genes, characteristic of methane-oxidizing (pmoA) and sulfide-oxidizing (APS) bacteria, were also identified. Metagenomic approach (3) revealed the carbon dioxide fixation via the rTCA and CBB cycle and results suggest that three metabolic types (iron, sulfide and methane oxidation) may co-occur within this community. According to in vivo experiments (4), evidence of exchanges from bacteria to the host was given by the first direct demonstration of nutritional transfers, this association being thus regarded as a true mutualism. The import of soluble microbial by-products does occur by permeation across the gill chamber integument rather than by the digestive pathway. Regarding the gut microbial community, our results indicated a wider permanent diversity than previously assumed and the presence of long microbial filaments directly in contact with gut epithelial cells inserted between microvillousities (5).

The authors thank the IFREMER, Région Bretagne, and Ouest Genopole, deep oases, CNRS, UBO, Belgian National Fund for Scientific Research and MAMBA project for their financial support.

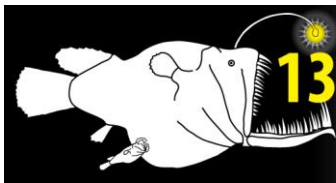
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International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

Thursday 6<sup>th</sup> December

Reproduction and Population 2

**POSTGLACIAL ISOLATION OF THE MEDITERRANEAN *CENTROSCYMNUS COELOLEPIS* REVEALS THE IMPORTANCE OF THE PILLARS OF HERCULES AS GEOGRAPHICAL BARRIER FOR DEEP SEA SHARKS.**

Catarino D<sup>1</sup>, Knutsen H<sup>2</sup>, Veríssimo A<sup>3,4</sup>, Sannæs H<sup>2</sup>, Jorde Per E<sup>2</sup>, Olsen E<sup>2</sup>, Menezes G<sup>1</sup>, Company JB<sup>5</sup>, Donavaro R<sup>6</sup>, Stefanni S<sup>1</sup>, Dell'Anno A<sup>5</sup>

<sup>1</sup> IMAR/DOP, University of the Azores, Horta, Faial, Portugal, <sup>2</sup> IMR, Institute of Marine Research, Flødevigen Marine Station, Arendal, Norway, <sup>3</sup> CIBIO, Research Center in Biodiversity and Genetic Resources, Vairão, Portugal, <sup>4</sup> VIMS, Virginia Institute of Marine Science, VA, USA, <sup>5</sup> CSIC, Institut de Ciències del Mar, Barcelona, Spain, <sup>6</sup> Department of Life and Environmental Sciences, Università Politecnica delle Marche, Ancona, Italy

The Portuguese dogfish (*Centroscymnus coelolepis*) is a medium size deep-water squaloid shark with a worldwide distribution. In the Mediterranean Sea the species inhabits deeper waters and the individuals here are substantially smaller and mature at younger age than their relatives in the Atlantic and Pacific Oceans. We used a combination of 11 microsatellite markers and a 554bp fragment of the mitochondrial DNA (mtDNA) Control Region (CR) to investigate the genetic population structure in this species. Eight sampling areas (United Kingdom, Azores, South of the Azores, Madeira, Portugal mainland, Mauritania, Mediterranean and Australia) were screened with microsatellites revealing an overall genetic heterogeneity within the study area, largely formed by a strong genetic barrier between the Atlantic and the Mediterranean Sea ( $F_{ST} = 0.1034$  to  $0.1307$ ,  $P < 0.001$ ). Within the Atlantic however, high levels of gene flow were detected ( $F_{ST} = -0.0016$  to  $0.0096$ ,  $P > 0.05$ ). Genetic heterogeneity between the Australian and the Atlantic collections was significantly different only for a few pairwise comparisons, with surprisingly low levels of genetic divergence given the large distance among the sampled areas ( $F_{ST} = 0.0000$  to  $0.0108$ ). The results from the mtDNA CR follow the same pattern as the microsatellite analysis, revealing no significant differences across Atlantic and Pacific oceans and a strong genetic barrier towards the Mediterranean Sea. The combined results from microsatellites and mtDNA suggests a single and isolated population of this deep-water shark species in the Mediterranean Sea which most likely became separated from the Atlantic population during the last glaciations when the Mediterranean deep-sea was colonized ca. 150 Ky ago.



*Tuesday 4<sup>th</sup> December*

*Biodiversity Pattern – Intermediate 1*

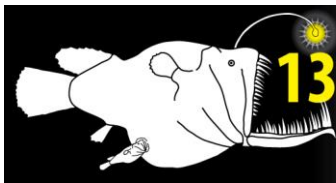
### **THE BIODIVERSITY AND ECOLOGY OF SENGHOR SEAMOUNT (N ATLANTIC)**

**Chivers A**<sup>1</sup>, Narayanaswamy B<sup>1</sup>, Lamont P<sup>1</sup>, Turnewitsch R<sup>1</sup>, Dale A<sup>1</sup>, Mair J.M.D. H<sup>2</sup>

<sup>1</sup> The Scottish Association for Marine Science, <sup>2</sup> Heriot-Watt University

Seamounts are often typified by highly rich and diverse communities of predominantly large suspension feeding organisms such as gorgonians and antipatharian corals, which are often the focus of seamount research. By comparison few studies have focused on the less enigmatic but no less important infauna. Morphologically diverse and often characterised by unique hydrodynamic regimes, seamounts provide a habitat for abundant and diverse macrofaunal communities, which, dependent upon local conditions may be typified by highly endemic fauna or widespread or cosmopolitan species. Communities may be influenced strongly by bathymetric gradients, shaping community structure, species diversity and standing stock in response to environmental gradients.

Senghor seamount is located in the northern Atlantic Ocean, 300 nm East of Senegal in the Cape Verde Archipelago. Macrofaunal sampling was undertaken during the R/V Meteor cruise M79/3 (November 2009). A multicorer and a boxcorer were used to take benthic macrofaunal samples from four transects (North, East, South and West), from the summit ~150 m to the base of the seamount ~3500 m. Macrofaunal standing stock appears to decline with depth across all transects from the summit to the base of the seamount in response to the decline of available organic material with depth. As expected, the macrofaunal communities are dominated by polychaetes at all depths, with the majority of remaining individuals characterized by a small number of classes such as tanaids, isopods and gastropods. Species diversity appears to reveal a parabolic relationship with depth, intermediate depths (1500 m) demonstrating highest species diversity.



International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

*Friday 7<sup>th</sup> December*

*Trophic and Process 4*

**INSIGHTS INTO THE TROPHIC ECOLOGY OF LARGE MESOPELAGIC FISHES FROM THE CENTRAL NORTH PACIFIC USING STOMACH CONTENT AND FATTY ACID BIOMARKER ANALYSES**

**Choy CA**<sup>1</sup>, Nichols PD<sup>2</sup>, Phleger CF.<sup>2</sup>, Drazen JC<sup>1</sup>

<sup>1</sup> University of Hawaii, Dept. of Oceanography, <sup>2</sup> CSIRO Marine and Atmospheric Research

Little is known about the basic biology and trophic ecology of large mid-trophic level mesopelagic fishes such as alepisaurids and gempylids. Over the past decade some of these species are increasing in abundance in the central North Pacific while commercially targeted tunas and billfishes have declined (Polovina et al. 2009). Whether or not these species all share a common (micronekton) prey base is unclear. Using traditional stomach content analysis (SCA) and fatty acid (FA) biomarker analysis in parallel, this study provides some of the first data on the trophic ecology of the mesopelagic fishes *Alepisaurus ferox*, *Lampris guttatus*, *Lepidocybium flavobrunneum*, *Gempylus serpens*, and information on their commercially targeted pelagic counterparts (*Thunnus obesus*, *T. albacares*, *Coryphaena hippurus*, *Xiphias gladius*).

~400 stomachs of *A. ferox*, *L. guttatus*, *L. flavobrunneum*, and *G. serpens* have been examined. All species consumed a variety of epipelagic and mesopelagic cephalopods, fishes and crustaceans and two species (*L. guttatus* and *A. ferox*) consumed substantial quantities of plastic debris.

FA profiles were created for eight species of predatory fishes and numerous species of potential micronekton prey (fishes, cephalopods, crustaceans, gelatinous organisms) collected from epi-/meso-/bathypelagic depths. FA profiles were also analysed in bulk zooplankton and suspended particulates across a large depth gradient. Initial analysis suggests strong groupings of FA profiles according to predator depth of forage/occurrence. We examine key trophic connections between predatory fishes and micronekton prey and contrast results between SCA and FA biomarkers, both of which provide unique perspectives to understanding trophic ecology in understudied deep ocean ecosystems.





*Friday 7<sup>th</sup> December*

*Conservation and Management 2*

## **CLOSED AREAS FOR DEEP-SEA HABITAT RECOVERY: A CASE OF SHUTTING THE DOOR AFTER THE HORSE HAS BOLTED?**

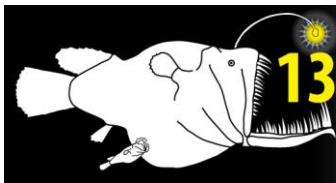
**Clark M**, Beaumont J, Stewart R, Rowden A, Bowden D

NIWA, Kilbirnie, Wellington, New Zealand

Deep-sea trawling typically uses heavy ground gear and nets that can cause considerable damage to benthic invertebrate communities on fishing grounds. This has been clearly documented for deep-sea corals such as *Lophelia pertusa* reefs in the North Atlantic Ocean, and their equivalent *Solenosmilia variabilis* on seamounts off New Zealand and Tasmania. An option for fisheries or environmental managers concerned with balancing sustainable fisheries with habitat conservation is to close areas that have been impacted, and allow the benthic communities to recover. In this paper we evaluate whether that is a realistic option.

Photographic surveys have been carried out on the "Graveyard Seamount Complex", a group of small deep-sea features off the east coast of New Zealand. They include seamounts that have been continually fished, fished and then closed to trawling, and never-trawled features. Comparable surveys have been conducted in 2001, 2006, and 2009. We present the results of this time series of surveys, building on a previous study that compared two-survey series off Tasmania and New Zealand. The more detailed analyses confirm that recovery is slow, at least on a time scale of decades. Spatial management needs to consider closing areas prior to any fishing impact, rather than after the event, if biodiversity is to be protected.





International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

**Friday 7<sup>th</sup> December**

**New Methods and Novel Techniques 4**

### **COLONIZATION EXPERIMENTS IN THE AZORES DEEP SEA**

**Colaço A<sup>1</sup>**, Carreiro e Silva M<sup>1</sup>, Hilário A<sup>2</sup>, Serrão Santos R<sup>1</sup>

<sup>1</sup> Larsys Center of IMAR from the University of Azores Department of Oceanography and Fisheries, Portugal, <sup>2</sup> Dept of Biology and CESAM, University of Aveiro

Our knowledge of deep-sea biodiversity has increased and changed in the last few years, partially because of the discovery and exploration of new ecosystems. The understanding of the functioning and interconnectivity between the different ecosystems is still scarce. Some of these newly discovered ecosystems are chemosynthetic based. The energy supply to these communities relies mostly on methane- and sulphide-oxidizing microbes, which are unique in their ability to satisfy their carbon and nitrogen needs from inorganic sources, and are capable of sustaining carbon-fixation for the whole community. Geophysical-driven emissions of these reduced compounds to the deep-seafloor (hydrothermal vents, methane seeps) are mostly ephemeral and discretely distributed. Similarly, massive organic inputs (carcasses, sunken wood) that harbour autotrophic symbioses closely related to the endemic vent and seep taxa are expected to induce sulphide enrichments over limited spatial and temporal scales.

We present the first results of a series of colonization designed to study several aspects of connectivity, biodiversity and functioning of different ecosystems in the Azores. During Hermione (EU-FP7) programme two types of colonization devices were deployed at Menez Gwen seamount (850 m) (which hosts an hydrothermal vent field, cold water coral reefs and gardens), at the Condor Seamount (850 m)(where an observatory-type studies are being developed, and that presents cold-water coral gardens and sponge massifs), and at Lucky Strike vent field (1700 m). One of the colonization devices consists of different substrates tied to the sides of a cage, the other are buckets filled with sterilized sediment sieved at 500  $\mu\text{m}$  with the substrates placed on top of the sediment. The experimental substrates were made of whale bone, wood, vent mussel (*Bathymodiolus azoricus*), *Charonia lampas* shells and coral skeletons (*Madrepora oculata* and *Errina dabneyi*). During the CARCACE project (FCT-QREN-COMPETE) a whale bone and a cow were sunken at the Condor seamount at 1000 meters.



*Tuesday 4<sup>th</sup> December*

*Sponsors Announcements*

## **THE INTERNATIONAL SEABED AUTHORITY AND MARINE SCIENTIFIC RESEARCH**

### **Cook A**

International Seabed Authority, Kingston, Jamaica

The International Seabed Authority is the international organization established as part of the United Nations Convention on the Law of the Sea through which governments organize and control activities related to the mineral resources in, and on, the seabed beyond national jurisdiction. These resources are currently polymetallic nodules, polymetallic sulphides and cobalt-rich crusts. Any mineral resource found in the future will also come under the remit of the Authority. As part of these activities the Authority has a responsibility to ensure effective protection for the marine environment from harmful effects which may arise from activities associated with mineral exploration and exploitation. In addition, the Authority has a role to promote and encourage the conduct of marine scientific research in the deep sea and to coordinate and disseminate the results of such research and analysis. Since its establishment in 1994, the Authority has made increasing efforts in this regard and some of these will be highlighted in the presentation along with some planned future activities including opportunities for collaboration with the marine scientific community.



*Tuesday 4<sup>th</sup> December*

*Biodiversity Pattern – Large Scale 4*

**PELAGIC FISH DISTRIBUTION OVER A MID-OCEAN RIDGE SYSTEM, WITH EVIDENCE OF DIEL VERTICAL MIGRATION BY THE BATHYPELAGIC FAUNA**

**Cook A**<sup>1</sup>, Sutton T<sup>1</sup>, Galbraith J<sup>2</sup>, Vecchione MI<sup>3</sup>

<sup>1</sup> Virginia Institute of Marine Science, College of William & Mary, Gloucester Point, VA, USA, <sup>2</sup> National Marine Fisheries Service, Northeast Fisheries Science Center, Woods Hole, MA, USA, <sup>3</sup> National Systematics Laboratory, National Marine Fisheries Service, National Museum of Natural History, Washington, DC, USA

The Census of Marine Life field project MAR-ECO aimed to understand the patterns and processes of the ecosystems associated with the northern Mid-Atlantic Ridge (MAR) between Iceland and the Azores. Initial expeditions in 2003 and 2004 were focused on mapping large-scale spatial distributions of deep-pelagic and demersal fauna. On a return expedition in 2009 we examined the diel vertical distribution of deep-pelagic fishes in a subarea of the MAR to understand the structure and connectivity of assemblages from the surface to 3000 m. Species composition, abundance/biomass, and diel vertical migration (DVM) patterns were characterized. A minimum of 75 species were collected, which represented eight assemblages as determined by multivariate analyses. The maximum in fish biomass was found below 1000 m, corroborating findings from the 2004 G.O. Sars expedition. The previously reported occurrence of bathypelagic taxa in the epipelagic zone was confirmed by sampling over a shallow seamount. Three major patterns of vertical distribution were observed: 1) a strong DVM was exhibited by zooplanktivorous fishes from the mesopelagic to the epipelagic at night; 2) several numerically dominant species were broadly distributed from 200 m to greater than 1000 m and showed no clear DVM; and 3) DVM by bathypelagic fishes into the mesopelagic zone was observed, contrary to expectation. This last finding may represent a previously unreported linkage explaining the occurrence of the bathypelagic biomass maximum observed over a mid-ocean ridge system.



*Thursday 6<sup>th</sup> December*

*Human Impacts 2*

**ROBERTS' REEF: AN ENIGMATIC COLD-WATER CORAL MOUND IN THE DEEP-, LOW-ARAGONITE-SATURATION-STATE GULF OF MEXICO.**

**Cordes E<sup>1</sup>**, Lunden J<sup>1</sup>, Georgian S<sup>1</sup>, Shedd W<sup>2</sup>, Roberts H<sup>3</sup>

<sup>1</sup> Temple University, <sup>2</sup> Bureau of Ocean Energy Management, <sup>3</sup> Louisiana State University

Deep-water corals will be among the first to feel the effects of ocean acidification. The continued shoaling of the aragonite saturation horizon will place deep-water coral reefs at risk in the near future. The deep-water coral *Lophelia pertusa* creates extensive reef-like structures between 300 and 600 m depth in the Gulf of Mexico, where aragonite saturation states are between 1.25 and 1.69. Among the recently discovered coral sites in the northern Gulf of Mexico is a cold-water coral carbonate mound with a nearly complete cover of living *L. pertusa* on the surface. Piston cores acquired on and off the mound reveal a pattern of episodic coral growth and mound formation. Water samples taken by ROV adjacent to the corals revealed elevated alkalinity and aragonite saturation state values, as compared to the generally low saturation state of the waters of the deep Gulf of Mexico. These anomalous alkalinity measurements may be attributed to the dissolution of carbonates in the mound's interior, and/or the subsurface oxidation of methane within the porous mound structure. This apparent alkaline seep in a relatively acidic body of water provides the opportunity for unique natural experiments on the effects of ocean acidification on scleractinian corals.



Wednesday 5<sup>th</sup> December

Discovery 2

## BIOLOGICAL ASSEMBLAGES OF THREE NEW MUD VOLCANOES ALONG DEEP-REACHING TRANSFORM FAULTS IN THE HORSESHOE ABYSSAL PLAIN (NE ATLANTIC)

Cunha MR<sup>1</sup>, Hilário A<sup>1</sup>, Vieira RP.<sup>1</sup>, Magalhães V<sup>2</sup>, Adão H<sup>3</sup>, Aranda da Silva A<sup>1</sup>, Ravara A<sup>1</sup>, Rodrigues C<sup>1</sup>, Terrinha P<sup>4</sup>, Hensen C<sup>5</sup>

<sup>1</sup> Departamento de Biologia & CESAM, Universidade de Aveiro, Portugal, <sup>2</sup> Departamento de Geociências & CESAM, Universidade de Aveiro, Portugal, <sup>3</sup> Universidade de Évora, Portugal, <sup>4</sup> Instituto Português do Mar e da Atmosfera & Instituto D. Luiz, Portugal, <sup>5</sup> IFM-GEOMAR, Germany

Previous work on the Gulf of Cadiz (S. Iberian Margin) has revealed several mud volcanoes sitting on the accretionary wedge and aligned along west-east trending transform faults. The source of fluids in these mud volcanoes is several kilometres below the seafloor and their geochemical composition indicates that they are affected, in different degrees, by oceanic crust alteration, implying that there is active flow connecting the oceanic basement and the seafloor. To date, such kind of hydrothermal circulation is only known for relatively young oceanic crust (< 60 Ma) and therefore the existence of a hydrological connection between old, sedimented oceanic crust and the seafloor is a phenomenon that may represent a (missing) link between hydrothermal vents at mid-ocean ridges and cold seeps at continental margins.

During the cruise M86/5 onboard RV Meteor, within the research program of SWIMGLO (PTDC/MAR/100522/2008), selected sites along the westward trending transform faults of the adjacent Horseshoe Abyssal Plain were investigated and three new mud volcanoes, Michael Ivanov, Abzu and Tiamat were discovered at ca. 4500 m depths on the lower continental rise. Initial findings showed the occurrence of chemosymbiotic metazoan hosts (*Acharax gadirae* and several *Frenulata* species) and a high diversity in meiofauna and macrofauna. Nematodes were particularly abundant but tanaids, amphipods, polychaetes and bivalves (Nuculanidae) were also well represented. An AUV survey further enabled mapping the distribution of *Frenulata* fields, bivalve shells and disturbed sediment patches on MV *Michael Ivanov*. The results are discussed in relation to previous knowledge on the Gulf of Cadiz seeps.



Thursday 6<sup>th</sup> December

Human Impacts 3

## BENTHIC FAUNA OF THE NAMIBIAN SHELF UNDER THREAT

Currie B<sup>1</sup>, Levin L<sup>2</sup>

<sup>1</sup> Namibian Ministry of Fisheries and Marine Resources, <sup>2</sup> Scripps Institution of Oceanography

The frequent incidence of hydrogen sulphide H<sub>2</sub>S on the inner shelf of Namibia's central coast, which presents in episodic bouts of hydrogen sulphide throughout the water column, is a characteristic and unique feature of the Northern Benguela upwelling regime. High concentrations of hydrogen sulphide occur in the surface sediments of the inner shelf, supporting mats of giant sulphide-oxidizing bacteria *Beggiatoa* and *Thiomargarita* species. Whilst recent research into the microbial sulphate reducing processes in these surface sediments has increased our knowledge of formation of the H<sub>2</sub>S, little is known of benthic faunal distribution, adaptations and responses in this extreme environment. Opportunistic benthic collections on the Namibian shelf sediments between 20°S and 27°S over the past four years reveal scanty and small-bodied benthic animals, comprising mainly polychaetes, molluscs and crustaceans with few echinoderms. Meiofauna comprises abundant nematodes and foraminifera. On the outer shelf and slope the size and penetration of benthic fauna increases. The distribution of faunal species is examined relative to biogeochemical parameters of overlying water column and surface sediment. Stable isotope data are being used to help characterize the macrobenthos role in shelf and slope food webs. Whilst interesting and in its infancy, study of the benthic environment and its role to the ecosystem has become urgent and critical due to intense pressures to remove sediment layers through dredge-mining Namibia's shelf sediments for phosphates.



*Thursday 6<sup>th</sup> December*

*Temporal Patterns 1*

## **A COMPARISON OF THE DAY TO DAY OF DEEP-SEA HYDROTHERMAL FAUNAL ASSEMBLAGES IN THE ATLANTIC AND THE NORTH-EAST PACIFIC – A MULTIDISCIPLINARY OBSERVATORY APPROACH**

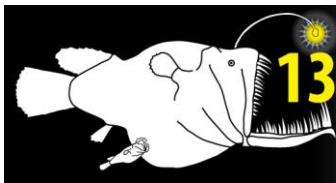
**Cuvelier D**, Sarrazin J, Laes A, Peton L, Sarradin MP

Ifremer, Centre de Brest, Department of Physical Resources and Deep-Sea Ecosystems (REM), France

Since the discovery of hydrothermal vents, our understanding of faunal vent assemblages is growing, however, their functional ecology and temporal dynamics remain less clear. Many critical features of these rapidly evolving ecosystems can only be understood through time-series observations. Several temporal variations studies have already been carried out at the Pacific and Atlantic hydrothermal vents but they are mostly based on yearly visits. The use of time-lapse cameras on the other hand has already demonstrated that sub-annual processes (e.g. semi-diurnal periodicities) also play a role in shaping hydrothermal vent communities and influencing their dynamics. Recently, the call from the scientific community for the development of novel techniques and approaches for studying the long-term temporal aspects of biotic and abiotic variables in different marine ecosystems has been put into practice through the installation of observatories.

An autonomous deep-sea observatory is currently up and running in the Atlantic Ocean (MoMAR at Lucky Strike on the Mid-Atlantic Ridge at 1700m depth) of which the ecological module (TEMPO) focuses on a hydrothermal *Bathymodiolus azoricus* mussel assemblage. Its first deployment took place in 2006 gathering video imagery, total dissolved iron concentrations (Fe) and temperature. Periodicities and rhythms in environmental variables spanning several months are unravelled using PCNM/MEM analyses, which decompose the time-series in sinusoidal waves. Significant scales and periods are thus revealed for all variables and tested within ecological models. Results on temporal variations for both fauna and environment are discussed. A similar module (TEMPO-mini), part of the cabled NEPTUNE observatory, was deployed in 2011 at 2186 m at Main Endeavour vent field in the northeast Pacific. The latter recorded imagery, temperature, Fe and oxygen of a *Ridgeia piscesae* tubeworm assemblage. Data analyses of similar time-spans between both modules will be presented, resulting in a first comparison of the dynamics at both ridges.





International

# 13<sup>th</sup> Deep-Sea Biology Symposium

Wellington, New Zealand 3 – 7 December 2012

*Tuesday 4<sup>th</sup> December*

*Evolution 2*

## **SPECTRAL TUNING IN THE EYE OF LANTERNFISHES (MYCTOPHIDAE).**

**de Busserolles F<sup>1</sup>, Hart N<sup>1</sup>, Hunt D<sup>1</sup>, Marshall J<sup>2</sup>, Collin S**

<sup>1</sup> University of Western Australia, <sup>2</sup> Queensland Brain Institute

Deep-sea organisms rely on different sensory systems for survival. In the mesopelagic zone, where the amount of light declines exponentially with depth and where bioluminescence predominates, vision becomes very important. However, in order to visualize objects in these low light conditions, and detect bioluminescent signals, the visual system of mesopelagic organisms is under tremendous selective pressure(s). Our study is focussed on visual specializations with respect to light (solar and bioluminescent) within the family Myctophidae. A yellow pigmented patch of retinal tissue was found in several species of lanternfishes that vertically migrate to the surface at night. The number, size, shape and position of this patch varies between species and in some cases was found to be sexually dimorphic. Following spectrophotometric studies, we confirmed that this pigmentation acts as a filter, absorbing short wavelengths (below 450 nm). At the level of the photoreceptors, microspectrophotometry and molecular biology revealed the presence of two rod visual pigments within a single type of photoreceptor (rods) with one pigments being long-wavelength-shifted. Several other deep-sea species possess lenticular yellow pigmentation, which is thought to enhance hue discrimination in some parts of the visual field, a selective advantage for detecting prey and predators. To our knowledge, this is the first observation of yellow retinal pigmentation in a deep-sea fish. The effect of this yellow pigment on the visual perception of these lanternfishes will be modelled and the results discussed in term of their ecology and behaviour.



Tuesday 4<sup>th</sup> December

Biodiversity Pattern – Intermediate 2

## BIODIVERSITY AND COMMUNITY COMPOSITION OF MACROFAUNA ASSOCIATED WITH MULTIPLE DEEP-SEA CORAL HABITATS IN THE GULF OF MEXICO

Demopoulos A<sup>1</sup>, Bourque J<sup>1</sup>, Frometa J<sup>2</sup>

<sup>1</sup> U.S. Geological Survey Southeast Ecological Science Center, Gainesville, FL, USA, <sup>2</sup> Jacobs Technology, Contracted to the U.S. Geological Survey, Southeast Ecological Science Center, Gainesville, FL, USA

Deep-sea scleractinian corals bioengineer a highly complex, three-dimensional substrate that can provide sheltered habitat, facilitate sediment accumulation and enhance colonization of encrusting fauna. While these systems can harbor significant levels of biodiversity, their community structure and function remain unclear. This work represents an ongoing study of the benthic ecology of deep-sea coral ecosystems (e.g., *Lophelia pertusa*) in the Gulf of Mexico (GOM) and is the first to quantitatively compare associated sediment macrobenthos (> 300 m). Study areas were located in three scleractinian habitats found at 350–500 m in the northern GOM within Bureau of Ocean Energy Management (BOEM) Lease Blocks VK826, VK906, and MC751. Using the ROV Jason II and submersible Johnson Sea-Link in 2009, quantitative in situ sediment cores were collected to compare taxonomic diversity, composition, and numerical abundance of macrofauna residing near deep-coral ecosystems to background communities residing in non-coral soft sediments. Macrofaunal diversity ( $H'$ ) was similar among all sampling locations. Densities ranged from 8,846 to 42,965 individuals  $m^{-2}$ , and were significantly greater near coral versus background sediments only at one site (VK826). However, community composition differed both among sites and between near-coral and background sediments. Polychaetes numerically dominated all samples, accounting for 70% of the total individuals near coral, whereas peracarid crustaceans were proportionally more abundant in the background cores (18%) than in those near coral (10%). Deposit-feeding polychaete families Oweniidae, Maldanidae, and Fauveliopsidae were more abundant near coral, accounting for 14% of the dissimilarity between the two habitats. Our results suggest that the enhanced habitat complexity associated with *L. pertusa* is supporting distinct communities in nearby soft sediments that differ from those reported from other deep-sea coral sites. The observed proximity effect suggests a turnover in benthic communities with distance away from the reef, the extent of which has yet to be determined.



*Thursday 6<sup>th</sup> December*

*Trophic & Process 1*

## **THE ROLE OF CARRION SUPPLY IN THE ABUNDANCE OF DEEP-WATER FISH OFF CALIFORNIA**

**Drazen J<sup>1</sup>, Bailey D<sup>2</sup>, Ruhl H<sup>3</sup>, Smith K<sup>4</sup>**

<sup>1</sup> University of Hawaii, <sup>2</sup> University of Glasgow, <sup>3</sup> University of Southampton, <sup>4</sup> Monterey Bay Aquarium Research Institute

Few time series of deep-sea systems exist from which the factors affecting abyssal fish populations can be evaluated. Previous analysis showed an increase in grenadier abundance, in the eastern North Pacific, which lagged epibenthic megafaunal abundance, mostly echinoderms, by 9–20 months. Subsequent diet studies suggested that carrion is the grenadier's most important food. Our goal was to evaluate if changes in carrion supply might drive the temporal changes in grenadier abundance. We analyzed a unique 17-year time series of abyssal grenadier abundance and size, collected at Station M, and reaffirmed the increase in abundance and also showed an increase in mean size resulting in a ~6 fold change in grenadier biomass. We compared this data with abundance estimates for surface living nekton (pacific hake and jack mackerel) eaten by the grenadiers as carrion. A significant positive correlation between Pacific hake (but not jack mackerel) and grenadiers was found. Hake seasonally migrate to the waters offshore of California to spawn. They are the most abundant nekton species in the region and the target of the largest commercial fishery off the west coast. The correlation to grenadier abundance was strongest when using hake abundance metrics from the area within 100 nm of Station M. No significant correlation between grenadier abundance and hake biomass for the entire California current region was found. Given the results and grenadier longevity, migration is likely responsible for the results and the location of hake spawning probably is more important than the size of the spawning stock in understanding the dynamics of abyssal grenadier populations. Our results suggest that some abyssal fishes' population dynamics are controlled by the flux of large particles of carrion. Climate and fishing pressures affecting epipelagic fish stocks could readily modulate deep-sea fish dynamics.



Thursday 6<sup>th</sup> December

Reproduction and Population 2

## SCAVENGING AMPHIPODS OF THE IBERIAN SUBMARINE CANYONS; A COMPARATIVE ANALYSIS AT THE COMMUNITY AND POPULATION LEVEL

Duffy G<sup>1,2</sup>, Horton T<sup>1</sup>, Shearer M<sup>2</sup>, Billett D<sup>1</sup>

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Submarine canyons have often been identified as hotspots of secondary production with the potential to house distinct faunal assemblages and idiosyncratic ecosystems. Within these deep-sea habitats, assemblages of scavenging fauna play a vital role in reintroducing organic matter from large food falls into the wider deep-sea food chain.

Free-fall baited traps were set at different depths within three submarine canyons on the Iberian Margin. Amphipods from the traps were identified to species level and counted. Scavenging amphipod assemblages were compared at different depths within each canyon, between individual canyon systems, and between the abyssal plain and submarine canyon sites. Samples from canyons were found to contain common abyssal plain species but in greater than expected abundances. Community composition differed significantly between the submarine canyons and abyssal plains. It is proposed that this is a result of the high organic carbon input into canyon systems owing to their interception of sediment from the continental shelf and input from associated estuarine systems.

Individuals of the dominant species, *Paralicella caperesca*, were dissected and measured to provide new insight into the population structure and reproductive ability of this understudied organism. These data were also used to compare the structure of populations from within submarine canyons to those of the abyssal plain.



*Friday 7<sup>th</sup> December*

*Conservation and Management 2*

## **COULD AN ORANGE ROUGHY FISHERY ACHIEVE MARINE STEWARDSHIP CERTIFICATION?**

**Dunn M**

NIWA, Wellington, New Zealand

Orange roughy fisheries are often held as one of the best examples of overfishing of a valuable, vulnerable, and long-lived deep sea fish. The history of orange roughy fisheries has been one of boom-and-bust, with fisheries depleted and then closed worldwide. Deep-sea trawl fisheries are also often highly damaging to benthic habitats. The Marine Stewardship Council (MSC) runs a third-party eco-labelling scheme that certifies fisheries as being adequately monitored and assessed, sustainable and environmentally responsible, and well managed. I will argue that, despite the apparent litany of failures, some existing orange roughy fisheries are close to satisfying MSC standards, and have the potential to be operated in a sustainable and environmentally responsible way.



*Friday 7<sup>th</sup> December*

*Conservation and Management 2*

**CONSERVATION ON THE HIGH SEAS – DEFINING ECOLOGICALLY AND BIOLOGICALLY SIGNIFICANT AREAS (EBSAS) IN THE SOUTH PACIFIC**

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CSIRO Marine and Atmospheric Research

The oceans cover 70% of the Earth's surface, and the majority of this area (or approximately half the Earth's surface) is in Areas Beyond National Jurisdiction (ABNJ). The international community provided a program of action for achieving sustainable development of the oceans, coastal areas and seas at the Rio Earth Summit in 1992 and in Johanassburg in 2002, however sustainable use of living resources on the high seas remains challenging. In 2008, the Conference of the Parties to the CBD adopted seven scientific criteria to identify ecologically or biologically sensitive areas (EBSAs) to enhance conservation and management measures and encouraged competent parties to conduct regional workshops. The first regional workshop held in Fiji in November 2011 was convened by the Secretariat of the Convention on Biological Diversity to identify potential EBSAs in the western South Pacific region. Experts from thirteen member nations of the Secretariat of the Pacific Regional Environment Programme, the Secretariat of the Pacific Community and eight international organisations identified 26 potential EBSAs in marine areas greater than 100 m deep. The workshop provided a successful first step in bringing together marine experts of this region to form partnerships that will continue to contribute to international efforts towards enhancing marine management and conservation. The workshop also identified an urgent need to facilitate capacity building in marine science and management in developing countries. In this paper we discuss the EBSA framework, the data for this region, results and lessons learned from this ABNJ conservation planning exercise, and look forward to future regional workshops.



*Tuesday 4<sup>th</sup> December*

*Biodiversity Pattern – Intermediate 3*

## **SPATIAL VARIATION IN THE MEGABENTHOS AT THE PORCUPINE ABYSSAL PLAIN**

**Durden J<sup>1</sup>, Ruhl H<sup>2</sup>, Bett B<sup>2</sup>, Billett D<sup>2</sup>**

<sup>1</sup> Ocean and Earth Science, University of Southampton, UK, <sup>2</sup> National Oceanographic Centre, Southampton, UK

Previous studies of the Porcupine Abyssal Plain (PAP) have focussed on temporal variability, and only very limited data have been available for robust spatial analysis. The PAP is not a homogeneous environment; it includes topographic highs (abyssal hills, 4600–4750 m depth) rising above the plain (4815 m depth), and variable concentrations of coarse sediments. Spatial heterogeneity in the megabenthos of the PAP in the relation to variations in sediment type and topography was assessed by analysing photographic transects, trawls, bathymetry and sediment core samples from eight locations around the PAP. Photos were analysed for faunal composition and biomass, lebenspurren density and seafloor coverage. Sediment particle size distributions at all sites were bimodal; ‘hill’ sites contained more coarse grains and fewer fine grains than ‘flat’ sites. Size distributions from different ‘flat’ sites were similar, but those from ‘hill’ sites were varied. Megafaunal communities at ‘hill’ sites had a higher abundance and diversity per area of sea floor than those at ‘flat’ sites. A greater proportion of filter feeders occurred at the ‘hill’ sites than at the ‘flat’ sites. An understanding of the spatial heterogeneity of these megabenthic communities will improve our understanding of time series analyses at the PAP and the extent to which abyssal time-series results can be extrapolated spatially.





*Friday 7<sup>th</sup> December*

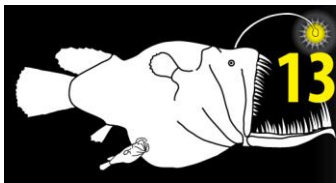
*New Methods and Novel Techniques 3*

#### **DEEP-SEA HARPACTICIDS: ARE CRYPTIC SPECIES A PROBLEM?**

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Whether species' ranges of deep-sea infauna are large or small is ecologically important. For example, if a species' range is on the scale of one thousand kilometers, students of the deep sea would want to evaluate how infauna are able to maintain genetic connectivity over such large distances. If species' ranges are on the scale of kilometers, then the deep sea harbors many species, and a student would want to evaluate how large numbers of similar species coexist in an environment that is considered relatively uniform and stable. Although species are traditionally identified by morphology, this approach can underestimate the true number of species present because of cryptic speciation. Similarly, DNA-sequencing techniques can underestimate the true number of species when inappropriate markers are used. For this study, we combined morphological and DNA-sequencing techniques to identify harpacticoid species present at eight stations spanning ~1500 km. We used the nuclear 18S ribosomal RNA gene and the mitochondrial cytochrome oxidase b gene to identify groups of harpacticoids that are genetically similar. By comparing these groups to independently identified morphological groups, we report the frequency of cryptic species among deep-sea harpacticoids and thus evaluate the utility of morphological characters alone to separate these species.



International

# 13<sup>th</sup> Deep-Sea Biology Symposium

Wellington, New Zealand 3 – 7 December 2012

Thursday 6<sup>th</sup> December

Plenary Presentation

## IMPACT TO DEEPWATER CORAL GARDENS FROM THE *DEEP WATER HORIZON* DISASTER

Fisher C<sup>1</sup>, Hsing P-Y<sup>1</sup>, Fu B<sup>1</sup>, Kaiser C<sup>2</sup>, Yoerger D<sup>2</sup>, Cordes E<sup>3</sup>, Roberts H<sup>4</sup>, Shedd W<sup>5</sup>, Shank T<sup>2</sup>, Cho W<sup>6</sup>, Larcom E<sup>1</sup>, Saunders M<sup>1</sup>, Brooks J<sup>7</sup>

<sup>1</sup> Pennsylvania State University, <sup>2</sup> Woods Hole Oceanographic Institution, <sup>3</sup> Temple University, <sup>4</sup> Louisiana State University, <sup>5</sup> Bureau of Ocean Energy Management, <sup>6</sup> Point Loma Nazarene University, <sup>7</sup> TDI Brooks International

The *Deepwater Horizon* disaster killed 11 men and by the time the Macondo well was capped more oil had been released into the marine environment than from any accidental oil spill in history. The effects of the oil that made it to the surface were often immediately apparent, although the long-term effects are still being studied. Determining the effects to deep-sea coral communities required an intensive and multidisciplinary effort, beginning with exploration to locate corals closer to the Macondo well, followed by documenting and quantifying the impact to the corals. As part of ongoing studies for the Bureau of Ocean Energy Management we conducted repeat visits to 10 known deep-water coral sites in October 2010, 6 months after the beginning of the spill. There was no apparent acute impact to corals at any of the sites >20 km from the Macondo well. However, we discovered a new site only 11 km away that exhibited widespread signs of recent deleterious impact in late 2010. Brown flocculent material removed from one coral contained hydrocarbons with fingerprints that match the oil from the Macondo well (White et al., 2012). Since that time we have continued our monitoring of the first impacted site we discovered and have documented some encouraging signs of recovery in some colonies as well as extensive tissue death and subsequent colonization of numerous other corals by hydroids. We have also conducted additional exploration using AUVs and towed camera systems, and discovered 6 additional sites with colonial coral communities that we have subsequently visited with ROVs. Some of these sites do not exhibit obvious and widespread signs of stress or impact, while at least one other does. This site is 13 km to the east of the other heavily impacted site and 6.5 km from the Macondo well.



Friday 7<sup>th</sup> December

Trophic and Process 3

**CROSS-BASIN HETEROGENEITY IN LANTERNFISH (FAMILY MYCTOPHIDAE) ASSEMBLAGES AND ISOTOPIC NICHES ( $\delta^{13}\text{C}$  and  $\delta^{15}\text{N}$ ) IN THE SOUTHERN TASMAN SEA ABYSSAL BASIN**

Flynn A<sup>1</sup>, Kloser R<sup>2</sup>

<sup>1</sup> Uni. Qld, CSIRO, Melbourne Museum, <sup>2</sup> CSIRO

A cross-basin (longitudinal) study of lanternfishes in the southern Tasman Sea abyssal basin during the austral winter of 2008 and 2009 found that mean biomass in the Western sector was higher than that in the Eastern sector, corresponding with cross-basin patterns in oceanographic heterogeneity and productivity. Dominant species over the abyssal basin differed from those previously recorded over the neighbouring continental slope. Vertical biomass profiles indicated diffuse night-time distributions in the Central sector and extensive diel vertical migrations in the Eastern sector. In the Western sector, macrocrustacean  $\delta^{13}\text{C}$  values were significantly higher, and  $\delta^{15}\text{N}$  significantly lower, than those in the Eastern sector. The results indicate a cross-basin difference in the primary productivity environment and  $^{15}\text{N}$  enrichment at the base of the foodweb. The cross-basin pattern in lanternfish  $\delta^{15}\text{N}$  values mirrored that for macrocrustaceans and was not correlated with standard length. Lanternfish  $\delta^{13}\text{C}$  values did not differ between sectors, but there were depth-wise differences, with values in the shallowest stratum (0–200 m) significantly higher than those in the deepest stratum (800–1000 m). Calculated trophic levels (TLs) of lanternfishes spanned the third trophic level and marked niche segregation was evident in the Eastern (mean TL 3.0–3.9) and Central (mean TL 2.5–3.6) sectors. Together, the results suggest that the Eastern and Western sectors are distinct sub-basin scale pelagic habitats, with implications for ecosystem modelling and future monitoring.



Tuesday 4<sup>th</sup> December

Autoecology 1

### SYMBIONT DIVERSITY IN THE TUBEWORM *RIDGEIA PISCESAE*: WHO'S IN, WHO'S OUT?

Forget N, Juniper SK

University of Victoria

Like many other symbiont-bearing species found at deep-sea hydrothermal vents, the northeast Pacific vestimentiferan tubeworm *Ridgeia piscesae* has no digestive system and relies on its association with chemolithoautotrophic bacteria for food. Most tubeworms harbour only one or two bacterial symbionts, and a study by Vrijenhoek (2010) suggests that only two gammaproteobacterial endosymbiont phylotypes exist among all vestimentifera examined to date, with a sequence divergence of around 4.3%. However, in the case of *R. piscesae*, morphological observations and limited molecular data suggested the presence of multiple symbionts in the trophosome. The goal of the present study was to test this hypothesis using a combination of 16S Sanger sequencing, 454 pyrosequencing and fluorescence in situ hybridization (FISH). Preliminary results suggest that most symbionts belong to the Gammaproteobacteria, followed by the Epsilonproteobacteria. Delta-, Alpha- and Betaproteobacteria phylotypes were also detected by Sanger sequencing, and pyrosequencing indicated the additional presence of a Bacteroidetes phylotype. Statistical analysis of the pyrosequences shows that symbiotic communities within adult tubeworms are more similar to each other than to symbiotic communities within new recruits, but no difference was detected between two contrasting tubeworm morphotypes ('short-fat' and 'long-skinny'). FISH confirmed the dominance of gammaproteobacterial symbionts in the *R. piscesae* trophosome and the presence of epsilonproteobacteria. We will also report a comparison of sequences obtained from free-living bacterial communities living in association with the tubeworm to determine the presence and relative abundance of the symbionts among free-living forms.



*Thursday 6<sup>th</sup> December*

*Temporal Patterns 1*

#### **EARLY SUCCESSION OF WHALE-FALL ECOSYSTEMS IN JAPANESE WATERS**

**Fujiwara Y<sup>1</sup>, Kawato M<sup>1</sup>, Miyazaki M<sup>1</sup>, Florence P<sup>2</sup>, Nagahori A<sup>1</sup>, Shinozaki A<sup>1</sup>, Yatabe A<sup>3</sup>, Maruyama T<sup>1</sup>**

<sup>1</sup> JAMSTEC, <sup>2</sup> IFREMER, <sup>3</sup> National Museum of Nature and Science, Tokyo

The deep sea is generally considered an oligotrophic environment with an average total organic carbon content in sediments of 0.5% by weight. Massive sporadic inputs of organic material into the deep sea, such as the recent oil spill in the Gulf of Mexico or the influx of terrigenous products transported by the tsunami in Japan, must have had a significant impact on the surrounding environments. Deadfalls of large nektonic animals are the more typical manner by which pulses of organic material reach the deep-sea floor. Whales contribute a large amount of organic material posthumously. The sediments directly underlying a sunken whale carcass experience an initial pulse of labile organic material equivalent to 2,000 years of background organic carbon flux. Little is known, however, about the decomposition process of sunken whale carcasses. Rare examples include two whale carcasses deployed off California. Aggregations of hagfish and some other scavengers have removed whale soft tissue at high rates (40–60 kg d<sup>-1</sup>). Here we conducted in situ deployments of whale carcasses in deep sea at depths from 500–1,000 m in Japanese waters. A swarm of pugnose eels was observed feeding on a sunken sperm whale carcass at a depth of 925 m in Sagami Bay. More than 90 % of soft tissues of the whale were consumed within 5 months of deployment and the estimated consumption rate was much higher than the previous studies. Another deployment of a baby sperm whale was also conducted at a depth of 489 m in the bay and detailed observations were performed immediately after the deployment. Results of time-lapse observations, physico-chemical measurements, and a time-series collection of vertical flux around the whale carcasses will be shown.



Thursday 6<sup>th</sup> December

Trophic and Process 2

## TROPHIC ECOLOGY OF DEEP-SEA ASTEROIDS FROM THE CONTINENTAL SLOPE OF EASTERN CANADA

Gale K<sup>1</sup>, Mercier A<sup>1</sup>, Hamel JF<sup>2</sup>

<sup>1</sup> Ocean Sciences Centre, Memorial University of Newfoundland, <sup>2</sup> Society for the Exploration and Valuing of the Environment

Asteroidea (sea stars) can be important predators in benthic communities and are often present in ecologically important and vulnerable deep-sea coral and sponge habitats. However, explicit investigations into the trophic ecology of deep-sea asteroids are rare. We investigated the diets of several species of deep-sea asteroid from the continental slope (~200–1500 m) of Newfoundland and Labrador, eastern Canada. Using a multifaceted approach, including live animal observations, stomach content analysis, and stable-isotope analysis, we present strong evidence that corals and sponges are common food items for two of our focal species, the deep-sea asteroids *Hippasteria phrygiana* and *Ceramaster granularis*. During experimental feeding trials, live *H. phrygiana* fed on several species of deep-sea soft coral and *C. granularis* fed on subtidal encrusting sponges. Gut content analysis of wild-caught individuals revealed sclerites from sea pens (e.g. *Pennatula* sp.) in the stomachs of both asteroid species. *H. phrygiana* also contained sclerites from at least two other species of octocoral and siliceous sponge spicules were present in the stomachs of *C. granularis*. The stable-isotope signatures ( $\delta^{15}\text{N}$  and  $\delta^{13}\text{C}$ ) of *H. phrygiana* and *C. granularis* are characteristic of high-level predators, with both species showing  $\delta^{15}\text{N}$  values ~4 ‰ (one trophic level) above four other asteroid species studied here and above published values for deep-sea corals in our study region. This study, which highlights the potential importance of sea stars as predators in deep-sea coral and sponge communities, is the first investigation of the diet and ecology for *Ceramaster granularis*, and the first for deepwater *Hippasteria phrygiana*.



*Thursday 6<sup>th</sup> December*

*Human Impacts 3*

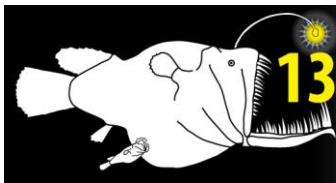
**THE SERPENT PROJECT: EXPLORING DEEP-SEA LIFE, ANTHROPOGENIC DISTURBANCE AND RECOVERY AT HYDROCARBON EXPLORATION SITES**

**Gates A, Jones D**

National Oceanography Centre

The SERPENT Project collaborates with industry to enable access to ROVs operating in deep water at hydrocarbon exploration locations. Over the ten years the project has been established, opportunistic observations and targeted visits to deep-sea drilling locations have increased the scope for biodiversity observations in the deep sea. The project has gathered samples and high resolution video and images at 100–3000 m depth from oil rigs and other industry infrastructure globally, among which have been many valuable records and behavioural insights. Some highlights are shown here. These locations are subject to physical disturbance from exploration drilling. Our study of 20 sites in the North-East Atlantic (Faroe-Shetland Channel and Norwegian Sea) shows that best practice exploration drilling consistently results in significantly reduced megafaunal abundance and diversity within 100 m of the source of disturbance. At three locations we show evidence for recovery of megafaunal assemblages. Close to the well, however, reduced diversity and abundance persists after 3 and 10 years highlighting the need for increased efforts to understand the impacts to the deep sea and the factors affecting recovery.





International  
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**Tuesday 4<sup>th</sup> December**

**Trench 2**

**EVOLUTIONARY RELATIONSHIPS IN TRENCH SPECIES OF THE GENUS *ELPIDIA* (HOLOTHUROIDEA, ELASIPODIDA, ELPIDIIDAE)**

**Gebruk A, Rogacheva A**

P.P. Shirshov Institute of Oceanology

Holothurians of the genus *Elpidia* are typical representatives of the ocean trench fauna. The genus comprises 22 species, of which 12 are endemic to trenches. Belyaev (1975) designated several species groups in the genus based mainly on the morphology of spicules. One of proposed groups included the trench species *E. kurilensis*, *E. birsteini* and *E. longicirrata*. The first occurs in the Aleutian, Kuril-Kamchatka and Japan Trenches. The second is known from the Kuril-Kamchatka and Idzu-Bonin, and the third occurs only in the Kuril-Kamchatka Trench.

We examined the phylogeny of the genus *Elpidia* based on matrix comprising 20 morphological characters coded for 22 terminal taxa, including 21 species of *Elpidia* and the outgroup taxon, *Psychroplanes convexa*. The strict consensus tree was obtained for four equally parsimonious trees (length = 33 steps).

Our results show that all species endemic to trenches group into a clade well derived on the phylogenetic tree. Within this clade supported by one clear synapomorphy, *E. kurilensis*, *E. birsteini* and *E. longicirrata* group together confirming the assumption of Belyaev. This group is the strongest supported on the consensus tree after the clade of the Arctic species of *Elpidia*. *E. hanseni* occurring in the Kuril-Kamchatka and Idzu-Bonin Trenches stays outside the clade of the north-west Pacific trench species. One more 'trench clade' is formed by *E. ninae* and *E. lata*, both occurring in the South-Sandwich Trench. Our data demonstrate that 1) the trench species in the genus *Elpidia* are most derived morphologically, and 2) evolutionary relationships among species occurring in the same or nearby trenches can be different: some species are closely related, others evolve separately.



*Monday 3<sup>rd</sup> December*

*Biodiversity Pattern – Large Scale 1*

**ABYSSAL SPECIES ARE EVERYWHERE – GEOGRAPHICAL DISTRIBUTION OF BENTHIC COPEPODA IN THE DEEP SEA**

Menzel L<sup>1</sup>, George KH<sup>2</sup>, Martínez Arbizu P<sup>2</sup>

<sup>1</sup> Senckenberg am Meer Wilhelmshaven, Abt. DZMB, <sup>2</sup> Senckenberg am Meer Wilhelmshaven, Abt. DZMB

Copepoda Harpacticoida are considered to be primarily bound to the sediment and to show limited mobility, since adults as well as juveniles of most species dwell in the sediment and are poor swimmers. Land masses and undersea mountain ranges are therefore considered to prevent species from dispersing. Nevertheless, some abyssal species of Harpacticoida have been recorded from mutually distant regions. However, investigations of large-scale species distribution patterns of Harpacticoida came to the fore only in recent years. Our extensive biogeographical studies are based on the largest data set on the distribution of deep-sea meiofauna at the species level. We included twelve regions in the South Atlantic, the North Atlantic, the Southern Ocean, the southern Indian Ocean, the Pacific Ocean, and the eastern Mediterranean Sea with altogether more than 4,000 specimens belonging to the Argastidae Por, 1986, one of the most abundant families of Copepoda Harpacticoida in the deep sea. The very wide, or even worldwide distribution of many abyssal species of Copepoda Harpacticoida showed that neither the topography of the sea bottom nor long distances seem to prevent species from dispersing in the deep sea.



**Tuesday 4<sup>th</sup> December**

**Trench 2**

## **HIGH TRIMETHYLAMINE OXIDE CONTENTS IN HADAL SNAILFISH (LIPARIDAE) INDICATE A DEPTH LIMIT FOR TELEOST FISHES**

**Gerringer M**<sup>1</sup>, Jamieson A<sup>2</sup>, Rowden A<sup>3</sup>, Drazen J<sup>4</sup>, Yancey P<sup>1</sup>

<sup>1</sup> Whitman College, USA, <sup>2</sup> University of Aberdeen, UK, <sup>3</sup> National Institute of Water and Atmospheric Research, New Zealand, <sup>4</sup> University of Hawai'i, USA

Trimethylamine N-oxide (TMAO), a protein-stabilizing osmolyte in many marine animals, occurs at only 40–70 mmol/kg in shallow-living teleost fishes, which, as osmoregulators, have much lower internal osmolalities than seawater (about 350 vs 1100 mosmol/kg for 35 ppt seawater). However TMAO has been found to increase with depth in muscles of numerous teleost families, reaching 261 mmol/kg in a macrourid from 4850 m. TMAO may be a 'piezolyte' ('pressure solute') because it can stabilize proteins against perturbations by hydrostatic pressure. Moreover, extrapolation of TMAO contents suggests that teleosts would become isosmotic at 8000–8500 m, perhaps explaining why no teleosts have been found below 8500 m. To test this hypothesis, five hadal liparids (*Notoliparis kermadecensis*; Kermadec snailfish) were caught by free-falling lander in the Kermadec Trench at 7000 m. Analysis revealed muscle TMAO to be  $423 \pm 42$  mmol/kg, fitting well with the extrapolation and consistent with the piezolyte hypothesis. We also measured osmolalities of liquid extracted from crushed muscles of the liparid and of fish previously collected from 500 to 3000 m in Monterey Bay (7 species, 3 families). Osmolalities of the latter increased with depth as predicted from TMAO contents ( $\text{mosmol/kg} = 326 + 0.0916 \cdot \text{depth}$ ;  $P < 0.0005$ ), extrapolating to isosmotic 1100 mosmol/kg at 8450 m. The liparid was almost isosmotic at  $1027 \pm 29$  mosmol/kg, supporting the hypothesis that TMAO accumulation sets the depth limit for teleosts at 8500 m or less.

Funding: Total Foundation (France) and National Science Foundation (USA).



*Wednesday 5<sup>th</sup> December*

*New Methods and Novel Techniques 2*

## **WHAT DO DEEP-SEA ANIMALS DO? A NEW FUNCTIONAL TRAIT CLASSIFICATION FOR DEEP-SEA FAUNA**

**Glover A**

The Natural History Museum, London

Biologists are under increasing pressure to demonstrate the value of deep-sea biodiversity to society. One important value is the functional role that biodiversity plays in maintaining ecosystem services. To study the 'function' of biological communities, we must investigate what it is that species actually do. That is, what is their ecological role in interacting with the environment and with other species – their functional traits. It is often assumed that we know rather little about the functional traits of deep-sea species, but this is to ignore 130 years of collecting and investigating. We have resolved to gather together available data in a new classification of functional traits for deep-sea species, and to make this available to the community for biological trait analysis. These classifications could be applied to combined faunal datasets to study, for example, the potential impacts of climate change on deep-sea ecosystem function.



Tuesday 4<sup>th</sup> December

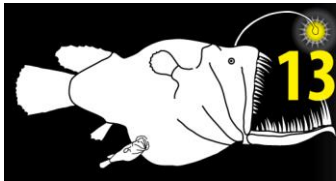
Biodiversity Pattern – Intermediate 3

## HARD-SUBSTRATE COLONIZATION EXPERIMENTS PROVIDE INSIGHT INTO MACROFAUNAL COMMUNITY PATTERNS AT EAST PACIFIC METHANE SEEPS

Grupe B<sup>1</sup>, Levin L<sup>1</sup>, Mendoza G<sup>1</sup>, Thurber A<sup>2</sup>

<sup>1</sup> Scripps Institution of Oceanography, <sup>2</sup> Oregon State University

Methane seeps are heterogeneous environments characterized by variation in reduced fluid flow, chemoautotrophy, specialized macrofauna, and a patchwork of hard substrate and soft sediment habitats. We asked which types of heterogeneity contribute to community and trophic patterns on hard substrates, which are much less studied than seep sediments. We deployed experimental substrates at Hydrate Ridge (Oregon margin) and Mound 12 (Costa Rica margin) for ten and thirteen months, respectively, testing the hypotheses that active fluid flow and substrate type structure communities at seeps. The substrates (seep carbonates, wood, bones, shells/tubes) mimicked those available in natural chemosynthetic ecosystems, and we predicted that the community trajectory on experimental carbonates would be most likely to resemble the in situ community. Fluid flow had a stronger effect on the community than substrate type and spatial effects at both locations. Gastropods, which dominate and graze upon bacteria on seep carbonates, rapidly colonized active substrates, reaching or surpassing in situ densities. Substrate type had a secondary effect on community development, and was mainly evident at Hydrate Ridge (*Osedax* colonizing bone, *Xylophaga* colonizing wood), while at Mound 12, carbonates and wood had similar communities with faunal isotopic patterns distinct from those on natural carbonates. Biodiversity was higher on active relative to inactive carbonates, while experimental substrates displayed opposite patterns with relatively high dominance and low diversity near active fluid flow. Results of these experiments indicate that community succession — and potentially recovery from disturbance — likely plays out over multiple years, which has implications for human activities on continental margins.



International

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*Tuesday 4<sup>th</sup> December*

*Biodiversity Pattern – Intermediate 2*

## **METAZOAN BIODIVERSITY PATTERNS OF THE DEEP-SEA WATER COLUMN**

**Haddock S<sup>1</sup>, Kiko R<sup>2</sup>**

<sup>1</sup> MBARI, <sup>2</sup> IFM-GEOMAR

We analyzed video records of 38 ROV dives with maximum depths of 2005 to 3973 m, spanning ten years of observations (2002–2011). These dives had been annotated to include 286,000 records of midwater organisms considered as taxonomic units (some to family, some to species). Each dive contained between 78 and 186 unique taxonomic concepts, allowing us to evaluate biodiversity of the bathypelagic realm in relation to shallower depths. We will apply a variety of diversity metrics to these data, including traditional measures and the Chao estimators, based on rarefaction. Patterns to be observed are differences in functional groups with depth, effects of the oxygen-minimum zone on diversity, and trends in water-column diversity with depth: whether it decreases or increases, and if trends appear continuous or punctuated.



*Monday 3<sup>rd</sup> December*

*Evolution 1*

## **EVOLUTIONARY HISTORY AND BIOGEOGRAPHICAL PATTERNS OF BARNACLES FROM HYDROTHERMAL VENTS**

**Herrera S**<sup>1,2</sup>, **Shank T**<sup>1</sup>

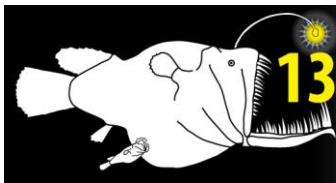
<sup>1</sup> Biology Department, Woods Hole Oceanographic Institution, Woods Hole, MA, USA, <sup>2</sup> MIT-WHOI Joint Program in Oceanography, Massachusetts Institute of Technology, Cambridge, MA, USA

Barnacles are some of the most conspicuous organisms in hydrothermal-vent ecosystems worldwide. Populations can reach extremely high densities, over one thousand individuals per meter square, and aggregations provide an important component to the flow of energy through ecosystems. Most putative barnacle species are endemic to particular ridge segments and arc basins, which suggests a role of habitat discontinuity as an important mechanism of speciation. The south-western Pacific region hosts the highest richness of putative chemosynthetic barnacle species and can be considered the center of chemosynthetic barnacle distribution.

Molecular phylogenetic analyses indicate that barnacles from chemosynthetic ecosystems form a monophyletic clade, suggesting that this group colonized these environments only once in recent evolutionary history. However, the relationships among more recently discovered morphospecies of vent barnacles remain unresolved. Given that barnacle species and populations are mostly restricted to contiguous vent fields, they represent a model to examine historical biogeographic patterns of origin, dispersal, and colonization of modern chemosynthetic fauna.

We utilized mitochondrial and nuclear genetic variants to examine the phylogenetic relationships of barnacle specimens collected from chemosynthetic environments throughout most of their currently known distribution. We will present a hypothesis of the evolutionary history of this group and will discuss it in terms of recently proposed biogeographical hypotheses for vent fauna. We will also present results of finer-scale genetic structure analyses performed with next-generation restriction-associated DNA sequencing data of populations from the recently discovered East Scotia Rise vent ecosystems.





International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

**Friday 7<sup>th</sup> December**

**PLENARY PRESENTATION**

## **HOW FAR DO LARVAE GO: DISPERSAL AND MPA DESIGN IN THE DEEP-SEA**

**Hilário A<sup>1</sup>, Metaxas A<sup>2</sup>, Colaço A<sup>3</sup>, Gollner S<sup>4</sup>, Levin L<sup>5</sup>, Mercier A<sup>6</sup>, Mestre N<sup>3</sup>, Ribeiro P<sup>3</sup>**

<sup>1</sup> Department of Biology & CESAM, University of Aveiro, Portugal, <sup>2</sup> Department of Oceanography, Dalhousie University, Canada, <sup>3</sup> Center of IMAR of the University of Azores, Department of Oceanography and Fisheries & LarSyS, Portugal, <sup>4</sup> DZMB Senckenberg Institute, Germany, <sup>5</sup> Center for Marine Biodiversity and Conservation, Scripps Institution of Oceanography, USA, <sup>6</sup> Ocean Sciences Centre, Memorial University of Newfoundland, Canada

One of the most challenging aspects of deep-sea ecology is to elucidate the processes that lead to specific geographic patterns in species distributions and the boundaries among ecosystems. One such process is connectivity amongst populations, which ensures gene flow and is essential in maintaining populations size and function, and in the recovery of populations from natural or anthropogenic disturbances. Population connectivity is therefore an integral part of the design of Marine Protected Areas (MPAs) since, to be effective: (1) they must act as sources of new individuals to other populations, mainly through larval dispersal; and (2) local larval supply and recruitment will ensure the recovery of closed areas/populations.

INDEEP (International network for Scientific investigation of deep-sea ecosystems), has brought together a team of biologists and oceanographers to address the issue of population connectivity within and across different deep-sea habitats. Here, we assess the current knowledge of direct observational and experimental estimates of larval duration in deep-sea populations in different habitats. Larval dispersal patterns along depth gradients and across basins and habitats will be examined for different taxa, and dispersal rates will be compared with rates from the closest taxonomic relatives that live in shallow water to determine whether they are taxonomically conserved (and could thus be extrapolated where data are scarce). We will incorporate larval duration in biophysical models, which include oceanographic data to estimate dispersal distances and pathways in the deep sea. Because the role of population connectivity in MPA design in shallow waters is relatively well established, larval dispersal distances in the deep sea will be compared with those in shallow systems. This will allow INDEEP to make recommendations on strategies for implementing MPAs in the deep sea.



*Thursday 6<sup>th</sup> December*

*Reproduction and Population 1*

## **LIFE HISTORY STRATEGIES IN OCEANIC SQUID**

**Hoving HJ**

Monterey Bay Aquarium Research Institute

The oceanic pelagic realm, the largest living space on our planet, is inhabited by a wide variety of cephalopods. Of the oceanic cephalopods, squids dominate the epi- meso- and bathypelagic zones, and their diversity peaks between 500 and 1500 m. Diversity at the family and generic levels is very high with 24 families and 69 genera, and 215 described squid species. Despite the importance of oceanic squid in marine foodwebs worldwide, knowledge on their life history strategies is biased towards commercially exploited epipelagic species, especially from the family of flying squid (Ommastrephidae). Species from these families only comprise ~10% of currently known squid species and are characterized by a high growth rate, a short lifespan (1 year or less) and repeated spawning in a short period at the end of the individual's life. Scientific evidence is accumulating that the life history strategies of members of the other 90% of oceanic squid species do not always follow this paradigm. In this talk I will present an overview of life history strategies of oceanic squid. I will correlate species' spawning strategies (synchronous or repeated spawning) and longevities with the depth of reproduction, in order to analyze if and how the adopted life history strategies of squid species change with increasing depth of occurrence. Deep-sea squid do not necessarily live life in the fast lane.



*Monday 3<sup>rd</sup> December*

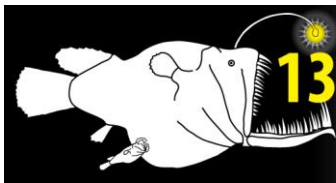
*Dispersal and Connectivity 1*

**INVESTIGATING POTENTIAL LARVAL DISPERSAL FROM A NE ATLANTIC SEAMOUNT (ANTON DOHRN) USING A LAGRANGIAN PARTICLE TRACING MODEL.**

Howell K<sup>1</sup>, Kirby I<sup>1</sup>, Nimmo-Smith A<sup>1</sup>, Read J<sup>2</sup>

<sup>1</sup> Plymouth University, <sup>2</sup> National Oceanography Centre, Southampton

Deep-sea population connectivity is poorly understood yet is central to developing our understanding of biogeography, biodiversity, speciation, and evolution of the deep-sea fauna. Seamounts provide a natural experimental setting in which to test questions relating to connectivity of populations as they are spatially isolated. They are also interesting systems in their own right with claims they act as stepping stones for larval dispersal and sources for neighbouring slope sinks. Potential connectivity of populations of a generic sessile benthic species with a lecithotrophic larva with a planktonic duration of 100 days was investigated. Larval movement to and from the Anton Dohrn Seamount (ADS) was simulated using a particle tracer model coupled to an oceanographic model. Larvae were released from 8 positions (corresponding to equally spaced compass points), at three depth bands (600, 1000, 1500 m), at monthly intervals over a 12-month period. The results suggest that populations on ADS are connected to the continental slope and neighbouring raised topographic features but only for species with a plankton larval duration of >50 days. The continental slope is the source of larvae to the seamount but Rosemary Bank, Lousy Bank and Rockall Bank are larval sinks. Population connectivity at the seamount is depth dependant with populations at mid slope (bathyal) depths becoming increasingly isolated as a result of poor larval dispersal potential via slower currents. These data suggest that seamounts may act a stepping stones for larval dispersal from the continental slope and as centres of speciation at mid slope depths.



International

# 13<sup>th</sup> Deep-Sea Biology Symposium

Wellington, New Zealand  3 – 7 December 2012

*Tuesday 4<sup>th</sup> December*

*Trench 2*

## **ABYSSAL AND HADAL BAIT-ATTENDING COMMUNITIES OF THE KERMADEC TRENCH (SW PACIFIC)**

**Jamieson A**<sup>1</sup>, Lacey N<sup>1</sup>, Piertney S<sup>1</sup>, Rowden A<sup>2</sup>, Clark M<sup>2</sup>

<sup>1</sup> University of Aberdeen, <sup>2</sup> National Institute of Water and Atmospheric Research

The Kermadec Trench, situated off the Northeast coast of New Zealand is one of only five hadal trenches that exceed 10,000 m. Within the HADEEP projects, three expeditions using baited cameras and traps have taken place with another two expeditions planned for 2013. This presentation will provide an overview of the biological sampling effort in the ultra-deep waters off New Zealand and report on various highlights including, amongst others, the first finding of the supergiant amphipod *Alicella gigantea* (Allicellidae) in the southern hemisphere, the first samples of the snailfish *Notoliparis kermadecensis* (Liparidae) in 59 years, and analysis of the scavenging-amphipod communities within the trench and in a trans-Pacific context. Furthermore, using the Kermadec Trench as a case study, we explore how the trench environment influences the distribution of benthic fauna.



Thursday 6<sup>th</sup> December

Trophic and Process 2

## DIFFERENCES IN BENTHIC FOOD-WEB STRUCTURE UNDER TWO CONTRASTING PRODUCTIVITY REGIMES: NE ATLANTIC VS W. MEDITERRANEAN.

Jeffreys R<sup>1</sup>, Lavaleye M<sup>2</sup>, Bergman M<sup>2</sup>, Duineveld G<sup>2</sup>

<sup>1</sup> University of Liverpool, <sup>2</sup> Royal Netherlands Institute of Sea Research (NIOZ)

Understanding food-web dynamics is central in comprehending ecosystem structure and function. To determine how food-web dynamics respond to differences in food supply, an accurate assessment of consumer diets is required. Here we use fatty-acid (FA) trophic biomarkers to ascertain trophic relationships and the nutritional status of benthic consumers. We compared the trophic dynamics of the megafauna under two contrasting productivity regimes, the NE Atlantic and the W. Mediterranean at a depth of 2000 m.

Particulate organic carbon fluxes to the seafloor were higher in the Atlantic site compared to the Mediterranean site, maximal fluxes being 20 mg C m<sup>-2</sup>d<sup>-1</sup> and 9 mg C m<sup>-2</sup>d<sup>-1</sup>, respectively. Chlorophyll-a concentrations in surficial sediments were higher in the Atlantic at 12 ng.cm<sup>-3</sup> compared to 4 ng.cm<sup>-3</sup> in Mediterranean. Megabenthic biomass and abundance were an order of magnitude higher in the NE Atlantic at 0.11 individuals m<sup>-2</sup> and 1.1 g m<sup>-2</sup> (wet weight) probably a result of the higher abundance of food at this site. The number of species observed in the Mediterranean was low (S=7) and the food web consisted of decapod crustaceans and fish. In the Atlantic a greater diversity of taxa were observed (S=49) with representatives from 10 phyla. Stable carbon and nitrogen isotope values point to typical deep-sea food webs at both sites, having four trophic levels with fish at the apex. In the Atlantic *Coryphaenoides* spp. had lower proportions of C<sub>20:4(n-6)</sub> and C<sub>22:6(n-3)</sub>, 48 % of the total FA, compared to 81% in the Mediterranean. This suggests that fish in the Mediterranean endure a higher degree of food limitation than their Atlantic counterparts. This was not observed in the FAs of invertebrate consumers. Differences were noted in FA profiles between feeding types. These results enable us to better understand how communities function under different productivity regimes.



**Monday 3<sup>rd</sup> December**

**Evolution 1**

**SYMPATRIC SPECIATION IN THE SEA: THE MANY FACES OF *ALVINICONCHA***

**Johnson S<sup>1</sup>, Tunnicliffe V<sup>2</sup>, VanDover C<sup>3</sup>, Schultz T<sup>3</sup>, Vrijenhoek R<sup>1</sup>**

<sup>1</sup> Monterey Bay Aquarium Research Institute, <sup>2</sup> University of Victoria, <sup>3</sup> Duke University Marine Laboratory

The Provannidae are a diverse group of gastropods that inhabit reducing environments in the deep-sea. Two genera, *Alviniconcha* spp. and *Ifremeria nautilei*, are reliant on symbiotic bacteria within their gill structures and are therefore restricted to hydrothermal vent habitats. These taxa have an interesting contrast in life-histories, where *I. nautilei* brood their “Waren’s” larvae, which later crawl away, and *Alviniconcha* spp. are broadcast spawners with planktotrophic development. Speciation patterns of these snails also differ, despite seemingly limited dispersal capabilities. *Ifremeria nautilei* shows little distinction among populations while *Alviniconcha* spp. is represented by six distinct lineages. Furthermore, *Alviniconcha* snails seem to have undergone sympatric speciation at several localities including the Fiji and Lau basins. We sequenced mitochondrial COI and the nuclear loci, ATPSa, ATPSb, H3, and EF1a to examine gene flow and intergradation among the different lineages from the Mariana Back-Arc, Fiji, Lau, and Manus basins and the Indian Ocean. We also examined the phylogenetic relationships among the distinct lineages in order to re-create the patterns of speciation throughout evolutionary history.



*Thursday 6<sup>th</sup> December*

*Human Impacts 2*

## **FUTURE REDUCTIONS IN GLOBAL-OCEAN BENTHIC BIOMASS PREDICTED AS A RESULT OF CLIMATE CHANGE**

**Jones D<sup>1</sup>, Ruhl H<sup>1</sup>, Yool A<sup>1</sup>, Wei CL<sup>2</sup>, Gehlen M<sup>3</sup>**

<sup>1</sup> National Oceanography Centre, United Kingdom, <sup>2</sup> Ocean Science Center, Memorial University of Newfoundland, Canada, <sup>3</sup> Laboratoire des Sciences du Climat et de L'Environnement, UMR CEA-CNRS-UVSQ, CEN de Saclay / L'Orme des Merisiers, France

The majority of mechanistic models predict global decreases in export production in 21<sup>st</sup>-century global warming simulations. This study provides an estimate of how decadal-to-century scale changes in global export production associated with global warming will influence benthic biomass in the open ocean. Biomass is predicted using accepted empirical relationships with the flux of particulate organic material and assessed in response to multi-model estimates of future (2090–2099) changes in export production using global warming simulations. Analysis using five fully coupled atmosphere ocean general circulation models suggests global reductions from current total benthic biomass between 2 and 10 megatons of carbon (1–9 % of current estimated total benthic biomass) with particular reductions in the North Atlantic and the northern sub-tropics in general. The Southern Ocean and some areas of upwelling may experience positive changes. It is expected that macrofaunal assemblages will suffer the greatest reductions, with major reductions in megafauna and meiofauna also predicted. These predicted major reductions in benthic biomass will likely have manifold ramifications for global deep-sea biology and may lead to wide-spread change in benthic ecosystems and the functions they provide.





*Wednesday 5<sup>th</sup> December*

*New Methods and Novel Techniques 1*

**AUTONOMOUS ECOLOGICAL SURVEYING OF THE ABYSS (AESA): TOWARDS A LANDSCAPE-SCALE PERSPECTIVE IN DEEP-SEA ECOLOGY**

**Bett B<sup>1</sup>**, Bailey D<sup>2</sup>, Durden J<sup>3</sup>, Billett D<sup>1</sup>, McPhail S<sup>1</sup>, Al Huvenne V<sup>1</sup>, Jones D<sup>1</sup>, Morris K<sup>1</sup>, Milligan R<sup>2</sup>, Ruhl H<sup>1</sup>

<sup>1</sup>National Oceanography Centre, University of Southampton Waterfront Campus, UK, <sup>2</sup>University of Glasgow, Institute for Biodiversity, Animal Health and Comparative Medicine, Glasgow, UK, <sup>3</sup>School of Ocean and Earth Science, University of Southampton, UK

Determining the distribution and abundance of life is challenging, especially in the deep sea where high pressure and other logistical challenges limit data availability to a tiny fraction of what is available for other systems. Features like hills, valleys, depressions, small rock outcrops, and biogenic mounds add to habitat complexity, but links between such features and the animals that live among them are very poorly resolved in abyssal-plain habitats using current methods. Life in and on the seafloor directly influences the burial of carbon and nutrient cycling — key ecosystem services. Man's exploitation of the deep sea continues to increase. Thus, spatial planning for responsible industrial activity in deep-sea environments and estimates of future change are based on rather limited information when compared to most other habitats. Previous results from a series of seven towed-camera surveys on the Porcupine Abyssal Plain (PAP) have indicated that the megafauna communities and habitat features on the abyssal hills surrounding our long-studied time-series site are quite distinct from those of the observatory site. Here we utilized a new camera system on the Autosub6000 autonomous underwater vehicle (AUV) to collect photographic transect and environmental data over an unprecedented range of scales from 1 m<sup>2</sup> to about 100 km<sup>2</sup> at PAP. The system uses a vertical camera creating overlapping seabed images, as well as a forward looking oblique camera that can quantify benthic-pelagic fish abundances. This extensive survey effort has allowed the kind of quantitative ecological analysis typically only possible in terrestrial habitats. We will also present developments into establishing a long-term AUV presence at key ecological research sites.



Tuesday 4<sup>th</sup> December

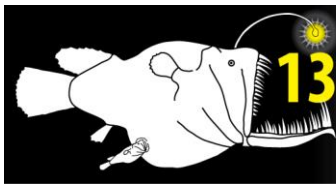
Evolution 2

## DIVERSITY OF HYDROTHERMAL VENT DECAPODS AT TOFUA ARC IN THE SOUTHWEST PACIFIC USING THE COI BARCODING

Kim SJ, Ju SJ

Korea Institute of Ocean Science & Technology

Decapods (i.e., shrimps and crabs) are among the most abundant and common organisms at vent fields. However, their identification based on morphological characteristics has often led to incorrect recognition of species due to the existence of sibling (or cryptic) taxa. DNA sequences are a useful tool for the identification of species and mitochondrial cytochrome c oxidase subunit I (COI) sequences are being widely used as the DNA barcode region for animals. It is primarily used to determine the appropriate thresholds in target taxa for species discrimination using COI. Vent decapods were collected from hydrothermal vent fields at Tofua Arc in the Southwest Pacific on April 2011 and February 2012 using ROV. The intra- and interspecific variations were calculated by Mega 5.05 using 44 COI sequences newly determined from vent shrimps and crabs with sequences of the family Alvinocarididae and Bythograeidae retrieved from GenBank. We defined the thresholds of the molecular operational taxonomic units (MOTU) for the family Alvinocarididae and Bythograeidae. Then 44 COI sequences were separated into six MOTUs; four crab groups (*Austinograea* sp., *Euryxanthops* sp., *Gandalfus puia*, *Xenograpsus* sp.) and two shrimp groups (*Nautilocaris saintlaurentae*, *Opaepele* sp.). These results will be very useful for assessing the evolutionary relationships and biogeographic distribution of vent-endemic organisms.



International

# 13<sup>th</sup> Deep-Sea Biology Symposium

Wellington, New Zealand 3 – 7 December 2012

**Tuesday 4<sup>th</sup> December**

**Autoecology 2**

## **A 3D INVESTIGATION OF THE MORPHOLOGY OF LEPETELLID LIMPETS (*LEPETELLA SIERRAI*): HYPOTHESES ON FEEDING ECOLOGY AND SYMBIOSIS**

**Judge J<sup>1</sup>, Haszprunar G<sup>2</sup>**

<sup>1</sup> University of California Berkeley, <sup>2</sup> Ludwig-Maximilians University Munich

The Lepetelloidea, a clade of small limpet-shaped gastropods, represents a case study in continental-margin and deep-sea diversification. Lineages in this clade have been found associated with a combination of different substrates, including hydrothermal vents, seeps, wood, whale carcasses, and additionally, polychaete tubes, elasmobranch egg cases, seagrass rhizomes, algal holdfasts, crab carapaces, and sponges. It is unclear how each lepetelloidean lineage utilizes its substrate; whether as a direct food source; a substrate to graze upon the microbial and fungal community; or a substrate that positions them in a reducing environment suitable for chemoautotrophic symbionts. Symbiosis is an obvious trait that would provide a lineage with a clear advantage in a nutrient-poor environment like the deep-sea, indicated by the prevalence of chemosymbiotic tube worms, mussels, and clams at hydrothermal vents. One lepetelloidean family, Lepetellidae, lives specifically on or inside empty polychaete tubes of the genus *Hyalinoecia*. The detailed morphology of a Mediterranean species, *Lepetella sierrai*, has been reconstructed from serial sections using the 3D modeling software AMIRA, and compared to other members of the genus. A unique alimentary tract, with huge oesophageal pouches, no true stomach, and an extensive multi-lobed midgut is shown. Additionally, a bacteriocyte system surrounding the entire mantle rim has been revealed via light microscopy and TEM. This is the first recognized evidence for a microbial symbiosis in lepetelloidean limpets. A hypothesis for a feeding ecology combining nutrition from the sugar phosphate polymer worm tube and chemoautotrophy is presented. Further investigation of this and other lepetelloidean feeding ecologies will contribute to uncovering the reasons behind the evolutionary success of this limpet clade that lives on a high diversity of substrates utilized by few other lineages.



*Monday 3<sup>rd</sup> December*

*Biodiversity Pattern – Large Scale 2*

**NEW ZEALAND'S DEEP-SEA ISOPOD CRUSTACEANS: SPATIAL PATTERNS OF DIVERSITY, ABUNDANCE AND COMPOSITION**

**Kaiser S<sup>1</sup>, Lörz AN<sup>2</sup>**

<sup>1</sup> University of Hamburg, <sup>2</sup> National Institute of Water & Atmospheric Research (NIWA)

Deep-sea areas constitute the largest habitat within New Zealand's exclusive economic zone. They comprise a great diversity of benthic habitats (such as ridges, seamounts and plateaus) and thus potentially harbour a great, yet largely unknown biodiversity. The Ocean Survey 2020 (OS 2020) was set up by the New Zealand government to map New Zealand's marine biodiversity. In the framework of the OS 2020 program benthic samples were taken in two contrasting regions, i.e. the Chatham Rise and Challenger Plateau. These two areas vary greatly in environmental settings (e.g. surface productivity and environmental variability), which may result in strongly contrasting community structures. Based upon both systematic and ecological approaches we use a key model group, isopod crustaceans, to examine faunal variation (in terms of abundance, biodiversity and composition) between the Chatham Rise and Challenger Plateau. This study denotes the first detailed investigation of the New Zealand deep-sea Isopoda and thus represents a significant contribution to the knowledge and understanding of New Zealand's deep-sea benthic biodiversity and its potential drivers.



*Tuesday 4<sup>th</sup> December*

*Biodiversity Pattern – Intermediate 2*

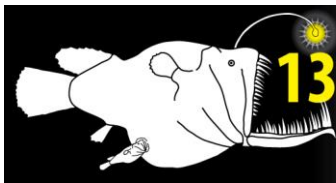
## **GIANT PROTISTS (XENOPHYOPHORES AND KOMOKIACEANS) FROM THE FERROMANGANESE NODULE FIELDS OF THE PACIFIC AND ATLANTIC OCEANS**

**Kamenskaya O<sup>1</sup>, Gooday A<sup>2</sup>, Tendal O<sup>3</sup>, Melnik V<sup>4</sup>**

<sup>1</sup> P.P.Sirshov Institute of Oceanology Russian Academy of Sciences Nakhimovsky pr. 36, Moscow 117997, <sup>2</sup> Ocean Biogeochemistry and Ecosystems, national Oceanography Centre, Southampton, European Way, Southampton SO14 3 ZH, United Kingdom, <sup>3</sup> Natural History Museum of Denmark, Universitetsparken 15, 2100, Copenhagen, Denmark, <sup>4</sup> Yuzhmorgeologiya State Scientific Centre, 20, Krymskaya St., Gelendzhik, 353461, Russia

Xenophyophores and komokiaceans (both groups are probably Foraminifera) were studied in trawl, grab and boxcore samples collected at two ferromanganese nodule fields in the Atlantic Ocean and two nodule fields in the Pacific Ocean. Special attention was given to the field in the Clarion-Clipperton Fracture zone (Eastern Pacific). Analyses of 38,600 seafloor photographs and fauna from 30 box-cores taken in the Russian Exploratory area of the Clarion-Clipperton ferromanganese nodule field revealed a diverse and abundant assemblage of these organisms. Xenophyophores, which are mainly of megafaunal size, were present in 70 % of the seafloor photographs. Their abundance averaged 1600 specimens per hectare, whereas the density of the next most common megafaunal group, the Actiniaria, did not exceed 170 specimens per hectare. The maximum density of xenophyophores was 12 specimens per m<sup>2</sup> (equal to 120000 specimens per hectare). In the box-cores, xenophyophores were found in 30 % of samples, while the Komokiacea, a group of mainly macrofaunal protists, occurred in 100 % of samples. A previous investigation revealed that the abundance and species diversity of metazoan macro- and meiobenthos increased when xenophyophores and komokiaceans were present, suggesting that these giant protists can structure benthic communities in nodule fields. Their study is particularly important in the light of planned mining in the deep sea and for understanding of recovery of the benthic communities after mining operations have ceased.

This work was supported by RFBR grant 12-04-01253a



International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

**Tuesday 4<sup>th</sup> December**

**Trench 1**

**TRENCH BIOLOGY: EXEMPLIFIED FROM THE JAPAN-BONIN-MARIANA TRENCHES CRUISES**

**Kitazato H**<sup>1</sup>, **Lecroq B**<sup>1</sup>, **Ohkawara N**<sup>1</sup>, **Oguri K**<sup>1</sup>, **Glud R**<sup>2</sup>, **Wenzhoefer F**<sup>3</sup>, **Gooday A**<sup>4</sup>

<sup>1</sup> Japan Agency for Marine-Earth Science and Technology, Japan, <sup>2</sup> Southern Denmark University, Denmark, <sup>3</sup> Max Planck Institute of Marine Microbiology, Germany, <sup>4</sup> National Oceanography Centre, UK

Among deep-sea realms, the trench is one of the least known and explored. In particular, deep trenches beyond 9,000 m are last-frontier regions, as they are difficult to visit without specific research gear. What kinds of organisms dwell in the deep trenches? Are there endemic species? What kinds of roles do trench ecosystems play? What kinds of material cycles take place in trenches? Plenty of questions have risen in relation to trench biodiversity and ecology.

JAMSTEC has long carried out deep trench research with several different technologies, such as ROV, ultra-deep lander-camera coring system and others. In 2002, we visited the Challenger Deep with ROV “KAIKO” and obtained push cores. We found that soft-walled foraminifers flourish at this deepest point in the world. The giant amphipod *Hirondellea gigas* is also distributed in the deep trenches of the north-western Pacific.

In 2010, we revisited the Challenger Deep with a free-fall type CTD-coring-camera system and ultra-deep profiling lander for taking surface undisturbed cores and measuring in-situ oxygen profiles. We found quite high concentrations of organic carbon and quite high microbial activity. Together with preliminary observations from the Japan Trench cruise in 2012, we shed light on the nature of deep-trench environments and their biology. We also plan to propose importance of “comparative trenchology”.



*Tuesday 4<sup>th</sup> December*

*Biodiversity Pattern – Intermediate 3*

## **DIVERSITY AND EVOLUTION OF NEW ZEALAND DEEP-SEA AMPHIPODA EXAMINED USING MOLECULAR METHODS**

**Knox M**<sup>1</sup>, **Hogg I**<sup>1</sup>, **Pilditch C**<sup>1</sup>, **Lörz AN**<sup>2</sup>, **Hebert P**<sup>3</sup>, **Steinke D**<sup>3</sup>

<sup>1</sup> University of Waikato, <sup>2</sup> National Institute of Water and Atmospheric Research, Wellington, <sup>3</sup> Biodiversity Institute of Ontario, University of Guelph, Canada

To assess patterns of diversity and evolution among species and populations in deep-sea habitats, we analysed mitochondrial DNA (COI) sequences from amphipod crustacean taxa inhabiting New Zealand's continental margins. Sampling stations were located on two prominent geomorphic features east and west of New Zealand, the Chatham Rise (n=15) and Challenger Plateau (n=5). Species-level diversity was assessed within the family Phoxocephalidae and compared with environmental variables. DNA sequences (n=297) revealed high overall diversity (n=49 MOTUs), as well as high beta diversity (28 MOTUs found at single station only). Cluster analyses of inter-station phoxocephalid composition revealed a group of highly similar stations, broadly distributed over the crest of Chatham Rise, probably in association with elevated food availability. Population-level differences were examined using three relatively abundant and widespread taxa and a further 61 taxa were used to assess average intra-specific genetic differences among stations. Similar levels of genetic divergence were found between eastern and western regions for all taxa. Based on molecular clock estimates, divergences most likely corresponded to isolation following landmass changes during the Pleistocene. This research highlights the value of molecular approaches, in particular COI sequences, for quantifying and comparing inter- and intra-specific diversity in under-sampled and/or under-studied taxa.





*Friday 7<sup>th</sup> December*

*New Methods and Novel Techniques 3*

## **EVALUATION OF GEOSPATIAL TOOLS FOR DELINEATING CONCENTRATIONS OF DEEP-SEA SPONGES**

**Knudby A<sup>1</sup>, Kenchington E<sup>2</sup>, Murillo J<sup>3</sup>**

<sup>1</sup> Department of Geography, Simon Fraser University, Burnaby, BC, Canada, <sup>2</sup> Ocean and Ecosystem Sciences Division, Department of Fisheries and Oceans, Bedford Institute of Oceanography, Dartmouth, NS, Canada, <sup>3</sup> Instituto Español de Oceanografía, Vigo, Spain

Maps of marine organisms are increasingly needed for spatial planning and conservation purposes. In the absence of complete census data, modelling approaches that produce maps from available point observations are necessary. Two broad approaches, spatial interpolation and habitat suitability modelling, can be distinguished. Spatial interpolation can yield accurate results where dense point observations are available, but errors increase in areas of strong environmental gradients and where few point data are available. Habitat suitability models overcome this by relying on a statistical model that predicts the organism parameter of interest from mapped environmental variables that quantify aspects of the organism's habitat. This removes the dependence on proximate observations, but introduces a dependence on the statistical relationship between the ecological parameter and its spatial predictors. Using research trawl data on sponge density we compare Kernel Density Analysis, the method currently used by Canada's Department of Fisheries and Oceans to delineate areas with significant deep-sea sponge aggregations, to two popular habitat suitability models (Maxent and Random Forest) and one spatial interpolation method (Universal Kriging). We evaluate their performances in areas with different densities of point observations and different environmental gradients, and quantify the influence of model selection on the predicted area of high-density sponge grounds. The relative merit of each approach, and the potential for hybrid approaches, is discussed.



Monday 3<sup>rd</sup> December

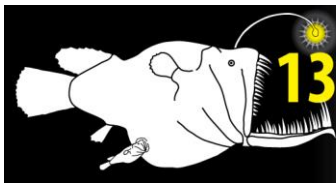
Evolution 1

**SMALL VESICOMYIDS (BIVALVIA: VESICOMYIDAE, VESICOMYINAE) VS LARGE-SIZE SYMBIOTROPHIC CONFAMILIAL RELATIVES**

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<sup>1</sup> P.P. Shirshov Institute of Oceanology, <sup>2</sup> MARUM – Center for Marine Environment Sciences and Faculty of Geosciences

*Vesicomya* Dall, 1886, the only genus of the subfamily Vesicomyninae, comprises 14 described and at least 8 undescribed species distributed worldwide from 400 m to 10,730 m depth. *Vesicomya* species were recorded in all studied deep-water trenches, reaching abundances of tens of thousands of specimens per trawl catch. Different from their famous confamilial relatives, large-size clams dominating chemosynthetic communities, representatives of *Vesicomya* are tiny bivalves with the shell length in the majority of species only about 5 mm. High abundances in deep-sea communities, affinities with chemosymbiotic molluscs and a previous finding of bacteria in gill tissue raise the question of symbiotrophy in *Vesicomya*. New results on stable carbon and nitrogen isotope composition, and data on the anatomy of the alimentary canal, do not corroborate the presence of chemoautotrophic endosymbionts in *Vesicomya*. Relationships of *Vesicomya* with genera of highly specialized chemosymbiotic large-size vesicomyids of the subfamily Pliocardiinae and possible evolutionary trends in the family are discussed.



International

# 13<sup>th</sup> Deep-Sea Biology Symposium

Wellington, New Zealand 3 – 7 December 2012

Tuesday 4<sup>th</sup> December

Autoecology 2

## THE LIMITS OF VISION: SPECIALISATIONS IN THE SMALL EYES OF THE DEEP-SEA BRISTLEMOUTH *CYCLOTHONE MICRODON* (TELEOSTEI)

Kuhar A<sup>1</sup>, Hart NS<sup>2</sup>, Collin SP<sup>3</sup>

<sup>1</sup> The University of Western Australia, <sup>2</sup> The University of Western Australia, <sup>3</sup> The University of Western Australia

The small bristlemouth *Cyclothone microdon* is said to be the most abundant vertebrate on earth, occurring in large numbers from the epipelagic (100 m) to the deep bathypelagic (2500 m) zones of the deep-sea. The present work investigates the importance of vision in this teleost fish, which possesses relatively small eyes, by examining the spacing, size and distribution of retinal neurons in order to assess this species' visual ecology. The eyes of *C. microdon* are characterised by their small size (1.1 mm in diameter), which have traditionally been described as "degenerate". The laterally-placed eyes have a ventral aphakic gap, a relatively large pupil, a spherical lens, but lack a reflective tapetum. A topographic analysis of the whole-mounted retina reveals a non-uniform hexagonal array of rod-like photoreceptors (4.8  $\mu\text{m}$  in diameter) with a peak density of 69,000 receptors/ $\text{mm}^2$  arranged in a concentric pattern of increasing cell density, culminating in an area in the dorso-temporal retina. A comparison of the number of photoreceptors and Nissl-stained ganglion cells at each topographic loci reveals a marked difference in summation across the retina (1:1 to over 7:1). Far from being degenerate, the small eyes of *C. microdon* show adaptations for optimising photon capture and low-light vision, which allows this species to perceive the movement of bioluminescent prey (particularly in the lower part of the frontal visual field).



Tuesday 4<sup>th</sup> December

Trench 2

## HADAL SERPULID POLYCHAETES: CALCAREOUS TUBEWORMS BEYOND THE ABYSS

Kupriyanova E<sup>1</sup>, Vinn O<sup>2</sup>, Taylor P<sup>3</sup>

<sup>1</sup> The Australian Museum, Sydney, Australia, <sup>2</sup> University of Tartu, Tartu, Estonia, <sup>3</sup> Natural History Museum, London, UK

Although the carbonate compensation depth (CCD) at 4000–5000 m is often proposed as a physiological barrier to deep-ocean colonization, many organisms with calcareous exoskeletons inhabit in the deepest oceanic trenches. Serpulid polychaetes inhabiting unprotected calcareous tubes are unlikely inhabitants of extreme depths, yet they are found at all oceanic depths from intertidal to hadal. We reviewed existing records of Serpulidae below 6000 m and examined the ultrastructure and mineralogical content of available hadal serpulid tubes to obtain insights into deep-sea biomineralisation. Species belonging to typical bathyal and abyssal genera (*Bathyditrupa*, *Bathyvermilia*, *Hyalopomatus*, and *Protis*) were collected from 6050 to 9735 m. However, only *Protis* spp. were found at 6200–9700 m. The hadal specimens of *Protis* have irregularly oriented prismatic (IOP) tube ultrastructures similar to those found in relatively shallow water representatives of the genus. We did not find any completely or partially decalcified hadal serpulid tubes, except for the deepest one (*Protis* sp. from 9700 m). Energy-dispersive X-ray analysis (EDX) revealed the presence of Mg, a proxy indicating that mineralogically the hadal tubes comprise only calcite with no aragonite. How serpulid polychaetes manage to calcify in spite of high energetic costs below the CCD, and how they protect their tubes from being completely dissolved at these extreme depths remain unexplained.



*Friday 7<sup>th</sup> December*

*Trophic and Process 4*

**LIPID AND FATTY ACID COMPOSITION OF *HIRONDELLEA DUBIA* (AMPHIPODA: LYSSIANASIDAE) FROM HADAL DEPTHS WITHIN THE KERMADEC TRENCH, SW PACIFIC**

Lacey N<sup>1</sup>, Jamieson A<sup>1</sup>, Pond D<sup>2</sup>, Mayor D<sup>1</sup>

<sup>1</sup> University of Aberdeen, <sup>2</sup> British Antarctic Survey

The hadal zone, deeper than 6 km, is primarily located within ocean trenches. Amphipods are a significant component of the fauna at these great depths, and are vital for the circulation and dispersal of organic material. Little is known of the physiology and ecology of hadal amphipods due to the difficulty involved with sampling. Lipids act as energy reserves for organisms, providing information on both nutritional inputs and energetic strategies. A total of 50 individuals of *Hirondellea dubia*, the dominant amphipod species within the Kermadec Trench, SW Pacific, were collected from 7014–9053 m depth. The samples were analysed in order to investigate their nutritional ecology, lipid physiology, reproduction and development and buoyancy. Total lipid, lipid composition and fatty-acid analysis of membrane and storage lipids are investigated to this effect.



*Thursday 6<sup>th</sup> December*

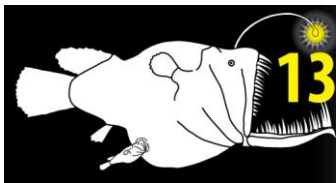
*Temporal Patterns 1*

#### **INTER-ANNUAL CHANGE IN THE ABYSSAL PLAIN – THE MACROFAUNAL RESPONSE TO CLIMATIC CHANGES**

**Laguionie-Marchais C<sup>1,2</sup>**, Billett DSM<sup>3</sup>, Paterson GLD<sup>2</sup>, Ruhl HA<sup>2</sup>, Thatje S<sup>1</sup>

<sup>1</sup> Ocean and Earth Science, University of Southampton, National Oceanography Centre, Southampton, European Way, Southampton, SO14 3HZ, UK, <sup>2</sup> Natural History Museum, Department of Zoology (Polychaete Group), London SW7 5BD, UK, <sup>3</sup> Ocean Biogeochemistry and Ecosystems, National Oceanography Centre, Southampton, European Way, Southampton, SO14 3HZ, UK

Under climate changing and the rise in deep-sea resources exploitation, characterising inter-annual variability in deep-sea community has become important. But, long-term observations from which inter-annual variation can be detected are scarce in deep sea. In recent years links between the processes at sea surface and change in deep-sea ecosystems have been observed. Thus, under temperate productive waters, abyssal habitats (> 4,000 m) receive seasonal pulsed inputs of fresh organic matter, as well as inter-annual variations. Two abyssal stations in the North East Atlantic (Porcupine Abyssal Plain) and the North East Pacific (Station M), both in areas with marked seasonal primary productivity, have been studied since 1989. Benthic community as exemplified by megafauna respond to climatically-driven changes in surface processes. Less is known about sediment macrofauna community temporal changes, which are made up of a more diverse group of fauna. This presentation is focused on macrofauna represented by polychaete worms (the most abundant macrofaunal taxon) from 1991 to 2005. It is the first time that St. M and PAP data have been conjointly studied ensuring a common statistical description. Using the two long-time series polychaete data sets, several taxonomic levels as well as relevant ecological descriptors such as rank abundance distribution, several questions were addressed: 1) Do polychaete community structure change at inter-annual scale? 2) Is macrofaunal change related to megafauna changes at the two stations? 3) Do global processes such as El Niño and the North Atlantic Oscillation affect macrofauna dynamics?



International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

*Tuesday 4<sup>th</sup> December*

*Autoecology 1*

**DISPERSAL CAPACITY AND SYMBIONT ACQUISITION IN *IDAS* SP., A SMALL CHEMOSYMBIOTIC MYTILID FROM DEEP-SEA ENVIRONMENTS**

Laming S<sup>1</sup>, Duperron S<sup>1</sup>, Cunha M<sup>2</sup>, Gaudron S<sup>1</sup>

<sup>1</sup> AMEX, University Pierre et Marie Curie, Paris 6, <sup>2</sup> CESAM, Universidade de Aveiro

Data on the dispersal capacity and connectivity of deep-sea metazoan populations in several oceanic regions, where seeps, hydrothermal vents and organic-falls are reported, remain absent or in poor supply. How specialised metazoans colonise these fragmented habitats is therefore a critical question. The bathymodiolin mussel *Idas* sp. has a patchy but ubiquitous distribution from the eastern Mediterranean to the Gulf of Cadiz, with a closely related species in the Gulf of Mexico. It thus represents an interesting model to study larval development, mode and dispersal potential of a deep-sea chemosymbiotic species. Samples are available from larval colonisation devices and sunken wood from various sites. Larval mode, maturation and gametogenesis are assessed by examining adult reproductive biology and larval/post-larval shell characteristics. In addition, the size-at-first-acquisition of symbionts and their transmission is assessed using correlative light-electron microscopy (CLEM) performed on the preserved larvae/juveniles of *Idas* sp. of varying size. CLEM permits direct corroboration of bacterial ultrastructure in FISH-identified bacterial symbionts, with better resolution on tissue compartmentalisation. *Idas* mussels, which have been shown to host multiple symbionts (sulphur-/methane-oxidising and methylotrophic), and which remain poorly resolved phylogenetically, are related to large *Bathymodiolus* occurring in vent or seep environments worldwide. Documenting larval dispersal, colonisation, and symbiont acquisition among and between populations of *Idas* provides an insight into the means by which biogeographic patterns are sustained and evolution has operated, and informs the resistance to disturbance occurring within habitats of this genus.





*Tuesday 4<sup>th</sup> December*

*Trench 2*

#### **ULTRA-DEEP SEQUENCING OF ULTRA-DEEP SEDIMENT**

**Lecroq B**<sup>1</sup>, Sinniger F<sup>2</sup>, Toyofuku T<sup>2</sup>, Nomaki H<sup>2</sup>, Ohkawara N<sup>2</sup>, Oguri K<sup>2</sup>, Kitazato H<sup>2</sup>

<sup>1,2</sup> Japan Agency for Marine-Earth Science and Technology (JAMSTEC). 2-15 Natsushima-cho. Yokosuka, Japan.

We propose to assess the foraminiferal richness of Mariana Trench sediment by Illumina ultra-deep sequencing. The environmental massive-sequencing approach consisted in getting numerous sequences of the global DNA extractions from environmental samples. This strategy is particularly applicable to the most remote point of the oceans since its biodiversity is dominated by tiny organisms that usually require time-consuming steps of isolation and observation under microscope before identification. RNA extractions have been included in analyses to distinguish in situ living organisms from extracellular DNA that could be conserved and carried long after the death of individuals. We present here foraminiferal richness obtained respectively from our extensive sequencing of DNA and RNA environmental extractions and we discuss the different compositions occurring at the bottom of the Trench on the one hand and on the slope on the other hand.



*Friday 7<sup>th</sup> December*

*New Methods and Novel Techniques 4*

## **IDENTIFYING ACTIVE FORAMINIFERANS IN THE SEA OF JAPAN USING DNA AND RNA-BASED METAGENETICS**

**Lejzerowicz F<sup>1</sup>, Voltsky I<sup>2</sup>, Pawlowski J<sup>1</sup>**

<sup>1</sup> University of Geneva, <sup>2</sup> Saint-Petersburg State University

DNA metagenetics is an efficient and rapid tool to describe the diversity of microbial eukaryotes at the deep-sea floor. However, the persistence of extracellular DNA in the surface deep-sea sediment skews analyses of ecological relevance by artificially extending the occurrence of some species. As an alternative, short-lived RNA molecules constitute a good proxy for the detection of active species at the moment of sampling. Here, we compared DNA and RNA-derived (cDNA) datasets representing the small-subunit ribosomal gene for studying the deep-sea benthic foraminiferal diversity. We analysed 257 ribosomal DNA and cDNA sequences obtained from seven unsieved sediments samples collected during the SoJaBio expedition to the Sea of Japan at depths ranging from 486 to 3665 m. The DNA and RNA-based approaches return similar taxonomic compositions of foraminiferal assemblages, but differed in some important points. First, the cDNA dataset was dominated by sequences of rotallids, suggesting that these calcareous species, some of which have also been stained by Rose Bengal, are the most active component of foraminiferal community. Second, the richness of monothalamous (single-chambered) foraminiferans was higher in DNA extracts from the deepest samples, confirming that this group of foraminifera is abundant but not necessarily very active in deep-sea sediments. Finally, the high divergence of undetermined sequences in cDNA dataset may indicate that they correspond to rare but active species, impossible to detect by traditional microscopic study. Our study demonstrates the reliability of the RNA-derived approach to detect active foraminiferal species and prompt its use in future high-throughput sequencing-based environmental surveys.



*Monday 3<sup>rd</sup> December*

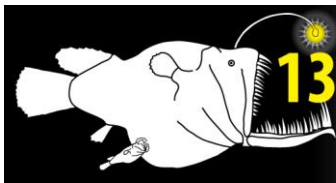
*Biodiversity Pattern – Large Scale 2*

**BIODIVERSITY, COMMUNITY STRUCTURE AND VERTICAL DISTRIBUTION OF PLANKTONIC CNIDARIANS IN THE CELEBES AND SULU SEAS**

**Lindsay D**<sup>1</sup>, Pagès F<sup>2</sup>, Grossmann M<sup>1</sup>, Nishikawa J<sup>3</sup>, Nishida S<sup>3</sup>

<sup>1</sup> JAMSTEC Japan, <sup>2</sup> ICM-CSIC Barcelona, Spain, <sup>3</sup> AORI, Japan

Plankton cnidarian biodiversity, community structure, vertical distribution and migration patterns were investigated in two marginal basins — at one station in each of the Celebes and Sulu Seas. These two seas are part of an island arc located in south-east Asia and although they are in close proximity, they are separated by a sill with only ~250 m of clearance above it. Primary productivity in the Sulu Sea was higher in the surface layers than in the Celebes Sea, and the water below ca. 600 m depth was relatively homogeneous with high temperatures (ca. 10° C) down to 1000 m depth. Contrastingly, the Celebes Sea was more oligotrophic and was filled mainly by Pacific Ocean water masses with water temperatures continuing to decline with depth to approach 5° C at 1000 m. The Celebes Sea station had more species of siphonophores (about 48) and less of medusae (about 10) compared to the Sulu Sea station with 39 siphonophores and 17 medusae, correlating well with the more typical oceanic nature of the Celebes Sea. Species diversity was correlated to physico-chemical water column parameters such as dissolved oxygen and temperature and the overall abundances and species richness in deep waters at the Sulu Sea station was low compared to the Celebes Station. The composition of the deep-water siphonophore community differed significantly with the occurrence of several species of the family Clausophyidae in the Celebes Sea but not a single specimen of this family at the Sulu Sea station.



International  
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*Tuesday 4<sup>th</sup> December*

*Evolution 2*

**DISTRIBUTION AND HABITAT SELECTIVITY OF DEEP-SEA CANYON NEMATODES**

Lins L<sup>1</sup>, Ingels J, Vanreusel A

<sup>1</sup> University of Ghent, <sup>2</sup> University of Ghent, <sup>3</sup> University of Ghent

Dispersal processes are known to influence assemblage dynamics of marine benthic invertebrates. Although without pelagic larvae and small in size, nematodes are found over wide geographical ranges and might be passively carried by water currents after resuspension events (caused by disturbance processes) and resettle as 'particles'. Such dislodgement is important for less-mobile taxa to achieve dispersal. The Whittard Canyon is a physically disturbed environment that receives high amounts of sediments and organic material coming from the shelf or surface waters, which could define the high abundances of meiofaunal groups found there. Selective settlement of nematodes was observed following a resuspension event under ex-situ experimental conditions using samples collected in the Whittard canyon at 812 m water depth. Three different types of energy sources (algae, bacteria, and sulphides) and two different controls (empty and azoic sediment) were offered to a nematode community sinking through the water column in three independent, simultaneously running experiments. The significant differences ( $p < 0.02$ ) between nematode assemblages demonstrated that nematodes are attracted by different energy sources. These experiments were combined with the analysis of the nematode community of the dominant species and the biogeochemical environment of background samples from the experimental site in order to study their habitat specificity and trophic interactions. The combination of background and experimental samples suggested that nematodes colonize empty patches selectively when descending in the water column, but whether they are attracted by food or by other attractants is still unclear.



Tuesday 4<sup>th</sup> December

Biodiversity Pattern – Intermediate 2

## THE LARGER PELAGIC CRUSTACEA OF THE GULLY SUBMARINE CANYON

Maclsaac K, Kenchington T, Kenchington E, Best M

Fisheries and Oceans Canada

The larger pelagic Crustacea of the Gully submarine canyon are described in detail for the first time. The Gully is the largest submarine canyon on the eastern seaboard of North America and Canada's first formal Marine Protected Area. Over seventy species were observed during three annual summer/fall surveys, from samples collected from the surface to the upper bathypelagic with an International Young Gadoid Pelagic Trawl. The fauna was dominated by cold temperate species typical of mid- to higher latitudes in the North Atlantic, with the northern krill *Meganyctiphanes norvegica*, the decapod *Eusergestes arcticus*, and the hyperiid *Themisto gaudichaudii* especially dominant at shallow to moderate depths. At least seventeen other species are new records for Canadian waters, including several species rarely reported worldwide, and taxonomic work is ongoing. The assemblage varied primarily with depth and the diel cycle, with only *M. norvegica* showing pronounced inter-annual variation in biomass and abundance. A limited comparison with the fauna over the adjacent continental slope indicated that species dominance structures differed, and that biomass, abundance, and species richness were greater inside the canyon. The total biomass and population size structure of *E. arcticus* in particular showed a positive "Gully effect", with more large animals inside the canyon than outside.



*Thursday 6<sup>th</sup> December*

*Human Impacts 3*

## **INVESTIGATING THE EFFECTS OF DEEP-SEA OIL SPILLS ON SEDIMENT COMMUNITY OXYGEN CONSUMPTION**

**Main CE**<sup>1</sup>, Ruhl HA<sup>2</sup>, Yool A<sup>2</sup>, Jones DOB<sup>2</sup>, Mayor DJ<sup>3</sup>

<sup>1</sup> University of Southampton, <sup>2</sup> National Oceanography Centre, Southampton, <sup>3</sup> Oceanlab, Institute of Biological and Environmental Sciences, University of Aberdeen

Crude oil spilled in the deep-sea results in potentially far-reaching anthropogenic impacts on an ecosystem that has barely been explored, let alone understood. The *Deepwater Horizon* oil spill in 2010 revealed our lack of knowledge of the effects of oil on deep-water sediment communities. Studying deep-sea sediment communities' functional responses to hydrocarbons will reduce these unknowns. This could help inform policy, as deep-sea drilling for oil continues with the potential for further accidental spills.

Oxygen uptake rates by biota were measured in the presence of hydrocarbons to indicate the effect of a deep-sea oil spill on this ecosystem function. Sediment cores with overlying bottom water were collected from 1000 m depth at an uncontaminated site in the Atlantic. The sediment communities were exposed to hydrocarbons by introducing serial dilutions of a water-accommodated fraction of crude oil that had been prepared using seawater also from ~1000 m depth. The cores, sealed in microcosms, were incubated *ex situ* at ambient bottom water temperature. Total oxygen uptake rates were measured in the microcosms over the duration of the incubations.

Multiple factors are considered in explaining variation of oxygen uptake, including the initial concentration of added monoaromatic hydrocarbons and an index of sediment fauna biomass.



*Thursday 6<sup>th</sup> December*

*Temporal Patterns 1*

**INFLUENCE OF SEASONAL AND EPISODIC EVENTS ON DEEP-SEA COMMUNITIES IN A SUBMARINE CANYON: FIRST RESULTS FROM THE NEPTUNE CANADA CABLED NETWORK.**

**Matabos M**, Ajayamohan RS, Juniper SK, Mihaly S, Gervais F

NEPTUNE Canada, University of Victoria

The NEPTUNE Canada (NC) undersea network has several camera and oceanographic instrument installations in Barkley Canyon, which incises the continental shelf in the northeast Pacific off Vancouver Island, Canada. The NC Barkley Canyon study area encompasses a wide range of environments from the continental shelf (400 m) to the continental slope (900 m), including a field of outcropping methane hydrates above a subduction zone. During the first two years of operations, researchers have been developing experimental approaches for combining camera observations with analysis of instrument data to study biological rhythms, bioturbation and responses of benthic organisms to environmental changes. An ongoing study of 12 months of camera recordings during 2011 is examining seasonal presence/absence patterns of mobile invertebrates and fishes. Quantitative data are used to focus on the short-term influence of a winter storm event that is associated with rapid changes in seawater properties at nearly 1000 m depth. Preliminary results show that benthic communities as deep as 900 m respond to surface winter storm events, with a shift from a shrimp-dominated community during the storm to a community dominated by buccinid gastropods after the event. The current data suggest that extreme weather events can propagate energy down to 800 m water depth and directly influence species migration along the continental slope. Also notable is a complete absence of echinoderms from the canyon floor for two periods of nearly 3 months each, in mid-winter and mid-summer. Results underline the importance of long-term continuous monitoring to understand temporal scales of changes in deep-sea communities, as well as the relative influence of cyclic (e.g. tides) vs. episodic events.





Thursday 6<sup>th</sup> December

Trophic and Process 1

**IS THE DEEP-SEA DIFFERENT? A CROSS-ECOSYSTEM STUDY INVESTIGATING HOW THE QUANTITY AND QUALITY OF ORGANIC MATTER INFLUENCE BENTHIC CARBON CYCLING**

Mayor D<sup>1</sup>, Thornton B<sup>2</sup>

<sup>1</sup> Institute of Biological and Environmental Sciences, Oceanlab, University of Aberdeen, UK, <sup>2</sup> The James Hutton Institute, Craigiebuckler, Aberdeen, UK

The composition of phytoplankton communities are changing in response to anthropogenic emissions and a changing climate. In turn, this is affecting the quantity and biochemical composition ('quality') of particulate organic matter (POM) exported to the seabed. Little is known about how these changes will affect the future role of marine sediments in global biogeochemical cycles. This study investigated how the quantity and quality of POM affected the rates and pathways of carbon cycling in three contrasting marine habitats; a temperate estuary (intertidal), Arctic shelf sediments (330 m) and the deep-seabed (1080 m). <sup>13</sup>C-labelled cultures of a lipid-rich diatom (*Chaetoceros radicans*) and lipid-poor haptophyte (*Phaeocystis* sp.) were used as representatives of high- and low-quality POM respectively. High- and low quantities of these two contrasting substrates were introduced to the seabed and the fate of the constituent C was quantified during ex-situ incubation experiments. This talk will explore the differences and similarities between carbon cycling in three spatially distinct ecosystems.



*Friday 7<sup>th</sup> December*

*Conservation and Management 1*

**CONSERVING THE DEEP-SEA AT VERY LARGE SPATIAL SCALES: PEW'S GLOBAL OCEAN LEGACY PROJECT**

Nelson J, Golder B, **Mazurek R**, Connell A

Pew Environment Group

Deep-sea habitats support a complex array of biological diversity in the ocean. Biogenic habitats formed by deep-sea corals and sponges are critical to numerous species by providing shelter, nursery areas, protection from currents and predators, and important breeding and spawning areas. Hydrothermal-vent zones have a density of organisms 10,000 to 100,000 times greater than the surrounding sea floor. Seamounts may act as navigational waypoints during migrations, provide animals with enhanced opportunities for feeding, and may serve as crucial breeding grounds. Despite their importance to ocean life, these deep-sea habitats are still mostly unexplored and are threatened by damage from fishing, oil extraction, and other activities. Since 2005 the Pew Environment Group's Global Ocean Legacy (GOL) project has been influential in the designation of over 1.5 million km<sup>2</sup> of highly-protected no-take marine reserves which protect important deep-sea habitats. Most recently, GOL has focused particular attention on the conservation of the deep-sea across the Pacific. In this presentation we will discuss the need for conservation of deep-sea areas at very large scales and the opportunity these areas offer as scientific reference sites.



*Friday 7<sup>th</sup> December*

*Trophic and Process 3*

## **THE ENERGETICS OF LIFE ON THE DEEP SEAFLOOR**

**McClain C<sup>1</sup>**, Allen A<sup>2</sup>, Tittensor D<sup>3,4</sup>, and Rex M<sup>5</sup>

<sup>1</sup>National Evolutionary Synthesis Center, Durham, NC, USA, <sup>2</sup>Dept. of Biological Sciences, Macquarie University, Sydney, Australia, <sup>3</sup>United Nations Environment Programme World Conservation Monitoring Centre, Cambridge, UK, <sup>4</sup>Microsoft Research Computational Science Laboratory, Cambridge, UK, <sup>5</sup>Dept. of Biology, University of Massachusetts, Boston, MA, USA

Life requires energy. The flux and transformation of energy influences processes and patterns across levels of biological organization. The deep oceans are especially energy-deprived systems because photosynthetically active radiation is non-existent and consequently primary production is virtually absent. The effects of this energy limitation impact ecological and evolutionary processes from the individual to the ecosystem. Yet this influence is incompletely understood. This meager knowledge of energetics in the deep sea is unfortunate considering rapid and accelerating decrease in oceanic primary production. I will discuss a framework to understand and link energetics across multiple scales of biological organization in the deep sea. This will include an overview of new research linking how species (dispersal, life history, metabolism, body size, lifespan) and community (patterns of community assembly, diversity, and standing stock) attributes are impacted by extreme limitation of chemical energy.



Wednesday 5<sup>th</sup> December

Discovery 1

**DISCOVERY OF A TUBEWORM-DOMINATED HYDROTHERMAL-VENT COMMUNITY IN THE SOUTH-WEST PACIFIC: SPECIES COMPOSITION, SPATIAL DISTRIBUTION AND BIOGEOGRAPHY**

Menot L, Piechaud N, Cambon-Bonavita MA, Galéron J, Fouquet Y

Ifremer, Brest, France

During summer 2010, the Futuna cruise explored the spreading centre, basin and volcanic zone, south of Futuna Island in the SW Pacific. Extensive seafloor mapping highlighted a previously unmapped caldera at 1420 m depth. Hydrothermal activity was evidenced by anomalies in temperature and turbidity profiles along CTD casts. Exploration of the caldera during six dives of the submersible Nautilie led to the discovery of a new hydrothermal site dominated by siboglinid tube worms.

Temperature in the near-translucent and diffusive fluid reached a maximum of 5.4°C, just 2.5°C above seawater temperature. Despite slow venting, the bush of tube worms harboured an abundant and characteristic vent fauna including alvinocaridid shrimps, large mytilids, galatheids and zoarcid fishes. The bush was surrounded by dense populations of sessile barnacles. Small gastropods were also found in abundance but *Ifremeria nautiliei* and *Alviniconcha hessleri*, the two large and dominant species in the nearby North Fiji and Lau basins were absent.

The composition and spatial distribution of this hydrothermal vent assemblage will be discussed in light of the known ecology of vent communities in the SW Pacific, and put in the biogeographical context and hypothesis as to the worldwide distribution of hydrothermal communities and main historical paths among biogeographical regions.



*Thursday 6<sup>th</sup> December*

*Temporal Patterns 1*

## **INCREASE OF LITTER AT THE ARCTIC DEEP-SEA OBSERVATORY HAUSGARTEN – INDIRECT EFFECT OF GLOBAL WARMING?**

Bergmann M, Klages M, **Kirstin M**

Alfred Wegner Institute for Polar and Marine Research

The deep ocean floor is the largest yet least-known habitat on Earth. Recent research highlights that persistent human waste (litter) has made it even to the remotest of areas on our planet: polar regions and the deep ocean floor. Nevertheless, little information is available about quantity and temporal trends of litter on the deep seafloor. To quantify litter inputs over time, we analysed images from the seafloor taken at the HAUSGARTEN observatory (79° N), located in the eastern Fram Strait at 2,500 m depth. Images were taken by a camera towed along the same transect in 2002, 2004, 2007, 2008 and 2011. Our results indicate that the proportion of images with litter doubled from 1.08 % in 2002 to 2.08 % in 2011. Similarly, if converted to a spatial scale litter quantities rose from 3,635 in 2002 to 7,710 litter items per km<sup>2</sup> in 2011. The major increase occurred between 2007 and 2011, when litter densities rose by one order of magnitude, similar to densities reported from a canyon near Lisboa. Plastic constituted the majority of litter (59 %) followed by a black fabric (11 %) and cardboard/paper (7 %). The majority of litter (66 %) was between 10 and 50 cm in size. 67 % of the litter was either entangled with or colonised by megafauna. The sponge *Cladorhiza gelida* (41 %) was most frequently entangled with litter followed by attached sea anemones (15 %). We discuss the possible harm to benthic biota and conclude that the observed increase in litter could be an indirect effect of global warming, which removes the sea-ice cover and opens the Arctic Ocean to the impacts of man's activities.



*Monday 3<sup>rd</sup> December*

*Dispersal and Connectivity 1*

## **CONNECTIVITY AND CONSERVATION OF SEAMOUNT COMMUNITIES: A SEASCAPE GENETIC APPROACH**

**Miller K<sup>1</sup>, England P<sup>2</sup>, Gunasekera R<sup>2</sup>**

<sup>1</sup> Institute of Marine and Antarctic Studies, Hobart, Tasmania, Australia, <sup>2</sup> CSIRO Marine and Atmospheric Research, Hobart, Tasmania, Australia

Understanding ecological processes in the deep sea remains one of the challenges of deep-sea biology, although information on population structure and early life history are critical for effective management and conservation of deep sea resources. Using a combination of population genetics and hydrodynamic modelling we have quantified the level of gene flow among deep sea populations of three invertebrate species with contrasting life histories: the solitary coral *Desmophyllum dianthus*, the colonial coral *Solenosmilia variabilis* and the squat lobster *Munida isos*. In addition we assessed the importance of sexual and asexual reproduction to the maintenance of populations (for the two coral species) as well as the level of genetic diversity in populations as a measure of resilience. Despite their differing dispersal potential, significant genetic subdivision was evident in all species at relatively small spatial scales (i.e. among seamounts within the same region;  $F_{ST} > 0.015$ ,  $p < 0.001$ ) indicating limited dispersal among seamounts. Genetic subdivision was also consistent with restricted dispersal of passive particles predicted using hydrodynamic modelling and genetic diversity was high. In combination, our results suggest that in the deep sea, as for many shallow water counterparts, that dispersal of marine invertebrate larvae will be limited. This finding has important consequences for management, including the likelihood of recruitment or spillover from marine protected areas, the spacing of MPAs if they are to act effectively as networks, as well as the recovery of areas impacted through natural or anthropogenic activities.



*Thursday 6<sup>th</sup> December*

*Human Impacts 3*

## **THE EFFECTS OF OIL PRODUCTION ON DEEP-WATER FISH COMMUNITIES IN WEST AFRICA: EARLY RESULTS FROM THE DELOS PROJECT**

**Milligan R<sup>1</sup>, Clarke J<sup>2</sup>, Polanski J<sup>3</sup>, Priede M<sup>3</sup>, Rowe G<sup>4</sup>, Ruhl H<sup>5</sup>, Smith K<sup>6</sup>, Walls A<sup>2</sup>, Bailey D<sup>1</sup>**

<sup>1</sup> University of Glasgow, <sup>2</sup> BP Exploration Ltd., <sup>3</sup> Oceanlab, University of Aberdeen, <sup>4</sup> Texas A&M University, <sup>5</sup> National Oceanography Centre, Southampton, <sup>6</sup> Monterey Bay Aquarium Research Institute

Very little is currently known about what long-term impacts deep-water (> 1000 m) oil production may have on the benthic environment and fauna. This is partly because our poor understanding of natural long-term changes in deep water systems but particularly because many new production sites are located in areas that have received little previous study. The Deep-ocean Environmental Long-term Observatory System (DELOS) monitoring stations were installed in February 2009 at the Greater Plutonio oil field in Angola to monitor and compare long-term environmental and biological changes over the lifetime of the oil production platform. Located at a depth of 1400 m, the observatories were designed to continuously record data from two sites: the 'near field' site, which is located 50 m from an active well and the 'far field' (control) site, located 15 km from any oil production activity.

Analysis of the time-lapse photographs from each platform between February 2009 and August 2011 shows no significant differences between stations in composition or abundance of the fish fauna. We did however detect the presence of two distinct assemblages of fish based on feeding type: the first was comprised predominantly of scavenging fish species, and the second comprised mainly of benthopelagic scavenging species. Shifts between these two assemblages were observed at both observatories, indicating temporal shifts in fish community composition over timescales of week-months. As these shifts occur at both the near- and far-field stations we suggest that these changes occur as a result of natural environmental changes, potentially driven by vertical changes in the distribution of an overlying oxygen-minimum zone.

### **Acknowledgements**

The authors would like to thank Dr Alan Jamieson (Oceanlab) for his assistance with the species identification, and Dr. Daniel Jones (NOC) for his assistance in describing and interpreting the effects of production activities seen in the images.

### **Sources of Funding**

This work has been funded by BP and NERC.





*Tuesday 4<sup>th</sup> December*

*Autoecology 2*

**DEVELOPMENT AND REPRODUCTIVE STRATEGY OF THE BONE-EATING WORM *OSEDAX JAPONICUS***

**Miyamoto N, Fujiwara Y**

Institute of Biogeosciences, Japan Agency for Marine-Earth Science and Technology

The bone-eating marine worm *Osedax* exclusively inhabits vertebrate bones. Its unique life style and morphology have fascinated scientists. The whole process of their development, however, has not been observed due to the difficulties of rearing larvae and induction of settlement on vertebrate bones. Here we report the post-embryonic development and settlement of *Osedax japonicus*. Fertilized eggs are spawned to the transparent mucus of a female and larvae swim out from the mucus at the trochophore stage. Larvae settle on whalebones, elongate their body and crawl around on the bones. Then, they secrete mucus to make the translucent cylindrical tube and two palps start to develop. Two weeks after settlement, extended palps of worms are seen from the outside of bones. The recruit of dwarf male is induced by rearing larvae with adult females. Six weeks after settlement, females start to spawn eggs to their mucus. Their short generation time should reflect their unique reproductive strategy.



*Friday 7<sup>th</sup> December*

*Conservation and Management 1*

## **SETTING GLOBAL CONSERVATION PRIORITIES FOR SEAMOUNTS: COUPLING DEEP SEA WITH PELAGIC CONSERVATION**

**Morato T<sup>1</sup>, Taranto G<sup>1</sup>, Kvile K<sup>1</sup>, Santos R<sup>1</sup>, Pitcher T<sup>2</sup>**

<sup>1</sup> University of the Azores, Portugal, <sup>2</sup> Fisheries Center, University of British Columbia, Canada

In the last twenty years, several global targets for protection of marine biodiversity have been adopted but have failed. The Convention on Biological Diversity (CBD) now aims at preserving 10 % of all the marine biomes by 2020. For achieving this goal, ecologically or biologically significant areas (EBSA) have to be identified in all biogeographic regions. However, the methodologies for identifying the best suitable areas are still to be agreed. Here, we propose a framework for applying the CBD EBSA criteria to locate potential ecologically or biologically significant seamount areas based on the best information currently available. The framework combines the likelihood of a seamount constituting an EBSA and its level of human impact and can be used to locate priority areas for seamount conservation at global, regional and local scales. This methodology allows the classification of individual seamounts into various portfolio conservation categories which can help optimizing management efforts toward the protection of the most suitable areas. The framework was tested against 1000 dummy seamounts with satisfactory results in terms of assigning seamount to proper EBSA and threats categories. Additionally, the framework was applied to about 200 seamounts that were assigned to sixteen different portfolio categories from low EBSA threats to very high EBSA threats. This framework is not designed to produce definite solutions in terms of EBSA selections but rather to give alternatives to prioritize choices based on management objectives. This framework also allows the identification of seamount EBSAs and threats considering different ecological groups in the pelagic, benthic of both realms. Therefore, this framework may represent an important tool to mitigate seamount biodiversity loss and to achieve the 2020 goals.



Thursday 6<sup>th</sup> December

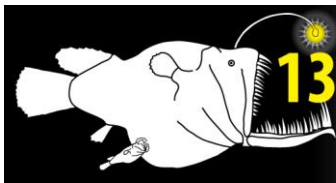
Temporal Patterns 1

## PARALLEL DECADAL VARIABILITY IN JUVENILE GROWTH RATES FOR NORTHERN AND SOUTHERN HEMISPHERE ORANGE ROUGHY POPULATIONS

Morrongiello J<sup>1</sup>, Thresher R<sup>1</sup>, Sloyan B<sup>1</sup>, Krusic-Golub K<sup>2</sup>, Shephard S<sup>3</sup>, Cerna F<sup>4</sup>, Minto C<sup>5</sup>, Nolan C<sup>5</sup>

<sup>1</sup> CSIRO Wealth from Oceans Flagship, GPO Box 1538, Hobart 7001 Australia, <sup>2</sup> Fish Aging Pty Ltd, Australia, <sup>3</sup> Galway-Mayo Institute of Technology, Galway, Ireland, <sup>4</sup> Instituto de Fomento Pesquero, Valparaiso, Chile, <sup>5</sup> Irish Sea Fisheries Board, Dublin, Ireland

We reconstruct trends over the last 150 years in growth rates of juvenile orange roughy (*Hoplostethus atlanticus*) collected in the SW Pacific (Tasman Sea), SE Pacific (off Chile) and NE Atlantic (Irish Sea) from analysis of otolith structure. Individual growth rates for this long-lived species were inferred from the widths of the first five annuli laid down by each individual. Collectively the data span a period from 1820 to 1992, covering similar ranges in all three areas. Mean growth rates differ between sites (on average, TS>IS>Chile) and vary widely among individuals at each. Nonetheless, there are surprisingly similar decadal trends for fish from all three. Comparison with coral proxies for the Tasman Sea population suggests this variability reflects long-term variation in temperatures in the intermediate water masses occupied by the species in each area. The similarity of the two Southern Hemisphere populations is consistent with a common origin of the Antarctic Intermediate Water inhabited by fish at the two sites. The similar variation in the Irish Sea population implies a globally acting mechanism that underlies intermediate depth water mass characteristics and environmental conditions for deep-sea biota in the two hemispheres.



International

# 13<sup>th</sup> Deep-Sea Biology Symposium

Wellington, New Zealand 3 – 7 December 2012

Thursday 6<sup>th</sup> December

Temporal Patterns 1

## TEMPORAL AND SPATIAL PATTERNS OF IN SITU COMMUNITY STRUCTURE USING TIME-LAPSE CAMERA SYSTEMS AT A VENT FIELD ON THE EAST PACIFIC RISE

Munro C<sup>1</sup>, Luther, III GW<sup>2</sup>, Lutz R<sup>4</sup>, Vetriani C<sup>4</sup>, Moore T<sup>3</sup>, Herrera S<sup>1</sup>, Shank T<sup>1</sup>

<sup>1</sup> Woods Hole Oceanographic Institution, <sup>2</sup> College of Earth, Ocean and Environment, University of Delaware, <sup>3</sup> College of Earth, Ocean and Environment, University of Delaware and Instituto Mediterraneo de Estudios, <sup>4</sup> Institute of Marine and Coastal Sciences, Rutgers University

High-resolution digital imagery obtained by time-lapse camera systems enables continuous in situ monitoring of faunal community structure and habitat use in the deep-sea. This presentation will discuss results of a time-lapse deployment from a site in the Tica vent field on the East Pacific Rise. We examined 956 images taken over a 47-hour period. In-situ temporal changes in fluid chemistry and temperature revealed the first in-situ evidence for potential “chemotaxis” in a hydrothermal vent-endemic species, the swarming amphipod *Halice hesmonectes*. Rapid changes in the flux of hydrogen sulfide and temperature coincide with the mass movement and measured density responses of amphipods to follow and occupy increasing concentrations of sulfide and elevated temperature. We link fluid chemistry, flux, and microseismicity to these faunal responses to hypothesize that these swarms track the gradients and concentrations of diffuse fluid venting in an effort to feed on higher concentrations of microbes. The temporal distribution of other mobile fauna, including brachyuran and galatheid crabs reflected differences in hydrothermal flux, temperature, and sulfide concentration. This study reveals new insights into changes in community structure, temporal and spatial scales over which they respond to environmental change.



*Wednesday 5<sup>th</sup> December*

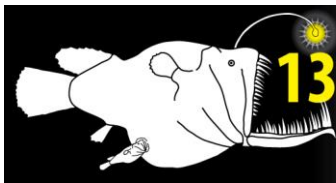
*Discovery 2*

## **FUNGAL DIVERSITY IN DEEP-SEA ENVIRONMENTS**

**Nagano Y<sup>1</sup>**, Nagahama T<sup>1,2</sup>, Konishi M<sup>1</sup>, Shimane Y<sup>1</sup>, Mori K<sup>1</sup>, Ohta Y<sup>1</sup>, Hatada Y<sup>1</sup>

<sup>1</sup> Institute of Biogeosciences, Japan Agency for Marine-Earth Science and Technology (JAMSTEC), <sup>2</sup> Department of Food and Nutrition, Higashi-Chikushi Junior College

As in other environments, micro-organisms are known to play an important role in deep-sea ecosystems. Since the first foray into deep-sea research, with the development of advanced instrumentation for sampling and researching life at great depths, the presence and ecological importance of deep-sea bacteria and archaea has been extensively researched and documented. In contrast, fungi, one of the most extremotolerant and ecologically important groups of micro-organisms, have been relatively underexplored in deep-sea environments. However, the presence of fungi in deep-sea environments, including deep marine subsurface and their ecological importance in the ecosystems is drawing attention recently. Many fungi have been isolated by culture-dependent methods from various deep-sea environments, with the majority showing similarity to terrestrial species. On the other hand, culture-independent methods have revealed many novel fungal phylotypes, including novel fungal lineages recently validated as the new phylum Cryptomycota. Cryptomycota is suspected to lack typical fungal chitin-rich cell walls and is suggested as one of the ancient lineages within the kingdom of fungi. Zoosporic fungi, including Cryptomycota, have been extensively detected, especially from hydrothermal vents and methane cold-seeps. Further investigation on deep-sea fungi is promising to provide key insights into the phylogenetic histories of fungi and their mechanisms of adaptation to extreme environments, and a better understanding of deep-sea ecosystems. Although the true abundance and importance of fungi in deep-sea ecosystems is still not yet fully understood, current knowledge on the diversity of fungi in deep-sea environments through recent studies will be discussed in this presentation.



International

# 13<sup>th</sup> Deep-Sea Biology Symposium

Wellington, New Zealand 3 – 7 December 2012

Thursday 6<sup>th</sup> December

Reproduction and Population 2

## GAMETOGENESIS AND POPULATION STRUCTURE OF A HYDROTHERMAL VENT GASTROPOD *LEPETODRILUS NUX* AT DIFFERENT VENT SITES IN OKINAWA TROUGH

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<sup>1</sup> Okinawa Institute of Science and Technology, <sup>2</sup> Japan Agency for Marine-Earth Science and Technology, <sup>3</sup> The University of Tokyo

The gastropod *Lepetodrilus nux* is the one of widely-distributed species in animal communities at deep-sea hydrothermal vents along Okinawa Trough. However, the biological life-history characteristics remain poorly understood for the species. In general, gametogenesis and population structure help to understand the supply-side effects on population dynamics, mainly addressing the following questions: (1) Do larvae exist in the water column at any time? (2) Do larvae of the species recruit continuously to certain habitats? In this study, we observed gonads of *L. nux* using histological techniques, and population structure using size-frequency analysis. *L. nux* individuals were collected from four different vent sites in Okinawa Trough, using suction sampler and the ROV Hyper-dolphin in 2011. As two *Lepetodrilus* spp. have been identified along Okinawa Trough, we first identified all *Lepetodrilus* individuals genetically. They did not differ genetically among vent sites in Okinawa Trough. Therefore, we conducted analysis as considering all samples as *Lepetodrilus nux*. *L. nux* exhibited different gametogenic stages within a gonad. Population structures showed polymodal size-frequency distributions. These results suggest *L. nux* may reproduce continuously thus larvae may exist in the water column at any time, but larvae may not recruit continuously in a certain area.



*Wednesday 5<sup>th</sup> December*

*Discovery 1*

## **DISCOVERIES MADE ON SEAMOUNTS ALONG THE SOUTHWEST INDIAN OCEAN RIDGE**

**Narayanaswamy B**<sup>1</sup>, Rogers A<sup>2</sup>, Paterson G<sup>3</sup>, Serpetti N<sup>1</sup>, Taylor M<sup>2</sup>, Woodall L<sup>3</sup>, Lamont P<sup>1</sup>, Chivers A<sup>1</sup>, Packer M<sup>3</sup>, Ferrero T<sup>3</sup>

<sup>1</sup> Scottish Association for Marine Science, <sup>2</sup> University of Oxford, <sup>3</sup> Natural History Museum, London

Little exploration has been undertaken on the seamounts in the Southwest Indian Ocean and consequently little is known regarding their biological ecosystems. At the end of 2011 the UK NERC funded expedition to the Southwest Indian Ocean took place, sampling five seamounts along the Ridge system. The seamounts located to the south and centre of the ridge lie in a region of high current velocities and enhanced primary production, whilst the more northerly seamounts lie under the Southern Indian Ocean gyre, a region of weak currents and low primary productivity. Although much reduced now, the seamounts have been the focus of an intense commercial deep-water trawl fishery. Two voluntary benthic protected areas are in force in this region.

The ROV Kiel 6000 was used to collect video and stills footage from each seamount, as well as samples of coral framework individual corals and where possible push cores were taken to sample the sediment infauna. The megacorer and HYBIS grab were also deployed wherever possible to collect infaunal macro- and meio- fauna. The video footage and stills images show a range of highly diverse and complex habitats on the seamounts. Numerous types of corals, sponges as well as lobsters, eels, sea stars and brittle stars to name but a few were observed. In addition, there was evidence of human impact from trawling with trawl scars, large areas of bare rock as well as lost fishing gear including lobster pots and gill nets.





Thursday 6<sup>th</sup> December

Reproduction and Population 2

#### A NEW METHOD FOR IN SITU MARKING TO STUDY GROWTH RATE OF HYDROTHERMAL VENT BIVALVES

Nedoncelle K, Lartaud F<sup>1</sup>, De Rafelis M<sup>2</sup>, Le Bris N<sup>1</sup>

Sorbonne Université – Pierre et Marie Curie

The set-up of an appropriate method adapted to deep environments was applied on hydrothermal-vent bivalves shells to investigate their growth rate variability in their natural environment. In situ chemical staining was used for the first time on the mussel *Bathymodiolus thermophilus* at 2500 m depth at 9°47' N on the East Pacific Rise vent field. Combined with high-resolution microincrement analysis, it allows to accurately determine the age and growth rate of the shells. The mark-and-recapture experiment conducted over 10 days shows that *B. thermophilus* mineralizes its shell according to a circalunidian rhythm and displays tide-related growth-rate variability. A von Bertalanffy growth-rate model was built for this species and highlights that the largest shell (21.45 cm) should be 19 years old, which corresponds to growth-rate change with ontogeny of 3.9–1.7 cm.yr<sup>-1</sup>. This growth pattern is consistent with a specific adaptation of *B. thermophilus* to the instability of the habitat, where major volcanic eruptions repeatedly disturb settled populations. Our model is supported by in situ observations of new colonization events between May 2010 and March 2012. These findings have relevance for studying population structure and recruitment in mytilid bivalves in the deep sea. Additionally, the method developed enables analysis of shell growth response to hydrothermal environmental variability.



*Thursday 6<sup>th</sup> December*

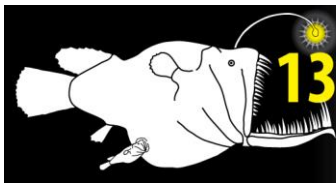
*Trophic and Process 1*

## **DEPTH VARIABILITY OF PARTICLE FLUXES AND IMPLICATIONS FOR THE ENERGY REQUIREMENTS OF DEEP-OCEAN BENTHIC COMMUNITIES**

**Nodder S<sup>1</sup>**, Duineveld G<sup>2</sup>, Northcote L<sup>1</sup>, Witbaard R<sup>2</sup>, Lavaleye M<sup>2</sup>

<sup>1</sup> National Institute of Water & Atmospheric Research (NIWA), <sup>2</sup> Royal Netherlands Institute for Sea Research, Texel, The Netherlands

Global models of particle flux often used in the construction of energy budgets for deep-ocean benthic communities generally assume a power law relationship whereby organic fluxes reduce exponentially with increasing depth. In natural systems, however, where fluxes have been measured at mid-water column and near-bottom depths over the same time-scales, it is apparent that such simplistic models do not always hold. Recent evidence from sediment traps moored continuously at 1500 m and at 50 m off the sea-bed (~2800–3100 m water depth) for more than a year (2009–11) in subtropical and subantarctic water masses to the east of New Zealand suggest that the near-bed fluxes of organic material are typically higher than those at mid-water depths over all time-scales (bi-weekly, monthly, seasonally, interannually). Thus, a single trap deployed at mid-water column depths does not provide a very robust estimate of the total organic flux that the benthos actually receives. Previous estimates of the energetic requirements of deep-sea communities, based on a single mid-water trap and benthic lander oxygen chambers deployed for a year at the same locations in 2000–01, suggested that there was a significant deficit in the carbon requirements of the benthos. Based on the new trap data, as measured 50 m above the seabed, it is apparent that a substantial proportion of this deficit will be alleviated by taking into account the total organic carbon flux to the sea-floor, with the realisation that particle fluxes are a horizontal as well as a vertical process.



International

# 13<sup>th</sup> Deep-Sea Biology Symposium

Wellington, New Zealand 3 – 7 December 2012

Friday 7<sup>th</sup> December

Trophic and Process 3

## IN SITU EXPERIMENTAL MEASUREMENTS OF CARBON FIXATION ON THE DEEP-SEA FLOOR

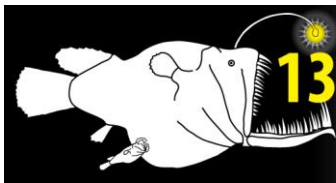
Nomaki H<sup>1</sup>, Inoue K<sup>2</sup>, Suga Hi<sup>1</sup>, Tsuchiya M<sup>1</sup>, Toyofuku T<sup>1</sup>, Kitazato H<sup>1</sup>, Nunoura T<sup>1</sup>

<sup>1</sup> JAMSTEC, <sup>2</sup> AORI, the University of Tokyo

With the exception of chemosynthetic communities, deep-sea benthic food webs are sustained by particulate organic matter derived from the water column. However, recent studies suggest that chemoautotrophic carbon fixation may also contribute to the deep-sea benthic ecosystems. However, there was no quantitative measurement of carbon fixation in a “normal” deep-sea floor.

Since 2008, we have measured organic carbon production rates by in situ incubation experiments using a <sup>13</sup>C-labelled sodium bicarbonate. The experiments were carried out at three different water depths (530 to 1145 m) of the Arabian Sea, 914 m depth of the Sea of Japan, complementary onboard experiments at the Sea of Japan, 1453 m of the Sagami Bay, and 5370 m depth of the western North Pacific. We also investigated effects of nutrient addition to the measured carbon fixation rates. Nutrients concentrations, carbon isotopic compositions of sediments and some protists, and microbial communities were investigated using incubated sediments.

Measured carbon fixation rates varied largely between oceanic settings: highest in the bathyal Sagami Bay and lowest in two deeper stations of the Arabian Sea and the abyssal plain of the western North Pacific. Organic carbon produced at the deep-sea floor corresponds up to 3 % of the particulate organic carbon flux from photic zone, suggesting substantial contribution of autochthonous carbon fixation in certain area. Nutrient additions significantly enhance the carbon fixation. Some benthic foraminifera were slightly labeled with <sup>13</sup>C, suggesting they partly rely on autochthonous organic carbon which is produced by chemoautotrophic microbes. These results require reconsideration of the traditional view that deep-sea benthic ecosystems are solely sustained by organic matters originated from the photosynthesis.



International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

*Tuesday 4<sup>th</sup> December*

*Autoecology 1*

**SYMBIOTIC DIVERSITY IN DEEP-SEA WOOD BORING XYLOPHAGAINAE CLAMS**

**Nunes-Jorge A, Dubilier N, Borowski C**

Max Planck Institute for Marine Microbiology, Bremen, Germany

Sunken wood can provide a valuable carbon source to the sea floor of both shallow and deep-sea waters. These organic falls are rapidly colonized by specialized organisms such as wood-boring bivalves that feed on the wood. Deep-sea wood-boring bivalves (family Pholadidae: subfamily Xylophaginae) occupy the same ecological niche as their shallow-water counterparts, the so-called shipworms (family Teredinidae). Both groups harbor symbiotic bacteria in their gills. While shallow-water shipworm symbionts have been identified as cellulolytic nitrogen-fixing Gammaproteobacteria, very little is known about the symbionts of deep-sea Xylophaginae.

This study focuses on the diversity and biogeography of symbionts in five species of deep-sea Xylophaginae. Our specimens were recovered from experimentally deployed wood-logs in 600–2300 m water depths at six locations that included sites in the deep Mediterranean as well as the northern and tropical Atlantic. Initial phylogenetic characterization of the symbionts based on 16S rRNA clone libraries revealed that the majority of the sequences clustered with the symbionts of the shallow-water Teredinidae. This suggests similar physiological properties, namely cellulase production and nitrogen fixation. In the deep-sea Xylophaginae, we regularly found two or more different symbiont phlotypes in single host individuals. Some host species contained closely related symbiotic phlotypes across geographical locations indicating host-specific symbiont distribution. Other phlotypes were more closely related in different host species co-occurring at the same location indicating geographic structuring of symbiont distribution rather than host specificity. Fluorescence In Situ Hybridization and in-depth 16SrRNA analyses will be the next step to better understand the distribution patterns and evolutionary history of symbioses in deep-sea wood-boring bivalves.



**Thursday 6<sup>th</sup> December**

**Reproduction and Population 1**

**REPRODUCTIVE BIOLOGY AND POPULATION STRUCTURE OF THE ALVINOCARIDID SHRIMP *RIMICARIS HYBISAE* AT HYDROTHERMAL VENTS ON THE MID-CAYMAN SPREADING CENTRE**

**Nye V, Copley J**

University of Southampton

Characterising the life-history biology of hydrothermal-vent species is a prerequisite for understanding the dynamics and distribution patterns of these insular populations. Recent studies have revealed spatial and temporal variation in the reproductive development of some species at hydrothermal vents (e.g. Copley et al., 2003). The alvinocaridid shrimp *Rimicaris hybisae* is an important component of the faunal assemblages at at least two deep-water hydrothermal-vent fields on the Mid-Cayman Spreading Centre (MCSC) (Connelly et al. 2012; Nye et al. 2012). Here we present novel data from recent explorations of hydrothermal vent fields at the MCSC, which contributes to our analyses of reproductive processes of macrofaunal invertebrates from MCSC vents, and the role of life-history on the distribution patterns of vent taxa. Our aim was to determine any spatial variation in the population structure and reproductive features of *R. hybisae* between known vent fields at the MCSC, and to compare our results with the data available for other alvinocaridid shrimps from vents and cold seeps. Six samples of *R. hybisae* were collected from different locations at the Beebe Vent Field (~2300 m) and the Von Damm Vent Field (~5960 m), MCSC, in January 2012. Population structure, minimum fecundity and oocyte size-frequency distributions were compared between sample locations to assess spatial variation. Our results are presented in the context of available data for other alvinocaridids. We anticipate that future analysis will enable us to determine any temporal patterns in the reproduction of *R. hybisae* and to elucidate further the life-cycle of this species.



*Monday 3<sup>rd</sup> December*

*Dispersal and Connectivity 2*

## **THE 'L' SUPERHIGHWAY: BATHYAL CONNECTIVITY ACROSS ATLANTIC, INDIAN AND SOUTH PACIFIC OCEANS**

**O'Hara T**

Museum Victoria, Melbourne, Australia

The existence of bathyal (200–3500 m) species with global distributions has been observed since the 19<sup>th</sup>-century Challenger Expedition. Subsequent taxonomy has both split species complexes and synonymised regional variants, and it is still difficult to generalise about bathyal species distribution and dispersal. The recent discovery of numerous additional species of bathyal ophiuroids (brittle stars) from southern Australia and New Zealand that are morphologically indistinguishable from populations in the North Atlantic has prompted the investigation of these species using modern molecular methods. Large-scale phylogeographies of widespread bathyal animals are rare because of the difficulty in sourcing appropriate material. However recent expeditions to the mid-Atlantic Ridge, Southern Atlantic, SW Indian Ocean, Australia, New Zealand, and throughout the SW Pacific has provided samples that will begin to address questions of lineage distribution, both geographically and bathymetrically. The results do not necessarily conform to expectations about what environmental factors or life-history characteristics may limit these distributions.



Wednesday 5<sup>th</sup> December

Biodiversity Pattern – Small 1

## DISTRIBUTION OF VESICOMYID BIVALVE SPECIES ASSOCIATED TO COLD SEEPS IN THE CONGO BASIN: SPATIAL OR DYNAMIC CONTROL?

Olu K<sup>1</sup>, Decker C<sup>1</sup>, Andersen A<sup>2</sup>, Arnaud-Haond S<sup>1</sup>, Caprais JC<sup>1</sup>, Khripounoff A<sup>1</sup>, Krylova E<sup>3</sup>, Marcon Y<sup>4</sup>, Ondréas H<sup>5</sup>, Rabouille C<sup>6</sup>

<sup>1</sup> Ifremer, <sup>2</sup> Université Paris 6, <sup>3</sup> Shirshov Institute, <sup>4</sup> MARUM, <sup>5</sup> Ifremer, <sup>6</sup> CEA

In the Congo basin there are cold seeps fuelled by fluids coming from buried paleo-turbidite channels and associated with giant pockmarks, at depths 600–3000 m, and seeps presumably related to rapid terrestrial organic matter recycling in the terminal lobes of the present-day active channel of the Congo, at 5000 m depth. The four explored pockmarks around 3000 m depth are colonised by large symbiont-bearing taxa. Whereas the same siboglinid and mytilid species were found on different pockmarks, vesicomys were presented by different species on different pockmarks. Previously we hypothesized bathymetric zonation for this family and suggested that the main factor for determination vesicomys species composition in the Gulf of Guinea could be depth. Nevertheless recently received data show that the species composition can be varied in the same depth range of different pockmarks. As hydrogen sulphide concentrations in the vesicomys aggregates vary among pockmarks, a chemical control could be superimposed to the bathymetry to explain vesicomys diversity and distribution.

In the pockmark Regab, *Christineconcha regab* is highly dominant and distributed all over the area, while *Laubiericoncha chuni* was restricted to areas of lower methane fluxes. These species differ by their morphology and physiology. *L. chuni* has long siphons allowing deeper location in the sediment to reach deeper sulphide levels. Moreover, *L. chuni* possess an intra-erythrocyte circulating hemoglobin with high oxygen binding affinity whereas *C. regab* has only myoglobin in its foot. In parallel, mosaic analysis revealed highly dynamic areas potentially related to transient fluxes that could favour *C. regab*. In the active seeps of terminal lobes the dominant species was usually *C. regab*, while *Abyssogena southwardae* was sampled in sites presently disconnected from the active channel.

The data suggest narrow ecological specialization of vesicomys. Environmental heterogeneity provides a base for local vesicomys diversity at least at generic level.





Monday 3<sup>rd</sup> December

Biodiversity Pattern – Large Scale 3

## DISTRIBUTION AND LIFE HISTORY OF SHOVELNOSE DOGFISH *DEANIA CALCEA* IN NEW ZEALAND WATERS

Parker S<sup>1</sup>, Jones E<sup>2</sup>, Clark M<sup>3</sup>, King K<sup>3</sup>

<sup>1</sup> NIWA Nelson, <sup>2</sup> NIWA Auckland, <sup>3</sup> NIWA Wellington, New Zealand

The shovelnose dogfish (or birdbeak dogfish, *Deania calcea* (Lowe, 1839)) is a common temperate squaloid elasmobranch occurring globally on upper continental or insular slopes from 500–1200 m depth. It is a common bycatch species in deepwater trawl and bottom longline fisheries in temperate regions of the eastern Atlantic and western Pacific oceans, and the Eastern south Pacific near Chile, although its global distribution and ecology are not well described. Concern about the productivity of deepwater chondrichthyans, and therefore vulnerability to impacts from fishing has been growing globally as studies show that some species have life history characteristics that depress their ability to recover quickly following exploitation. Spatial analysis of survey and fishery observer data spanning more than 30 years shows discrete depth distributions and spatially segregated sex and reproductive stage distributions. Pregnant females are only found around the North Island while putative pupping grounds are identified on western Chatham Rise. Of the deepwater dogfish found in New Zealand, *D. calcea* is the most abundant, yet basic biological information about distribution and productivity, especially age, gestation period, and frequency are still lacking. Although difficult to conduct, the studies needed to validate the ageing methodology (dorsal spine sections) and to document gestation period should be a high priority for this and other deepwater elasmobranch species.



*Wednesday 5<sup>th</sup> December*

*Biodiversity Pattern – Small 1*

**THE DISTRIBUTION AND DIVERSITY OF HETEROTROPHIC PROTISTS IN A METHANE SEEP ECOSYSTEM OFF THE COAST OF OREGON**

**Pasulka AL.**<sup>1</sup>, Orphan VJ<sup>2</sup>, Steele JA<sup>2</sup>, Chadwick G<sup>2</sup>, Connon S<sup>2</sup>, Landry MR<sup>1</sup>, Levin LA<sup>1</sup>

<sup>1</sup> Scripps Institution of Oceanography, UCSD, <sup>2</sup> California Institute of Technology

Heterotrophic protists are critical components of marine ecosystems; they influence carbon cycling as well as ecosystem structure and function by consuming prokaryotic microorganisms and recycling nutrients. Until recently, protozoan communities, particularly ciliates and flagellates, have been largely uncharacterized in deep-sea chemosynthetic ecosystems. Therefore, our current understanding of the role heterotrophic protists may have in structuring chemosynthetic communities or in methane biogeochemical cycling is limited. An important first step in understanding the ecology of marine protists in chemosynthetic ecosystems is characterizing their distribution and diversity within these environments. In this study, we explored how various sources and scales of heterogeneity (e.g., substrate type, chemical gradients, and biological interactions) structured protistan communities in a deep-sea methane seep at Hydrate Ridge, Oregon. We sampled sediments and carbonate rocks from 600 and 800 m water depths. Using terminal restriction fragment length polymorphism (T-RFLP) in conjunction with 18S rRNA sequencing, we characterized the composition and diversity of heterotrophic protists along biogeochemical gradients in seep sediments. While clam beds and bacterial mats are both common features in seep environments, they exhibit different pore water chemical gradients (e.g., methane and sulfide) and prokaryotic communities (potential prey sources). Based on T-RFLP, we found that protistan composition and diversity varied with depth in the sediments. However, these depth patterns differed in sediments below bacterial mats vs. clam beds. Clone libraries revealed that ciliates were the dominant non-rhizoid protists. Additionally, sulfide concentration appears to be an important factor in determining distributional patterns of heterotrophic protists at methane seeps.



*Wednesday 5<sup>th</sup> December*

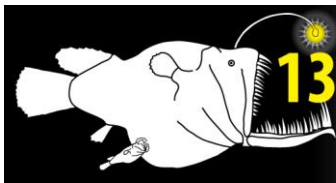
*Biodiversity Pattern – Small 2*

#### **CHARACTERISING HABITAT COMPLEXITY — USING MICROCT SCANNERS TO STUDY CORAL FRAMEWORKS**

**Paterson G**<sup>1</sup>, Ahmed F<sup>1</sup>, Serpetti N<sup>2</sup>, Taylor M<sup>3</sup>, Ferrero T<sup>1</sup>, Narayanaswamy B<sup>2</sup>, Lamont P<sup>2</sup>, Woodall L<sup>1</sup>, Packer M<sup>1</sup>, Rogers A<sup>3</sup>

<sup>1</sup> Natural History Museum, <sup>2</sup> Scottish Association for Marine Science, <sup>3</sup> University of Oxford

Habitat heterogeneity is seen as a major factor in the structuring and persistence of biological assemblages, particularly their diversity and abundance. Yet despite this seeming importance there has been little focus on the mechanisms which underpin such links. Here we present initial results from a study to assess habitat heterogeneity and complexity in deep-water coral habitats. This initial phase assesses how to measure and categorise the structural complexity of a coral framework using micro-CT-scanner to create 3-D models of coral samples from a range of seamounts in the SW Indian Ocean Ridge. Using a micro-CT scanner allows us to measure accurately various components of the coral framework such as surface area, (i.e. living area), branching level (i.e. habitat complexity) and the various volumes of cavities within the framework (i.e. macrofaunal burrowing rates). Surface area is important to organisms which use coral as a substratum while cavity space is important for those animals which use the coral as refuge or as living space. This latter measure lends itself to fractal analyses and the results can be related back to the different size elements of the associated fauna. We explore how these results can be scaled to larger coral structures and reefs. Understanding the mechanisms which link habitat heterogeneity and diversity is a crucial step in explaining its importance in conservation.



International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

**Monday 3<sup>rd</sup> December**

**NZ Context Plenary**

**DEEP-SEA RESEARCH IN THE NEW ZEALAND REGION, 1865–1965**

**Pawson Dave**, Pawson Doris

National Museum of Natural History, Smithsonian Institution, Washington, DC, USA

Between 1865 and 1965, New Zealand deep-sea research featured great discoveries, memorable incidents, and extraordinary personalities. Based upon published and unpublished materials, and some personal experiences, an attempt is made to convey the distinctive flavour of this pioneering century. The era began with the founding of the Colonial Museum (now Te Papa), and ended with the coming of age of the New Zealand Oceanographic Institute (now NIWA).

In 1874, the HMS Challenger was the first research ship to occupy deep-sea (> 180 m) stations near New Zealand. Challenger collected more than 220 new species of animals in the region, and New Zealand became the type locality for several iconic deep-sea species. Other well-known visiting deep-sea vessels included the *Dana* (1930), *Discovery II* (1932), *Galathea* (1952), *Vitjaz* (1958), and *Eltanin* (early 1960s). Early New Zealand government vessels, such as *Hinemoa* and *Amokura*, also made significant contributions. Of great importance were relatively inexpensive local investigations by the New Zealand universities from the late 1940s to the 1960s. These, and some other modest programs, employed some astonishingly small vessels, which retrieved samples of fishes and invertebrates from great depths. By 1965, the New Zealand Oceanographic Institute, the Marine Department, and the Dominion Museum (Te Papa) had occupied several hundred deep-sea biological stations, and New Zealand's role in deep-sea research was well established.



*Monday 3<sup>rd</sup> December*

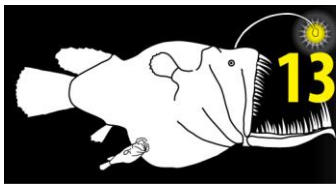
*Dispersal and Connectivity 2*

#### **HIGH-THROUGHPUT POPULATION GENETICS IN A DEEP-SEA HYDROTHERMAL-VENT LIMPET**

**Plouviez S<sup>1</sup>, Ball B<sup>1</sup>, Clark J<sup>1</sup>, O'Neill E<sup>2</sup>, Weisrock D<sup>2</sup>, Cunningham C<sup>3</sup>, Van Dover C<sup>1</sup>**

<sup>1</sup> Nicholas School of the Environment, Duke University Marine Laboratory, 135 Duke Marine Lab Road, Beaufort, NC 28516, USA, <sup>2</sup> Department of Biology, University of Kentucky, 101 Thomas Hunt Morgan Building, Lexington, KY 40506, USA, <sup>3</sup> Biology Department, Duke University, 130 Science Drive, Durham, NC 27708, USA

Estimating dispersal capabilities of deep-sea species is a major challenge. Larval life history of deep-sea species is poorly understood, making direct estimation of dispersal difficult. Population-genetic studies, or how populations are genetically connected among each other, can help in estimating those dispersal capabilities. Due to the limited development of molecular markers, most of the population genetic studies on deep-sea species have used a single mitochondrial gene (cytochrome oxidase I, COI) to infer connectivity among populations. However, the utility of this gene by itself is limited. Because it is usually inherited only maternally, COI can only trace female migration and does not detect potential recombinants between populations or between species. Some recent studies have started to compare a few nuclear genes with the COI gene, allowing more rigorous studies of connectivity. In our study, we have used a Next Generation Sequencing approach to infer population connectivity and phylogeography on a deep-sea hydrothermal vent limpet from the southwest Pacific.



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Thursday 6<sup>th</sup> December

Human Impacts 3

**CHANGES IN BIOMASS AND POPULATION SIZE STRUCTURE OF DEMERSAL DEEP-SEA FISHES OF THE PORCUPINE SEABIGHT AND ABYSSAL PLAIN (ICES SUBAREA VII), NORTH EAST ATLANTIC OCEAN; IMPACTS OF A DEEP WATER FISHERY?**

**Priede I (Monty)**<sup>1</sup>, Godbold JA<sup>2</sup>, Bailey DM<sup>3</sup>, Collins MA<sup>4</sup>, Gordon JDM<sup>5</sup>, Spallek W<sup>6</sup>

<sup>1</sup> Oceanlab, University of Aberdeen, <sup>2</sup> National Oceanography Centre, Southampton, UK, <sup>3</sup> Faculty of Biomedical and Life Sciences, University of Glasgow, UK., <sup>4</sup> Government House, Port Stanley, Falkland Islands, <sup>5</sup> Scottish Association for Marine Science, Oban, UK, <sup>6</sup> Faculty of Earth Science & Environmental Management, University of Wroclaw, Poland

A time series from 1977–1989 and 2000–2002 of scientific trawl surveys in the Porcupine Seabight and adjacent Abyssal Plain of the NE Atlantic was analysed to assess changes in demersal fish biomass and length frequency. These two periods coincide with the on-set of the commercial deep-water fishery in the late 1970s and the on-set of the regulation of the fishery in the early 2000s and allowed us to investigate changes in the relationship between total demersal fish biomass and depth between the pre- and post commercial fishing periods, changes in the biomass ( $\text{kg.km}^{-2}$ ) depth distribution and length frequency distribution of the most dominant fish species. Our results show a decline in total demersal fish biomass of 36 % within the depth range of the commercial fishery (< 1500 m). Whilst there were significant declines in target (*Coryphaenoides rupestris*) and non-target (e.g. *Coryphaenoides guentheri* and *Antimora rostrata*) species, not all species declined significantly. Changes in the overall length-frequency distribution were detected for two species (*Coryphaenoides armatus*, *Synphobranchus kaupii*), but only at depths greater than 1800 m (outside the maximum depth for commercial trawling). This suggests that whilst there is evidence for likely fisheries impacts on the biomass distribution of the demersal fish population, species-specific impacts are highly variable. It is clear that changes in population structure can extend beyond the depth at which fishing takes place, highlighting the importance for also considering the indirect effects on deep-sea fish populations.



*Thursday 6<sup>th</sup> December*

*Reproduction and Population 2*

## **REPRODUCTIVE BIOLOGY AND RECRUITMENT IN THE DEEP-SEA FISH COMMUNITY OF THE NORTH-WESTERN MEDITERRANEAN CONTINENTAL MARGIN**

Fernandez-Arcaya U<sup>1</sup>, Ramirez-Llodra E<sup>1</sup>, Rotllant G<sup>2</sup>, Recasens L<sup>1</sup>, Aguzzi J<sup>1</sup>, Flexas M<sup>3</sup>, García Jose A<sup>1</sup>, Sánchez A<sup>4</sup>, Company Joan B<sup>1</sup>

<sup>1</sup> Institut Ciències del Mar, CSIC, Barcelona, Spain, <sup>2</sup> IRTA, San Carles de la Ràpita, Spain, <sup>3</sup> GRC Geociències Marines, Uni. Barcelona, Spain

Reproductive temporal patterns are presently unknown in the majority of deep water continental margin fishes. In the deep ecosystem of the Blanes submarine canyon (western Mediterranean) and its adjacent open slope we conducted trawl sampling surveys between 300 and 1750 m depth in different seasons in order to assess, for the most abundant species, the occurrence of the following patterns: (1) temporal pattern in the reproductive process and its relationships with depths and (2) preferential depth stratum for the general recruitment of the fish community. In order to establish a potential cause-effect relationship between timing of reproduction and organic matter inputs, we also used data from sediment traps gathered at the same temporal frequency as trawling. We detected the occurrence of temporization in the reproductive activity of 14 species. In middle slope (i.e. 800–1350 m), a very marked seasonal reproduction during autumn-winter was observed, while reproductive activity was spread over all seasons in shallower and deeper areas (i.e 300–800 m and below 1350 m). Moreover, a link between the distribution of nepheloid layers and the distribution of juveniles was observed, suggesting a possible trophic linkage between high concentration of particulate matter and the first stages of development. These results coincide with those already reported for megabenthic species of crustaceans decapods in the same area, suggesting the occurrence of a general temporization in reproduction related to depth.





*Wednesday 5<sup>th</sup> December*

*New Methods and Novel Techniques 2*

**TAKING THE LABORATORY INTO THE DEEP: IN SITU MIDWATER OXYGEN CONSUMPTION MEASUREMENTS AS A TOOL TO ADDRESS THE CHANGING VERTICAL DISTRIBUTION OF THE SERGESTID SHRIMP, *SERGESTES SIMILIS*, IN MONTEREY BAY, CALIFORNIA.**

**Reisenbichler K, Robison B**

<sup>1</sup> MBARI

The expanding oxygen minimum zone (OMZ) in Monterey Bay, California has been accompanied by changes in the vertical distribution centers of a number of midwater species, including the vertically migrating shrimp, *Sergestes similis*. The in situ midwater respirometry system (MRS) developed at MBARI is a promising tool for studying the oxygen consumption rates and limitations of mesopelagic animals within the range of oxygen concentrations at which they are normally found. It also has the capability of manipulating environmental conditions within the chambers (e.g., pH and oxygen concentration). By measuring respiration rates at depth, we can eliminate the variables introduced during traditional laboratory measurements (e.g., reduced pressure, animal perturbation during transfer, and variable seawater chemistry) to more directly ascertain the importance of oxygen concentration in determining the vertical distribution of these species. This presentation will describe the preliminary results of in situ respiration rate measurements and acidifications experiments of *S. similis* and compare them to those obtained in the lab.



*Monday 3<sup>rd</sup> December*

*Evolution 1*

## **ON THE PHYLOGENY OF MACROSTYLIDAE (ISOPODA) AND THEIR POSITION AMONGST THE JANIROIDEA**

**Riehl T**

University of Hamburg, Zoological Museum

The deep-sea isopod family Macrostylidae is very old and derived. It is characterized by a large number of apomorphies of which many have been attributed to a burrowing or tubicolous lifestyle. Unique statocysts located in the pleotelson and a tagma specialized for burrowing, the fossosome, are among these.

Since their first recognition in the late 19<sup>th</sup> century, it has been found closely related to Munnopsidae, Desmosomatidae and Nannoniscidae. Today, molecular data suggest a general affinity between all four families, but the phylogenetic position of each taxon showed dependence on the method of inference and the DNA marker used. Furthermore, additional potential sister taxa were suggested by the genetic analyses, such as Janirellidae, Mesosignidae and the aberrant genus *Xostylus*. Overall, the evidence remains contradictory. Despite its common occurrence and more than 80 described species from all world oceans, no revision of the family has yet been conducted and Macrostylidae remains monotypic.

First results of a new attempt to infer relationships within Macrostylidae and the family's position among the Janiroidea is presented. It is based on molecular data and improved taxon sampling. Ancient divergence was detected within Macrostylidae and the family has been found most closely related to Mesosignidae, Janirellidae and *Xostylus*, contradicting previous hypotheses. The results are compared with and discussed on the background of their morphology.



*Wednesday 5<sup>th</sup> December*

*New Methods and Novel Techniques 1*

**COMBINING LANDSCAPE ECOLOGY AND SPECIES-ENVIRONMENT RELATIONSHIPS FOR IMPROVED HIGH-RESOLUTION HABITAT MAPPING IN THE DEEP SEA**

**Robert K, Jones D, Huvenne V**

National Oceanography Centre

Creation of habitat maps, describing both biotic and abiotic components of marine ecosystems, is an important step for effective management. However, collecting biological information is time consuming and full coverage cannot usually be achieved. Examining species-environment relationships is of interest as environmental characterization is facilitated by acoustic surveys. To create habitat maps, fine-scale species-environment relationships can be modelled and used to map out species distributions, or bathymetric and backscatter maps can be classified into 'regions' of similar acoustic signatures for which characteristic species are identified. In this study, we combined both approaches. Sediment interpretation maps were created using sidescan sonar information collected with an automated underwater vehicle on the Rockall Bank, NE Atlantic. Megabenthic invertebrate abundances were extracted from imagery transects collected by a remotely operated vehicle. We used canonical ordination techniques to examine the relationships between fine-scale sediment characteristics extracted from the imagery as well as landscape metrics describing the patch mosaic structure of the area surrounding each image, derived from the sediment interpretation maps. We found fine-scale sediment characteristics to explain 45 % of the variation in species composition. However in the absence of such information, landscape descriptors of sediment interpretation maps still explained 20 % of the variation, and their spatial arrangement provided information regarding areas of higher biodiversity. As one of the rare landscape ecology studies performed in deeper marine environments, our study suggests that it is not only the fine-scale environmental relationships which are of importance, but also the broader spatial context in which habitat patches are present.



*Thursday 6<sup>th</sup> December*

*Human Impacts 2*

## **THE CONSEQUENCES OF EXPANDING OXYGEN-MINIMUM ZONES FOR MESOPELAGIC ANIMALS**

**Robison B**, Reisenbichler K, Sherlock R, Walz K

Monterey Bay Aquarium Research Institute

Oxygen-minimum zones (OMZs) are expanding both vertically and geographically on a global scale. Exposure to hypoxia affects different species in different ways, and the cumulative effects of continuing OMZ expansion are likely to yield significant changes in affected mesopelagic communities. Based on a 16-year time series of quantitative video transects in Monterey Bay, California we see the following changes as probable consequences of OMZ expansion:

Hypoxia-tolerant species will find their habitats expanded, albeit tempered by changes in the upper layers which may affect the food supply at depth.

Compression of upper mesopelagic and vertically migratory species into a narrower, more-illuminated depth range will expose them to greater pressure from visually-cued predators.

Species that do not undertake diel vertical migrations will face continuous exposure to lower ambient oxygen.

Some species will be displaced vertically, while others will not. This will result in the fragmentation and reassembly of communities, establishing new patterns of competition and interaction.

Gelatinous predators, because of their apparent tolerance of hypoxia, may increase in abundance.

High-performance top predators with high oxygen requirements may re-locate geographically, while opportunistic, hypoxia-tolerant species may replace them.



Tuesday 4<sup>th</sup> December

Autoecology 1

## A BACTERIUM'S-EYE VIEW OF CHEMOSYNTHETIC SYMBIOSES IN BIVALVES FROM THE EAST ATLANTIC COLD SEEPS

Rodrigues CF<sup>1,2</sup>, Cunha MR<sup>1</sup>, Génio L<sup>1</sup>, Olu K<sup>3</sup>, Duperron S<sup>2</sup>

<sup>1</sup> Departamento de Biologia & CESAM, Universidade of Aveiro, <sup>2</sup> Université Pierre-et-Marie-Curie, UMR 7138 (UPMC CNRS IRD MNHN), Systématique Adaptation, Evolution, <sup>3</sup> Laboratoire Environnement Profond, Département Etudes des Ecosystèmes Profonds, Centre Ifremer de Brest

The study of several cold seep sites from East Atlantic (Gulf of Guinea, Gulf of Cadiz) and eastern Mediterranean has revealed the occurrence of several chemosymbiotic bivalves. Some species are new to science, endemic or yet not found in other sites, whereas others are shared among sites. Moreover, the same (or sister) species have been found on both sides of Atlantic, strengthening the hypothesis of a trend towards Amphi-Atlantic distribution observed in several metazoan groups. As the study of the bivalve species associated with these environments rises, so do the study of bacteria associated with these bivalves, which aims to understand the evolution of “symbiotic systems” and their level of adaptability. Targets of our studies include symbionts of the less studied species within family Thyasiridae, smaller vesicomyid bivalves and species of the complex clade Bathymodiolinae. As the diversity of bacteria involved in symbiosis with thyasirids, or the high similarity among all bacterial phylotypes from vesicomyids is revealed, the links between species from all these different areas are explored. Results from Bathymodiolinae show a very complex picture of associations between bacteria and mussels, with the sympatric species “*Bathymodiolus mauritanicus*” and *Idas*-like specimens sharing a sulphur-oxidising symbiont, and specimens of a single *Idas* species from three distinct locations displaying different associations with bacteria.

Data presented here (known distribution, ecology, and symbiotic interactions) will help to understand the link between bacteria and metazoans from the different areas, and infer about their dispersion and evolution.



Monday 3<sup>rd</sup> December

Biodiversity Pattern – Large Scale 2

**GLOBAL BIOGEOGRAPHY OF ABYSSAL SEA-CUCUMBERS; SPECIES DISTRIBUTIONS, POPULATION GENETICS AND THE IMPORTANCE OF ECOLOGICAL AND HISTORICAL FACTORS.**

Ross E<sup>1</sup>, Billett D<sup>2</sup>, Gubili C<sup>1</sup>, Ruhl H<sup>2</sup>, Bett B<sup>2</sup>, Huvenne V<sup>2</sup>, Jones D<sup>2</sup>, Tyler P<sup>1</sup>, Rogacheva A<sup>3</sup>

<sup>1</sup> School of Ocean and Earth Sciences, University of Southampton, UK, <sup>2</sup> National Oceanography Centre, Southampton, UK, <sup>3</sup> Shirshov Institute of Oceanology, Moscow, Russia

Knowledge of the environmental factors driving species distributions in the deep-sea is essential for a better understanding of the biogeography of the abyssal benthos. Local-scale time series studies have highlighted the possible importance of food supply (quantity, quality, temporal variation) on the community structure of the megabenthos at regional scales. This study analysed the global distributions of elasipodid holothurians from online databases of Natural History Collections, cruise reports and published literature. Distribution data were mapped against a number of environmental variables thought to be potentially important for the biogeography of the holothurians, including temperature, oxygen, salinity, and the total input, seasonality and inter-annual variability of POC flux. Differences in the global distributions of the major elasipodid families were compared and their environmental tolerances were investigated in relation to known responses at time-series sites.

Progress for species-level biogeographic studies is reliant on reliable taxonomic information which correctly delimits species ranges. Cryptic speciation is capable of undermining such research. Therefore population genetic analyses of two species of apparently cosmopolitan Elasipodida — *Psychropotes longicauda* and *Oneirophanta mutabilis* — were conducted using CO1 and 16S molecular markers. Levels of geographic structuring were studied in order to identify whether cryptic speciation may hamper species-level biogeographic studies of the Elasipodida.



Friday 7<sup>th</sup> December

Conservation and Management 1

## USE OF PREDICTIVE HABITAT MODELLING TO ASSESS THE DISTRIBUTION AND EXTENT OF THE CURRENT PROTECTION OF 'LISTED' DEEP-SEA HABITATS

Ross R, Howell K

Plymouth University, UK

Global declines in biodiversity have resulted in the establishment of marine protected area (MPA) networks. Currently area closures for the protection of 'listed' deep-sea habitats are based on maps of recorded presence of species considered indicative of that habitat. Recently it has been shown that predictive habitat modelling, rather than species modelling, may provide more reliable estimates of habitat extent. With political bodies setting percentage protection targets, habitat predictive distribution maps may then be used to assess current protection measures. This study uses combined predictive modelling methods (GAMs and Maximum Entropy) to produce distribution maps of three listed habitats in the NE Atlantic: *Lophelia pertusa* (Linnaeus, 1758) reef, *Pheronema carpenteri* (Thomson, 1869) aggregations, and *Syringammia fragilissima* (Brady, 1883) aggregations. Models use presence and absence data with terrain parameters derived from the GEBCO 30 arc-second grid as predictor variables, and are validated using repeated 70% /30% data splits, using AUC and threshold dependent assessment methods. Within the current MPA network in the NE Atlantic, 23% (*Lophelia pertusa* reef), 2% (*Pheronema carpenteri* aggregations) and 6% (*Syringammia fragilissima* aggregations) of the area predicted as suitable for each listed habitat are currently contained within protected areas.





Tuesday 4<sup>th</sup> December

Biodiversity Pattern – Intermediate 1

## SIGNIFICANT DEEP-SEA CORAL AND HARDBOTTOM HABITATS ON THE WEST FLORIDA SLOPE, EASTERN GULF OF MEXICO

Ross S<sup>1</sup>, Brooke S<sup>2</sup>

<sup>1</sup> Univ. of North Carolina at Wilmington, <sup>2</sup> Marine Conservation Institute, USA

Deep-sea corals (DSC) and the communities they support appear to be more scattered and less abundant in the Gulf of Mexico (GOM) than elsewhere in the North Atlantic Ocean. The structure-forming scleractinian coral *Lophelia pertusa* is the dominant deep coral in the GOM (most common at depths of 300-600 m), but it rarely forms bioherms in the GOM, and most DSCs are attached directly to hard substrata. Until recently, it was thought that the most extensive DSC communities occurred in the north-central GOM; however, between 2008 and 2010 five research cruises documented widespread DSC habitats and fauna on the West Florida Slope (WFS) in the eastern GOM. Multibeam sonar surveys of the WFS revealed hundreds of mounds and ridges, many newly discovered. Some of these were subsequently surveyed using underwater vehicles (submersible and ROVs), and those above 525 m depths were usually capped with abundant living coral colonies, dominated by *L. pertusa*, with evidence of bioherm formation. A north-south trending rocky scarp, over 191 km long, also provides abundant hard substrata which supported a diverse community of gorgonian and antipatharian corals. We recorded 39 taxa of fishes on or near these deep reef habitats, 29 of which were only observed in close association with the reef habitat. Sixty-seven taxa of invertebrates were documented, most also from the reef habitats compared with near-by non-reef habitat. New records of fauna to the GOM are discussed. This part of the WFS now appears to have the most extensive coverage of living DSC in the GOM. It is a complex region which requires additional surveys to better understand the influences of oceanography and geology on the occurrence of DSC and to facilitate conservation of these diverse ecosystems.



*Wednesday 5<sup>th</sup> December*

*Biodiversity Pattern – Small 1*

**SMALL-SCALE VARIATIONS OF HYDROTHERMAL FAUNAL ASSEMBLAGES ON THE TOUR EIFFEL EDIFICE (MID-ATLANTIC RIDGE) IN RELATION TO ABIOTIC CONDITIONS**

Sarrazin J<sup>1</sup>, de Busserolles F<sup>2</sup>, Fabri MC<sup>1</sup>, Guilini K<sup>3</sup>, Ivanenko VN<sup>4</sup>, Legendre P<sup>5</sup>, Morineaux M<sup>1</sup>, Vanreusel A<sup>3</sup>, Sarradin PM<sup>1</sup>

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Hydrothermal-vent ecosystems are characterized by differing faunal compositions, with variations in species density, diversity and dominance, depending on the geographic locations and intrinsic abiotic factors. On the Tour Eiffel hydrothermal edifice (Lucky Strike vent field, Mid-Atlantic Ridge), twelve microhabitats colonized by the bivalve *Bathymodiolus azoricus* and the shrimp *Mirocaris fortunata* were studied in order to elucidate fauna-habitat relationships. The major objective of this study was to get an integrated view on the structuring effects of several abiotic factors (temperature, pH, total dissolved sulfide, iron and copper concentrations) on the vent community at the scale of a single edifice and to evaluate their role on faunal diversity at a local scale.

A richness of 41 macrofaunal and 29 meiofaunal taxa was found. Two groups of microhabitats emerged when looking at the fauna. Interestingly, this corresponds to the presence of contrasting environmental conditions. Indeed, the shrimps *Mirocaris fortunata* and the nematode genus *Halomonhystera* were found in microhabitats with higher hydrothermal inputs while the mussels *Bathymodiolus azoricus* and the nematode genus *Cephalochaetosoma* were associated to milder conditions. The Tegastidae, which represented the dominant copepod family, were most abundant in low temperature microhabitats. Multivariate statistical analyses (RDA) confirmed these observations. The diversity appears to be higher in the less extreme microhabitats but whether the observed pattern is due to the local abiotic conditions or to the structuring effects of the mussels remains to be clarified.



*Tuesday 4<sup>th</sup> December*

*Biodiversity Pattern – Large Scale 4*

## **SQUAT LOBSTER DEPTH DISTRIBUTION IN THE SOUTHWEST PACIFIC**

**Schnabel K<sup>1</sup>, Bostock H<sup>1</sup>, Ahyong S<sup>2</sup>**

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Squat lobsters (Decapoda: Anomura: Galatheoidea and Chirostyloidea) show distinct differences in depth distribution worldwide, with the family Munidopsidae occurring to greatest depths (> 4000 m) compared to Chirostylidae and Galatheidae reaching maximum depths of ~ 1500 m. Here, we combine an examination of the depth distributions for nearly 500 squat lobster species in the light of a recent biogeographic analysis for the southwest Pacific region that shows distinct regional assemblages from east to west (eastern Australia to French Polynesia) and from north to south (Vanuatu to Macquarie Ridge). However, whether these regional differences coincide with differences in depth distributions across taxa has not yet been studied. Observations are presented in the context of regional bathymetry, physical and chemical oceanography and biological associations. Strong trans-Tasman faunal connections between New Zealand and Australian squat lobster communities are maintained across latitudes and depths and it is clear that, overall, the southwest Pacific region presents a highly dynamic and complex ecological system.



Tuesday 4<sup>th</sup> December

Biodiversity Pattern – Large Scale 4

## DISTRIBUTION OF SELECTED MUNNOPSIDAE (CRUSTACEA, ISOPODA, ASELOTA) SPECIES AROUND ICELAND LINKED TO LONG-TERM OCEANOGRAPHIC DATA

Schnurr S<sup>1</sup>, Brandt A<sup>2</sup>, Brix S<sup>1</sup>, Fiorentino D<sup>2</sup>, Jochumsen K<sup>3</sup>, Malyutina M<sup>4</sup>, Quadfasel D<sup>3</sup>, Svavarsson J<sup>5</sup>

<sup>1</sup> German Centre for Marine Biodiversity Research (DZMB), Senckenberg Research Institute, <sup>2</sup> University of Hamburg, Biocentrum Grindel Zoological Museum, <sup>3</sup> University of Hamburg, Institute of Oceanography, <sup>4</sup> A.V. Zhirmunsky Institute of Marine Biology FEB RAS, <sup>5</sup> University of Iceland, Institute of Biology

Based on samples of the BIOICE (Benthic Invertebrates of Icelandic Waters; 1991–2004) and IceAGE (Icelandic Animals: Genetics and Ecology; since 2011) projects diversity, composition and distribution of selected isopod genera of the family Munnopsidae Lilljeborg, 1864 around Iceland were studied. The area around Iceland is climatically of great importance and thus located in a zoogeographic key position, which is highly influenced by the Greenland-Scotland Ridge. This submarine barrier, which extends from Greenland to Scotland, constrains the water exchange between the northern North Atlantic and the Nordic Seas. Additionally, water exchanges through the ridge are of major importance for the regional climate, the regional climate of northern Europe and the global thermohaline circulation. Data from the NISE (Norwegian Icelandic Seas Experiment) project were used to model the long-term near-bottom mean temperature and salinity values. A quite diverse composition of Munnopsidae occurs within the research area. Of the six munnopsid genera examined in this study, 15 species were identified. In all 10,787 individuals were determined, the majority of specimen belonging to the genus *Eurycope* Sars, 1864. Some species were either restricted to areas north (four) or south (three) of the ridge, while most species (eight) were present on both sides of the ridge. The distributional patterns of the evaluated munnopsid genera are heavily influenced by depth. Temperature and water mass appear to play a less important role in driving the distributional pattern of Munnopsidae whereas salinity and sediment type do not appear to influence the species distribution within the study area.



*Friday 7<sup>th</sup> December*

*New Methods and Novel Techniques 3*

## **THE IMPACT OF EXPERTS' INTER- AND INTRA-OBSERVER AGREEMENTS ON COMPUTATIONAL OBJECT CLASSIFICATION IN IMAGES FROM THE DEEP SEAFLOOR OF THE HAUSGARTEN OBSERVATORY**

**Schoening T<sup>1</sup>, Bergmann M<sup>2</sup>, Purser A<sup>3</sup>, Gutt J<sup>2</sup>, Dannheim J<sup>2</sup>, Taylor J<sup>4</sup>, Nattkemper T W.<sup>1</sup>, Boetius A<sup>5</sup>**

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Far-sighted marine research institutions around the globe are capturing images from the seafloor at a scale of hundreds of thousands. Only a small part of these data have been accessed to date, as manual analyses are time-consuming and automated evaluation approaches are still under development. Machine learning and neural networks have been identified as a promising algorithmic approach to automate analysis of images from the seafloor. These algorithms need ground-truth data about the objects to be detected. As the information provided by one human expert lacks reproducibility, the expertise of a group of individuals has to be employed to collect training data as well as to evaluate the performance of an automated detection.

In this paper we show that the inter- and intra-observer agreements of these human experts is a critical factor for the training of a learning architecture and has shown to be conditional to image quality for some object classes. A supervised automated detection approach is evaluated where five experts marked the positions of eight distinct object classes within seventy images taken at the HAUSGARTEN observatory (eastern Fram Strait, Arctic). Support Vector Machines were trained to detect and classify objects in the images with an overall sensitivity of 0.87 and precision of 0.67. A detailed comparison of the human expert agreements showed interesting correlations with the system's performance and pointed us towards new strategies for (semi-) automated underwater image analysis.



*Tuesday 4<sup>th</sup> December*

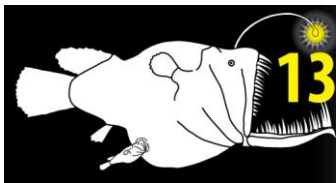
*Autoecology 2*

## **IN SITU BURROW CASTING REVEALS NEW CLUES TO THE DEEP-SEA BIOLOGY**

**Seike K<sup>1</sup>, Jenkins R<sup>2</sup>, Watanabe H<sup>3</sup>, Nomaki H<sup>3</sup>, Sato K<sup>4</sup>**

<sup>1</sup> Atmosphere and Ocean Research Institute, University of Tokyo, <sup>2</sup> Graduate school of Environment and Information Science, Yokohama National University, <sup>3</sup> Institute of Biogeosciences, Japan Agency for Marine-Earth Science and Technology, <sup>4</sup> Department of Earth and Planetary Science, University of Tokyo

Burrows produced by endobenthos are particularly important in seafloor environment, because they mix sediments, disrupt microstratigraphy, influence the biogeochemistry of seafloor sediment, and harbor other small organisms and microbes in the structure. Although the deep sea is the largest ecosystem on Earth, burrow morphology in the environment remains poorly understood because of the logistical challenges: Burrows have been observed in core samples. However, the soupy mud of the deepwater seafloor surface deforms the original burrow morphology during coring. In addition, it is generally not possible to retrieve cores from unconsolidated sandy and gravelly sediments. Large organisms in the sediment often show escaping movements, downward or upward, during coring, thereby disrupting the original burrow structures or life positions. Furthermore, the observable volume is limited due to the size of the core and the device used for analysis. We overcame these problems by in situ burrow casting — an extremely useful approach to understanding the burrow morphology. Here we report large burrow's morphology obtained by in situ burrow casting at a hydrocarbon-seep site and a non-seep site at water depths of 1173 and 1455 m, respectively. Deep and complex burrows are abundant at both sites, indicating that the burrows introduce oxygen-rich seawater into the deep reducing substrate, thereby influencing benthic metabolism and nutrient fluxes, and providing an oxic microhabitat for small organisms. This is, to our knowledge, the first study to examine in situ burrow morphology at the deep-sea, providing new clues to deep-sea ecological research.



International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

*Friday 7<sup>th</sup> December*

*Conservation and Management 2*

**ECOLOGICAL ADAPTIONS OF MACRO-EPIFAUNA ON DEEP-SEA CORALS IN THE SOUTHWEST INDIAN OCEAN**

**Serpetti N**<sup>1</sup>, Chivers A J<sup>1</sup>, Lamont PA<sup>1</sup>, Narayanaswamy BE<sup>1</sup>, Rogers AD<sup>2</sup>, Taylor ME<sup>2</sup>, Paterson GLJ<sup>3</sup>, Woodall LC<sup>3</sup>, Packer M<sup>3</sup>, Ferrero TJ<sup>3</sup>

<sup>1</sup> Scottish Association for Marine Science, <sup>2</sup> University of Oxford, <sup>3</sup> The Natural History Museum - London

Deep-water seamount systems are characterised by unique abiotic characteristics in terms of geographic distribution, topographic profiles and hydrographical properties. These exclusive properties can stimulate genetic divergence leading to genetically “isolated” areas that host highly endemic and specialised fauna. Physical, biological and geological processes can also connect isolated populations in particular in contiguous regions such as ocean ridges with numerous seamounts, promoting genetic connectivity of communities via dispersal. Seamounts are characterised by high species richness represented by high endemism with a few cosmopolitan species, often associated with habitat-forming corals. Deep-sea corals provide a heterogeneous habitat structure for a group of taxa that developed diverse mutualistic, commensalistic, or parasitic relationships with varying degrees of specificity to their host corals.

The area investigated in this study consists of five seamounts located on the Southwest Indian Ridge that extends south westwards between South Africa and Antarctica. The north-east part of the ridge is located in a region of weak currents and low productivity contrary to the south-west region. The contiguity of these seamounts supplied us with a great opportunity to analyse species variations, ecological adaptations and genetic flow across the ridge and evaluate the effect of environmental variables on them. We sampled several coral species with diverse multi-dimensional structures (scleractinians forming cold-water coral reefs and octocorals, stylasterids and antipatharians forming coral gardens) and analysed their macro-epifaunal associations (including isopods, amphipods, tanaids and polychaetes), connectivity, evolution and endemism. The results will be discussed in terms of ecological adaptations, biological diversity and ecosystem vulnerability to anthropogenic impact.





*Monday 3<sup>rd</sup> December*

*Dispersal and Connectivity 2*

**CORAL ECOSYSTEM DIVERSITY IN THE DEEP GULF OF MEXICO: HOST CORAL-INVERTEBRATE SYMBIONT RELATIONSHIPS AND THE GENETIC CONNECTIVITY OF DEEP-SEA CORAL ECOSYSTEMS**

**Shank T<sup>1</sup>**, Cordes E<sup>2</sup>, Quattrini A<sup>2</sup>, Cho W<sup>1</sup>, Herrera S<sup>1</sup>, Heyl T<sup>1</sup>, Munro C<sup>1</sup>, Hsing PY<sup>3</sup>, Demopolous A<sup>4</sup>, Fisher C<sup>3</sup>

<sup>1</sup> Woods Hole Oceanographic Institution, <sup>2</sup> Temple University, <sup>3</sup> United States Geological Survey, <sup>4</sup> Pennsylvania State University

Deep-sea corals provide habitat structure for an array of species that have developed diverse symbiotic relationships with relative specificities to their host corals. Growing intensities of fisheries, in addition to oil extraction from seamounts and hydrocarbon-rich continental margins, place a premium on understanding the processes controlling coral ecosystems. We examined more than fifteen long-term observation stations of DSC communities in the deep Gulf of Mexico and additional sites ranging from 10 to 200+ miles from the wellhead of the Deepwater Horizon (DWH) incident. We documented patterns between particular invertebrates and their host corals via imaging, morphological and molecular systematic/phylogenetic approaches and are assessing levels of associate connectivity across hosts and locations through faunal and time-series larval trap collections. More than 720 coral-associated invertebrates (including shrimp, amphipods, anemones, barnacles, and crabs) were sampled and >120 representatives of these sampled taxa were morphologically and genetically identified. We have identified >80 coral-community associated morphospecies (predominantly crustaceans, 27 species and echinoderms, 15 species) from six phyla living on > 18 coral hosts, including octocorals, black corals, and scleractinian corals. Associates hosted only by dead coral skeleton (e.g., barnacles and polychaetes) were also observed. Genetic identifications have revealed fidelity in some groups to be high (e.g., specific ophiuroid species only inhabiting specific species of octocoral), suggesting that symbionts may be obligate to their coral hosts. Differences in coral associate composition varied with depth and biogeographic location within the Gulf, yet show marked similarities with coral-associate composition and relationships in deepwater coral ecosystems around the world.



*Wednesday 5<sup>th</sup> December*

*New Methods and Novel Techniques 1*

**CAPTURING EPISODIC EVENTS IN THE DEEP-SEA COMMUNITY USING A CONTINUOUSLY MONITORING INSTRUMENT SUITE**

**Sherman A, Smith K**

Monterey Bay Aquarium Research Institute

The deep ocean covers two-thirds of the earth's surface; unfortunately this vast ecosystem is difficult to study because of the technical and financial challenges of sampling with adequate temporal resolution. Continuous long-term monitoring of the deep-sea ecosystem is critical for assessing the impact of climate change on this environment. With this goal in mind, a suite of instruments were developed and deployed over the past two decades to measure the biological processes at a long-term time-series study site in the NE Pacific. These instruments include: a time-lapse camera, a benthic rover, and moored sediment traps. The time-lapse camera captures one image every hour, and each image encompasses a 20 m<sup>2</sup> area of the sea floor. The Benthic Rover is a bottom-transiting autonomous underwater vehicle that drives from site to site, measuring sediment community oxygen consumption (SCOC). Finally, two sediment traps, located at 600 and 50 m above the seafloor, collect sinking particulate matter. All three instruments were deployed at 4000 m and collected continuous measurements between November 2011 and June 2012. The resulting data showed an unprecedented "spring bloom" of salp (*Salpa* spp.) carcasses and fecal material that sank to the seafloor, stimulating a significant increase in SCOC when compared to previous years. This bloom was evident in all instrument datasets. In addition to bloom events, this instrument suite detects seasonal and inter-annual changes in food supply and fauna populations. Such long time-series studies provide much needed information on how climate change is impacting the deep-sea ecosystem.



*Friday 7<sup>th</sup> December*

*New Methods and Novel Techniques 4*

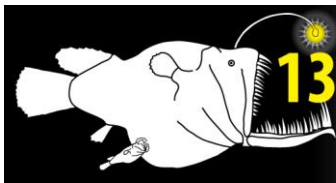
## **UNCOVERING ABYSSAL COMMUNITIES USING HIGH-THROUGHPUT SEQUENCING. WHERE ARE WE AND WHAT TO EXPECT?**

**Sinniger F<sup>1,2</sup>**, Creer S<sup>3</sup>, Maruyama T<sup>1,2</sup>, Fujikura K<sup>1</sup>, Kitazato H<sup>1</sup>

<sup>1</sup> Japan Agency for Marine-Earth Science and Technology, <sup>2</sup> Global Oceanographic Data Center, Nago, Okinawa, Japan, <sup>3</sup> Molecular Ecology and Fisheries genetics group, ECW, Bangor University, Gwynedd, United Kingdom

Deep-sea seafloor sediments are one of the most widespread and homogeneous habitat on Earth. However, the biodiversity of the deep-sea communities remains largely unknown and the cosmopolitanism of its inhabitants remains an open question. Among deep-sea communities, meiofauna (organisms between 500 (1000) and 44 (31)  $\mu\text{m}$  living on/in the sediments) remains poorly known in comparison to other groups and environments. Meiobenthic organisms play an important role in the ecosystem and impact significantly on sedimentary sea floor and the surrounding water masses. In addition, short life cycle and high turnover make meiobenthic communities good candidates to be used as bio-indicators of environmental disturbance. However, characterisation of meiobenthic diversity is problematic due to several factors such as convergent morphology, small size of the organisms and lack of specialist taxonomists.

Metagenetics is the part of metagenomics consisting in sequencing homologous markers from environmental DNA. This method offers new perspectives to investigate the taxonomic composition of the communities inhabiting marine sediments. Meiobenthos metagenetics allow the analysis of taxonomic richness and distribution across multiple phyla in parallel. Here I will present the results obtained from environmental DNA extracted from abyssal sediments. Those results show that metazoan meiobenthic communities diversity can be characterised using minimal sample volumes and a surprising low bias of planktonic DNA compared to the expectations. The results are compared with other recent studies using different methodologies to assess the impact of factors such as sample size and processing and to clarify the potential use of such methods in applied deep-sea research.



International

# 13<sup>th</sup> Deep-Sea Biology Symposium

Wellington, New Zealand 3 – 7 December 2012

Thursday 6<sup>th</sup> December

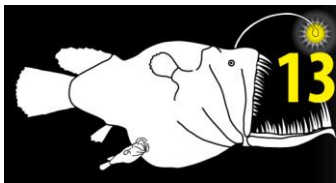
Trophic and Process 1

## MASSIVE KRILL FALLS AND HIGH MACROFAUNAL ABUNDANCE IN DEEP-SEA FJORDS ALONG THE WEST ANTARCTIC PENINSULA (WAP)

Smith C<sup>1</sup>, Derocher M<sup>1</sup>, Seifer C<sup>1</sup>, Honig D<sup>2</sup>, Grange L<sup>1</sup>

<sup>1</sup> University of Hawaii at Manoa, <sup>2</sup> Duke University Marine Laboratory

Glacio-marine fjords are widespread in temperate-polar latitudes, and produce cold, isolated deep-sea habitats on continental margins. These deep fjord ecosystems may be heavily modulated by glacial ice, meltwater and terrigenous sediments, causing ecosystem structure and function to be highly sensitive to climate warming. Recent studies suggest that fjords along the central WAP, including Andvord Bay and Flandres Bays, are intense hotspots of pelagic biomass, attracting enormous aggregations of keystone species such as krill and feeding humpback whales. However, the deep benthic ecosystems underlying these pelagic hotspots remain very poorly studied. During krill/humpback whale aggregations in Andvord and Flandres Bays in May-June 2011, we conducted photographic surveys, megacoring, and trawling to evaluate krill falls and macrobenthic community structure in 500–700 m deep fjord basins. Photographic and trawl surveys indicated that carcasses of krill, *Euphausia superba*, occurred widely over the fjord floors (an area > 100 km<sup>2</sup>) at densities of 2–58 carcasses m<sup>-2</sup>. Krill carcasses were mostly adults > 5 cm in length and in various stages of decomposition, suggesting that krill falls had been occurring for days to weeks. We estimate that the total number of krill carcasses at the combined fjord floors exceeded 200 x 10<sup>6</sup> individuals, with a total krill-carcass biomass > 200 metric tons. Megafauna and macrofauna feeding on krill carcasses included anemones, asteroids and syllid polychaetes. Macrofaunal abundances and diversity were high in Andvord Bay (the only fjord cored intensively) compared to similar depths on the open margin. Massive aggregations of krill and feeding humpback whales have been observed repeatedly (2009, 2010 and 2011) in the WAP fjords, raising the possibility that migrating krill provide regular horizontal nutrient subsidies from sinking carcasses and moults to deep fjord benthos. Because these deep fjords can be both oceanographically isolated and highly productive, they may promote speciation of benthos around Antarctica.



International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

Friday 7<sup>th</sup> December

Trophic and Process 4

**INVESTIGATION OF DEEP-SEA ECHINOID FEEDING ECOLOGY IN THE NE ATLANTIC: IMPLICATIONS FOR DEEP-SEA CORAL ECOSYSTEMS**

Stevenson A<sup>1</sup>, Gröcke D<sup>2</sup>, Mitchell F<sup>3</sup>

<sup>1</sup> Center for the Environment, School of Natural Sciences, Trinity College, Dublin, Ireland, <sup>2</sup> Department of Earth Sciences, Durham University, Durham, DH1 3LE, UK, <sup>3</sup> Department of Botany, School of Natural Sciences, Trinity College, Dublin, Ireland

In shallow waters, echinoids play an important role in nutrient redistribution and tropical coral reef stability, yet in the deep-sea their role remains unknown. Stable isotope analyses (SIA) were performed on echinoid muscle, echinoderma, and gonad to evaluate their feeding strategies in deep-sea habitats. Eight species (*Gracilechinus elegans*, *Gracilechinus alexandri*, *Echinus affinis*, *Cidaris cidaris*, *Tromikosoma uranus*, *Phormosoma placenta*, *Sperosoma grimaldii*, and *Araeosoma fenestratum*) were collected on the Irish and French continental margins. Gut content and video analyses were performed in conjunction with SIA.

Similar high  $\delta^{15}\text{N}$  signatures were observed across all tissues and species, suggesting that deep-sea echinoid species feed at the same trophic level and primarily maintain an omnivorous diet. However,  $\delta^{13}\text{C}$  signatures span a large range, indicating that echinoids may be partitioning food sources within the sediment. This may perhaps allow for coexistence and maintenance of the high diversity of echinoids observed in deep-sea environments. A large shift (3–5 ‰) was observed between  $\delta^{13}\text{C}$  signatures of muscle and echinoderma compared to the gonads, suggesting a seasonal shift in diet whereby reproductive periods of deep-sea echinoids are likely regulated by surface nutrient deposition.

Gut content and video observations show evidence of *Lophelia-Madrepora* bioerosion by four echinoid taxa. In the presence of *Lophelia-Madrepora* reefs, echinoids may preferentially engage in bioerosion of the coral infrastructure to supplement a nitrogen poor diet. Because echinoid bioerosion is a limiting factor for reef growth and hasn't been described in present day deep-sea coral reefs, these taxa may yet play an important role within deep-sea ecosystems.



*Monday 3<sup>rd</sup> December*

*Biodiversity Pattern – Large Scale 3*

## **THE DEEP-PELAGIC BIOME OF THE ATLANTIC OCEAN: CHARACTER AND ECOLOGICAL DISCRETENESS OF THE MESO- AND BATHYPELAGIC FISH FAUNAS**

**Sutton T**<sup>1</sup>, Bergstad OA<sup>2</sup>, Bucklin A<sup>3</sup>, Burghart S<sup>4</sup>, Cook A<sup>1</sup>, Falkenhaus T<sup>2</sup>, Hopkins T<sup>4</sup>, Porteiro F<sup>5</sup>, Schiel S<sup>6</sup>, Torres J<sup>4</sup>, Vecchione M<sup>7</sup>, Wiebe P<sup>8</sup>

<sup>1</sup> Virginia Institute of Marine Science, <sup>2</sup> Institute of Marine Research, Flødevigen, HIS, Norway, <sup>3</sup> Department of Marine Science, University of Connecticut, Groton, CT, USA, <sup>4</sup> College of Marine Science, University of South Florida, St. Petersburg, FL, USA, <sup>5</sup> Departamento de Oceanografia e Pescas, Universidade dos Açores, Horta,, <sup>6</sup> Alfred-Wegener-Institut Für Polar- und Meeresforschung, Bremerhaven, Germany, <sup>7</sup> NMFS National Systematics Laboratory, National Museum of Natural History, <sup>8</sup> Woods Hole Oceanographic Institution

Global synthetic analyses have revealed that deep-sea inventories are far from complete, nowhere more so than in the bathypelagic biome. This data gap served as the impetus for recent deepwater surveys, many of which have altered our perceptions of pelagic ecosystems. Here we examine data from four deep-pelagic (0–5000+ m) sampling programs in the Atlantic (60° N–25° S) in order to assess the fish communities with respect to faunal distinctiveness and ecological connectivity. Quantitative analyses give contrasting pictures with respect to faunal composition and ecosystem operation. Geometric abundance class analyses reveal that the faunal character of meso- and bathypelagic biomes is fundamentally dissimilar; the former exhibit a much higher proportion of common species, the latter a higher portion of rarer species. From an energetics perspective, however, the bathy- and mesopelagic biomes appear highly interconnected. Approximately 70 % of species collected below 1000 m are also found in the mesopelagial, and in some cases the epipelagial. These species comprised 66 to > 90 % of individuals collected below 1000 m in the regions sampled. Thus, the “spanning” taxa add considerably to the ichthyofaunal diversity of the world ocean below 1000 m, and appear to be the vectors that support the diverse array of holobathypelagic fishes. Data from the four regions studied suggest that classic pelagic biogeographic boundaries do not apply to bathypelagic realm, as shared species are the rule rather than the exception. Last, cumulative species curves suggest we are far from understanding the true complexity of the bathypelagic biome.



Thursday 6<sup>th</sup> December

Trophic and Process 2

## SCAVENGER DIVERSITY AND SCAVENGING RATES AT JELLYFISH-FALLS AND FISH-FALLS AT THE DEEP-SEA FLOOR

Sweetman A<sup>1</sup>, Jones D<sup>2</sup>, Smith C<sup>3</sup>

<sup>1</sup> Norwegian Institute for Water Research (NIVA), <sup>2</sup> National Oceanography Center, Southampton, UK, <sup>3</sup> University of Hawaii at Manoa, USA

In recent years, a number of studies have described accumulations of moribund jellyfish at the deep seafloor off Oman, the Ivory Coast, the Sea of Japan and deep-sea fjords. These collective observations suggest that gelatinous zooplankton carcasses (hereafter referred to as jelly-falls) may provide an important transport vector for carbon and nitrogen to the deep seafloor, because jellyfish are renowned for their ability to rapidly form massive, yet often short-lived blooms. Mass mortality of blooming jellyfish could therefore become very important for deep-sea energetics on local scales that match the scale of jellyfish blooms in overlying waters.

Decomposing jelly-falls may have both positive and negative impacts on seafloor habitats. If large numbers of jellyfish accumulate in a relatively small area at the seafloor, the low energy content of the gelatinous detritus may lead to scavenging fauna choosing to feed on higher energy content food-sources, causing a build-up of impermeable gelatinous detritus at the seafloor, and a reduction in oxygen flux into sediments. Alternatively, if supplementary food is in short supply, and the scavenging fauna has a substantial supply of jellyfish detritus, jelly-falls may enhance the abundance and biomass of scavenging fauna at the seafloor. However, to the best of our knowledge, no studies exist that have assessed scavenger biodiversity and scavenging rates of jelly-falls at the deep-sea floor and compared scavenger dynamics to processes around deep-sea fish-falls.

To assess scavenging rates of jellyfish versus fish foods, we will conduct scavenger experiments at 1300 m depth in the Sognefjord in October 2012 using two identical landers equipped with time-lapse cameras and standardized jelly-fish (*Periphylla periphylla*) and mackerel baits. This talk will show-case experimental in-situ results on scavenger identities and scavenging rates measured from the mass difference between the initial and final weight of the standardized bait blocks.





*Thursday 6<sup>th</sup> December*

*Human Impacts 2*

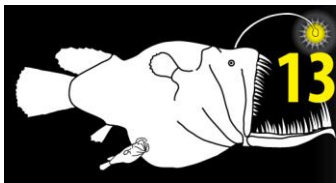
**DON'T ROCK THE BOAT:**

**IMPACTS OF A LOST SHIPPING CONTAINER ON THE DEEP-SEA BENTHOS OF THE MONTEREY BAY NATIONAL MARINE SANCTUARY, CA**

Taylor J<sup>1</sup>, DeVogelaere AP<sup>2</sup>, Burton E J<sup>2</sup>, Frey O<sup>2</sup>, Lundsten L<sup>1</sup>, Kuhnz L<sup>1</sup>, Whaling P J<sup>1</sup>, Lovera C<sup>1</sup>, Buck KR<sup>1</sup>, Barry JP<sup>1</sup>

<sup>1</sup> Monterey Bay Aquarium Research Institute, <sup>2</sup> Monterey Bay National Marine Sanctuary

Intermodal containers are lost at sea along international shipping routes in considerable numbers; an estimated 10,000 per year. Carrying a wide assortment of cargo, and covered with paint of varying composition and often-uncertain toxicity, lost containers can take centuries to degrade. During a storm in Feb 2004, 24 standard metal intermodal containers (12.2 x 2.4 x 2.6 m) fell off Chinese Merchant Vessel M/V *Med Taipei* along the central coast of California. Monterey Bay Aquarium Research Institute (MBARI) scientists discovered one of these containers at 1281 m depth in the Monterey Bay National Marine Sanctuary, in June 2004. To assess the ecological condition of the site, it was revisited during a March 2011 research cruise in collaboration with the Monterey Bay National Marine Sanctuary (MBNMS). During this revisit, sediment core samples and high-definition video transects were taken from a radius up to 500 m from the container. Results show that the appearance of this intermodal container has caused significantly ( $p < 0.05$ ) lower megafauna  $\alpha$ -biodiversity (within-site) as far as 50 m from the container, with even greater reduction ( $p < 0.01$ ) in biodiversity on the container itself and up to 1 m from its base. High megafauna  $\beta$ -diversity (between-site) is indicated by distinct community compositions between the container's hard substrate, the sediment at its base, and the sediment  $> 1$  m from its base. Furthermore, the composition of communities on and  $\leq 1$  m from the container was skewed towards fewer fast-growing, short-lived ("weedy") species, at higher densities. Preservation of biodiversity is an important consideration when evaluating the impact of a foreign habitat on an ecosystem. Our results suggest the biodiversity of an area of deep-sea benthos nearly 10,000 m<sup>2</sup> has been impacted by the appearance of this shipping container.



International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

**Monday 3<sup>rd</sup> December**

**Dispersal and Connectivity 1**

**HIGH CONNECTIVITY OF SHRIMP ACROSS LARGE SPATIAL SCALES AND DISTINCT CHEMOSYNTHETIC HABITATS**

**Teixeira S<sup>1,2</sup>, Olu K<sup>1</sup>, Serrão E<sup>2</sup>, Arnaud-Haond S<sup>1</sup>**

<sup>1</sup> Department “Environnement Profond”, REM/EEP/LEP Laboratoire, Centre de Brest de l’IFREMER, Plouzané, France, <sup>2</sup> Centre of Marine Sciences, CIMAR, University of Algarve, Campus of Gambelas, Faro, Portugal

Despite high endemism at the species level, deep-sea vents and cold seeps have been reported to share related taxa, in fact the dominant biomass at these ecosystems are the polychaete annelids, bivalve molluscs, gastropod molluscs and the shrimp family Alvinocarididae.

We studied several species of Alvinocarid species in order to assess the pattern of migration or genetic divergence across large spatial distances and between cold seeps and hydrothermal vents habitats. Indeed, *Alvinocaris muricola* is one of the few species that, based on morphological criteria, is expected to be shared between seeps and vents along the Atlantic Equatorial belt. We used sequences of mitochondrial cytochrome c oxidase I (COI, 710bp), of nuclear 18S rRNA gene, and several microsatellite loci designed for *Rimicaris exoculata* (Teixeira et al. 2011b) and *Chorocaris* sp (Zelnio et al. 2010) to analyze genetic structure within populations of each species and divergence among closely related taxa (as described based on morphological characters). Using the mitochondrial and nuclear sequences obtained and adding sequences already available at Genbank, we assessed the monophyletic nature of distinct but closely related taxa, therefore adding a molecular component to the morphological identifications of the different species of the Alvinocarididae family. We then added the microsatellite data to further investigate the connectivity of the *Alvinocaris* shrimp across the Atlantic equatorial belt.

We found that the Alvinocarididae shrimp group in four major clades, the composition of each clade not supporting the taxonomic classification based mainly on morphology. More importantly, the analysis of the *Alvinocaris* shrimp of the Atlantic belt region revealed a surprisingly high and/or recent connectivity between the hydrothermal vents of the Mid Atlantic Ridge and cold seeps studied from both sides of the Atlantic.



*Tuesday 4<sup>th</sup> December*

*Biodiversity Pattern – Large Scale 4*

**MINIMUM RANGE SIZES OF SEDIMENT-DWELLING SPECIES IN THE DEEP SEA: INSIGHTS FROM HARPACTICOID COPEPODS**

**Thistle D**, Easton E, Spears T

Florida State University

Estimates of species' minimum range sizes in the deep sea vary from the size of the sampler that collected them to thousands of kilometers. Range size is important because, if most species have kilometer-scale ranges, deep-sea biologists should concentrate on how such specialized species evolved and persist. If most species have 1000-kilometer-scale ranges, deep-sea biologists should concentrate on how gene flow is maintained over enormous distances. We are using morphological and gene-sequencing methods to estimate the minimum ranges of harpacticoid species on the continental rise along the west coast of the USA, applying both techniques to the same individuals. We "broke the blind," that is, we compared the morphology-based species designations and gene-sequencing-based species designations when  $n=136$ . We found that three of the 21 species for which we had both kinds of data had 1000-kilometer ranges. Just before the meeting, we will again break the blind and will report on whether or not our preliminary results hold in a larger data set.



*Thursday 6<sup>th</sup> December*

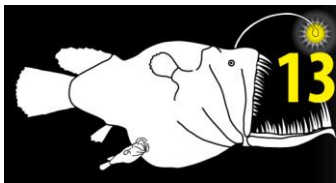
*Temporal Patterns 1*

**MILLENNIAL SCALE VARIABILITY IN SOUTHERN HEMISPHERE INTERMEDIATE WATER MASS TEMPERATURES FROM ANALYSIS DEEP-SEA CORAL PROXIES**

**Thresher R<sup>1</sup>**, Fallon S<sup>2</sup>, Neil H<sup>3</sup>, McRae C<sup>4</sup>, Wilson N<sup>4</sup>, Richter de Forges S<sup>5</sup>, Correge T<sup>6</sup>, Marriott P<sup>3</sup>, Tracey D<sup>3</sup>, Gurney R<sup>1</sup>

<sup>1</sup> CSIRO Wealth from Oceans Flagship, <sup>2</sup> ANU, <sup>3</sup> NIWA, <sup>4</sup> CSIRO Process Science and Engineering, <sup>5</sup> IFREMER, <sup>6</sup> Univ. de Bordeaux

Little concrete is known about environmental conditions of the deep Southern Ocean and adjacent seas prior to the onset of detailed instrumental records in the 1990s. Historical data covering a longer period are critical not only for better parameterising existing ocean-climate models but also provide a context for the ecology of what is often a very long-lived deep sea biota. To help fill this gap, we have examined skeletal chemistry and growth rates of deep-sea corals collected at Intermediate Water depths from sea mounts in the SW Pacific, producing detailed temperature proxies spanning the last millennium and growth rate records since the Last Glacial Maximum (ca. 20,000 years Before Present). The data indicate regionally coherent temperature variability at ca. 1000 m depth over the last 1300 years, with conditions relatively stationary until about 1500 AD and thereafter a irregular long-term cooling at Intermediate depths. The coral proxy suggests that modern day temperatures at these depths are among the coolest since ca. 700 AD. To put this in a longer context, we have begun analysis of growth rates of radiocarbon-dated sub-fossil colonial corals collected on sea mounts off SE Australia. The combination of these data, plus the proxy records for the last millennium, imply that conditions at Intermediate depths have changed substantially in the last several centuries, and hence that inferences drawn about the ecology of deep-sea species that are based on modern conditions may not characterise those prevalent during their recent evolutionary or ecological history.



International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

*Thursday 6<sup>th</sup> December*

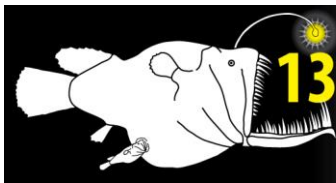
*Trophic and Process 2*

**WARM MUD AT THE CHILE TRIPLE JUNCTION: A METHANE LADDER BETWEEN STEPPING STONES?**

**Thurber A**<sup>1</sup>, Levin L<sup>2</sup>, Blackman D<sup>2</sup>, German C<sup>3</sup>, Shank T<sup>3</sup>, Grupe B<sup>2</sup>, Frieder C<sup>2</sup>, Sellanes J<sup>4</sup>, Lilley M<sup>5</sup>, Dowell E<sup>1,6</sup>

<sup>1</sup> Oregon State University, <sup>2</sup> Scripps Institution of Oceanography, <sup>3</sup> Woods Hole Oceanographic Institution, <sup>4</sup> Universidad Catolica del Norte, Chile, <sup>5</sup> University of Washington, <sup>6</sup> University of North Carolina at Chapel Hill

The deep sea of Southern Chile remains largely unknown yet hosts one of the few spots on the planet where hydrothermal-vent and cold-seep habitats may co-occur. Here we describe a warm-mud habitat recently discovered at the Chilean Triple Junction, a location where an actively-spreading ridge is being subducted underneath a continental margin. Occurring with 40 km of a methane seep and at 2900 m water depth, hydrothermally-heated fluid passes through and warms the overlying sediment blanket. Unlike most reducing habitats there were no obvious surface manifestations of the underlying hydrothermal activity. Instead haphazard collection revealed that > 8° C temperatures were present within 10 cm of the sediment surface at multiple locations along a scarp above the triple junction. The overlying water contained nM quantities of methane and had a slight temperature increase compared to ambient temperatures (20 mC degree increase measured in situ 2 m above bottom and 10° C degrees measured ex situ at the sediment surface). The sediment community was composed of a diversity of large protists (including xenophyophores) as well as metazoan fauna that are common either in the deep sea, reducing habitats, or both. Symbiont-bearing fauna were limited to frenulates although a diversity of recently settled bivalves with potential seep or vent affinities were also recovered. Chemosynthetic energy, including methane, fueled a subset of the community, including both syllid and frenulate annelids. The metazoan and microbes communities will be used to place this warm-mud community from an unexplored region of the globe in our understanding of reducing habitat biogeography, potentially providing insight into the evolutionary connections among reducing habitats. As this location hosts moderately-elevated temperatures and methane it provides an intermediate “hybrid” habitat that may function as a ladder between the stepping stones created by vents and seeps.



International

# 13<sup>th</sup> Deep-Sea Biology Symposium

Wellington, New Zealand  3 – 7 December 2012

*Wednesday 5<sup>th</sup> December*

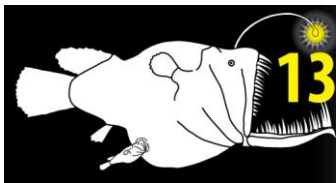
*Plenary Presentation*

## **THE DEEP SEA AS A TESTBED FOR ECOLOGICAL THEORY**

**Tittensor D<sup>1</sup>**

<sup>1</sup> Dalhousie University, Canada

The deep ocean has a number of unique characteristics, such as its extreme energy limitation, that make it ideal for testing ecological theories. I share some thoughts on why it is well positioned as another 'replicate' to test the generality of our ecological understanding, give some examples and describe work in progress on applying models, and make some suggestions for avenues worthy of further exploration.



International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

*Thursday 6<sup>th</sup> December*

*Trophic and Process 2*

**INSIGHTS IN FAUNAL FEEDING STRATEGIES IN THE BENTHIC FOOD WEBS: A COMPILATION OF ISOTOPE TRACER DATA**

van Oevelen D<sup>1</sup>, Woulds C<sup>2</sup>, Soetaert K<sup>1</sup>

<sup>1</sup> Royal Netherlands Institute for Sea Research (NIOZ-Yerseke), <sup>2</sup> University of Leeds

Benthic fauna in soft sediments is fuelled by detritus from primary production in the upper ocean. Upon deposition on the seafloor, the fresh phytodetritus is diluted by a large stock of sedimentary detritus, resulting in a mixture where detritus lability is inversely related to detritus stock size. Climate change is expected to reduce the quantity and change the composition of phytodetritus input to the seafloor. In order to predict how benthic communities will respond to these changes, it is crucial to understand feeding strategies of benthic fauna. One of the most sensitive methods to study the fate of fresh phytodetritus on the seafloor is by tracing the incorporation of <sup>13</sup>C-labelled algae by benthic fauna. Although many studies have been conducted, the data have however not been consistently compared.

Here, we present an overview of tracer experiments from 23 study sites ranging from 0–5000 m of water depth. The data set consists of > 900 assimilation rates of <sup>13</sup>C-labelled phytodetritus by meio- and macrofauna, spanning an individual size range of eight orders of magnitude. Striking findings are 1) incorporation rates vary between faunal compartments, indicating different feeding strategies, 2) incorporation rates are typically 1–2 orders of magnitude lower as compared to respiration rates, suggesting that fresh phytodetritus represents a limited carbon source for most fauna and 3) unlike feeding theory suggests, incorporation rates decreases with organism size and 4) assimilation rate of labile detritus decreases with depth, suggesting increased specialization on lower quality detritus with increasing water depth.





*Monday 3<sup>rd</sup> December*

*Biodiversity Pattern – Large Scale 1*

**FREE-LIVING NEMATODES ASSOCIATED WITH CHEMOSYNTHETIC HABITATS : A LARGE SCALE INTEGRATED ANALYSIS ON DISTRIBUTION AND DIVERSITY PATTERNS**

**Vanreusel A, De Groote A, Pape E, Van Campenhout J, Lins L, Guillini K, Ingels J**

University Ghent

We performed an integrated analysis based on datasets, obtained from the North East Atlantic margin, the West African margin, the Northeast American margin and the East Mediterranean. We showed that nematodes are often thriving in the sulphidic sediments of deep cold seeps, with standing stock values occasionally exceeding largely the numbers at background sites, while they are showing low diversity, and high dominance of a single species. We further analysed the major scales of turnover in biodiversity considering comparisons within habitats, between habitats, between seeps from the same region and between regions. We identified differences in regional diversity between different areas and identified the proportion of unique and ubiquitous taxa. We also provided evidence that shallow water relatives, rather than typical deep-sea taxa, have successfully colonized the reduced sediments of seeps at large water depth. Therefore, we further applied molecular techniques to identify the connectivity between different populations both between different seep sites and with shallow-water populations.



*Monday 3<sup>rd</sup> December*

*Evolution 1*

## **THE ENIGMA OF HIGH SPECIES DIVERSITY IN WOOD-BORING BIVALVES**

**Voight J**

Field Museum of Natural History, Chicago, IL, USA

Deep-sea wood-boring bivalves of the Xylophaginae (Pholadidae) are diverse and enigmatic. Especially surprising is the large number of sympatric species. Although these taxa must bore into wood or other vegetation on the seafloor to survive, and deep-sea wood appears to us to be rare, small, and temporally unpredictable, how can high levels of species diversity be sustained?

Two mechanisms likely allow species co-occurrence, either in microsympatry or in the same ocean basin. First, in larger wood blocks, species partition substrate by time. The first colonist species are under strong selection for maximum reproductive output, a strategy that leaves individuals vulnerable to predation. Species that colonize later are more predator-resistant, as evidenced by terminal hooks or sheaths that protect their siphons and extend individual life spans.

A second mechanism that may increase species diversity functions within ocean basins. Species with attached miniatures, revealed by T. Haga and Ockelman and Dinesen in 2011 to be dwarf males, are significantly more common near landmasses than at the same depths farther offshore. A determining factor may be how long vegetation of different sizes floats. Small pieces of vegetation are apt to sink close to shore; large ones will likely float longer and go farther out to sea. Nearshore species frequenting small pieces of wood must avoid self-fertilization, but the limited space and food provided by small substrate preclude survival of two full-sized individuals. The evolution of dwarf males addresses both problems for nearshore species, but would be maladaptive in offshore species that frequent logs that offer sufficient substrate to support large reproductively active populations.



*Wednesday 5<sup>th</sup> December*

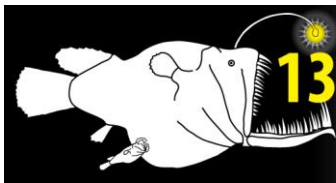
*New Methods and Novel Techniques 1*

### **INNOVATIONS IN SEEP EXPLORATION: REMOTE AUV OPERATIONS FROM A SHORE-BASED CENTER**

**Wagner J<sup>1</sup>, Brothers L<sup>2</sup>, German C<sup>3</sup>, Kaiser C<sup>3</sup>, Yoerger D<sup>3</sup>, Van Dover C<sup>1</sup>**

<sup>1</sup> Duke University Marine Laboratory, <sup>2</sup> U.S. Geological Survey, <sup>3</sup> Woods Hole Oceanographic Institution

The 2012 Okeanos Explorer/Sentry AUV cruise pioneered unprecedented deep-sea research techniques — AUV operations controlled remotely, not from the ship, but from shore hundreds of miles away. Exploration of the Blake Ridge Diapir system was conducted off the US East Coast, seeking seeps and other chemosynthetic communities. Substantial mapping undertakings constructed bathymetry data, sub-bottom profile, and complete photomosaic coverage of this diapir. However, the team of scientists directing operations and analysing data was participating through a “virtual cruise” based in Rhode Island, USA, at NOAA’s Exploration Command Center. An extensive volume of data was relayed ship to shore, both in real time and in large overnight transfers, completing one of the most significant data transfers during an on-going cruise. Shared communication channels were multifaceted, including telepresence, intercoms, and live chats. Through these data and communication lines, scientists on shore were constantly engaged and maintained an up-to-date following of the ship’s activities. This novel approach to deep-sea research creates revolutionary opportunities for scientists to participate in and learn from cruises, in addition to reducing costs. Further, without berth limitations, the shore-based research approach increases the possibility of extensive multidisciplinary teams collaborating toward tackling deep-sea research questions in real time. The Sentry AUV cruise at Blake Ridge represents a collaborative joining of the NOAA Okeanos Explorer Program, National Science Foundation (NSF), and Woods Hole Oceanographic Institution (WHOI). Successes during Okeanos Explorer’s Blake Ridge mission pave the way to continue expanding the versatility and practicality of sharing ship-to-shore data, communications, and now even land-based AUV control for the future.



International

# 13<sup>th</sup> Deep-Sea Biology Symposium

Wellington, New Zealand 3 – 7 December 2012

*Tuesday 4<sup>th</sup> December*

*Biodiversity Pattern – Intermediate 1*

## **BETA DIVERSITY IN ECHINODERMS IS STRUCTURED BY SPATIAL TURNOVER ALONG A BATHYMETRIC GRADIENT IN THE PORCUPINE SEABIGHT AND ABYSSAL PLAIN**

**Wagstaff M<sup>1</sup>**, Howell K<sup>2</sup>, Bett B<sup>3</sup>, Billett D<sup>3</sup>, Brault S<sup>1</sup>, Stuart C<sup>1</sup>, Rex MI<sup>1</sup>

<sup>1</sup> University of Massachusetts Boston, USA, <sup>2</sup> University of Plymouth, UK, <sup>3</sup> National Oceanography Centre, Southampton, UK

Beta diversity in the deep sea has previously been interpreted as a consequence of species turnover. Recently developed metrics allow for beta diversity along an environmental gradient to be decomposed into two processes, spatial replacement (turnover) and nestedness due to species loss. In macrofaunal molluscan assemblages, both processes occur, but vary in relative importance with depth. Turnover predominates at bathyal depths, but abyssal faunas are significant nested subsets of bathyal faunas. This result, coupled with evidence on dispersal ability and population density, supports the theory that source-sink dynamics help maintain abyssal biodiversity. Here, we examine spatial replacement and nestedness in asteroids and holothurians in the Porcupine Seabight and Abyssal Plain. Unlike mollusks, spatial turnover is the dominant trend along the depth gradient and there is no evidence for the operation of source-sink dynamics to maintain abyssal diversity in these two classes. Holothurians are mainly deposit feeders and show no decline in diversity with depth that might implicate source-sink dynamics. Asteroids however do show a decrease in species diversity with depth. Predatory asteroids are replaced by deposit feeders as less energy becomes available to support higher trophic levels. It is now clear that both turnover and nestedness occur along a bathymetric gradient and that their roles can vary with depth and among taxa. In echinoderms it appears that turnover predominates and that abyssal diversity is a consequence of adaptation to the deep-sea and not a result of source-sink dynamics.



*Tuesday 4<sup>th</sup> December*

*Biodiversity Pattern – Intermediate 3*

## **BIODIVERSITY OF DEEP-SEA HYDROTHERMAL VENT FAUNA AND ITS RELATIONSHIPS TO ENVIRONMENTS IN OKINAWA TROUGH**

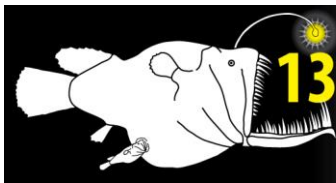
**Watanabe H**<sup>1</sup>, Yamamoto M<sup>1</sup>, Ogura T<sup>1,2</sup>, Takahashi Y<sup>1,2</sup>, Yahagi T<sup>3</sup>, Nakamura M<sup>4</sup>, Seo M<sup>3</sup>, Kojima S<sup>3</sup>, Watsuji T<sup>1</sup>, Takai K<sup>1</sup>

<sup>1</sup> Japan Agency for Marine-Earth Science and Technology, <sup>2</sup> The Graduate School of Marine Science and Technology, Tokyo University of Marine Science and Technology, <sup>3</sup> Atmosphere and Ocean Research Institute, University of Tokyo, <sup>4</sup> Okinawa Institute of Science and Technology, <sup>5</sup> Kyushu University

Flourish assemblages of deep-sea hydrothermal vent fauna associated with steep environmental gradient formed by high temperature venting fluid containing high concentration of metals and the other kinds of chemicals. The Okinawa Trough, is a backarc basin which has started rifting from the southern part 2 My ago, and at least nine hydrothermal vent fields has been discovered along the NE-SW spreading axis. Multi-disciplinary investigation was carried out in five of nine vent fields to find out the relationships between biodiversity and environments in the Okinawa Trough.

In the five hydrothermal vent fields, quantitative faunal sampling and simultaneous environmental measurements using sensors including a newly developed D-Pote (a Deep-sea Potentiostat) were carried out at more than two points in each vent field, during the NT11-20 cruise of R/V Natsushima / ROV Hyper-Dolphin. Biodiversity was evaluated based on the collected faunal samples and the relationships between faunal composition and environmental factors such as temperature, depth, salinity, and concentrations of oxygen and sulphide compounds were examined statistically.

Biodiversity of the vent fauna was relatively low in the northern part of the Okinawa Trough, where vent fields are located in relatively shallow area (< 1000 m depth). On the other hand, in the southern, relatively deep (> 1000 m depth) and older part, vent communities of relatively high biodiversity corresponding with great variation of concentration of sulphide compounds were observed. The present results suggested that the correspondence of the biodiversity, environmental diversity, and geological history of hydrothermal vent fields in the Okinawa Trough.



International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

*Friday 7<sup>th</sup> December*

*Trophic and Process 4*

**SPATIAL DIFFERENCES IN SOUTHERN OCEAN HYDROTHERMAL VENT FOOD WEBS: INFLUENCES OF CHEMISTRY, MICROBIOLOGY AND PREDATION ON TROPHODYNAMICS.**

**Wigham B<sup>1</sup>**, Reid W<sup>1</sup>, Sweeting C<sup>1</sup>, Polunin N<sup>1</sup>, Zvirglmaier K<sup>2</sup>

<sup>1</sup> Newcastle University, UK <sup>2</sup> Technische Universitaet Muenchen, Germany

The hydrothermal vents on the East Scotia Ridge (ESR) are the first to be explored in the Antarctic and are dominated by large peltospirid gastropods, stalked barnacles (*Vulcanolepas* n. sp.) and yeti crabs (*Kiwa* n. sp.). Samples were collected at two vent fields (E2, E9) with contrasting vent fluid chemistries to describe trophic interactions and identify potential carbon fixation pathways using stable isotopes. The lightest  $\delta^{13}\text{C}$  were in peltospirid gastropods (E2 = -30.1‰, E9 = -31.2‰) and indicated carbon fixation via the Calvin-Benson-Bassham (CBB) cycle by a single species of gamma-Proteobacteria housed within the gills. The heaviest  $\delta^{13}\text{C}$  were in *Kiwa* n. sp. (E2 = -19.2‰, E9 -10.6‰), which mirrored that of the epibionts on the ventral setae. Large differences in *Kiwa* n. sp.  $\delta^{13}\text{C}$  were potentially the result of site differences in epibiont community (E2 epibionts = mix of gamma- and epsilon-Proteobacteria, E9 epibionts = epsilon-Proteobacteria) and in turn the relative contribution of carbon fixed via the reductive tricarboxylic acid (rTCA) and CBB cycles assimilated by *Kiwa* n. sp. Site differences in carbon fixation pathways were traced into higher trophic levels e.g. a stichasterid asteroid that predaes on *Kiwa* n. sp. Sponges and anemones at the periphery of E2 assimilated a proportion of photosynthetic primary production but this was not observed in vent fauna from E9. The differences in  $\delta^{13}\text{C}$  and  $\delta^{34}\text{S}$  values of vent fauna at E2 and E9 sites suggest possible differences in the relative contribution of photosynthetic primary production and chemoautotrophic carbon fixation via CBB and rTCA cycles to the hydrothermal vent food webs.



Friday 7<sup>th</sup> December

Trophic and Process 3

## NATURAL IRON FERTILISATION IS REFLECTED IN THE STABLE ISOTOPIC COMPOSITION OF CARBON IN DEEP-SEA HOLOTHURIANS

Wolff G<sup>1</sup>, Fisher E<sup>1</sup>, Billett D<sup>2</sup>, Smythe M<sup>1</sup>

<sup>1</sup> University of Liverpool, <sup>2</sup> National Oceanography Centre, Southampton

Natural iron fertilisation influences the flux of particulate organic carbon (POC) to the abyss around the Crozet Plateau in the Southern Indian Ocean<sup>1</sup>. To the north and east of the Crozet Islands, where surface waters are fertilised by iron (+Fe), the POC flux (3000 m) is approximately 2.5x greater than in the region underlying high nutrient-low chlorophyll (HNLC) waters to the south. This is reflected in the benthic megafaunal biomass (ca. 4000 m), which is ca. 3.5 times higher at the +Fe site<sup>2</sup>. Major differences in the taxa at the +Fe and HNLC sites reveal how surface oceanic conditions and the chemical composition (quality) of the POC flux to the sea floor change and structure deep-sea benthic communities<sup>2</sup>.

Here, we present the stable isotopic (SI) signatures of carbon and nitrogen in the dominant megafauna, the holothurians, collected from the +Fe and HNLC sites at Crozet.  $\delta^{13}\text{C}$  compositions reflect the trophic niches of the holothurian species, ranging from +8 to 14 ‰ at the two sites. However,  $\delta^{13}\text{C}$  SIs differ by > 7 ‰ between +Fe and HNLC (e.g. *Abyssocucumis* sp.; -14 ‰ and -21 ‰ at +Fe and HNLC, respectively), while in POC and sedimentary organic carbon (SOC) samples,  $\delta^{13}\text{C}$  differs by only ca. ~2 ‰ between the same sites<sup>3</sup>. Compound specific isotopic analyses (CSIA) of fatty acids and sterols in holothurian tissues from the two sites confirm that their bulk  $\delta^{13}\text{C}$  signatures better reflect the differing productivity of overlying waters than do POC and SOC. Lipids in the most selective feeders at +Fe are strongly enriched in  $^{13}\text{C}$ . We provide evidence that the deep-sea fauna retain an integrated carbon signature that most best represents differences in overlying productivity and  $\text{pCO}_2$  at the +Fe and HNLC sites, which shows their potential as a sentinel for environmental change in the deep ocean.

- 1 Pollard, R. T. et al. (2009) Southern Ocean deep-water carbon export enhanced by natural iron fertilization. *Nature* 457: 577–U581, doi:10.1038/nature07716.
- 2 Wolff, G. A. et al. (2011) The Effects of Natural Iron Fertilisation on Deep-Sea Ecology: The Crozet Plateau, Southern Indian Ocean. *PLoS One* 6, doi:10.1371/journal.pone.0020697.
- 3 Hernandez-Sanchez, M. T. et al. (2012) Signature of organic matter exported from naturally Fe-fertilised oceanic waters. *Deep Sea Research Part I: Oceanographic Research Papers* 65: 59–72, doi:10.1016/j.dsr.2012.02.007.





*Monday 3<sup>rd</sup> December*

*Biodiversity Pattern – Large Scale 3*

#### **MEIOFAUNAL COMMUNITY ASSESSMENT OF SEAMOUNTS ON THE SOUTHWEST INDIAN OCEAN RIDGE**

**Woodall L<sup>1</sup>**, Ferrero T<sup>1</sup>, Packer M<sup>1</sup>, Paterson G<sup>1</sup>, Serpetti N<sup>2</sup>, Narayanaswamy B<sup>2</sup>, Taylor M<sup>3</sup>, Rogers A<sup>3</sup>

<sup>1</sup> Natural History Museum, London, <sup>2</sup> Scottish Association for Marine Science, Oban, <sup>3</sup> University of Oxford, Oxford

Biodiversity and species' ecological function are two biological factors that define ecosystems. The marine ecosystem, especially the deep sea, is poorly documented and the Southwest Indian Ocean Ridge (SWIR) is noted as a particularly data deficient region. Rich with seamounts, it is vulnerable to on-going pressure from the fishing industry and the new threat of mineral mining. Seamounts on the SWIR are numerous and diverse, extending from sub-polar waters in the SW to those beneath subtropical seas in the SE. The ridge also follows a productivity gradient. Therefore the study of the fauna provides an excellent opportunity in which to explore the role of diversity drivers such as: primary production and disturbance, both anthropogenic (fishing) and natural (hydrodynamic regime), together with factors such as temperature, depth and oxygen concentration.

Nematodes are poorly known from seamounts but have the potential to provide important information on how disturbance and productivity affect seamount infaunal communities. Here we present an assessment of nematode community assemblages from the same depth across the SWIR seamounts and thus across a productivity gradient, using both morphological and molecular techniques. In this talk we present the results of our study on: 1) whether disturbance and productivity gradients affect nematode assemblages, 2) biogeographic patterns of nematodes across the SWIR.



*Monday 3<sup>rd</sup> December*

*Biodiversity Pattern – Large Scale 2*

**BETA DIVERSITY IN THE DEEP-SEA – PATTERNS OF COMMUNITY COMPOSITION TURNOVER FOR BATHYAL SPECIES AROUND AUSTRALIA AND NEW ZEALAND**

**Woolley S<sup>1,2</sup>, O'Hara T<sup>1</sup>**

<sup>1</sup> Museum Victoria, <sup>2</sup> School of Botany, University of Melbourne

The biogeography of bathyal species (200–2500 m) across Australia, New Zealand and the globe is still unresolved. A key component of benthic marine biogeography is spatial turnover of species among populations and regions. Describing patterns of community composition will contribute to testing the hypothesis that beta diversity increases with geographic distance in bathyal communities. This study uses distributions of Ophiuroidea (brittle stars) to model beta diversity across Australia and New Zealand. These patterns are compared spatially to highlight regional and interregional change in species distributions. Describing patterns of beta-diversity will help inform conservation efforts in deep-sea, by highlighting regions of uniqueness and biogeographic breaks around Australia and New Zealand.



*Monday 3<sup>rd</sup> December*

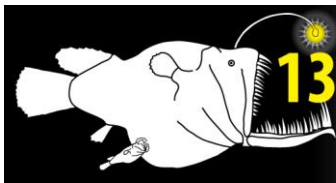
*Biodiversity Pattern – Large Scale 1*

## **PATTERNS AND CONTROLLING FACTORS OF SPECIES DIVERSITY IN THE ARCTIC OCEAN**

**Yasuhara M**<sup>1</sup>, Hunt G<sup>2</sup>, van Dijken G<sup>3</sup>, Arrigo KR<sup>3</sup>, Cronin TM<sup>4</sup>, Wollenburg JE<sup>5</sup>

<sup>1</sup> The University of Hong Kong, <sup>2</sup> Smithsonian Institution, <sup>3</sup> Stanford University, <sup>4</sup> US Geological Survey, <sup>5</sup> Alfred Wegener Institute for Polar and Marine Research

Large-scale diversity patterns in the deep sea are reasonably well known including polar-low, tropical-high latitudinal diversity patterns in gastropods, bivalves, isopods, foraminifera, ostracods, etc. Unimodal depth diversity gradients also appear to be a prevailing pattern. Paleoecological studies revealed that glacial-low and interglacial-high diversity is fairly common pattern in deep-sea environments. However, the underlying mechanisms controlling diversity are still controversial. Here we present new Arctic Ocean results using large ostracod and foraminiferal datasets that document Arctic large-scale diversity patterns with respect to latitude and water depth, and compare them with ecological and paleoecological records in other oceans. This comparison suggests that the underlying mechanisms causing observed species diversity patterns are unexpectedly complex. Mechanisms driving deep-sea species diversity are most likely different among regions (for example, North Atlantic, North Pacific, Arctic, and Southern Oceans) and for different taxonomic groups (for example, isopods, gastropods, bivalves, echinoderms, nematodes, foraminifera, and ostracods). The most important factors influencing diversity are particulate organic matter flux, bottom-water temperature, and, to a lesser degree, seasonality of surface productivity. Ice cover may be also important in the polar seas.



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# 13<sup>th</sup> Deep-Sea Biology Symposium

Wellington, New Zealand 3 – 7 December 2012

Monday 3<sup>rd</sup> December

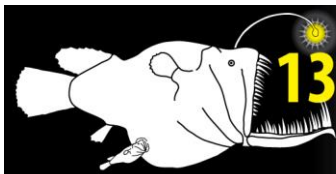
Dispersal and Connectivity 2

## DISPERSAL TRAJECTORIES OF COLD-SEEP TUBEWORM LARVAE (*LAMELLIBRACHIA LUYMESI*) PREDICTED BY OCEAN MODELS AND EMPIRICAL DATA ON LARVAL DEVELOPMENT

Young C<sup>1</sup>, He R<sup>2</sup>, Eggleston D<sup>2</sup>, Li Y<sup>2</sup>, Qian H<sup>2</sup>, Leong P<sup>3</sup>, Manahan D<sup>3</sup>

<sup>1</sup> Oregon Institute of Marine Biology, Univ. of Oregon, <sup>2</sup> Dept. of Marine, Earth and Atmospheric Sciences, North Carolina State University, <sup>3</sup> Department of Biological Sciences, University of Southern California

*Lamellibrachia luymesii*, a common siboglinid tubeworm associated with methane seeps, occurs over a limited geographic range in the Northern Gulf of Mexico where metapopulations demonstrate little genetic structure. However, the species is also found as far south as Guyana and morphologically indistinguishable congeners are known from Barbados, Chile, Uruguay and the Mediterranean. To determine if long-distance larval dispersal is likely, we used LTRANS, a Lagrangian transport model, to simulate trajectories of larvae originating from seeps at the South American sites and on the Louisiana Slope. Biological parameters for the models (zygote buoyancy, larval swimming speed, zygote and larval metabolism, larval thermal tolerance and planktonic larval duration) were measured or inferred from in vitro cultures. Because reproduction appears to be continuous in this species, we ran simulations during several times of year. Over a three-week larval period, simulated larvae from the Gulf of Mexico dispersed as far as 300 km, which was far enough to seed both extremes of the Gulf distribution, but not the nearest known downstream seeps on the Blake Plateau or in the eastern Atlantic. Ontogenetic vertical migration mediated by zygote buoyancy and larval swimming had only a modest effect on dispersal distance when compared with passive drifting at the adult depth. There was no dispersal difference among months. Larval connectivity among widely disjunct populations appears very unlikely within a single generation. If these populations are connected genetically, the dispersal models suggest the existence of undiscovered seeps that could serve as stepping stones along the South American margin and in the Caribbean Sea.



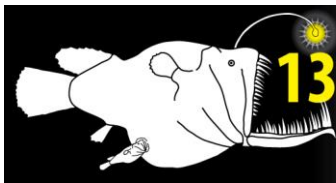
International

**13<sup>th</sup> Deep-Sea Biology Symposium**

Wellington, New Zealand  3 – 7 December 2012

# Poster Abstracts

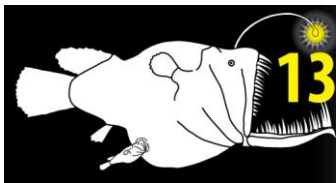
**Alphabetical by  
Presenting Author  
Surname**



International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

**Poster Listing**

- P1**  
GENETIC DIVERSITY AND CONNECTIVITY OF *MUNIDOPSIS* SPP., A SQUAT LOBSTER FROM WESTERN PACIFIC BACK-ARC BASINS  
Aleí F
- P2**  
BATHYMETRIC AND TEMPORAL CHANGES IN SUPRABENTHIC ASSEMBLAGES FROM THE BLANES CANYON AND ADJACENT SLOPE (IBERIAN MARGIN, NW MEDITERRANEAN)  
Cunha M
- P3**  
DISTINCT MEGABENTHIC STRUCTURE-FORMING COMMUNITIES WITHIN THE MAKAPU’U DEEP-SEA CORAL BED  
Baco A
- P4**  
A SYNTHESIS OF GENETIC CONNECTIVITY IN DEEP-SEA FAUNA AND IMPLICATIONS FOR MPA DESIGN  
Baco A
- P5**  
ASSOCIATED SPECIES OF TWO DEEP-SEA PENNATULACEAN CORALS IN THE NORTHWEST ATLANTIC  
Baillon Sandrine
- P6**  
COURTSHIP, EGG LAYING, DEVELOPMENT AND FEEDING OF THE DEEP-SEA POLYCHAETE *OPHRYOTHROCHA*  
Baillon S
- P7**  
PIECING TOGETHER CORALS AND BOTTOM TRAWLS  
Baird SJ
- P8**  
PREDICTING PRESENT AND PAST DISTRIBUTIONS OF DECAPOD SHRIMPS IN THE SOUTHERN OCEAN  
Basher Z
- P9**  
INTERANNUAL CHANGES IN MEGAFUNA FROM THE ARCTIC OBSERVATORY 'HAUSGARTEN' BETWEEN 2002 AND 2012  
Bergmann M
- P10**  
RECENT ADVANCES IN NEW ZEALAND CEPHALOPOD RESEARCH: AN OVERVIEW  
Bolstad K



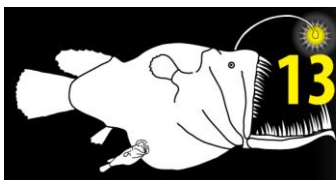
International

# 13<sup>th</sup> Deep-Sea Biology Symposium

Wellington, New Zealand 3 – 7 December 2012

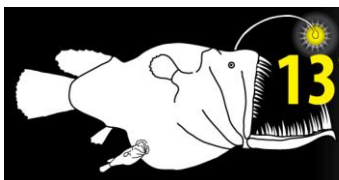
- P11**  
**DISTRIBUTION, POPULATION STRUCTURE, REPRODUCTION, AND DIET OF *OPHIOLIMNA ANTARCTICA* (LYMAN, 1879) FROM KEMP CALDERA IN THE SOUTHERN OCEAN**  
Boschen R
- P12**  
**COLD SEEP COMMUNITIES ON THE HIKURANGI MARGIN, NEW ZEALAND**  
Bowden D
- P13**  
**EVOLUTION OF THE DEEP-SEA ENVIRONMENT WITH REFERENCE TO THE BATHY- ABYSSOPELAGIC CALANOID COPEPOD FAMILY: MEGACALANIDAE**  
Bradford-Grieve J
- P14**  
**SYSTEMATIC REVIEW OF WHIP-LASH SQUID (CEPHALOPODA: MASTIGOTEUTHIDAE) FOUND IN NEW ZEALAND WATERS**  
Braid H
- P15**  
**DEEP OCEAN CURRENTS AFFECT SHALLOW REEF EVOLUTION**  
Bromfield K
- P16**  
**DEEP-SEA CARBON SEQUESTRATION USING CROP RESIDUE: PRELIMINARY OBSERVATIONS OF A BALE OF CORN STOVER IN 3100 M DEPTH OVER 2.5 YEARS.**  
Buck K
- P17**  
**REPRODUCTION STRATEGY IN DEEP-SEA EPIZOIC SCALPELLID BARNACLES**  
Buhl-Mortensen L, Høeg J
- P18**  
***RIMICARIS EXOCULATA* GUT EPIBIONT COMMUNITIES ALONG THE MID-ATLANTIC RIDGE HYDROTHERMAL VENT SITES**  
Cambon-Bonavita MA
- P19**  
**ACQUISITION OF EPIBIOTIC BACTERIA ALONG THE LIFE CYCLE OF THE HYDROTHERMAL SHRIMP *RIMICARIS EXOCULATA***  
Cambon-Bonavita MA
- P20**  
**INORGANIC CARBON FIXATION AND NUTRITIONAL TRANSFERS IN THE HYDROTHERMAL VENT HOLOBIONT *RIMICARIS EXOCULATA***  
Cambon-Bonavita MA





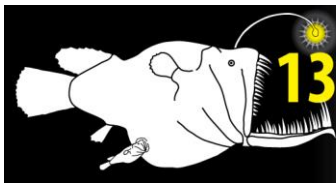
International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

- P21**  
**THE DEEP-SEA *RIMICARIS EXOCULATA* SHRIMP GILL CHAMBER EPIBIOSIS REVISITED BY METAGENOMICS AND DISCOVERY OF ZETAPROTEOBACTERIAL EPIBIONTS**  
Cambon-Bonavita MA
- P22**  
**POLYCHAETE FEEDING GUILD COMPOSITION OF A MACROBENTHIC POLYCHAETE COMMUNITY, SENGHOR SEAMOUNT (N ATLANTIC)**  
Chivers A
- P23**  
**OCEAN ACIDIFICATION DIFFERENTIALLY AFFECTS THE PHYSIOLOGY AND GENE EXPRESSION PROFILES OF COLD-WATER SCLERACTINIANS AND OCTOCORALS**  
Colaço A
- P24**  
**THE AZORES MARINE PARK: TOWARDS THE PROTECTION OF THE DEEP SEA**  
Colaço A
- P25**  
**COMPOSITION AND DISTRIBUTION OF FAUNA AT A HYDROTHERMAL VENT FIELD ON THE SOUTHWEST INDIAN RIDGE**  
Nye V
- P26**  
**INSIGHTS INTO THE POPULATION DYNAMICS OF THE DEEP-SEA CORAL GENUS *PARAMURICEA* IN THE GULF OF MEXICO**  
Cordes E
- P27**  
**MAPPING THE BATHYAL ICHTHYOFAUNA DIVERSITY IN THE GORRINGE BANK (NE ATLANTIC)**  
R. Cunha M
- P28**  
**DEEP WATER HOLOTHUROIDS FROM THE ROSS SEA AND ADJACENT ISLANDS AND SEAMOUNTS, WITH DESCRIPTIONS OF NEW SPECIES BASED ON MORPHOLOGICAL AND MOLECULAR PHYLOGENY**  
Davey N
- P29**  
**A REVIEW OF THE CAUDINID SEA CUCUMBERS OF NEW ZEALAND, WHAT WE FOUND IN THE DEEP WATERS**  
Davey N
- P30**  
**GLOBINS IN VESICOMYID BIVALVES AS AN ADAPTATION TO HYPOXIC ENVIRONMENTS**  
Decker C



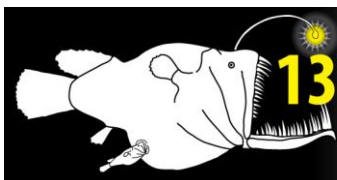
International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

- P31**  
**FOOD-WEB STRUCTURE OF COLD-WATER CORAL ECOSYSTEMS IN THE GULF OF MEXICO REVEALED BY DELTA-13C AND DELTA-15N ANALYSIS**  
Demopoulos A
- P32**  
**A NEW GENUS AND SEVERAL NEW SPECIES OF DEEP-SEA BAMBOO CORALS (ISIDIDAE) FROM NEW ZEALAND WATERS: A TAXONOMIC AND MOLECULAR APPROACH**  
Dueñas L
- P33**  
**POPULATION STRUCTURE OF THE SCAVENGING AMPHIPOD, *ABYSSORCHOMENE ABYSSORUM*, AT BATHYAL DEPTHS ON THE MID-ATLANTIC RIDGE IN THE VICINITY OF THE CHARLIE-GIBBS FRACTURE ZONE**  
Duffy G
- P34**  
**MEGAFAUNAL COMMUNITY STRUCTURE IN THE SUBMARINE CANYONS OF SOUTHERN CALIFORNIA**  
Duffy G
- P35**  
**COMMUNITY COMPOSITION OF SCAVENGING AMPHIPODS AT BATHYAL DEPTHS ON THE MID-ATLANTIC RIDGE**  
Duffy G
- P36**  
**LIVE AND DEAD DEEP-SEA BENTHIC FORAMINIFERAL FAUNAS FROM TWO SUBMARINE CANYON AREAS (NE ATLANTIC)**  
Duros P
- P37**  
**LIVING IN COCKAIGNE: REPRODUCTION OF *EURYCOPE SPINIFRONS* GURJANOVA, 1933 (ISOPODA: MUNNOPSIDAE) IN THE DEEP SEA OF JAPAN AND COMPARISON TO THE ISOPOD FAUNA IN THE ADJACENT KURIL TRENCH AREA**  
Elsner N
- P38**  
**THE SQUID GENUS *TEUTHOWENIA* IN NEW ZEALAND WATERS: SYSTEMATICS, ECOLOGY AND BIG, GOOGLY EYES**  
Evans A
- P39**  
**BATHYMETRIC PATTERNS OF FREE-LIVING NEMATODE DIVERSITY AND ABUNDANCE IN THE SEA OF JAPAN**  
Fadeeva N, Mordukhovich V
- P40**  
**PHYLOGENETIC ANALYSES OF THE DEEP-SEA OCTOCORALS *CORALLIUM* AND *PARAGORGIA* BASED ON WHOLE MITOCHONDRIAL GENOMES**  
Figueroa D, Baco A



International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

- P41**  
**TROPHIC MODES OF FORAMINIFERA IN THE ARABIAN SEA: EVIDENCE FROM STABLE ISOTOPE ANALYSIS.**  
Jeffreys R
- P42**  
**A ZOOGEOGRAPHY OF LANTERNFISHES (FAMILY MYCTOPHIDAE) IN THE EASTERN-SOUTHEASTERN AUSTRALIAN REGION AND COMPARISONS WITH PHYSICOCHEMICAL BIOGEOGRAPHY**  
Flynn A
- P43**  
**HABITAT AND COMMUNITIES OF COMMON DEEP-SEA ASTEROIDS FROM NEWFOUNDLAND AND LABRADOR, CANADA**  
Gale K
- P44**  
**LARVAL DISPERSAL OF DEEP-SEA MUSSELS: INSIGHTS FROM TRACE ELEMENT FINGERPRINTS**  
Cunha MR
- P45**  
**FAUNISTIC RESEARCH ON METAZOAN MEIOFAUNA FROM SEAMOUNTS — A REVIEW**  
George KH
- P46**  
**A NEW SPECIES OF ANCORABOLIDAE (CRUSTACEA: COPEPODA: HARPACTICOIDA) FROM THE CAMPOS BASIN, BRAZIL, INCLUDING A PHYLOGENETIC REVIEW OF THE TAXON *POLYASCOPHORUS* GEORGE, 1998**  
George KH
- P47**  
**CHARACTERIZATION OF A MONOPHYLUM *ECHINOCLETODES* LANG (COPEPODA: HARPACTICOIDA: ANCORABOLIDAE), DISPLACEMENT OF *E. BODINI* DINET AND *E. WALVISI* DINET INTO *CLETODES* BRADY (CLETODIDAE), AND PRESENTATION OF TWO NEW SPECIES**  
George KH
- P48**  
**ARGESTINAE POR, 1986, THE FIRST RECOGNIZED SUPRAGENERIC MONOPHYLUM WITHIN ARGESTIDAE SENSU POR, 1986 (CRUSTACEA, COPEPODA, HARPACTICOIDA)**  
George KH
- P49**  
**MODELLING *LOPHELIA PERTUSA* DISTRIBUTION IN THE GULF OF MEXICO**  
Georgian S
- P50**  
**USING NEW TECHNOLOGIES TO IDENTIFY DEEP-SEA SPECIES: MARINE LIFE FIELD GUIDE IBOOK**  
Gervais F



International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

P51

A NEW POLYNOID POLYCHAETE AND HOLOTHURIAN ASSOCIATION FROM THE MID-ATLANTIC RIDGE

Glover A

P52

THREE SPECIES OF *OSDAX* FROM THE DEEP SOUTHERN OCEAN

Glover A

P53

DISTRIBUTION OF *CALANUS* IN ARCTIC-ATLANTIC BORDER AREA: EXPATRIATION AND POTENTIAL COLONIZATION

Gluchowska M

P54

HUSBANDRY OF COLD-WATER CORALS IN AQUARIA: COLLECTION AND CARE REQUIREMENTS

Godinho A

P55

BENTHIC FORAMINIFERAL SQUATTERS INHABITING THE TESTS OF OTHER FORAMINIFERA

Laguionie-Marchais C

P56

THE DEEP-SEA OSTRACODA COLLECTED OFF SOUTHERN ICELAND DURING THE THE ICEAGE PROJECT

Grimm M

P57

DEEP-SEA MACROFAUNAL ECOLOGY AND BIODIVERSITY OF THE WHITTARD SUBMARINE CANYON

Gunton L

P58

PHYLOGENOMICS OF DEEP-SEA OCTOCORALS: NEW APPROACHES TO SOLVE LONG-STANDING PROBLEMS

Herrera S

P59

PREDICTION OF DEEP-SEA SESSILE BENTHIC EPIFAUNA ACROSS THE KERGUELEN PLATEAU

Hibberd T

P60

THE WORLD REGISTER OF DEEP-SEA SPECIES

Higgs N

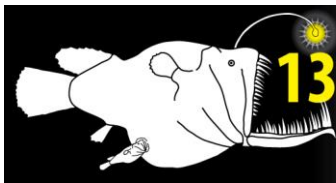
P61

COLD-WATER CONNECTIVITY: MICROSATELLITE DEVELOPMENT IN THE OCTOCORALS *EUNICELLA VERRUCOSA* AND *ALCYONIUM DIGITATUM*

Holland L



- P62**  
**CATALOGUING THE DEEP SEA**  
Howell K
- P63**  
**DEEP-SEA OCTOPUSES FROM SOUTHEAST PACIFIC OCEAN**  
Ibáñez C
- P64**  
***OPISTHOTEUTHIS* SPECIES (CEPHALOPODA: OPISTHOTEUTHIDAE) FROM BATHYAL ZONE OF SOUTHEASTERN PACIFIC OCEAN**  
Ibáñez C
- P65**  
**MBARI'S DEEP-SEA GUIDE: FINDING MEANING IN A MULTI-DECADAL DATABASE OF DEEP-SEA OBSERVATIONS**  
Jacobsen Stout N
- P66**  
**TROPHIC MODES OF FORAMINIFERA IN THE ARABIAN SEA: EVIDENCE FROM STABLE ISOTOPE ANALYSIS**  
Jeffreys R
- P67**  
**AUTONOMOUS ECOLOGICAL SURVEYING OF THE ABYSS (AESAs): TOWARDS A LANDSCAPE SCALE PERSPECTIVE IN DEEP-SEA ECOLOGY**  
Jones D
- P68**  
**SELECTION OF HOUSEKEEPING GENE FOR QUANTITATIVE RT-PCR NORMALIZATION IN THE HYDROTHERMAL VENT SHRIMP *NAUTILOCARIS SAINTLAURENTAE***  
Kim SJ, Ju SJ
- P69**  
**A NEW SPECIES OF THE FAMILY CALLIANASSIDAE (CRUSTACEA: DECAPODA: AXIIDAE) FROM VENT FIELDS AT TOFUA ARC IN THE SOUTHWEST PACIFIC**  
Kim SJ
- P70**  
**ESTABLISHING AN ABYSSAL ECOLOGY OBSERVATORY ON THE NEPTUNE CANADA UNDERSEA NETWORK**  
Juniper K
- P71**  
**DEEP-SEA TREASURES - MACROBENTHIC ASSEMBLAGES OF THE TROPICAL PACIFIC NODULE PROVINCE (CLARION-CLIPPERTON FRACTURE ZONE)**  
Kaiser S



International

# 13<sup>th</sup> Deep-Sea Biology Symposium

Wellington, New Zealand 3 – 7 December 2012

P72

**THE INFLUENCE OF CHEMOSYNTHETIC ECOSYSTEMS ON NEMATODE COMMUNITY  
STRUCTURE AND BIOMASS IN THE DEEP EASTERN MEDITERRANEAN SEA.**

Kalogeropoulou V

P73

**$\alpha$  and  $\beta$  DIVERSITY OF HARPACTICOID COPEPODS AROUND THE RYUKYU AND KURIL TRENCHES, NORTH-WEST PACIFIC**  
Kitahashi T

P74

**ARE MESOZOIC SHALLOW-WATER SERPULIDS (ANNELIDA, POLYCHAETA) ANCESTORS OF THE RECENT DEEP-SEA FAUNA?**

Kupriyanova E

P75

**SHAKEN BUT NOT STIRRED: RESPONSE OF A DEEP-SEA NEMATODE COMMUNITY TO A ONE-OFF PHYSICAL DISTURBANCE  
EVENT**

Leduc D

P76

**IN THE (SEA)BED WITH INDUSTRY: WHY DEEP-SEA BIOLOGISTS MUST ENGAGE IN INTERCOURSE (WITH THE COMMERCIAL  
SECTOR)**

Levin L

P77

**AMAZING AMPHIPODA OF NEW ZEALAND'S VASTLY UNKNOWN DEEP-SEA**

Loerz AN

P78

**BENTHIC ASSEMBLAGE STRUCTURE AND ENVIRONMENTAL DRIVERS ON MONOWAI SEAMOUNT, KERMADEC VOLCANIC  
ARC**

Long N

P79

**PHYLOGENY OF SERGESTIDAE AND ALVINOCARIDIDAE**

Lunina A

P80

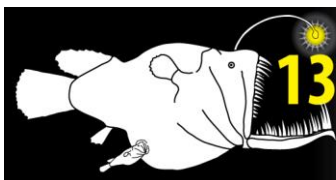
**PREDICTING TRAJECTORIES OF DISSOLVED HYDROCARBONS IN THE DEEP-SEA USING A 3-DIMENSIONAL GENERAL  
CIRCULATION MODEL OF THE OCEANS**

Main C

P81

**EXPLORING THE DEEP-WATER MEDITERRANEAN BIODIVERSITY:  
IN SITU OBSERVATIONS IN THE SANTA MARIA DI LEUCA COLD-WATER CORAL PROVINCE**

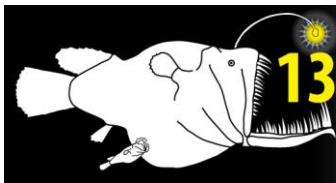
Maiorano P



International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

- P82**  
**THE HIGHLIGHTS OF THE JOINT RUSSIAN/GERMAN DEEP-SEA EXPEDITION SOJABIO (SEA OF JAPAN BIODIVERSITY STUDIES) IN 2010**  
Malyutina M, Brandt A
- P83**  
**EXTENDING THE WORLD'S LONGEST ECOLOGICAL TIME-SERIES OBSERVATION OF A HYDROTHERMAL VENT FIELD**  
Marsh L
- P84**  
**DEEPFORAMS – DEEP-SEA FORAMINIFERAL STUDIES ON THE PORTUGUESE MARGIN**  
Cunha MR
- P85**  
**BIONOD: A FRENCH-GERMAN CRUISE TO STUDY SPECIES DISTRIBUTION AND BIODIVERSITY PATTERNS ACROSS POLYMETALLIC NODULE FIELDS IN THE NORTH-EAST PACIFIC**  
Menot L
- P86**  
**INTERANNUAL CHANGES IN THE BENTHIC MEGAFUNAL COMMUNITY IN THE EASTERN FRAM STRAIT**  
Meyer K
- P87**  
**HYDROTHERMAL AND ADJACENT DEEP-SEA FAUNAL ASSEMBLAGES AT SOUTHERN LAU BACK-ARC BASIN REVEALED BY HIGH-RESOLUTION VIDEO IMAGE**  
Min WG
- P88**  
**MEIOBENTHOS COMMUNITY IN HYDROTHERMAL VENT AND ADJACENT DEEP-SEA BED ON THE SOUTHERN LAU BACK-ARC BASIN**  
Min WG
- P89**  
**COMMUNITY STRUCTURES OF MEIOBENTHOS AND DISTRIBUTIONAL PATTERNS OF NEMATODE ASSEMBLAGE ON THE DEEP SEAFLOOR OF KODOS AREA IN THE CLARION-CLIPPERTON FRACTURE ZONE (NE PACIFIC)**  
Min WG
- P90**  
**COMMUNITY STRUCTURES AND DISTRIBUTIONAL PATTERNS OF MEIOBENTHOS ON THE DEEP SEAFLOOR AND CONTINENTAL SLOPE OF EAST SEA (SEA OF JAPAN)**  
Min WG
- P91**  
**METAZOAN MEIOFAUNA FROM THE NORTH-WESTERN SLOPE OF THE SEA OF JAPAN**  
Mordukhovich V, Fadeeva N



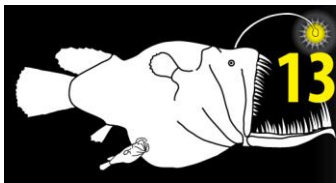


International

# 13<sup>th</sup> Deep-Sea Biology Symposium

Wellington, New Zealand  3 – 7 December 2012

- P92**  
**THE ENIGMATIC NECKER RIDGE: INSIGHTS INTO FAUNA AND COMPARISON TO THE HAWAIIAN ARCHIPELAGO**  
Morgan N
- P93**  
**WHAT HAPPENED TO THE GOOSE BARNACLES?**  
Narayanaswamy B
- P94**  
**SEAMOUNT CARBONATE COMMUNITIES**  
Narayanaswamy B
- P95**  
**GAS FLUXES THROUGH CHEMOSYNTHETIC ECOSYSTEM LIVING IN THREE AREAS OF THE GULF OF GUINEA (EQUATORIAL ATLANTIC OCEAN)**  
Olu K
- P96**  
**NEW DATA ON SABLEFISH *ANOPLOPOMA FIMBRIA* POPULATION STRUCTURE WITHIN THE RUSSIAN WATERS BASED ON GENETIC RESEARCH USING DNA-MARKERS**  
Orlov A
- P97**  
**DISTRIBUTION AND BIOLOGY OF DEMERSAL FISHES BASED ON RESULTS OF DEEP-WATER EXPLORATORY TRAP FISHERY IN THE RUSSIAN NORTHWESTERN PACIFIC**  
Orlov A
- P98**  
**FORMALDEHYDE UTILIZATION BY DEEP-SEA BACTERIA AND ITS IMPLICATION IN CHEMOSYNTHESIS**  
Sujith PP
- P99**  
**PROGRESS ON TAXONOMIC KNOWLEDGE OF SOME DOMINANT POLYCHAETE SPECIES FROM PORCUPINE ABYSSAL PLAIN SUSTAINED OBSERVATORY (PAPSO), NE ATLANTIC OCEAN**  
Paterson G
- P100**  
**REVISION OF TAXONOMIC CHARACTERS ON ABYSSAL BITENTACULATE CIRRATULIDS (POLYCHAETA: CIRRATULIDAE)**  
Paterson G
- P101**  
**ECOLOGICAL FUNCTION OF THE MID-ATLANTIC RIDGE**  
Priede I (Monty)



International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

P102

OBSERVATIONS ON TORQUARATORID ACORN WORMS (HEMICHORDATA, ENTEROPNEUSTA) FROM THE NORTHERN MID-ATLANTIC RIDGE WITH DESCRIPTIONS OF A NEW GENUS AND THREE NEW SPECIES

Priede I (Monty)

P103

REDISCOVERED SPECIES AND NEW BATHYMETRICAL RANGES OF BATHIAL ECHINODERMS IN THE WESTERN MEDITERRANEAN SEA

Ramirez-Llodra E

P104

DAY-NIGHT AND INTERNAL-TIDAL ACTIVITY RHYTHMS IN DEEP-SEA BLACK COD (*ANOPILOPOMA FIMBRIA*) AND HAGFISH (*EPTATRETUS* SP.) BY NEPTUNE VIDEO-MONITORING AT BARKLEY CANYON (CANADA)

Ramirez-Llodra E

P105

SIMULATED DEEP-SEA HYDRODYNAMIC BENTHIC REGIMES MODULATE *NEPHROPS NORVEGICUS* BURROW EMERGENCE

Ramirez-Llodra E

P106

IMPEDIMENT BE RESOURCE: SEXUAL DIMORPHISMS IN DEEP-SEA ISOPOD CRUSTACEANS

Riehl T

P107

MEGAFaUNA DIVERSITY IN THE CLARION-CLIPPERTON FRACTURE ZONE: PRELIMINARY DATA OF THE BIONOD PROJECT

Rogacheva A

P108

DEEP-SEA INVERTEBRATES OF NEW ZEALAND: DIVERSITY, TOOLS AND OPPORTUNITIES

Schnabel K

P109

POLYNOIDEA POLYCHAETES SPECIES ASSOCIATIONS WITH DEEP-SEA CORALS AND THEIR CONNECTIVITY ACROSS THE SOUTHWEST INDIAN OCEAN RIDGE

Serpetti N

P110

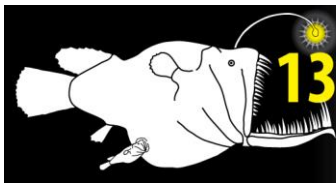
MEIOFAUNAL COMMUNITIES IN THE LEVANTINE BASIN (EASTERN MEDITERRANEAN): THE EFFECT OF DEPTH AND DISTANCE-TO-COAST ON DISTRIBUTION PATTERNS

Sevastou K

P111

CONTROLS ON HADAL MEGAFaUNAL COMMUNITY STRUCTURE: A SYSTEMATIC EXAMINATION OF PRESSURE, FOOD SUPPLY, TOPOGRAPHY, AND EVOLUTION

Taylor H



International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

P112

**NEMATODE COMMUNITY STRUCTURE IN A HYDROTHERMAL VENTING FIELD IN MYOJIN KNOLL, A SEAMOUNT ON THE IZU-OGASAWARA ARC, THE WESTERN NORTH PACIFIC OCEAN**

Setoguchi Y

P113

**NEMATODE ASSEMBLAGE FROM DEEP-SEA POLYMETALLIC NODULE AREA OF THE CENTRAL INDIAN OCEAN BASIN**

Singh R

P114

**THEY ARE EVERYWHERE! ON WORLDWIDE DISTRIBUTION OF DEEP-SEA COPEPOD AND NEMATODE SPECIES**

Singh R

P115

**MACROFAUNAL SPECIES DIVERSITY ALONG THE WESTERN ANTARCTIC PENINSULA DEEP CONTINENTAL SHELF AND THE IMPLICATIONS OF CLIMATE CHANGE**

Smith C

P116

**BIODIVERSITY, CONNECTIVITY AND ECOSYSTEM FUNCTION IN ORGANIC-RICH WHALEBONE AND WOOD-FALL HABITATS IN THE DEEP SEA**

Smith C

P117

**DEEP-SEA URCHIN (*STRONGYLOCENTROTUS FRAGILIS*) PHYSIOLOGY AND BEHAVIOR ARE IMPAIRED BY OCEAN ACIDIFICATION AND HYPOXIA, ULTIMATELY REDUCING REPRODUCTIVE CAPACITY**

Taylor J

P118

**COMPARATIVE POPULATION GENETICS OF TWO HYDROTHERMAL-VENT-ENDEMIC SPECIES, *CHOROCARIS* SPP. AND *OLGASOLARIS TOLLMANNI* FROM SOUTHWEST PACIFIC BACK-ARC BASINS**

Thaler A

P119

**SPECIATION OF PROVANNA SPP. (GASTROPODA: PROVANNIDAE) IN THE DEEP-SEA CHEMOSYNTHETIC COMMUNITY AROUND JAPAN**

Tomomi O

P120

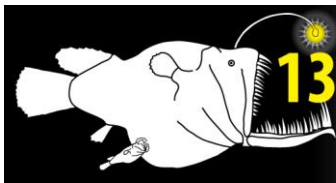
**POTENTIAL EFFECTS OF OCEAN ACIDIFICATION ON HABITAT FORMING DEEP-SEA CORALS IN THE NEW ZEALAND REGION**

Tracey D

P121

**OBSERVER AND RESEARCH TRAWLS DISCOVER NEW SPECIES IN THE NEW ZEALAND REGION**

Tracey D



International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

**P122**

**DEEP WATER ATLANTIC ZOOPLANKTON PASSAGE TO THE ARCTIC — STEP BY STEP TRACK.**

Trudnowska E

**P123**

**OXYGEN MINIMUM ZONE INFLUENCES CARBON FLOWS THROUGH DEEP-SEA SEDIMENT ECOSYSTEMS: A MODELLING STUDY**

Van Oevelen D

**P124**

**COPEPODS OF THE SOUTHERN OCEAN: DO CRYPTIC SPECIES EXIST?**

Vereshchaka A

**P125**

**CAN INTRA-POPULATION VARIATION IN TROPHIC ECOLOGY OF ROCKALL TROUGH DEEP-SEA FISHES BE EXPLAINED BY BODY SIZE?**

Wigham B

**P126**

**THE SUCCESSFUL SCALE WORMS (APHRODITIFORMIA, POLYCHAETA) — HOW CAN THEY BE EVERYWHERE (IN THE SEA)?**

Wiklund H

**P127**

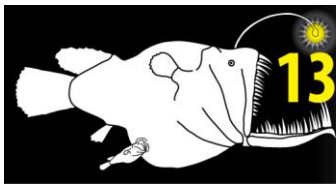
**AN UNIQUE ISOPOD CRUSTACEAN ASSEMBLAGE ASSOCIATED WITH WOOD IN THE DEEP-SEA BENTHIC ENVIRONMENT**

Wilson GDF

**P128**

**DISTRIBUTION AND POPULATION GENETIC STRUCTURE OF VENT SHRIMPS IN THE OKINAWA TROUGH**

Yahagi T



International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

**P1**  
**GENETIC DIVERSITY AND CONNECTIVITY OF *MUNIDOPSIS* SPP., A SQUAT LOBSTER FROM WESTERN PACIFIC BACK-ARC BASINS**

Alei F, Thaler A, Plouviez S, Van Dover C  
Duke University Marine Lab

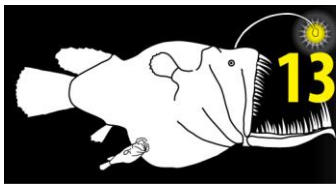
Deep-sea hydrothermal vents are patchy, dynamic ecosystems that host specialized communities. In southwest Pacific back-arc basins, vents are distributed non-linearly, occurring in small fields throughout spreading centers. Population genetic studies at hydrothermal vents tend to focus on biomass-dominant species that host chemoautotrophic endosymbionts. This study examines the population structure and connectivity of the squat lobster, *Munidopsis* spp., a species known to occur in abundance in some Pacific vent communities but that can also be found associated with other deep-sea habitats. Samples were collected from hydrothermal vents in Manus Basin, Papua New Guinea, at multiple spatial scales, from a few hundred meters to tens of kilometers, at both active and inactive vent sites. We used a partial cytochrome-C-oxidase subunit I gene (COI) to infer population structure and assess connectivity among sampling sites. While single gene studies such as this do not provide a comprehensive picture of population structure and connectivity, they constitute a first step, allowing the identification of cryptic species and evaluating coarse patterns of genetic differentiation over evolutionary time scales.

**P2**  
**BATHYMETRIC AND TEMPORAL CHANGES IN SUPRABENTHIC ASSEMBLAGES FROM THE BLANES CANYON AND ADJACENT SLOPE (IBERIAN MARGIN, NW MEDITERRANEAN)**

Almeida M<sup>1</sup>, Company J<sup>2</sup>, Lampadariou N<sup>3</sup>, Cunha M<sup>1</sup>

<sup>1</sup> Universidade de Aveiro, Portugal, <sup>2</sup> Institut de Ciències del Mar (ICM), Spain, <sup>3</sup> Hellenic Centre for Marine Research, Heraklion, Crete, Greece

Suprabenthos is an important component of the BBL (Benthic Boundary Layer) faunal assemblage. It has an important trophic role in deep-sea ecosystems because is a food source of deep-water fishes and other megabenthic groups, such as decapod crustaceans). Therefore, studies on suprabenthic assemblages are crucial to a better understanding of deep-sea communities. Most studies on suprabenthic assemblages of the northwestern Mediterranean have been dedicated to slope depths and particular settings (e.g. submarine canyons). In the Blanes canyon suprabenthic fauna was sampled in order to investigate environmental gradients and the possible effect of catastrophic events (e.g. DSWC) on species composition and community structure. Bathymetric transects at seasonal and inter-annual temporal scales were conducted in the Blanes Canyon and adjacent open slopes in the framework of multiple projects (RECS, PROMETEO, BIOFUN, DOSMARES). Samples were collected using an automatic opening and closing suprabenthic Macer-Giroq sledge and environmental factors (e.g. nutrient contents, salinity, temperature) influencing faunal distribution were also recorded. The material collected is being currently studied. Here we present the first results comparing the macrofauna collected during several cruises in 2003–2004 and 2008–2009 covering a deep-range from 500 to 2000 m. Taxonomic composition, faunal abundance and biomass, biodiversity and community structure in relation to environmental drivers will be discussed.



International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

**P3**

**DISTINCT MEGABENTHIC STRUCTURE-FORMING COMMUNITIES WITHIN THE MAKAPU'U DEEP-SEA CORAL BED**

Long D<sup>1,2</sup>, Baco A<sup>1</sup>

<sup>1</sup> Florida State University, <sup>2</sup> Temple University

Seamounts are largely unexplored undersea mountains rising abruptly from the ocean floor, which can support an increased abundance and diversity of organisms. Deep-sea corals are important benthic structure-formers on hard substrates in these habitats; however, most past work addressing deep-sea coral and seamount communities have not considered the role of small-scale variation. Corals and sponges in the Makapu'u deep-sea coral bed (4.3 km<sup>2</sup>), offshore of Oahu, Hawaii, were mapped from ~ 320–530 m depth. The physical environment was surveyed at multiple spatial scales to relate biotic patterns with abiotic variables and to test the hypothesis of differing communities in the northern and southern regions of the bed. This hypothesis was partially supported, with distinct regional communities within the same depth zone, likely manifesting via local hydrological changes. Despite the narrow range examined, depth was found to be the strongest structuring gradient, and different relief and substrate types hosted unique assemblages. This work yields new insight on the spatial ecology of seamounts and points out that community changes can occur over relatively narrow depth ranges and can be structured by small-scale physiography.

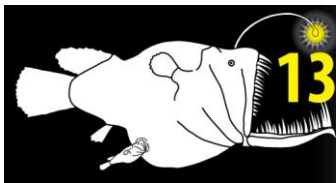
**P4**

**A SYNTHESIS OF GENETIC CONNECTIVITY IN DEEP-SEA FAUNA AND IMPLICATIONS FOR MPA DESIGN**

Baco A<sup>1</sup>, Etter R<sup>2</sup>, Ribeiro P<sup>3</sup>, von der Heydn S<sup>4</sup>, Shank T<sup>5</sup>, Metaxas A<sup>6</sup>

<sup>1</sup>Florida State University, USA, <sup>2</sup>University of Massachusetts Boston, USA, <sup>3</sup>University of the Azores, Portugal, <sup>4</sup>Stellenbosch University, South Africa, <sup>5</sup>Woods Hole Oceanographic Institution, USA, <sup>6</sup>Dalhousie University, Canada

With anthropogenic impacts increasingly advancing into deeper waters, there is interest in establishing deep-sea marine protected areas or reserves. One of the key concepts for MPA design is an understanding of connectivity and scales of dispersal of the taxa of interest. It has been hypothesized that deep-sea taxa are able to disperse greater distances than are shallow water taxa, which would imply MPA networks could be more widely spaced, however this has not been tested. As part of a larger synthesis on connectivity in the deep sea via the INDEEP program Connectivity Working Group, we are compiling population genetic studies of deep-sea benthic invertebrates. The data from these studies are being reanalysed using two methods that have been used to derive dispersal distance from genetic data in syntheses of shallow water taxa. We will present preliminary results of this synthesis and discuss the results in comparison to estimates of dispersal in shallow water, as well as the implications for deep-sea MPA design. We will also highlight priorities for research to better understand genetic connectivity of key deep-sea habitats.



International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

P5

**ASSOCIATED SPECIES OF TWO DEEP-SEA PENNATULACEAN CORALS IN THE NORTHWEST ATLANTIC**

Baillon S<sup>1</sup>, Hamel JF<sup>2</sup>, Mercier A<sup>1</sup>

<sup>1</sup>Ocean Sciences Centre, Memorial University, St John's, Newfoundland and Labrador, <sup>2</sup>Society for the Exploration and Valuing of the Environment (SEVE), Portugal Cove, St Philips, Newfoundland and Labrador, Canada

Deep-sea coral ecosystems are biodiversity hotspots, similar to their tropical reef counterparts. To date, analyses of species associated with deep-sea corals have largely centred on scleractinians and gorgonians growing on hard bottoms, although the importance of soft corals fields is increasingly being recognized. *Anthoptilum grandiflorum* and *Halipteris finmarchica* are two sea pens (Octocorallia: Pennatulacea) common on soft bottoms along the continental slope of eastern Canada. They were found to harbour four major species. Redfish (*Sebastes* spp.) larvae occurred on both sea pens, exclusively in April-May. A parasitic copepod, *Lamippe bouligandi* was consistently found in the polyp wall of *A. grandiflorum* and another unidentified copepod was observed at the base of the polyp gastrovascular cavity in *H. finmarchica*. An epibiotic sea anemone was also found on *H. finmarchica*. Other species that were recorded occasionally including shrimp larvae (*Pandalus montagui*) and fish eggs (*Lycodes esmarkii*). Stable-isotope analyses ( $\delta^{13}\text{C}$  and  $\delta^{15}\text{N}$ ) indicated that *H. finmarchica* and its epibiotic sea anemone likely share a diet of pelagic invertebrates and particulate organic matter. The associated copepods showed a significant enrichment in  $\delta^{15}\text{N}$  suggesting that they are either feeding directly on sea pen tissue or on the partly digested prey of their host. While the number of associates species appears to be lower in sea pens than in hard-bottom corals, they range from obligatory (parasitic copepods) to facultative associates (sea anemone) and include important functional links (redfish larvae), suggesting that sea pens make a moderate yet key contribution to the enhancement of biodiversity while acting as a structural habitat.

P6

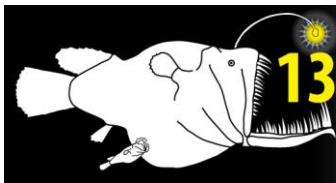
**COURTSHIP, EGG LAYING, DEVELOPMENT AND FEEDING OF THE DEEP-SEA POLYCHAETE OPHRYOTROCHA**

Hamel JF<sup>1</sup>, Baillon S<sup>2</sup>, Mercier A<sup>2</sup>

<sup>1</sup> Society for the Exploration and Valuing of the Environment (SEVE), 21 Phils Hill Road, Portugal Cove-St. Philips (Newfoundland and Labrador), A1M 2B7, Canada, <sup>2</sup> Ocean Sciences Centre (OSC), Memorial University, St. John's, (Newfoundland and Labrador), Canada, A1C 5S7

To our knowledge, this is the first account of a complete life cycle in a deep-sea polychaete, a species of the genus *Ophryotrocha* collected off northeast Newfoundland (eastern Canada) between 500–1500 m depth. Monitoring of live specimens under laboratory conditions showed that they fed on the peduncle of live sea pens (*Anthoptilum grandiflorum* and *Halipteris finmarchica*). They also ingested decaying organic matter but never fed on any other deep-sea coral species tested, including nephteids and scleractinians. *Ophryotrocha* sp. exhibited seasonal feeding between April and February, followed by a reproductive season between February and May. This sequence was consistent over the two years of study. *Ophryotrocha* sp. is gonochoric and mating behaviour (early February) involves pairs of individual of opposite sex attached head to tail for several hours to days. Transparent gelatinous masses containing 80–110 eggs are laid from mid-February to late March. Propagules develop in the mass until the 1-chaetiger larvae emerge 30–45 days post-laying at a temperature of 1° C. Juveniles constitute ~40–45 % of the eggs laid, suggesting that part of the spawn is used as nutrient supply. After emerging, juveniles remain aggregated and are guarded by adults for a few days before they disperse. When removed from parental care, all offspring in the gelatinous mass died before emergence. The new generation reached sexual maturity in 9–10 months and were ready to reproduce the following February. Cases of segmenting adult worms were also observed. In total, two complete semelparous generations developed successively during our study.





International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

**P7**

**PIECING TOGETHER CORALS AND BOTTOM TRAWLS**

**Baird SJ**, Tracey D, Mormede S

National Institute of Water & Atmospheric Research

Coral specimens are returned from commercial trawling effort in New Zealand waters by government observers. Many represent coral taxa protected under New Zealand legislation under broad taxonomic orders: Anthoacthecata (family Stylasteridae only), Antipatharia, Gorgonacea [now included in order Alcyonacea], and Scleractinia. A set of samples or catches of these corals from research sampling and fisheries bycatch was modelled with available and relevant environmental variables using boosted regression trees in an attempt to describe important influences of the environmental space preferred by protected corals. Two separate analyses were carried out for depths relative to middle depths and deepwater trawling (200–2000 m): one by order (the level at which the corals are managed under New Zealand law) and the second by four broad “functional groups” (defined by physical structure and provision of habitat). The results are described in relation to past and current bottom trawling activity and patterns, with discussion on the appropriateness of the data and analytical methods.

**P8**

**PREDICTING PRESENT AND PAST DISTRIBUTIONS OF DECAPOD SHRIMPS IN THE SOUTHERN OCEAN**

**Basher Z<sup>1</sup>**, Costello M, Bowden D

<sup>1</sup> Leigh Marine Laboratory, The University of Auckland, <sup>2</sup> National Institute of Water and Atmospheric Research (NIWA) Ltd

We have mapped the distribution of decapod shrimps (*Nematocarcinus lanceopes*, *Notocrangon antarcticus* and *Chorismus antarcticus*) around the Southern Ocean using up to date known location records extracted from biodiversity databases and recent survey cruises. Species distribution models using MaxEnt shows predicted distribution of the shrimps in unsurveyed areas of Southern Ocean shelf, slope and deep-sea regions. Influence of environmental variables in the model shows variation of predictive performance of the model algorithm and variable ranking between global and regional scales. We modelled potential past geographic distribution maps of these species during Last Glacial Maxim. This model also identified prospective refugia locations in the Southern Ocean during LGM, which could acted as seeding populations for re-colonization of the present circum-Antarctic distributions of shrimps after the glaciation period. We will present preliminary results from a collaborative research to verify these links between populations in identified potential refugia locations with present day distributions using genetic and molecular techniques.



**P9**  
**INTERANNUAL CHANGES IN MEGAFUNA FROM THE ARCTIC OBSERVATORY 'HAUSGARTEN' BETWEEN 2002 AND 2012**

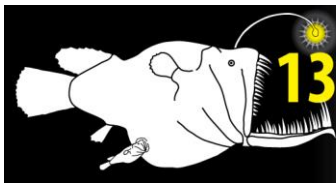
**Bergmann M**, Bauerfeind E, Soltwedel T, Klages M  
Alfred Wegner Institute for Polar and Marine Research

Although megafaunal organisms play an important role in benthic ecosystems little is known about their temporal dynamics. Here, we assessed the interannual dynamics of megafaunal organisms from the HAUSGARTEN observatory in the eastern Fram Strait, an area where the effects of climatic forcing are particularly evident. We analysed four congruent camera transects taken in 2002, 2004, 2007 and 2011. Environmental parameters were measured in order to be able to put our faunal results into an environmental context. Our results indicate that although the densities of megafaunal taxa show different patterns over time, most exhibit an overall decrease between 2002 and 2007 and total megafaunal densities decreased from 2002 to 2004 to 2007 (12.16 to 7.41 ind.m<sup>-2</sup>). Although suspension feeder densities also decreased, predator/scavenger and deposit feeder densities declined to such an extent that suspension feeders accounted for almost 100 % of the megafauna in 2007. In 2011, however, total megafaunal densities and the densities of different trophic groups approached the initial levels. Surprisingly, the number of dropstones increased in 2011. The patterns observed concur with a very low local ice cover and phytodetrital input in 2006 followed by an increase in ice cover and phytodetritus. Our results indicate the importance of ice-related export of particles to the deep seafloor and highlight the need for time-series transects, especially in an era when productive marginal ice zones tend to disappear with the receding sea ice.

**P10**  
**RECENT ADVANCES IN NEW ZEALAND CEPHALOPOD RESEARCH: AN OVERVIEW**

**Bolstad K**  
Auckland University of Technology

A higher diversity of octopus and squid has been reported from New Zealand waters than from those of any other country to date, and new taxa are identified with some frequency. In addition to the valuable commercial species, many locally occurring deep-sea squid species play important roles in the diets of other economically, ecologically, culturally and inherently biologically valuable animals including fish, marine mammals, and seabirds. However, the ecology and systematics of the squids themselves are often poorly understood; a number of recent and ongoing research projects have been undertaken to help redress this lack of information. Emphasis has been placed on squid families with high local diversities (Cranchiidae, Mastigoteuthidae), particularly unstable systematics (Chroteuthidae, Octopoteuthidae, Onychoteuthidae), and high importance in marine mammal diets (e.g., Histioteuthidae). In addition to clarifying the true composition of the local cephalopod fauna, this research aims to provide useful information for ecological work on these animals' predators and prey. Because squid are known to respond quickly to changing environmental pressures, particularly in ecosystems disrupted by anthropogenic and/or meteorological events, improving our understanding of New Zealand's teuthofauna should be a priority in monitoring and managing our marine environment.



International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

**P11**  
**DISTRIBUTION, POPULATION STRUCTURE, REPRODUCTION, AND DIET OF *OPHIOLIMNA ANTARCTICA* (LYMAN, 1879) FROM KEMP CALDERA IN THE SOUTHERN OCEAN**

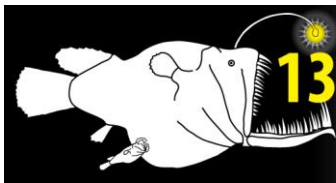
**Boschen R**, Tyler P, Copley J  
University of Southampton

A large population of *Ophiolimna antarctica* (Lyman, 1879) was discovered at 1546 m in Kemp Caldera, a topographic feature with active hydrothermal venting at the southern end of the South Sandwich Islands, Southern Ocean. The distribution, population structure, reproduction, and diet of *Ophiolimna antarctica* were investigated. *O. antarctica* were found predominantly on basalt with an over-dispersed distribution. The mean density was 17 individuals m<sup>-2</sup> with a range of 9–24 individuals m<sup>-2</sup>. There was a bimodal population structure, with separate juvenile and adult peaks. Sexes were separate and the sex ratio was not significantly different from equality. The maximum oocyte diameter was 520 µm, suggesting direct or lecithotrophic development, whilst individual females reproduced asynchronously. Stomach contents revealed a varied diet indicative of omnivory, including crustacean fragments, flocculate material, diatoms, forams, fish scales and ophiuroid tissue and spines. There was no influence of the nearby hydrothermal vents on the diet of *O. antarctica*. The ecology of *O. antarctica* is consistent with what is known for other Antarctic and deep-sea ophiuroid species.

**P12**  
**COLD SEEP COMMUNITIES ON THE HIKURANGI MARGIN, NEW ZEALAND**

**Bowden D**<sup>1</sup>, Rowden A<sup>1</sup>, Thurber A<sup>2</sup>, Baco A<sup>3</sup>, Levin L<sup>4</sup>, Smith C<sup>5</sup>  
<sup>1</sup> NIWA, Wellington, <sup>2</sup> Oregon State University, Corvallis, USA, <sup>3</sup> Florida State University, Tallahassee, USA, <sup>4</sup> Scripps Institution of Oceanography, La Jolla, USA, <sup>5</sup> University of Hawai'i at Manoua, Honolulu, USA

Cold seeps are sites where hydrocarbon (usually methane)-enriched fluids emerge from the seabed at or near ambient temperature. These sites are colonised by distinctive communities of animals which exploit energy derived either directly or indirectly from chemosynthetic bacteria that metabolize methane or sulphides. The existence of cold seeps in New Zealand waters was first inferred from fishery bycatch in the early 1990s but it was not until a joint US-NZ research voyage in 2006 that sites on the Hikurangi Margin, east of the North Island, were located and sampled by scientific survey. To date, three research voyages have explored the ecology of these seeps, using acoustic and seismic tools to detect and map the sites, and cameras, epibenthic sledges, and corers to sample the fauna. We present a synthesis of results from this work, describing relationships between the physical and biological characteristics of the known sites, a hypothetical succession sequence from first colonisation to senescence, and impacts and potential future threats to the communities from trawl fisheries and gas hydrate extraction.



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Wellington, New Zealand 3 – 7 December 2012

**P13**

## **EVOLUTION OF THE DEEP-SEA ENVIRONMENT WITH REFERENCE TO THE BATHY- ABYSSOPELAGIC CALANOID COPEPOD FAMILY: MEGACALANIDAE**

**Bradford-Grieve J**

National Institute of Water and Atmospheric Research

In this paper I employ my experience as a biological oceanographer and calanoid copepod taxonomist and systematist to explore the evolution of deep-sea pelagic environments in geological time. I use these ideas to interpret what environmental change has meant to bathypelagic and abyssopelagic faunas using the family Megacalanidae and the Calanoida in general as my example. I discuss the relationships between environmental evolution and the evolution of the Calanoida. I will highlight the significance of specific adaptations and how these may have fitted copepods for recent as well as future environments.

**P14**

## **SYSTEMATIC REVIEW OF WHIP-LASH SQUID (CEPHALOPODA: MASTIGOTEUTHIDAE) FOUND IN NEW ZEALAND WATERS**

**Braid H, Bolstad K**

Auckland University of Technology

Squids of the family Mastigoteuthidae are bathypelagic and some species have circumglobal distributions. They are prey to commercially important fish species such as orange roughy and hoki. Based on decreasing bycatch incidence in commercial fishing nets, one species appears to be nationally endangered. Unfortunately, the threat classification of other species around New Zealand is unknown because they have either not been identified or described; mastigoteuthid taxonomy is notoriously controversial, with many species descriptions based on single, badly damaged specimens. In addition, specimens frequently lose their skin and tentacles (heavily relied on by previous authors for identification) upon capture. An integrative taxonomic approach has been attempted for New Zealand material in order to clarify the local representatives of this family. Important morphological characters appear to be photophore distribution, fin shape, funnel and mantle locking cartilage, and body proportions. These characters have suggested a preliminary distinction between the genera *Mastigoteuthis* and *Idioteuthis*. Several methods have been used in an effort to extract DNA sequences from formalin-fixed tissue from museum specimens. Though only three species of mastigoteuthid squid had previously been reported in New Zealand, six known species have presently been identified, and several additional, possibly new species also occur locally.



**P15**  
**DEEP OCEAN CURRENTS AFFECT SHALLOW REEF EVOLUTION**

**Bromfield K**  
Environmental Protection Authority

Predicting ecosystem effects resulting from physical changes is problematic given the complexity of ecological interactions. However, correlations between faunal changes in Neogene coral reef communities from Papua New Guinea, Indonesia and Fiji, with known physical changes provide a greater understanding of their evolutionary response to global patterns of change. The period encompassed by the study reflects a time of extreme climatic variability. From the mid-Miocene, the climate can be summarised as: (1) climatic optimum prior to 14.7 Ma, characterised by minimal global ice volume (2) long-term cooling from 14.7 to 13.9 Ma, and (3) an "Icehouse" period after 13.9 Ma. During the Pliocene (~5.3–2.6 Ma), the Walker Cycle was significantly weaker than Present and the Indo-Pacific experienced near permanent El Niño conditions. Additional tectonic stressors from ongoing restriction of the Indonesian Throughflow (ITF) drove changing ocean circulation. The responses of reefal corals during these changes are two-fold: faunal turnover and a structural transition from domination by massive to ramose forms. Prior to restriction of the ITF, currents through this pathway were stronger, and periodically reversed such that during the past ~17 Ma there may have been a pathway for the exchange of genetic material between Fiji and Indonesia. In contrast, Papua New Guinea has been oceanographically isolated in a separate eddy of currents associated with the ITF. Oceanographic isolation may account for the anomalously high numbers of extinct, unique and largely endemic species recorded from Papua New Guinea.

**P16**  
**DEEP-SEA CARBON SEQUESTRATION USING CROP RESIDUE: PRELIMINARY OBSERVATIONS OF A BALE OF CORN STOVER IN 3100 M DEPTH OVER 2.5 YEARS.**

**Buck K, Whaling P, Lovera C, Barry J**  
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The notion that mankind can ameliorate rising atmospheric CO<sub>2</sub> levels by sequestering crop residue in the deep-sea has recently been proposed and bandied about by several research groups. Amongst some of the unanswered questions proposed for this large-scale undertaking, the refractive nature of the crop residue and any broader effects of the residue on the local to regional sediment community remain largely unknown. We availed ourselves of our operational capabilities to deploy a 8'x 4'x 4' bale of corn stover in April 2009 at 3100 m depth 50 nautical miles off the central California coast. We revisited the site in Oct. 2011 and measured the oxygen gradient leading into the bale using an O<sub>2</sub> probe. In addition, we collected sediment cores along transects in the vicinity of the bale to assess related patterns in the biomass of bacteria, meiofauna and macrofauna. The bale was intact, had a conspicuous galatheid assemblage putatively feeding on the thiotrophic bacterial mats growing on the surface. A profile of oxygen in the bale made with an Aanderra O<sub>2</sub> optode showed a diminution of the O<sub>2</sub> to 10 % of ambient just 10 cm from the outside surface of the bale. Bacterial and meiofaunal populations showed significant enhancements < 1 m from the bale when compared to cores taken 1–100 m away from the bale. Macrofaunal populations showed no trend. These preliminary findings demonstrate that the projected hypoxia/anoxia within the bale exists, likely slowing the stover degradation and that the effects of the bale on the sediment is limited to the immediate vicinity of the bale.

P17

**REPRODUCTION STRATEGY IN DEEP-SEA EPIZOIC SCALPELLID BARNACLES**

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<sup>1</sup> Institute of Marine Research, Bergen, Norway, <sup>2</sup> Department of Cell Biology and Zoomorphology, Biological Institute, University of Copenhagen

We present new information on the reproduction strategy of the deep sea scalpellid barnacles *Verum brachiumcancri* and *Weltnerium nymphocola* associated with decapods and pycnogonids. The size and development of larvae, morphology of the dwarf male, its position in the female receptacle, and the degree of infection is documented. Reproduction strategy is compared with the three other scalpellids — *Ornatoscalpellum stroemii*, *Arcoscalpellum michelotianum* and *Scalpellum scalpellum*. The main obstacles for the propagules are; to reach a suitable substratum (host) or to find a female/hermaphrodite and for the reproduction to be successful, these are related to the constraints to reproduction and dispersal represented by their habitat. For both species the development to cypris larva take place inside the female and they have only a single dwarf male deeply inserted in the female receptacles. A similar reproduction strategy is found in the deep-sea species *O. stroemii* associated to corals. A surprising and new observation was that the dwarf male of *V. brachiumcancri* had a long and well-developed penis that can release the sperm close to the eggs inside the female. The morphology of dwarf males has been studied but observations on how they are adapted to the female/hermaphrodite morphology are scarce. Our findings indicate a connection between the presence of only a single dwarf male deeply inserted in the receptacle and the existence of a long and specialized penis to secure fertilization. The challenge to overcome the huge distances between suitable substratum and conspecifics is something epizoic scalpellids shares with many deep-sea organisms.

P18

**RIMICARIS EXOCULATA GUT EPIBIONT COMMUNITIES ALONG THE MID-ATLANTIC RIDGE HYDROTHERMAL VENT SITES**

**Cambon-Bonavita MA<sup>1</sup>, Durand L<sup>1</sup>, Roumagnac M<sup>1</sup>, Cueff-Gauchard V<sup>1</sup>, Jan C<sup>2</sup>, Guri M<sup>3</sup>, Crassous P<sup>4</sup>, Zbinden M<sup>4</sup>, Arnaud-Haond S<sup>5</sup>**

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The deep-sea hydrothermal vent shrimp *Rimicaris exoculata* harbours an enlarged gill chamber colonised by a dense and complex epibiont community. This shrimp ingests chimney particles and its gut houses an autochthonous and distinct microbial community. A trophic role has been suggested for both communities. This species dominates hydrothermal ecosystems megafauna all along the Mid-Atlantic Ridge regardless of contrasted geochemical conditions prevailing in them. This work intends to analyse the possible environmental conditions influence on the distribution and composition of its gut microbial community. This community associated with *R. exoculata* specimens collected at four hydrothermal vent sites (Rainbow / TAG / Logatchev / Ashadze) was analysed through 16S rRNA surveys, and microscopic observations (TEM, SEM and FISH analyses). The filamentous epibionts inserted between the gut epithelial cells microvilli, and revealed in a previous study, were observed on all examined specimens. The results indicated the gut microbial community was restricted to Deferribacteres, Mollicutes, Epsilonproteobacteria and in a lesser extent Gammaproteobacteria groups, regardless of the site. As in the previous studies, Deferribacteres and Mollicutes-related epibionts were highly specific to the host. At the ecotype level, a single Deferribacteres phylotype was retrieved at all sites but four Mollicutes-related OTUs were retrieved, one of them being only identified on the Rainbow specimens. Evolutionary relationships were analysed at the ribotype level among these autochthonous communities using median-joining networks. The topology of ribotypes networks illustrated a community diversification possibly following demographic expansions suggesting a more ancient evolutionary history at Rainbow. Hypotheses on the gut epibiont role and transmission pathways are proposed.





P19

**ACQUISITION OF EPIBIOTIC BACTERIA ALONG THE LIFE CYCLE OF THE HYDROTHERMAL SHRIMP *RIMICARIS EXOCULATA***

**Cambon-Bonavita MA<sup>1</sup>, Guri M<sup>2,3</sup>, Durand L<sup>1</sup>, Zbinden M<sup>5</sup>, Crassous P<sup>4</sup>, Shillito B<sup>5</sup>**

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The caridean shrimp *Rimicaris exoculata* dominates the fauna at several Mid-Atlantic Ridge hydrothermal vent sites. This shrimp has an enlarged gill chamber, harboring a dense ectosymbiotic community of chemoautotrophic bacteria associated with mineral oxide deposits. Until now, their acquisition is not fully understood. At three hydrothermal vent sites, we analyzed the epibionts diversity at different moult stages and also in the first stages of the shrimp life (eggs, hatched eggs (with larvae) and juveniles). Hatched eggs associated with young larvae were collected for the first time directly from gravid females at the Logachev vent site during the Serpentine cruise. An approach using 16S rRNA clone libraries, scanning and transmission electron microscopy and fluorescent in situ hybridization was employed. Molecular results and microscope observations indicated a switch in the composition of the bacterial community between early *R. exoculata* life cycle stage (egg libraries dominated by the Gammaproteobacteria) and later stages (juvenile/adult libraries dominated by the Epsilonproteobacteria). We hypothesized that the epibiotic phylotype composition could vary according to the life stage of the shrimp. Our results confirmed the occurrence of a symbiosis with Gamma and Epsilonproteobacteria, but more complex than previously assumed. We revealed the presence of active type I methanotrophic bacteria colonizing the cephalothorax of shrimps from the Rainbow site. They were also present on the eggs from the Logachev site. This could be the first “epibiotic” association between methanotrophic bacteria and hydrothermal vent crustacean. We discuss possible transmission pathways for epibionts linked to the shrimp life cycle.

Guri M., Durand, L., Cueff-Gauchard, V., Zbinden, M., Crassous, P., Shillito, B., Cambon-Bonavita, M.A. (2012) Acquisition of epibiotic bacteria along the life cycle of the hydrothermal shrimp *Rimicaris exoculata*. *The ISME Journal* 6: 597–609.





P20

**INORGANIC CARBON FIXATION AND NUTRITIONAL TRANSFERS IN THE HYDROTHERMAL VENT HOLOBIONT *RIMICARIS EXOCULATA***

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The shrimp *Rimicaris exoculata* dominates some hydrothermal vent ecosystems of the Mid-Atlantic Ridge and is thought to be a primary consumer harbouring a chemoautotrophic bacterial community in its gill chamber. Previous works inferred these epibionts as sulphide-, methane-, iron- and hydrogen-oxidizers [1, 2]. In vivo experiments were carried out in pressurized aquarium with isotope-labelled inorganic carbon in the presence of various electron donors and with radiolabelled organic compounds, chosen as potential by-products of bacterial metabolisms available for feeding the host. The epibionts do fix inorganic carbon by chemoautotrophy but, at least a large part of them appears to be able to switch between electron donors, or to heterotrophy, according to environmental conditions. They also seem to be capable of electron donor internal storage that could supply the chemosynthetic metabolisms in deprived electron donor conditions. Evidence of exchanges from bacteria to the host was given by the first direct demonstration of nutritional transfers; this association being thus regarded as a true mutualism. The import of soluble microbial by-products does occur by permeation across the gill chamber integument rather than by the digestive pathway. *R. exoculata* might be now regarded as a real holobiont (sum of the metabolic and genetic abilities of a host and associated bacteria) supported by gill chamber and gut [3] resident microbial communities to exploit several energy sources, increasing its fitness in an extreme environment.

[1] Zbinden M., Shillito B., Le Bris N., De Villardi de Montlaur C., Roussel E., Guyot F., Gaill F., Cambon-Bonavita M.A. (2008). New insights in metabolic diversity among the epibiotic microbial communities of the hydrothermal shrimp *Rimicaris exoculata*. *Journal of Experimental Marine Biology and Ecology* 359: 131–140.

[2] Guri M., Durand, L., Cueff-Gauchard, V., Zbinden, M., Crassous, P., Shillito, B., Cambon-Bonavita, M.A. (2012) Acquisition of epibiotic bacteria along the life cycle of the hydrothermal shrimp *Rimicaris exoculata*. *The ISME Journal* 6: 597–609.

[3] L. Durand, M. Zbinden, V. Cueff-Gauchard, S. Duperron, E. Roussel, B. Shillito and M.A. Cambon-Bonavita (2010). Microbial diversity associated with the hydrothermal vent shrimp *Rimicaris exoculata* gut and occurrence of a resident microbial community. *FEMS Ecology* 71:291–303.



P21

**THE DEEP-SEA *RIMICARIS EXOCULATA* SHRIMP GILL CHAMBER EPIBIOSIS REVISITED BY METAGENOMICS AND DISCOVERY OF ZETAPROTEOBACTERIAL EPIBIONTS**

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<sup>1</sup> IFREMER, Centre de Brest, REM/EEP/LMEE, Technopôle Brest-Iroise, BP 70, 29280 Plouzané, France, <sup>2</sup> Université de Bretagne Occidentale, UMR 6197-Laboratoire de Microbiologie des Environnements Extrêmes (LMEE), Institut Universitaire Européen de la Mer (IUEM), Place Nicolas Copernic, 29280 Plouzané, France, <sup>3</sup> Max Planck Institute for Marine Microbiology, Celsiusstrasse 1, 28359, Bremen, Germany, <sup>4</sup> Jacobs University Bremen gGmbH, Campus Ring 1, 28759 Bremen, Germany, <sup>5</sup> School of Biological Sciences, Bangor University, Bangor, Gwynedd, Wales, UK, <sup>6</sup> CNRS, LMEE, Technopôle Pointe du diable, BP 70, 29280 Plouzané, France

The shrimp *Rimicaris exoculata* thrives on deep-sea hydrothermal chimneys along the Mid-Atlantic Ridge (MAR). *R. exoculata* harbors a dense community of epibiotic bacteria in its gill chamber, which is dominated by filamentous Epsilon- and Gammaproteobacteria. We used metagenomics on specimens from the Rainbow hydrothermal vent site on the MAR to investigate the epibiont metabolism. The Epsilon- and Gammaproteobacteria epibionts harbored sulfur oxidation (sox) and hydrogenase genes indicating that reduced sulfur compounds and hydrogen could power chemolithoautotrophy by both epibionts. We identified carbon dioxide fixation genes of the reductive tricarboxic acid (rTCA) cycle in the epsilonproteobacterial epibionts and of the Calvin-Benson-Bassham (CBB) cycle in the gammaproteobacterial epibionts. Furthermore, the epsilonproteobacterial epibionts had two distinct denitrification systems (nas/nir and nap/nrf) indicating adaption to varying environmental nitrate concentrations. In addition virulence gene homologues and genes for surface attachment were found, providing insights into molecular mechanisms of host-epibiont interactions. Likewise, potential genes for host nutritional and detoxification processes were identified that ensure the shrimp's survival in its hostile hydrothermal vent habitat. Both epibionts exhibited niche differentiations, which allows them to avoid direct competition and enhances the fitness of their *Rimicaris* host by allowing it to cope with a broader range of environmental conditions in its dynamic habitat. Unexpectedly the metagenome harbored sequences affiliated to the iron-oxidizing Zetaproteobacteria, which could explain the presence of thick iron oxyhydroxide deposits in the gill chamber. We showed the presence of Zetaproteobacteria by fluorescence in situ hybridization (FISH) and thereby provide the first evidence for a Zetaproteobacteria-invertebrate association.



P22

**POLYCHAETE FEEDING GUILD COMPOSITION OF A MACROBENTHIC POLYCHAETE COMMUNITY, SENGHOR SEAMOUNT (N ATLANTIC)**

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<sup>1</sup> The Scottish Association for Marine Science, <sup>2</sup> Heriot-Watt University

Polychaetes are often an important constituent of deep-sea benthic macrofaunal communities, usually dominating assemblages by more than 70 %. The focus of seamount research is however often upon the larger mega-epifaunal elements of seamount communities such as predominantly large suspension feeding organisms (porifera, gorgonians, antipatharian corals), as such limited information exists within the literature regarding seamount polychaete community assemblages. Consequently little is known about the feeding guild composition of seamount polychaete functional groups, and how this is influenced by bathymetric and environmental gradients, sediment grain size, current velocities and availability of organic material. Grouping of polychaetes into feeding guilds based upon their level of motility (motile, discreetly motile and sessile) and feeding modes (carnivorous, filter feeder, herbivore, surface deposit-feeder and herbivores) is often a useful way of analysing polychaete communities. Senghor seamount is located in the northern Atlantic Ocean, 300 nm East of Senegal in the Cape Verde Archipelago. Sampling of the polychaete fauna was undertaken during the R/V Meteor cruise M79/3 (November 2009). A multicorer and a boxcorer were used to take benthic macrofaunal samples from four transects (North, East, South and West), from the summit ~150 m to the base of the seamount ~3500 m. Carnivorous polychaetes appear to dominate summit and north upper slope stations followed by herbivores and then subsurface deposit feeders. All remaining stations across all four transects are dominated by surface deposit feeding polychaetes.

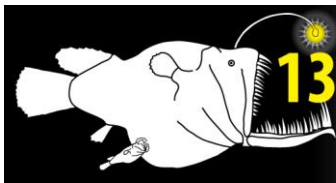
P23

**OCEAN ACIDIFICATION DIFFERENTIALLY AFFECTS THE PHYSIOLOGY AND GENE EXPRESSION PROFILES OF COLD-WATER SCLERACTINIANS AND OCTOCORALS**

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Larsys- Center of IMAR from the University of Azores- Department of Oceanography and Fisheries

Ocean acidification as a consequence of the rising atmospheric pCO<sub>2</sub> is predicted to affect marine calcifying organisms. While potential effects of future levels of pCO<sub>2</sub> on tropical coral species has been relatively well studied, there is currently limited information on their effects on cold-water corals. Here we describe two experiments to compare the calcification, basal metabolism (measured as respiration rates), biochemistry (proteins, lipids and carbohydrates) and gene expression responses of the azooxanthellate solitary coral *Desmophyllum dianthus* and the gorgonian *Dentomuricea* sp. at pH levels of their natural environmental (pH = 8.1) with those predicted for the year 2100 (pH = 7.8). Corals were collected from 200 and 450 m depth in the Azores (NE Atlantic) and maintained in aquaria under controlled pH levels using a CO<sub>2</sub>-bubbling system in flow-through aquaria under constant water temperature, over a period of 1 to 8 months. Calcification rates were measured using the buoyant weight and the alkalinity anomaly techniques. Gene expression profiles were studied by means of RT-PCR, targeting representative genes involved in biomineralization, cellular stress and metabolism. Calcification rates did not significantly differ between treatments for both coral species, although respiration rates were slightly enhanced under acidified conditions for *D. dianthus*, but depressed for *Dentomuricea* sp. In addition, there was a noticeable increase in tissue necrosis in *Dentomuricea* sp. under lower pH conditions, but no observable difference for *D. dianthus*. The differential gene expression profiles supported the participation of specific stress-related genes during physiological responses to the experimental variations of pH. The reasons for the differential response of scleractinians and octocorals to pH variations are discussed. This study demonstrates how the use mRNA expression-based tools can assist in better understanding the response of cold-water corals to ocean acidification.



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P24

**THE AZORES MARINE PARK: TOWARDS THE PROTECTION OF THE DEEP SEA**

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Portugal, with its archipelagos of the Azores and Madeira, has one of the largest European Exclusive Economic Zones (EEZ) and a continuous continental shelf embracing almost 4 million km<sup>2</sup>. Most of the the seafloor corresponds to deep-sea habitats including abyssal plains, mid-ocean ridges, subduction zones, seamounts, hydrothermal-vents, cold-seeps, mud-volcanoes, canyons, sponge-aggregations, cold-water coral reefs and gardens, etc. The jurisdiction over such a diverse area, the promising economic opportunities of mineral resources and bioprospection potential for pharmaceutical and industrial applications increases the nation's deep-sea stakeholders responsibility, towards sustainable use and preventive impacts on the biodiversity and habitats of the deep-sea. It is upon interdisciplinary scientific teams of biologists, chemists, geologists, oceanographers and geophysicists to develop research lines leading to innovation capable of generating economic opportunities for the society. On the other hand, it is upon political, industrial and economic groups to identify, implement, verify and comply with resource exploitation practices allowing new profitable activities without generating unsustainable impacts on the seafloor habitats. These extended habitats and ecosystems have been the target of scientific and jurisdictional research leading to concomitant plans of conservation. Based on OSPAR and IUCN Guidelines for creation of MPAs, a set of areas at the Azores EEZ, (hydrothermal vent fields Lucky Strike and Menez Gwen; the seamounts Dom João de Castro and Sedlo), were designated for protection from 2005 to 2009. Equally Portugal committed with OSPAR the designation of deep-sea areas across the Mid-Atlantic-Ridge, the Rainbow vent field, the Mid-Atlantic-Ridge North of Azores, the Altair and Antialtair seamounts, as MPA for the OSPAR network. OSPAR parties agreed to protect the water column above in the 2010 Bergen meeting. The Azores Government created the Azores Marine Park to integrate all the areas. The process leading to its legal creation is reviewed and discussed.

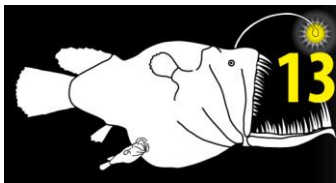
P25

**COMPOSITION AND DISTRIBUTION OF FAUNA AT A HYDROTHERMAL VENT FIELD ON THE SOUTHWEST INDIAN RIDGE**

Copley J<sup>1</sup>, Marsh L<sup>1</sup>, Nye V<sup>1</sup>, Huhnerbach V<sup>2</sup>, Rogers A<sup>3</sup>, Chen C<sup>3</sup>, Roterman N<sup>3</sup>, Glover A<sup>4</sup>, Shank T<sup>5</sup>

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The Dragon Vent Field (37°47' S, 49°39' E, depth ~2800 m) is the first active vent field to be visually confirmed on the ultraslow-spreading SW Indian Ridge (SWIR). In November 2011 we undertook the first ROV dives to this vent field to determine the composition and distribution of its fauna. The large size (> 20 m tall) of sulfide edifices at the Dragon Vent Field is consistent with well-established hydrothermal activity at the site. Faunal species present include taxa known from vents on the neighbouring Central Indian Ridge (CIR), such as the alvinocaridid shrimps *Rimicaris kairei* and *Mirocaris indica*, the "scaly-foot" peltospiroid gastropod, *Bathymodiolus* mussels, and eolepadid barnacles. However, several common CIR taxa were not observed at the Dragon Vent Field, and the fauna also exhibit some affinities with vents on the East Scotia Ridge (ESR) in the Southern Ocean. These Southern Ocean affinities include a new species of peltospiroid gastropod common to both localities, and *Kiwa* crabs morphologically similar but divergent in COI sequence to a new species from ESR vents. Furthermore, the abundances of several taxa at the Dragon Vent Field contrast with their occurrence at other long-lived vent fields, such as low numbers of *Rimicaris kairei* around "black smoker" sources. Using precision ROV videography, we surveyed the microdistribution of fauna on three sulphide edifices that exhibited differing levels of hydrothermal activity, from which we quantify the zonation of assemblages and propose a successional sequence for fauna at a vent field on the SWIR.



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**P26**  
**INSIGHTS INTO THE POPULATION DYNAMICS OF THE DEEP-SEA CORAL GENUS *PARAMURICEA* IN THE GULF OF MEXICO**

Doughty C, Quattrini A, Cordes E  
Temple University

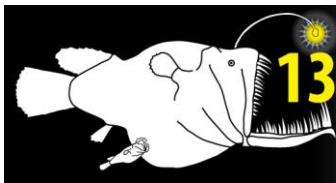
Species in the genus *Paramuricea* are common in deep waters (>200 m) of the Gulf of Mexico. *Paramuricea* spp. increase habitat heterogeneity and provide substrate for numerous faunal associates. In light of the *Deep-Water Horizon* oil spill in the Gulf, it has become apparent that data on population dynamics within this genus are critically needed. To date, at least one species of *Paramuricea* (*P. biscaya*) has been documented to be negatively impacted by the spill. Using remotely operated vehicles, we documented the abundances and size frequencies of *Paramuricea* across 22 sites at depths of 250–2500 m. In addition, molecular barcoding (mt COI+igr+msh) and microsatellite loci were used to delineate species boundaries. Furthermore, microsatellites were analyzed to determine population structure in *Paramuricea biscaya*. Results suggest that seven mitochondrial haplotypes are present and appear to be segregating into different depths zones [(type C: < 280 m) (type E: 280–445 m) (type A: 445–550 m) (type B1-4: 800–2500 m)]. At any one site, abundances ranged from a single colony (GC246, 894 m) to 523 colonies (AT357, 1050 m). Abundance data of observed in situ *Paramuricea* spp. were mapped with bathymetric data to aid in determining habitat preference. Size frequencies measured range from 0–5 cm (DC673) to 100–105cm (GC852) with median heights varying per site. Size frequencies observed indicated variable recruitment patterns. Lack of small colonies (< 10 cm) at many of the sites for *Paramuricea biscaya* suggests limited recent recruitment. In contrast, at AT357 small (< 10 cm) colonies were abundant. Pairing height frequencies with growth rate data of *P. biscaya* reveals relative age of populations. Overall, abundance and height frequencies illustrate that populations of the slow-growing *Paramuricea* species are rare and exhibit low recruitment rates, making them even more susceptible to anthropogenic threats.

**P27**  
**MAPPING THE BATHYAL ICHTHYOFAUNA DIVERSITY IN THE GORRINGE BANK (NE ATLANTIC)**

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Departamento de Biologia & CESAM, Universidade de Aveiro

The Gorringe Bank, located in the Euroasian and African plate convergence, 150 nautical miles WSW of Portugal, is formed by the Gettysburg and Ormond seamounts which rise from over 5000 m to a few tens of meters depth. Several surveys were undertaken in the Gorringe seamounts during the last years, but little is known about deep-water fish diversity. Following the E/V Nautilus Exploration Program, the Gorringe Bank was revisited and an annotated photographic technique was applied. Based on 131 hours of ROV-based surveys in both seamounts, a collection of about 4832 photographs of the seafloor was taken covering a depth range of 3022 m. This non-extractive method is particularly crucial to incorporate in situ data and avoid disturbance or damaging sensitive communities. The list of 48 fish species ascribed to 32 families includes the common reef fish species — *Muraena helena*, *Conger conger*, *Anthias anthias*, *Serranus atricauda*, *Epinephelus marginatus* — but also typically deep-sea species such as the blackbelly rosefish (*Helicolenus dactylopterus*), mediterranean slimehead (*Hoplostethus mediterraneus*), angler fish (*Lophius* sp.), the false boarfish (*Neocyttus helgae*) and tripod fishes (*Bathypterois* sp.). Other taxa, including scavenging demersal fish, deep-water sharks and rays were recorded and the ongoing work confirms new and relevant data on the ichthyofauna of the Gorringe Bank. The image analysis enabled an exhaustive characterization of fish assemblages and their habitats and retrieved depth as the most significant correlate with fish diversity and distinctness. Our results support the view of the Gorringe Bank seamounts as biodiversity hotspot and their possible biogeographic importance as “stepping stones”.





International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

**P28**

**DEEP-WATER HOLOTHUROIDS FROM THE ROSS SEA AND ADJACENT ISLANDS AND SEAMOUNTS, WITH DESCRIPTIONS OF NEW SPECIES BASED ON MORPHOLOGICAL AND MOLECULAR PHYLOGENY.**

**Davey N**<sup>1</sup>, O'Loughlin M<sup>2</sup>, Van den Spiegel D<sup>3</sup>, Pauley G<sup>4</sup>

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Voyages to the Ross Sea and adjacent seas were undertaken by NIWA (New Zealand) 2001–2008. Extensive holothuroid collections were made from > 1000 m, much of this sampling deeper than any previous sampling. Morphological systematic examination was initially undertaken. Tissue samples were then taken for all 2004 and 2008 material for DNA extraction and sequencing. Thirteen new species have been described based on a combination of the morphological and molecular genetic data. This increases and updates the known number of species in the Antarctic (164 by O'Loughlin et al. 2010). New species have been erected for *Molpadia* Risso, 1826, *Elpidia* Théel, 1876, *Pseudocnus* Panning, 1949, *Peniagone* Théel, 1882, *Pannychia* Théel, 1882, *Taeniogyrus* Semper, 1867, *Ellipinion* Hérouard, 1923 and *Trachythyone* Studer, 1876. The genetic data have indicated additional cryptic species within this recent collection. However the morphological characteristics have not yet distinguished the cryptic species adequately and further erection of new species has not been appropriate based on the single gene data. However, molecular phylogeny indicates abyssal Ross Sea cryptic species for *Laetmogone wyvillethomsoni*, *Benthodytes sanguinolenta* and *Psolidiella mollis*. Phylogenetic trees will be presented for a selection of species, and the insights that this analysis provide for speciation in the Antarctic deep sea discussed.

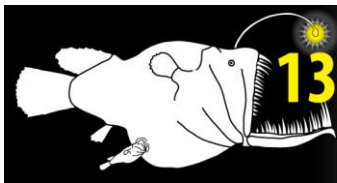
**P29**

**A REVIEW OF THE CAUDINID SEA CUCUMBERS OF NEW ZEALAND, WHAT WE FOUND IN THE DEEP WATERS**

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The Invertebrate collection (NIC) at the National Institute of Water and Atmospheric Research Ltd (NIWA) in Wellington, New Zealand holds many lots of sea cucumbers in the family Caudinidae Heding, 1931. Much of this material was collected from coastal areas in the 1960's and 70's. The majority of the specimens were considered to be *Paracaudina chilensis* (Müller, 1950). However, as NIWA voyages started to explore the deeper canyons and plateaus, much more Caudinidae material began to emerge. A detailed systematic study of this New Zealand Caudinidae material was undertaken following O'Loughlin et al. (2011) revision of the genus *Paracaudina* Heding, 1932. Much of the deeper material resulted in being systematically different to the predominantly coastal *Paracaudina chilensis*. Five species of Caudinidae occur in New Zealand waters. Two new species are described in the *Paracaudina* genus. These are from depths greater than 500 m in the Hikurangi margin, Kaikoura Basin and Chatham Rise. The deep water species *Hedingia albicans* (Théel) is discussed also.



International

# 13<sup>th</sup> Deep-Sea Biology Symposium

Wellington, New Zealand 3 – 7 December 2012

P30

## GLOBINS IN VESICOMYID BIVALVES AS AN ADAPTATION TO HYPOXIC ENVIRONMENTS

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Vesicomylid bivalves are one of the most abundant and diverse symbiotic taxa that form dense aggregates in both cold-seep and hydrothermal ecosystems: about one hundred different species have yet been described. In the cold seeps of the Gulf of Guinea, on the giant Regab pockmark, two vesicomylid species have been sampled. *Christineconcha regab* (Krylova & Cosel, 2011) is distributed all over Regab pockmark, while *Laubiericoncha chuni* (Cosel & Olu, 2008), is only present at the south-western part of the pockmark, exposed to lower methane concentrations. Vesicomylids live in symbiosis with chemoautotrophic bacteria and use carbon compounds produced by their symbionts. The latter need in turn oxygen, carbon dioxide and sulphide for their metabolism that are transported through the bivalves' hemolymph. All tissues of *L. chuni* are colored by its red blood, whereas *C. regab* has clear hemolymph. To compare the ability towards hypoxia of these two species in reduced and hypoxic environments, we searched for oxygen-carriers, like globins in both species. *L. chuni* possesses an intrerythrocyte circulating hemoglobin and a myoglobin in its foot, whereas *C. regab* has only myoglobin in its foot. Both hemoglobins and myoglobins have a monomeric structure but differ in the globin number and molecular weight. Oxygen binding affinity is higher for the circulating hemoglobin. No cooperativity, no Bohr effect, but a temperature effect is observed for both globins. We present here the comparative analysis of these globins, and discuss how they could play a role in the adaptation to hypoxia and influence the distribution of the two vesicomylid species.

P31

## FOOD-WEB STRUCTURE OF COLD-WATER CORAL ECOSYSTEMS IN THE GULF OF MEXICO REVEALED BY DELTA-13C AND DELTA-15N ANALYSIS

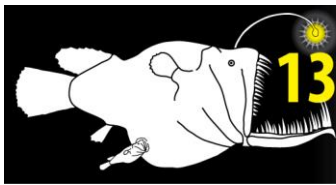
Demopoulos A<sup>1</sup>, McClain-Counts J<sup>1</sup>, Ross S<sup>2</sup>, McIver T<sup>2</sup>, Nizinski M<sup>3</sup>

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The trophic structure of deep-sea coral ecosystems is poorly understood. Stable carbon and nitrogen isotope analyses (SIA) provide time-integrated estimates of food resources and trophic levels of the assimilated diet. We used SIA to identify carbon sources and characterize the trophic structure of coral-associated fishes and invertebrates in *Lophelia pertusa* habitats located in the Gulf of Mexico. Four sites were investigated from 2007-2010, three on the continental slope off Louisiana and the fourth on the West Florida Slope (WFS).

SIA revealed a simple food web, encompassing 4-5 trophic levels. At all sites,  $\delta^{15}\text{N}$  of *L. pertusa* was similar to other corals, as well as several mobile invertebrate taxa, including crabs and urchins. Similar  $\delta^{15}\text{N}$  values indicate these taxa may feed at the same trophic levels suggesting some level of trophic redundancy within deep-sea coral ecosystems. In addition to SIA, prey was identified from gut content analyses (GCA) performed on four fishes (*Conger oceanicus*, *Hoplostethus occidentalis*, *Helicolenus dactylopterus*, *Grammicolepis brachiusculus*,) and these data were compared to SIA data. Overall, SIA results supported GCA. For example, a crab- and shrimp-dominated diet of *C. oceanicus* and *H. occidentalis* was supported by both GCA and SIA. In some instances, GCA did not reflect SIA results. A crustacean-based diet was predicted for *H. dactylopterus*, but stomachs contained mostly pyrosomes, followed by squids, fish, and shrimp. Both stomachs examined from *G. brachiusculus* (n=2) were empty; however, SIA indicated a diet similar to *H. occidentalis*, potentially small shrimp. While GCA provided a snapshot of food items consumed by these fishes, stable isotope results yielded a longer-term perspective of their assimilated diet, providing insight into potential carbon sources when GCA results were ambiguous. Thus, SIA indicated freshly exported phytoplanktonic production serves as the basal carbon source fuelling these deep-sea coral ecosystems.





International

# 13<sup>th</sup> Deep-Sea Biology Symposium

Wellington, New Zealand 3 – 7 December 2012

P32

## A NEW GENUS AND SEVERAL NEW SPECIES OF DEEP-SEA BAMBOO CORALS (ISIDIDAE) FROM NEW ZEALAND WATERS: A TAXONOMIC AND MOLECULAR APPROACH

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Bamboo corals (Isididae) belong to a very diverse group of octocorals, but they are still poorly understood. Their study through taxonomy, ecology and evolutionary approaches has been a difficult task because of the extreme environments they inhabit and the difficulty of obtaining good quality samples. However, new undescribed species have been commonly collected as part of invertebrate by-catch studies from commercial fisheries. In this study we describe one new genus and four new species of deep-sea bamboo corals from New Zealand waters using both morphological and molecular approaches. Samples were obtained through the New Zealand Government Observers Program that is active throughout New Zealand deepsea regions including the Ross Sea (Antarctica). The four bamboo coral species are described based on their gross general morphology and DNA comparisons. For the general morphological description we used macro-structural characters such as branching pattern, color and polyp arrangement, along with axis architecture and sclerite shape and arrangement. Additionally, we amplified three mitochondrial genes, 16S, IGR4 and MSH1, which corroborated their status as new taxa and elucidated closely related species. The first two new species belong to the subfamily Mopseinae. One is characterized as an orange bushy colony, with tall polyps and rather unornamented sclerites. The second represents a new genus and is white and has highly ornamented sclerites. The other two species belong to the subfamily Keratoisidinae and the genus *Keratoisis*. One is characterized as having big, highly armed conical polyps and the second has very long, smooth internodes with an unusual nacreous lustre.

P33

## POPULATION STRUCTURE OF THE SCAVENGING AMPHIPOD, *ABYSSORCHOMENE ABYSSORUM*, AT BATHYAL DEPTHS ON THE MID-ATLANTIC RIDGE IN THE VICINITY OF THE CHARLIE-GIBBS FRACTURE ZONE

Duffy G<sup>1,2</sup>, Horton T<sup>1</sup>, Shearer M<sup>2</sup>

<sup>1</sup> National Oceanography Centre, Southampton, <sup>2</sup> University of Southampton

Through their role in recycling organic carbon from large food-falls, scavenging amphipods form a vital component of the secondary production cycles that support numerous deep-sea ecosystems. In spite of this our understanding of the ecology of these organisms is still severely lacking. A concerted effort in the field has furthered our understanding of these organisms and the factors affecting their distribution at the community level but few studies have examined the factors affecting population structure and distribution.

The ECOMAR project provided a unique opportunity to study scavenging amphipod communities at a single depth (~2500 m) across four geographically separated study-sites at the Mid-Atlantic Ridge over a four-year period. Distinct assemblages were found at each site with significant differences in species composition north and south of the Charlie-Gibbs Fracture Zone (CGFZ). All samples collected were dominated by the lysianassoid amphipod *Abyssorchomene abyssorum*. The finding of this common abyssal scavenger species at all sites provided an opportunity to study these organisms at a higher resolution, at the population level. Population structure was found to vary between sites with the clearest trend being between the site north and south of the CGFZ. Individuals from the northern sites were on average much smaller than those in the south due to an increased proportion of small juveniles and hatchlings. The differences seen can be tied to variability in surface production over the sites and reflects differences seen in species composition observed between sites.



**P34**

**MEGAFUNAL COMMUNITY STRUCTURE IN THE SUBMARINE CANYONS OF SOUTHERN CALIFORNIA**

Duffy G<sup>1</sup>, Lunsten L<sup>2</sup>, Kuhnz L<sup>2</sup>, Paull C<sup>2</sup>

<sup>1</sup> National Oceanography Centre, Southampton, <sup>2</sup> Monterey Bay Aquarium Research Institute

Submarine canyons have been studied to a very limited extent in spite of their important biological roles as hotspots of secondary production and organic matter conduits between the shelf and the deep sea. The heterogeneity and rugged terrain of submarine canyons makes them difficult to sample using traditional means such as trawling, however the recent application of remotely operated vehicles (ROVs) has proved successful in studying these important environments. A number of ROV surveys were conducted in five submarine canyons off Southern California during research expeditions in 2005 and 2010. Video transects from a range of depths were analysed to produce presence/absence data of megafaunal animals for each site and a comparison of benthic communities at various depths, locales, and canyons was performed. No difference was found between canyons based on the level of sediment transport activity, however there was significant variation in biological community composition and abundance between water depths. These depth-related trends are in agreement with the findings of previous studies and are likely tied to depth-correlated variables such as hydrostatic pressure, temperature, salinity, and oxygen concentration.

**P35**

**COMMUNITY COMPOSITION OF SCAVENGING AMPHIPODS AT BATHYAL DEPTHS ON THE MID-ATLANTIC RIDGE**

Horton T<sup>1</sup>, Thurston Mi<sup>1</sup>, Duffy G<sup>1,2</sup>

<sup>1</sup> National Oceanography Centre, Southampton, <sup>2</sup> University of Southampton

This study focussed on a section of the Mid-Atlantic Ridge with one pair of sampling sites at 49° N and the other at 54° N, north and south of the CGFZ and east and west of the ridge, at a water depth of 2500 m. 16 baited-trap samples of necrophagous amphipods were collected during three research cruises on the R.R.S. *James Cook* in 2007, 2009 and 2010. Amphipods of the superfamily Lysianassoidea are numerically dominant and taxonomically diverse and form the most important group of necrophages in most deep-sea environments. A total of 39 scavenging species from 253,306 specimens were identified at the four supersites over the four-year study period. Less than half of the entities could be ascribed to known species. More than 25 % of the species recorded were found at all of the superstations, supporting the view that necrophagous amphipods are highly mobile, widely distributed animals, found in all oceans. The number of lysianassoid species (31) was higher than expected when compared with other studies of necrophagous amphipods, particularly as all sampling was done at one depth (2500 m). Deep-sea scavenging amphipods are generally thought to have low diversity and previous studies have supported this view. Samples were large with some traps containing more than 40,000 specimens. The most abundant species, *Abyssorchomene abyssorum*, dominated all trap samples with percentage compositions over 90% at the NE sites in 2009–2010. Univariate and Multivariate analyses indicated a significant difference in community composition and species richness between the northern and southern stations. There are at least 15 new species to be described from the ECOMAR samples, and particular effort is required in the genus *Paracallisoma* and the genus *Tryphosella*.



P36

**LIVE AND DEAD DEEP-SEA BENTHIC FORAMINIFERAL FAUNAS FROM TWO SUBMARINE CANYON AREAS (NE ATLANTIC)**

**Duros P**<sup>1</sup>, Fontanier C<sup>2,3</sup>, Metzger E<sup>2</sup>, Jorissen F<sup>2</sup>, de Stigter H<sup>4</sup>, Cesbron F<sup>2</sup>, Deflandre B<sup>3</sup>, Schmidt S<sup>3</sup>, Buscail R<sup>5</sup>, Zaragosi S<sup>3</sup>  
<sup>1</sup> JSPS PDF/ BioGeos, JAMSTEC, Yokosuka, Japan, <sup>2</sup> BIAF, CNRS UMR 6122 LPGN, Angers University, 2 bd Lavoisier, 49 045 Angers Cedex, France., <sup>3</sup> EPOC, CNRS UMR 5805, Avenue des Facultés, 33405 Talence Cedex, France., <sup>4</sup> Royal NIOZ, P.O. Box 59, 1790 AB Den Burg - Texel, The Netherlands., <sup>5</sup> CEFREM, University of Perpignan, 52, Avenue Paul Alduy, 66860 Perpignan Cedex, France., <sup>6</sup> Univ PM, Via Breccia Bianca, 60131 Ancona, Italy.

The first aim of this study was to assess the impact of various abiotic parameters (e.g. organic matter) on the ecological characteristics of living benthic foraminifera in Whittard and Cap-Ferret canyons (Bay of Biscay). These canyons exhibit different sedimentary dynamics. In fact, organic and inorganic sediment particles are mainly transported by gravity flow processes within Whittard canyon and by resuspension events along Cap-Ferret canyon. Consequently, a faunal comparison between both canyons allowed us to investigate a putative effect of sedimentary disturbance. Faunas from adjacent slopes were also studied. The results show that canyon axes concentrate preferentially organic matter compared to adjacent environments. Therefore, faunas found within canyons are abundant and diverse. However, a gravity flow deposition at the deeper part of Whittard canyon may have resulted in the development of a peculiar fauna strongly dominated by only one species (*Quinqueloculina seminula*) which seems to constitute an early recoloniser. Such pioneer species were not observed at Cap-Ferret indicating more quiescent conditions. The second aim was to study the dead fauna and to compare them with the living ones. This comparison shows that transport processes of foraminiferal tests within canyon axes and biological processes lead to differences between both faunas. Along Whittard canyon, transport seems to occur by gravity mechanisms, whereas suspension events induced by high currents may be responsible for transport of foraminifera at Cap-Ferret. In the case of canyons affected by important sedimentary disturbance, such as Whittard canyon, dead fauna could provide a possible historical record of sedimentary disturbances.

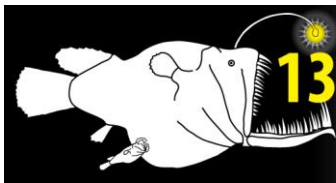
P37

**LIVING IN COCKAIGNE: REPRODUCTION OF *EURYCOPE SPINIFRONS* GURJANOVA, 1933 (ISOPODA: MUNNOPSIDAE) IN THE DEEP SEA OF JAPAN AND COMPARISON TO THE ISOPOD FAUNA IN THE ADJACENT KURIL TRENCH AREA**

**Elsner N**<sup>1</sup>, Golovan O<sup>2</sup>, Malyutina M<sup>2</sup>, Brandt A<sup>1</sup>

<sup>1</sup> University of Hamburg, Hamburg, Germany, <sup>2</sup> Zhirmunsky Institute of Marine Biology, Vladivostok, Russia

*Eurycope spinifrons* Gurjanova, 1933 is the only free-living isopod found below 2500 m in the deep Sea of Japan, but it occurs in high abundance there. This provides an excellent opportunity to study the population structure of a deep-sea isopod. In our studies we found that at the depths below 2500 m, adults of *E. spinifrons* grow larger than at the depth of 500 m. Additionally, female body length correlates positively with the number of carried eggs, suggesting a higher reproduction rate at these depths. The gut content revealed that *E. spinifrons* mainly consumes diatoms. The conditions in this area are favourable: anoxic conditions until about 8,000 years ago eliminated the true deep-sea fauna there and obviously only few opportunistic species have managed to colonize the deep bathyal and abyssal depths of the Sea of Japan, thus competition is low and food is relatively plentiful for a deep-sea ecosystem. The Russian-German cruise to the Sea of Japan (SoJaBio) in the summer of 2010 where *E. spinifrons* for this study was sampled was followed by the German-Russian cruise to the Kuril Trench area (KuramBio) in the summer of 2012. Because biodiversity is so low in the Sea of Japan and the deep sea communities are adjacent, yet completely separated from each other, a comparison between the materials of both cruises reveals interesting differences.



International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

**P38**

**THE SQUID GENUS *TEUTHOWENIA* IN NEW ZEALAND WATERS: SYSTEMATICS, ECOLOGY AND BIG, GOOGLY EYES**

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<sup>1</sup> Auckland University of Technology, <sup>2</sup> University of Auckland

Cranchiid squids are trophically important in New Zealand waters, but their systematics are notoriously unstable, complicating efforts to report their ecological roles accurately. Herein, a revised description of the cranchiid genus *Teuthowenia* is proposed, with a focus on *T. pellucida*, the locally resident species. A detailed description of its complete life cycle is given, and several important ecological factors are discussed in addition to its trophic role, such as fecundity and sexual dimorphism. One of the genus' most distinctive physical characters is the large, bulbous eyes. As these animals are believed to undergo an ontogenetic habitat shift, with some life stages residing primarily in the deep sea, a detailed histological investigation of the eyes is underway. Initial results show structural change of retinal photoreceptors throughout maturation. It is possible that the cellular structure of these light sensors could be connected to the depth at which the squid lives. Teuthid eye structure is a little-researched topic, and the eye structure of *T. pellucida* appears different from that reported for other squid taxa (most of which have been coastal, shallow-water species). This novel research will therefore further our understanding of visual abilities of deep-sea squid.

**P39**

**BATHYMETRIC PATTERNS OF FREE-LIVING NEMATODE DIVERSITY AND ABUNDANCE IN THE SEA OF JAPAN**

Fadeeva N, Mordukhovich V

Far Eastern Federal University

Biota some areas of the Sea of Japan slope are only recently explored, although their true extent and geographical coverage are still not fully established. Nematode abundance and diversity patterns were analyzed from the upper subtidal down to the bathyal zone of the Sea of Japan (up to 3367 m). At the deepest stations the most dominant families were Xyalidae (about 30%), Chromadoridae (about 20%) and Trefusiidae (about 20%). The observations point to an exchange of nematode species between shallow-water habitats and deep-sea areas of the Sea of Japan. At the same time, analysis of the nematofauna of the Sea of Japan revealed the transition in composition and structure of the nematodes communities along the bathymetric gradient. Several diversity indices were calculated, both weighted for species richness and equitability. The analysis showed that there was a non-linear relationship between depth and diversity. Some biogeochemical variables of the sediments were analyzed in conjunction with structural and functional diversity of nematodes. Densities of nematodes were comparable with those at similar water depths in the other Pacific areas.



P40

**PHYLOGENETIC ANALYSES OF THE DEEP-SEA OCTOCORALS *CORALLIUM* AND *PARAGORGIA* BASED ON WHOLE MITOCHONDRIAL GENOMES**

**Figueroa D, Baco A**

Florida State University

Molecular phylogenetic analyses of octocorals have shown that the current morphological taxonomic classification of these organisms needs to be revised. One group of corals in need of such revision are the families Coralliidae and Paragorgiidae. These families share several taxonomically important characters and it has been suggested that the Coralliidae may be a derived branch of the Paragorgiidae. There is also uncertainty in the classification of the two genera that make up the Coralliidae, *Corallium* and *Paracorallium*. Molecular analyses suggest that the genus *Corallium* is paraphyletic, with the *Paracorallium* as one of two internal clades.

We sequenced the whole mitochondrial genome of five species of *Paragorgia* and of five species of *Corallium* to achieve two objectives: 1) To elucidate the phylogenetic relationship of Paragorgiidae and Coralliidae; and 2) to determine whether *Corallium* and *Paracorallium* are monophyletic. Our study shows that all five species of Coralliidae share the two mitochondrial gene arrangements previously discovered in *Corallium konojoi* and *Paracorallium japonicum*; and that the *Corallium konojoi* arrangement is also found in the Paragorgiidae. Analyses of the intergenic spacers suggest that the *konojoi* arrangement is the product of a single evolutionary event instead of two independent ones. Our phylogenetic reconstruction based on all the protein coding genes and ribosomal RNAs of the mitochondrial genome shows that the Coralliidae are a monophyletic sister branch to the Paragorgiidae, rather than a derived branch. This work agrees that the Coralliidae should be divided into two genera, however the members of those two genera need to be reevaluated.

P41

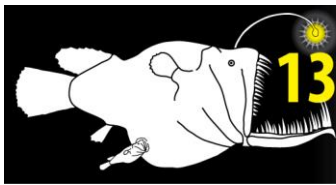
**TROPHIC MODES OF FORAMINIFERA IN THE ARABIAN SEA: EVIDENCE FROM STABLE ISOTOPE ANALYSIS.**

Fisher E<sup>1</sup>, Jeffreys R<sup>1</sup>, Gooday A<sup>2</sup>, Larkin K<sup>3</sup>, Wolff G<sup>1</sup>, Billett D<sup>2</sup>

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The Arabian Sea is an area of high productivity with the highest recorded fluxes of organic matter (OM) to the deep ocean<sup>1,2</sup>. This provides an abundant food source for fauna at the seafloor. An intense oxygen minimum zone (OMZ) also provides a potential source of chemosynthetic based nutrition<sup>3</sup>. We compared the trophic ecology of foraminifera on the Oman and Pakistan margins (140–3153 m water depth) of the Arabian Sea using stable isotope analysis (SIA). Organic carbon concentrations of surficial sediments were higher on the Oman margin (3–5 %) compared to Pakistan (1–3 %) and sedimentary OM quality estimated from the hydrogen index was also higher off Oman (300–400 mg HC/mg TOC) compared to Pakistan (< 250 mg HC/mg TOC).  $\delta^{13}\text{C}$  and  $\delta^{15}\text{N}$  values of sediments were similar on both margins (-20 ‰ and 8 ‰, respectively). Foraminifera had large ranges of  $\delta^{13}\text{C}$  values (from -22.3 ‰ to +2.1 ‰ on the Oman margin and from -29 ‰ to +0.1 ‰ off Pakistan), suggesting that they utilise multiple food sources. Foraminifera had nitrogen isotope values (-11.5 ‰ to 10.6 ‰ on the Oman margin and -3.9 ‰ to 27.3 ‰ off Pakistan), suggesting that some species (e.g. *Globobulimina* and *Karreriella* sp.) utilise denitrification on the Pakistan Margin and other species may feed on chemosynthetic bacteria within the OMZ on the Pakistan margin (e.g. *Uvigerina* ex gr. *semiornata*)<sup>4</sup> and Oman margin (e.g. *Chilostomella* sp.) and even below the OMZ on the Oman margin (e.g. *Ammolagena clavata*). At the time of sampling, a carpet of jelly detritus, including whole jellyfish carcasses (*Crambionella orsini*) was seen across the Oman margin transect<sup>5</sup>. We suggest that these may provide a source of chemosynthetic bacteria for foraminifera at these sites. Foraminifera are quite capable of utilising chemosynthetic and photosynthetic food sources, despite heavily depleted oxygen concentrations.





International

# 13<sup>th</sup> Deep-Sea Biology Symposium

Wellington, New Zealand 3 – 7 December 2012

P42

## A ZOOGEOGRAPHY OF LANTERNFISHES (FAMILY MYCTOPHIDAE) IN THE EASTERN-SOUTHEASTERN AUSTRALIAN REGION AND COMPARISONS WITH PHYSICOCHEMICAL BIOGEOGRAPHY

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<sup>1</sup> Uni. Qld, CSIRO, <sup>2</sup> Uni. Qld

In this first attempt to model the distributions of a mesopelagic fish family at this scale in the eastern-southeastern Australian region (10° S to 57° S), lanternfish species occurrence records spanning a period from 1928 to 2010 were collated. Generalised Additive Models (GAMs) were used to investigate species-habitat relationships and depth interactions of environmental covariates for selected species. The results of GAMs were used to inform the selection of environmental covariates used in presence-only models (MAXENT) that were required in order to model all species over the full study area. A four-region zoogeographic scheme is hypothesised: Coral Sea region, Subtropical Lower Water region, Subtropical Convergence/South Tasman region and Subantarctic region. The major frontal systems of the Tasman Front, Subtropical Convergence and Subantarctic Front represented zoogeographic boundaries. An additional boundary at ~25° S (coined the 'Capricorn' boundary) was adopted from one of the existing biogeographic schema to delineate the Coral Sea from Subtropical Lower Water regions. Lanternfish zoogeographic regions are congruent with some aspects of two existing biogeographic schema in the region that were derived from physicochemical properties. However, neither existing physicochemical biogeographic scheme alone reflects lanternfish distributions. Zoogeographic regions are discussed in context with the paleoceanographic setting and hypotheses of speciation that may be useful for future phylogeographic studies.

P43

## HABITAT AND COMMUNITIES OF COMMON DEEP-SEA ASTEROIDS FROM NEWFOUNDLAND AND LABRADOR, CANADA

Gale K<sup>1</sup>, Gilkinson K<sup>2</sup>, Hamel JF<sup>3</sup>, Mercier A<sup>1</sup>

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Although they are among the most common mobile megafauna in deep-sea benthic communities, little is known about the ecology of most deep-water asteroids (sea stars). As a first step towards understanding the importance of asteroids in bathyal communities, we present data on the distributions and habitats of several species and their co-occurrence with other benthic invertebrates from the continental slope (~200–2400 m) of Newfoundland and Labrador (NL), Canada. We analyzed invertebrate bycatch records collected by Canada's Department of Fisheries and Oceans (DFO) during multi-species trawl surveys in NL since 2007 and combined this data with video surveys taken from the remotely operated vehicle ROPOS in July 2007. We established a preliminary framework for the geographic range and habitat (depth, substrate type) of approximately 20 asteroid species and their association with other invertebrate megafauna in this region. Most of the asteroids in our study region were found on silt or mud substrates and individuals were often observed in close association with sponges and corals. *Ceramaster granularis* was observed feeding on sponges, *Tremaster mirabilis* and *Hippasteria phrygiana* were observed feeding on the coral *Acanthogorgia armata*, and some suspension-feeding asteroids (order Brisingida) used tall gorgonians as habitat. This work provides an empirical baseline for the species composition of benthic invertebrate megafauna throughout the continental slope of Newfoundland and, combined with parallel studies of diet and ecology, sheds light on the importance of asteroids as predators in deep-sea communities.



P44

#### LARVAL DISPERSAL OF DEEP-SEA MUSSELS: INSIGHTS FROM TRACE-ELEMENT FINGERPRINTS

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Documenting larval dispersal strategies, colonization, and connectivity among populations is mandatory to understand biodiversity, biogeographic patterns, persistence and evolution in highly fragmented deep-sea habitats. Direct observations of marine larval dispersal require labour-intensive methods that are even more demanding to carry out in the deep sea. Indirect approaches using microchemical signatures in hard parts (e.g. fish otoliths, mollusc statoliths and shells) are developing fast in near shore environments, but remain poorly explored in deep-sea ecosystems. Elemental fingerprinting lies on the principle that variations in environmental conditions (temperature, salinity, seawater chemistry) are recorded by the elemental composition of calcified structures, generating natural geochemical tags. Microchemistry of larval structures (retained after settlement) can be used to identify the location where the hard part was formed, thus allowing reconstruction of larval origin of settled juveniles. This work intends to investigate the extent to which elemental fingerprinting can be used to track mussel larvae from patchy and ephemeral deep-sea habitats. Bathymodiolin mussels (*Bivalvia*: Mytilidae) are abundantly found at deep-sea chemosynthetic habitats worldwide. Yet, the mechanisms driving species diversity and distribution of these ubiquitous bivalves are far from being completely understood. Specimens of *Idas* aff. *modiolaeformis* were collected from wood blocks deployed at mud volcanoes in the Gulf of Cadiz, and were also recovered from a natural wood-fall in the Gorringe seamounts (NE Atlantic). *Idas* species have typical mytilid D-shaped embryonic shells and large larval shells, suggesting a planktotrophic larval stage, while juveniles and adults are benthonic. Inductively coupled plasma mass spectrometry with laser ablation was used to measure trace element (e.g. <sup>43</sup>Ca, <sup>24</sup>Mg, <sup>55</sup>Mn, <sup>57</sup>Fe, <sup>88</sup>Sr, <sup>208</sup>Pb, <sup>238</sup>U) concentrations in embryonic and juvenile mussel shells. Here we present preliminary results of site-specific elemental signatures found in small deep-sea mussels.

P45

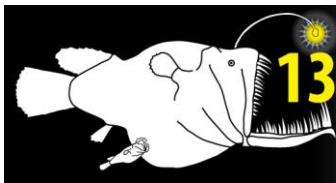
#### FAUNISTIC RESEARCH ON METAZOAN MEIOFAUNA FROM SEAMOUNTS — A REVIEW

George KH

Senckenberg am Meer, DZMB

The number of biological investigations focusing on meiofauna from seamounts is significantly low compared to studies dealing with seamount plankton, fish, and benthic mega- and macrofauna. World-wide, just eight seamounts have been object of meiobenthic investigation. First taxonomic and biogeographic studies on meiobenthos were realized on the Great Meteor Seamount (northeast Atlantic) in the 1970s. A decade later, the focus turned towards ecological aspects, switching to north-eastern Pacific seamounts, while disregarding the Atlantic elevations. Since the beginning of the 21<sup>st</sup> century, an increase of taxonomic as well as chorological, biogeographic and other faunistic topics can again be noted. In particular Atlantic seamounts moved into the scope of meiobenthic research. To date, 357 meiobenthic species have been reported from seamounts, distributed over nine from totally 26 registered major taxa, and with Copepoda Harpacticoida presenting the highest number of registered species ( $S = 215$ ), followed by Tardigrada ( $S = 35$ ) and Nematoda ( $S = 32$ ). The major part of collected species (92.2 %) has not been reported from other localities, pointing perhaps to a remarkable potential of endemism. Forty-seven species from seamounts have been described so far. The present contribution reviews the scientific research on seamount meiofauna of the past > 40 years, including remarks on fundamental questions like e.g. the potential role of seamounts as stepping stones/staging posts or “trapping stones” for meiofauna.





International

# 13<sup>th</sup> Deep-Sea Biology Symposium

Wellington, New Zealand 3 – 7 December 2012

P46

## A NEW SPECIES OF ANCORABOLIDAE (CRUSTACEA: COPEPODA: HARPACTICOIDA) FROM THE CAMPOS BASIN, BRAZIL, INCLUDING A PHYLOGENETIC REVIEW OF THE TAXON *POLYASCOPHORUS* GEORGE, 1998

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A new species of the genus *Polyascopephorus* George, 1998 (Copepoda, Harpacticoida, Ancorabolidae), collected from the Grussaí Canyon (Campos Basin, Brazil, South Atlantic), is described in the present contribution, and increases the number of *Polyascopephorus* species to three. A detailed phylogenetic analysis reveals that *P. monoceratus* sp. nov. shares the following generic apomorphies: (i) lateral posterior cephalic processes bifurcate, (ii) significant diminution of leg 1 endopod, (iii) furcal rami rounded on outer apical margin, and (iv) furcal apical setae IV, V, VI displaced to inner apical edge of furcal ramus. Within the genus, *P. monoceratus* sp. nov. has five derived characters that justify its establishment as a distinct species: a) first abdominal somite (genital double-somite in female) with single cuticular process dorsally at posterior margin, b) branches of female lateral bifurcate cephalic processes of the same size, c) furcal seta VII plumose on distal half, d) male leg 1 lacking endopod, e) leg 2 exopod segment 3 terminal setae bare, geniculate. While *P. gorbunovi* (Smirnov, 1946) and *P. martinezi* George, 1998 were collected from arctic areas, the finding of *P. monoceratus* sp. nov. off Brazil extends the generic distributional range to the South Atlantic ocean.

P47

## CHARACTERIZATION OF A MONOPHYLUM *ECHINOCLETODES* LANG (COPEPODA: HARPACTICOIDA: ANCORABOLIDAE), DISPLACEMENT OF *E. BODINI* DINET AND *E. WALVISI* DINET INTO *CLETODES* BRADY (CLETODIDAE), AND PRESENTATION OF TWO NEW SPECIES

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The findings of two new species of Harpacticoida (Crustacea, Copepoda), namely *Echinocletodes voightae* sp. nov. (Ancorabolide Sars) and *Cletodes meyerorum* sp. nov. (Cletodidae sensu Por) permitted a thorough phylogenetic re-examination of the genus *Echinocletodes* Lang, 1936, whose membership in Ancorabolidae has been increasingly queried in the past decade. *E. voightae* sp. nov. was sampled in wood-falls in the Gorda Ridge (NE Pacific Ocean). It resembles the type species *E. armatus* T. Scott, 1903, with which it shares eight clear-cut synapomorphies. In contrast, the remaining two species *E. bodini* Dinet, 1974 and *E. walvisi* Dinet, 1974 that were collected in the deep Angola Basin (SE Atlantic) do not have in common any of the mentioned synapomorphies. Instead, they show significant correspondence with the second described species *Cletodes meyerorum* sp. nov., which on its part can doubtlessly assigned to *Cletodes* Brady, 1972, due to two apomorphies presented by that genus. Consequently, both *E. bodini* and *E. walvisi* are displaced from *Echinocletodes* to *Cletodes*. That step confirms at the same time the monophyly of *Echinocletodes* that now encloses two species.



**P48**  
**ARGESTINAE POR, 1986, THE FIRST RECOGNIZED SUPRAGENERIC MONOPHYLUM WITHIN ARGESTIDAE SENSU POR, 1986 (CRUSTACEA, COPEPODA, HARPACTICOIDA)**

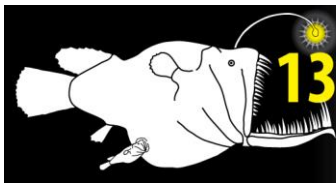
**George KH**  
Senckenberg am Meer, DZMB

The family Argestidae (Copepoda, Harpacticoida) was established by Por, 1986. It is commonly considered as typical representative of deep-sea meiobenthos, playing an even dominant role within deep-sea harpacticoid copepods. In the past years, an increasing number of faunistic and biogeographic studies related to deep-sea Harpacticoida focused on Argestidae because of their ubiquity and high relative abundance in deep-sea samples. Thus, it is expected that results from faunistic and biogeographic investigation on Argestidae might perhaps be generalized and assigned to at least all deep-sea Harpacticoida and perhaps even to other meiobenthic deep-sea taxa. Nevertheless, the monophyly of the family is far from being verified; recent Argestidae are united because of diagnostic rather than phylogenetic characteristics. The missing phylogenetic characterization of Argestidae is for instance one reason for the remarkable difference of both genus and species numbers (15–20, and 77–96, respectively) provided by several authors, staying those taxa side by side but absolutely disordered and neglecting any phylogenetic relation. Furthermore, it is obvious that without previous phylogenetic elucidation, meaningful investigations on Argestidae remain impossible and even dispensable. Recently, several studies aimed to clear up the systematic relationships inside Argestidae. While some authors concentrate on relations within single genera, others started discovering those between different genera. Here, evidence for a monophylum that is formed by two genera, namely *Argestes* Sars, 1910 and *Fultonia* T. Scott, 1902, is presented. Both genera are represented by four species each, all of which sharing the following derived characteristics: 1) body densely covered with small cuticular spinules; 2) female antennula with very strong seta terminally on 6th segment; 3) sensilla arising dorsally at thoracic somites remarkably elongate. As this combination of features is unique in Argestidae, they are regarded as autapomorphies for a suprageneric monophylum combining *Argestes* and *Fultonia* and named Argestinae Por, 1986.

**P49**  
**MODELLING *LOPHELIA PERTUSA* DISTRIBUTION IN THE GULF OF MEXICO**

**Georgian S, Cordes E**  
Temple University

*Lophelia pertusa* is the dominant habitat forming cold-water coral in the Gulf of Mexico (GoM), however its spatial distribution and environmental tolerances are not yet fully understood. In the GoM, *L. pertusa* is threatened by resource extraction, destructive fishing practices, and ongoing ocean acidification. It is crucial to gain a better understanding of the environmental factors that currently constrain the distribution of *L. pertusa*. We employed a Maximum Entropy (Maxent) modelling approach, which couples species occurrence data with environmental parameters to delineate niche and predict spatial distributions. Physical seafloor characteristics, including rugosity, slope, aspect, curvature, and bathymetric position index were derived from high resolution multibeam bathymetry for two sites within the GoM lease block Viosca Knoll, VK826 and VK906. Maxent models were developed to determine the ability of these features to explain *L. pertusa* distribution. At VK826, depth (46.7 %) and rugosity (26 %) contributed the most information to the model (mean area under the curve =  $0.978 \pm 0.002$ , binomial test,  $p < 0.001$ ), while bathymetric position index (39 %) and rugosity (30.5 %) were the strongest drivers of distribution in the VK906 model (mean area under the curve =  $0.969 \pm 0.04$ , binomial test,  $p < 0.001$ ). At both sites, *L. pertusa* preferentially occurred on steep slopes and elevated seafloor features. When the VK826 model was applied to the VK906 site, it accurately predicted >95% of known occurrences but overpredicted occurrences in areas where *L. pertusa* does not occur. The model was groundtruthed in an unexplored region of the VK826 site and accurately predicted two previously unknown *L. pertusa* mounds.



International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

**P50**

**USING NEW TECHNOLOGIES TO IDENTIFY DEEP-SEA SPECIES: MARINE LIFE FIELD GUIDE IBOOK**

**Gervais F**

NEPTUNE Canada

The NEPTUNE Canada cabled network gathers live data from instruments deployed and connected on the seafloor in the North East Pacific, off Vancouver Island (BC, Canada). Over the first two years of operations, NEPTUNE Canada has collected thousands of digital photos and hundreds of hours of high-definition video both during installation dives and from underwater cameras installed across our subsea network between 800 km and 2,700 m depth. The lack of an authoritative reference adapted to the study area of NEPTUNE Canada limited our ability to identify species observed underwater imagery. NEPTUNE Canada has developed a visual identification guide to help improve the quality of real-time video and photo annotations during the cruises, and in subsequent studies of archived imagery. The guide brings a common and scientifically valid language for quick and more accurate identification of macrofaunal and megafaunal species. Beginning as a print catalogue with the help of twenty experts around the world, the guide has become an electronic book that incorporates in situ photos and video sequences to aid identifications. This unpublished image collection, that will continue to grow, provides a unique opportunity to build a database on deep-sea species in the Northeast Pacific. NEPTUNE Canada invites experts of deep-sea species to contribute to the identification and classification of currently unknown species included in the guide. Available for free through iBook store, the Marine Life Field Guide iBook presents more than a hundred different taxa that are commonly observed during our dives or by our underwater cameras.

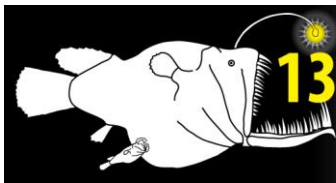
**P51**

**A NEW POLYNOID POLYCHAETE AND HOLOTHURIAN ASSOCIATION FROM THE MID-ATLANTIC RIDGE**

Shields M<sup>1</sup>, Glover A<sup>2</sup>, Wiklund H<sup>2</sup>

<sup>1</sup> Oceanlab, University of Aberdeen, <sup>2</sup> The Natural History Museum, London

The polychaete family Polynoidae is well known as being commensal, and species belonging to the family are often found associated with echinoderms and tube or burrow-building animals. Most work published on commensal polynoids is from shallow water and very little is known about polynoid associations in the deep sea. Presented here we describe a new deep-sea association between the polynoid, *Eunoe bathydomus* (Ditlevsen, 1917) and the holothurian *Deima validum validum* Théel, 1879 from the Mid-Atlantic Ridge, North Atlantic. In addition, for the first time in the deep-sea more than one polynoid specimen has been found living on a single holothurian host. There are potential ecological benefits from the association but it remains unclear what are the main ecological benefits for *E. bathydomus* being associated with *D. validum validum*. Genetic data demonstrates that *E. bathydomus* has a distribution ranging across the Mid-Atlantic Ridge over a distance of 72 km, which could have been facilitated by hitchhiking on holothurians. Additional taxonomic records of polynoid species from the Mid-Atlantic Ridge are also presented. All specimens were recovered by the remotely operated vehicle Isis during the RRS James Cook cruise JC48 in summer of 2010 as part of the NERC funded ECOMAR project.



International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

**P52**

**THREE SPECIES OF *OSEDAX* FROM THE DEEP SOUTHERN OCEAN**

Amon D<sup>1,2</sup>, Glover A<sup>2</sup>, Wiklund H<sup>2</sup>, Copley J<sup>1</sup>

<sup>1</sup> University of Southampton, U.K., <sup>2</sup> Natural History Museum, London, U.K.

We describe three new species of the siboglinid worm, *Osedax*, discovered inhabiting a whale skeleton found in the East Scotia Sea. The new species are abundant on the bones of a natural Minke whale carcass (*Balaenoptera acutorostrata*) serendipitously found at a depth of 1444 m in a seafloor caldera in close proximity to active hydrothermal vents. Two of these species are new to science and the other has been observed once previously off Smith Island in the Bransfield Strait. The three *Osedax* species belong to the 'nude-palp' clade and were observed to prefer whale bones in the skeleton with lower lipid content. We discuss here the detailed biology, ecology and phylogeny of these remarkable animals.

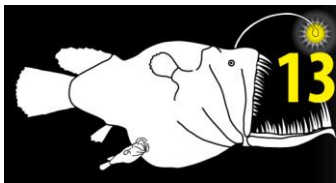
**P53**

**DISTRIBUTION OF *CALANUS* IN ARCTIC-ATLANTIC BORDER AREA: EXPATRIATION AND POTENTIAL COLONIZATION**

Gluchowska M<sup>1</sup>, Kwasniewski S<sup>1</sup>, Falk-Petersen S<sup>2</sup>, Hop H<sup>2</sup>

<sup>1</sup> Institute of Oceanology, Polish Academy of Sciences, <sup>2</sup> Norwegian Polar Institute

The Arctic is experiencing climate-induced environmental changes, mainly due to increasing temperature and volume of Atlantic waters flowing into the Arctic. It results in shifts of water masses and hydrological fronts and consequently changing the distribution of associated zooplankton communities. Fram Strait is the most important, and the only deep passage between the Arctic Ocean and the Greenland–Iceland–Norwegian Sea system. The dynamics of physical and biological characteristics of the water masses makes this region well suited for studying relationships between zooplankton distribution and physical properties of the water. Where Arctic and Atlantic water masses meet, the boreal copepod *Calanus finmarchicus*, the Arctic shelf-associated *C. glacialis* and the Arctic *C. hyperboreus* co-occur. Under continuing warming and strengthening of the Atlantic Inflow, expansion range of *C. finmarchicus* into the Arctic and its marginal seas is expected in the future. Simultaneously endemic species, such as *C. glacialis* could be negatively impacted due to the loss of the sea ice and associated algae production. Here we present observations on hydrography, distribution and abundance of the three key *Calanus* species in a border area between Arctic and Atlantic regimes, as found in the Fram Strait and in north-western Spitsbergen waters. Zooplankton samples were collected within the KongHau project (The Kongsfjord-Hausgarten transect case study: Impact of climate on Arctic marine community structures and food webs) at 62 stations with Multi Plankton Sampler (0.180 mm mesh size) in vertically stratified manner from bottom to surface in summers 2009-2011.



International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

P54

**HUSBANDRY OF COLD-WATER CORALS IN AQUARIA: COLLECTION AND CARE REQUIREMENTS**

Godinho A<sup>1</sup>, Braga-Henriques A<sup>1</sup>, Baylina N<sup>2</sup>, Carreiro-Silva M<sup>1</sup>

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Little is known on the behavior, biology and physiology of cold-water corals, mainly due to the difficulties in accessing their natural habitat. Therefore, aquarium-based studies are of major importance to overcome this obstacle and improve our knowledge on these organisms. The IMAR-DOP/UAÇ in collaboration with the Oceanário de Lisboa has developed aquarium systems to maintain and conduct experiments with cold-water corals (Corallab). Here we describe the system and its functions. Maintaining healthy deep-sea corals in aquaria is challenged by their specific needs in terms of temperature, water flow, water quality and feeding. At IMAR-DOP/UAÇ we have successfully maintained 13 species of cold-water corals belonging to four different taxonomic groups (scleractinians, ocotocorals, antipatharians and zoanthids), many of which have been maintained in captivity for more than two years. Corals have been collected from 200–500 m deep in the Azores region using submersibles, ROVs or as by-catch during longline fishing operations. Aquaria design and husbandry techniques presented here may be useful for other marine institutions that are interested in maintaining cold-water corals for experimentation.

P55

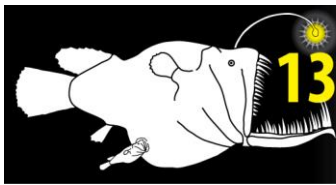
**BENTHIC FORAMINIFERAL SQUATTERS INHABITING THE TESTS OF OTHER FORAMINIFERA**

Laguionie-Marchais C, Rothe N, Gooday A

National Oceanography Centre, Southampton

There are scattered references in the literature, dating back more than 100 years, to foraminifera that occupy the tests of other benthic or planktonic foraminifera on an obligate or opportunistic basis. Many of these records refer to monothalamous (single-chambered) forms. More recently, Gooday (1986, *Deep-Sea Research* 33, 1345–1373) found numerous novel monothalamous foraminifera inhabiting empty globigerinacean shells in samples from the Porcupine Seabight (NE Atlantic). These forms construct various kinds of agglutinated structures (e.g. branched and unbranched tubes and lumps) on the exterior of the host shell and appear to be obligate inhabitants. Within the framework of the ECOMAR project, we recently discovered similar organisms occupying globigerinacean shells at bathyal depths (~2,500 m) at four sites (NW, NE, SW, SE) on the Mid-Atlantic Ridge (49° N, 53° N). One form, assigned to the poorly known genus *Hospitella*, comprises a series of brown, organic-walled 'pseudochambers', which occupy the chambers of the host shell and end in a tubular extension that projects externally. Another form, described as a new genus and species, has a cell body enclosed in a very thin, organic wall and containing numerous stercomata and iron-rich xanthosomes. This organism constructs a short, slightly tapered or conical, finely-agglutinated structure on exterior of the host shell. A variety of other forms, including allogromiid-like cells, compact masses of stercomata and protoplasm, and agglutinated spheres, were found within planktonic shells. Together, they represented 18 % (NW site) 38 % (NE site), 39 % (SE site), and 46 % (SW site) of 'live' (stained) foraminifera at the ECOMAR sites, suggesting that inhabitant foraminifera may contribute significantly to deep-sea biodiversity. Similar forms may be responsible for some of the unknown foraminiferal 'Operational Taxonomic Units' revealed by recent molecular studies of deep-sea sediments (Lecroq et al., 2011. PNAS doi: 10.1073/pnas. 1018426108). These poorly known protists clearly warrant closer attention and taxonomic effort.





International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

**P56**

**THE DEEP-SEA OSTRACODA COLLECTED OFF SOUTHERN ICELAND DURING THE THE ICEAGE PROJECT**

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The IceAGE Project aims to study the biodiversity (classical taxonomy, phylogeography and ecological modelling) in the climatic sensitive region around Iceland (Brix et al. 2012). The first IceAGE cruise was in September of 2011 and collected samples from 241 stations in 31 working areas off Iceland, from the continental shelf to the abyss. The abiotic data was collected using a CTD, which was deployed in all stations. Other cruises are planned for the future, including the IceAGE II in 2013. Here, we study the Ostracoda, Crustaceans which have one of the most complete fossil records and represent important proxies in palaeoenvironmental reconstructions. Our objective is to analyse EpiBenthic Sledge (EBS) samples from one deep and one shallow region off Southern Iceland, and also study on MULTICorer (MUC) sample of the same deep region as the EBS sample. We will compare the deep and shallow faunas and will also compare the faunas collected from both gears (EBS and MUC) in the deep sea. Since we just began to sort the EBS samples, we still do not have results to discuss, otherwise, we will be intensively working in this project in the next months and will have results to show to the deep-sea scientific community in December 2012.

**P57**

**DEEP-SEA MACROFAUNAL ECOLOGY AND BIODIVERSITY OF THE WHITTARD SUBMARINE CANYON**

**Gunton L**<sup>1</sup>, Gooday A<sup>2</sup>, Glover A<sup>3</sup>, Bett B<sup>2</sup>

<sup>1</sup> University of Southampton, <sup>2</sup> National Oceanography Centre, <sup>3</sup> The Natural History Museum

Submarine canyons are deep incisions in the continental slope. These major topographic features are difficult to sample due to the rugged terrain and dynamic conditions found inside them. Submarine canyons are major sources of habitat heterogeneity on continental margins. This increased heterogeneity, when compared to that of the adjacent slope and abyssal plain, is believed to enhance deep-sea benthic biodiversity and create a biomass hotspot inside the canyon. However, an increase in species diversity inside canyons compared to that of the adjacent slopes has not been universally supported by all studies, possibly reflecting different physical processes acting inside different canyons. The Whittard canyon is located on the Irish margin in the North East Atlantic, and encompasses water depths from 200m to 4000m. In this talk, I present results from an analysis of benthic macrofauna (> 300 µm). Three sites were sampled inside the canyon and one site on the adjacent slope, all being at a depth of 3500 m. The dominant macrofauna taxa at all four sites (inside and outside the canyon) were Polychaeta and Copepoda. Samples also contained Tanaidacea, Sipunculua, Ophiuroidea, Bivalvia, Amphipoda, Aplacophora, Bivalvia, Cumacea and Ostracoda. The Tanaidacea were found in relatively higher abundance on the adjacent slope compared to inside the canyon. Polychaeta were then identified to family level to further understand diversity at the site, also to compare diversity within the Polychaeta to macrofaunal class level diversity. This project will contribute to understanding of benthic species biodiversity and distribution on continental margins incised by submarine canyons. This knowledge will also enable us to better understand biogeography and macroecological patterning on deep-sea continental margins generally.



**P58**

**PHYLOGENOMICS OF DEEP-SEA OCTOCORALS: NEW APPROACHES TO SOLVE LONG-STANDING PROBLEMS**

**Herrera S<sup>1,2</sup>, Shank T<sup>1</sup>**

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The subclass Octocorallia is one of the least-studied groups within the phylum Cnidaria. In general, the taxonomy, phylogenetic relationships and population-level variability within this group are poorly understood. Morphologically-based species identification and classification are extremely challenging for non-specialists, and are difficult to replicate among taxonomists. Variations in octocoral colony architecture and micro-skeletal structures have been historically used as diagnostic characters. Studies over the last 15 years have shown that many of these morphological traits keep little to no correspondence with the patterns of relatedness inferred using low-variability mitochondrial and ribosomal DNA sequence markers. As such, these traditional molecular markers have been remarkably insufficient to resolve relationships at all taxonomic levels within the octocorals. These have been long-standing problems with no solution, leaving fundamental questions regarding species differentiation, classification, and biogeography of cold-water octocorals unresolved. Recent technical advances allow the implementation of next-generation sequencing technologies for the rapid detection and genotyping of genome-wide Single Nucleotide Polymorphisms (SNPs) in non-model organisms. These technologies open a new frontier in molecular studies, not only providing rich information for species identifications and taxonomy, but also the promise of providing profound insights into the population genomics, phylogeography, and evolution of deep-sea species. We employed Restriction-site-Associated DNA sequencing (RAD-seq) to identify SNPs in individuals from seven putative bubblegum coral species (Paragorgiidae), and from chrysogorgid, primnoid and pennatulid outgroups. We recovered 89,559 RAD loci across their genomes. Through phylogenomic analyses we produced a completely resolved evolutionary tree for the paragorgiids. Our approach demonstrates the great potential of RAD-seq for untangling the genetic relationships of deep-sea organisms, particularly those that have traditionally been difficult to study due to low levels of genetic variation.

**P59**

**PREDICTION OF DEEP-SEA SESSILE BENTHIC EPIFAUNA ACROSS THE KERGUELEN PLATEAU**

**Hibberd T**

Australian Antarctic Division

Sessile benthic invertebrates like sponges and corals form key components of marine biodiversity in the deep Southern Ocean. However, their distribution and extent across seascapes, and factors influencing their spatial ecology, are not well understood. In this study, benthic data from the southern Kerguelen Plateau, within the Heard Island and McDonald Islands (HIMI) region, were used to assess the potential causal relationship between sessile benthic epifauna and their associated environments, and to evaluate for the first time the efficacy of these bio-physical surrogacy relationships for extrapolating the distribution and biomass of sessile epifauna across seascapes of the deep Southern Ocean (200–2500 m depth). Quantitative samples of benthos and the co-located attributes of the environment were used to parameterise models for 16 key sessile groups. A Generalised Linear Modelling (GLM) framework was used to evaluate potential surrogacy relationships, and to subsequently predict biomass of sessile fauna across synoptic data layers of the causal surrogate(s). The GLM revealed consistent and predictable relationships between distribution and biomass of 10 groups, and either depth or geomorphology (or both). Synoptic data of depth and geomorphology were subsequently used within the GLM to predict the distribution of biomass of these correlated groups across the southern Kerguelen Plateau. Estimates revealed that the biomass of sessile epifauna were most prevalent above 300 m, and where physical parameters are likely to provide favourable attachment and feeding conditions, like on western banks, south facing slopes and around Heard Island. In the depth range from 500–1000 m, biomass of sessile groups was lower and patchier, and below 1000 m the seabed appeared relatively devoid of these taxa. This framework provides a valuable tool for estimating plausible upper and lower bounds of the biomass of sessile epifauna where biological specimens have not been collected, offering data upon which to assess impacts and assist with managing biodiversity.





P60

#### THE WORLD REGISTER OF DEEP-SEA SPECIES

Higgs N<sup>1</sup>, Horton T<sup>2</sup>, Glover A<sup>1</sup>

<sup>1</sup> Natural History Museum, London, <sup>2</sup> National Oceanography Centre, Southampton

A key first step towards better online information with regard deep-sea biology is an up-to-date and continuously maintained species list that uses current taxonomy. In order to carry out deep-sea biological research – in particular biodiversity research, the identification of deep-sea taxa is also required. There is a problem with accessing the resources required to identify these taxa, with the keys and guides often old /out of print or difficult to find. Here we outline a collaborative project with INDEEP, World Register of Marine Species (WoRMS) the Natural History Museum and the National Oceanography Centre, Southampton, to improve access to deep-sea species information. We aim to create a comprehensive list of identification guides (online keys, monographs and papers) that will be integrated with a new online portal: World Register of Deep-Sea Species. This portal will link directly to the creation of a deep-sea field 'app' (led by A. Glover, NHM) and the sourcing of guides and keys to deep-sea fauna (led by T Horton, NOC). This will be an invaluable tool for marine scientists seeking to identify their material. By linking to an authoritative and updated name database (WoRMS) we maintain a consistent taxonomy. All deep-sea biologists will be able to use this web-site as a rapid tool to search for deep-sea species, create deep-sea species lists and browse using an up-to-date taxonomy. Together these three projects will ultimately create a useful taxonomic reference tool, a new image database of deep-sea species, and a field guide 'in your pocket' for use in the lab or field. By collaborating with WoRMS, our taxonomy will be maintained by the WoRMS network of taxonomic editors. The World Register of Deep-Sea Species will thus be the most up-to-date database of deep-sea taxonomy.

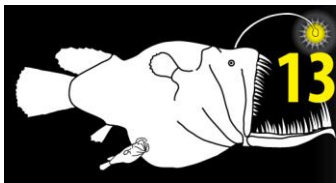
P61

#### COLD-WATER CONNECTIVITY: MICROSATELLITE DEVELOPMENT IN THE OCTOCORALS *EUNICELLA VERRUCOSA* AND *ALCYONIUM DIGITATUM*

Holland L<sup>1</sup>, Dawson D<sup>2</sup>, Horsburgh G<sup>2</sup>, Krupa A<sup>2</sup>, Stevens J<sup>1</sup>

<sup>1</sup> University of Exeter, <sup>2</sup> NERC Biomolecular Facility, University of Sheffield

Microsatellites, or simple sequence repeats (SSRs), are short tandem repeats of DNA motifs of 2–10 nucleotides that are highly polymorphic, multi-allelic, and co-dominant making them a popular marker for inference of intrapopulation structure. As such, we have developed microsatellite panels de novo for the temperate octocorals *Eunicella verrucosa* (pink sea fan) and *Alcyonium digitatum* (dead man's fingers) and used them to assess connectivity across the range of each species in the NE Atlantic. Both species are subject to damage via commercial fishing activity in the UK, and *E. verrucosa* (deemed 'vulnerable' on the IUCN red list) is subject to targeted conservation effort within the UK 2012 MPA network. At present, no genetic assessment of population structure within either species has been conducted using microsatellites. *Eunicella verrucosa* has an extensive distribution from western Africa to western Ireland and a depth within this range spanning epi-mesoplagic zones (4–500 m), of which the UK constitutes the most northerly and shallow portion of its range (whereas the UK forms the central portion of the range of *A. digitatum*). Therefore, the microsatellites can also be used to explore connectivity of this species within the context of marginal populations at their latitudinal limits. The panels were developed using an enrichment approach and 82 potential loci for *E. verrucosa* and 54 for *A. digitatum* were tested, resulting in development of 14 and 10 loci multiplexes for each species respectively. The selected loci included di-, tri-, tetra- and pentanucleotide repeats. Alleles per locus ranged between 2–18 (*E. verrucosa*) and 2–39 (*A. digitatum*). Properties of the microsatellites and resultant data, which contradicted our expected patterns of connectivity for each species, are presented. In addition, difficulties encountered during microsatellite development are discussed, including evidence for duplicate microsatellite regions, null alleles and deviations from Hardy-Weinberg equilibrium.



International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

**P62**

**CATALOGUING THE DEEP SEA**

Davies J<sup>1,2</sup>, Howell K<sup>2</sup>, Guillaumont B<sup>3</sup>, Hourigan T<sup>4</sup>

<sup>1</sup> IFREMER, Centre de Brest, DEEP/LEP, BP 70, 29280 Plouzané, France, <sup>2</sup> Marine Ecology and Biology Research Centre, University of Plymouth, Plymouth, UK, <sup>3</sup> Deep Sea Coral Research and Technology Program, NOAA Fisheries Service, Silverspring, Washington DC, USA

The use of photo-imagery as a non-destructive sampling tool in the deep sea is growing, particularly where hard substrata and highly sensitive habitats have become the focus of research attention. Identification of species is often difficult from imagery, especially when lacking specimens, but organisms can be identified as distinct Operational Taxonomic Units (OTUs), or morphotypes. Morphospecies can relate to varying taxonomic levels, from species, family, up to higher taxa. The use of morphospecies allows a greater resolution to be obtained from the data, and can be standardised across research institutes by using standardised terms, or a catalogue. Such a catalogue has been developed by the University of Plymouth for the Rockall Trough region of the NE Atlantic. However, the catalogue is limited in its scope and the web delivery site is extremely basic. This project will build on this preliminary image catalogue and broaden its scope to include newly collected data from the Bay of Biscay and the western Atlantic, as well as providing a more user friendly web delivery site. The project represents an on going partnership between Ifremer, NOAA and the University of Plymouth. New image data has been obtained from Ifremer's extensive programme of survey work in the Bay of Biscay and will be supplemented by additional data collected from the Rockall Trough region and imagery acquired by NOAA from the Western Atlantic. Incorporation of these new data represent a significant improvement on the original deep-sea species catalogue as much of these new in situ image data have been ground-truthed through the collection of physical specimens. In addition to developing the image based species catalogue the project aims to further advance the field of using imagery as a sampling tool through providing guidance on species identification from image data, key diagnostic features for specific groups, and advice on dealing with difficult groups such as the sponges. These new features will be delivered through a new web based portal that will allow greater interaction between users and data providers.

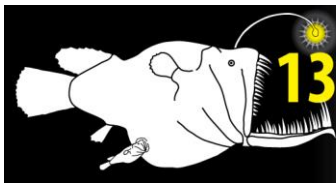
**P63**

**DEEP-SEA OCTOPUSES FROM SOUTHEAST PACIFIC OCEAN**

Ibáñez C<sup>1</sup>, Peña F<sup>1</sup>, Pardo-Gandarillas MC<sup>1</sup>, Poulin E<sup>1</sup>, Sellanes J<sup>2</sup>

<sup>1</sup> Universidad de Chile, <sup>2</sup> Universidad Católica del Norte

Deep-sea octopods inhabit the continental shelves to abyssal zones in all oceans of the world. In the southeastern Pacific Ocean the state of knowledge of this group is still deficient. However, the gradual increase in deep-sea research has helped to discover and describe new findings to the science. This study reports the octopus specimens collected on the continental shelf and slope of Chile (241–1482 m) between 29°S to 45°S. The specimens were obtained by bottom trawling (Agassiz trawl) from three cruises onboard AGOR Vidal Gormaz in 2004, 2006 and 2007, and one cruise onboard R/V Melville during 2010. We described their morphology, sequencing of mitochondrial DNA (16S rRNA, COI and COIII) was performed). Phylogenetic analyses, considering also available sequences at Genbank, suggest the presence of three species belonging to the family Octopodidae. Morphological and phylogenetic analyses confirm that these species correspond to the genera *Muusoctopus* and *Graneledone*. One of these species, *Muusoctopus longibrachus*, was the most recurrent for these latitudes, while the other two species are less frequent.



International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

**P64**  
**OPISTHOTEUTHIS SPECIES (CEPHALOPODA: OPISTHOTEUTHIDAE) FROM BATHYAL ZONE OF SOUTHEASTERN PACIFIC OCEAN**

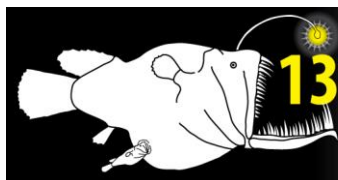
Pardo Gandarillas MC, Ibáñez C, Poulin E  
Universidad de Chile

The cirrate octopods (Cephalopoda: Cirrata) are the most abundant cephalopods in the deep sea between 300 to 7500 m. In this group is *Opisthoteuthis*, one of the most diverse, comprising nineteen valid species. *Opisthoteuthis* is the shallowest-distributed cirrate genus and all the species are closely associated with the bathyal bottom. We compare morphological and molecular data of *Opisthoteuthis* species from the SE Pacific Ocean deep sea based on three specimens collected from the coast of central Chile (33° S), at bathyal depths between 337 and 512 m. We sequenced the mitochondrial gene 16S rRNA to compare with another species and infer the phylogenetic position of these specimens from Chile using parsimony, likelihood and bayesian methods. Phylogenetic analysis confirmed the monophyly of the family Opisthoteuthidae and revealed that *Opisthoteuthis* sp. from Chile is the sister species of *Opisthoteuthis* from North Pacific Ocean.

**P65**  
**MBARI'S DEEP-SEA GUIDE: FINDING MEANING IN A MULTI-DECADAL DATABASE OF DEEP-SEA OBSERVATIONS**

Jacobsen Stout N, Kuhn L, Lundsten L, Schlining B, Schlining K, von Thun S, Matsumoto G  
MBARI

The Monterey Bay Aquarium Research Institute (MBARI) maintains a well-established database of deep-sea observations recorded by its remotely operated vehicles (ROVs) during 25 years of operations. The associated database and software system (Video Annotation and Reference System (VARS)) represents an evolution of collective knowledge and serves as an investigative tool that has facilitated hundreds of deep-sea research publications. From this unique time series dataset, MBARI's video annotation team has developed the Deep-Sea Guide (DSG). This interactive, web-based system allows for the correlation and visualization of vast amounts of imagery, descriptive and environmental data from multiple sources by providing tools for searching, identifying, and examining occurrence data (e.g., depth, time, abundance) for biological, geological and experimental observations. Basic features include searching and browsing by name, image, or taxonomic relationship, customizable comparison tables, access to unique descriptive entries, and links to references and taxonomic authorities. Also included are quality assessment metrics, which enable more precise characterization of taxa and better understanding of how data collection and analysis methods can be optimized. Delving deeper into mining this temporally and spatially rich dataset, standardized data products are created to provide a variety of data snapshots (e.g. raw or normalized depth distribution histograms for any observed taxa) allowing for efficient review and analysis. These new tools are delivering quantitative and qualitative information required for biodiversity assessment studies within MBARI's research locations and could provide context for and contribute to modeling of studies farther afield. In a continuing effort to refine sampling and analysis methods, overcome technological challenges, and improve the effective exchange of information, deep-sea community members are encouraged to contact MBARI's video analysis team to explore potential collaborations. Examples of current research using the DSG will be highlighted and system demonstrations will be available.



International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

P66

**TROPHIC MODES OF FORAMINIFERA IN THE ARABIAN SEA: EVIDENCE FROM STABLE-ISOTOPE ANALYSIS**

Fisher E<sup>1</sup>, Jeffreys R<sup>1</sup>, Gooday A<sup>2</sup>, Larkin K<sup>3</sup>, Wolff G<sup>1</sup>, Billett D<sup>2</sup>

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The Arabian Sea is an area of high productivity with the highest recorded fluxes of organic matter (OM) to the deep ocean<sup>1,2</sup>. This provides an abundant food source for fauna at the seafloor. An intense oxygen minimum zone (OMZ) also provides a potential source of chemosynthetic based nutrition<sup>3</sup>. We compared the trophic ecology of foraminifera on the Oman and Pakistan margins (140–3153 m water depth) of the Arabian Sea using stable isotope analysis (SIA). Organic carbon concentrations of surficial sediments were higher on the Oman margin (3–5 %) compared to Pakistan (1–3 %) and sedimentary OM quality estimated from the hydrogen index was also higher off Oman (300–400 mg HC/mg TOC) compared to Pakistan (< 250 mg HC/mg TOC).  $\delta^{13}\text{C}$  and  $\delta^{15}\text{N}$  values of sediments were similar on both margins (-20 ‰ and 8 ‰, respectively). Foraminifera had large ranges of  $\delta^{13}\text{C}$  values (from -22.3 ‰ to +2.1 ‰ on the Oman margin and from -29 ‰ to +0.1 ‰ off Pakistan), suggesting that they utilise multiple food sources. Foraminifera had nitrogen isotope values (-11.5 ‰ to 10.6 ‰ on the Oman margin and -3.9 ‰ to 27.3 ‰ off Pakistan), suggesting that some species (e.g. *Globobulimina* and *Karreriella* sp.) utilise denitrification on the Pakistan Margin and other species may feed on chemosynthetic bacteria within the OMZ on the Pakistan margin (e.g. *Uvigerina* ex gr. *semiornata*)<sup>4</sup> and Oman margin (e.g. *Chilostomella* sp.) and even below the OMZ on the Oman margin (e.g. *Ammolagena clavata*). At the time of sampling, a carpet of jelly detritus, including whole jellyfish carcasses (*Crambionella orsini*) was seen across the Oman margin transect<sup>5</sup>. We suggest that these may provide a source of chemosynthetic bacteria for foraminifera at these sites. Foraminifera are quite capable of utilising chemosynthetic and photosynthetic food sources, despite heavily depleted oxygen concentrations.

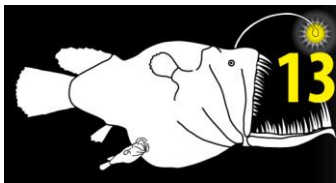
P67

**AUTONOMOUS ECOLOGICAL SURVEYING OF THE ABYSS (AES): TOWARDS A LANDSCAPE SCALE PERSPECTIVE IN DEEP-SEA ECOLOGY**

Jones D<sup>1</sup>, Bett B<sup>1</sup>, Bailey D<sup>2</sup>, Durden J<sup>3</sup>, Billett D<sup>1</sup>, McPhail S<sup>1</sup>, Huvenne V<sup>1</sup>, Morris K<sup>1</sup>, Milligan R<sup>2</sup>, Ruhl H<sup>1</sup>

<sup>1</sup> National Oceanography Centre, Southampton <sup>2</sup> University of Glasgow, Glasgow, UK <sup>3</sup> School of Ocean and Earth Science, University of Southampton, National Oceanography Centre, Southampton, UK

Determining the distribution and abundance of life is challenging, especially in the deep sea where high pressure and other logistical challenges limit data availability to a tiny fraction of what is available for other systems. Features like hills, valleys, depressions, small rock outcrops, and biogenic mounds add to habitat complexity, but links between such features and the animals that live among them are very poorly resolved in abyssal plain habitats using current methods. Life in and on the seafloor directly influences the burial of carbon and nutrient cycling – key ecosystem services. Man's exploitation of the deep sea continues to increase. Thus, spatial planning for responsible industrial activity in deep-sea environments and estimates of future change are based on rather limited information when compared to most other habitats. Previous results from a series of seven towed camera surveys on the Porcupine Abyssal Plain (PAP) have indicated that the megafauna communities and habitat features on the abyssal hills surrounding our long-studied time-series site are quite distinct from those of the observatory site. Here we utilized a new camera system on the Autosub6000 autonomous underwater vehicle (AUV) to collect photographic transect and environmental data over an unprecedented range of scales from 1 m<sup>2</sup> to about 100 km<sup>2</sup> at PAP. The system uses a vertical camera creating overlapping seabed images, as well as a forward looking oblique camera that can quantify benthic-pelagic fish abundances. This extensive survey effort has allowed the kind quantitative ecological analysis typically only possible in terrestrial habitats. We will also present developments into establishing a long-term AUV presence at key ecological research sites.



International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

P68

**SELECTION OF HOUSEKEEPING GENE FOR QUANTITATIVE RT-PCR NORMALIZATION IN THE HYDROTHERMAL VENT SHRIMP NAUTILOCARIS SAINTLAURENTAE**

Kim SJ, Ju SJ

Korea Institute of Ocean Science & Technology

Deep-sea vent invertebrates are known to tolerate a wide range of temperatures and pressures but a few studies have been conducted the analysis of relative genes expression effected on environmental stresses in vent organisms. A vent shrimp *Nautilocaris saintlaurentae* was collected by ROV named MAGNUM (Oceanering International, Inc.) at Tofua Arc (depth 1018 m) in the Southwest Pacific on 15 April 2011. Before genes expression experiments were assessed using the real-time qRT-PCR for evaluating physiological status of *N. saintlaurentae*, it was carefully evaluated whether a certain housekeeping gene (HKG) is stably expressed in the experimental system under study. Five commonly used HKGs (small subunit ribosomal RNA (SSU), ribosomal protein isoform 8 (RPL8), ribosomal protein S2 (RPS2), glyceraldehyde-3-phosphate dehydrogenase (GAPDH) and  $\beta$ -actin) were partially sequenced in *N. saintlaurentae*. Then PCR primer pairs were specifically designed and tested in real-time qRT-PCR assays. The expression of these potential reference genes was examined in 12 samples from six individuals that incubated at 4°C for 96 hours in-situ. The stability of five HKGs was determined using Ct mean value and geNorm software. RPL8 and RPS2 appeared as the most reliable reference genes with low M values (less than 0.4) for the normalization of qRT-PCR data in *N. saintlaurentae*.

P69

**A NEW SPECIES OF THE FAMILY CALLIANASSIDAE (CRUSTACEA: DECAPODA: AXIIDAE) FROM VENT FIELDS AT TOFUA ARC IN THE SOUTHWEST PACIFIC**

Ahn DH<sup>1</sup>, Kim SJ<sup>2</sup>, Ju SJ<sup>2</sup>, Min GS<sup>1</sup>

<sup>1</sup> Inha University, <sup>2</sup> Korea Institute of Ocean Science & Technology

A population of ghost shrimp was isolated from sediments of vent fields collected by TV grab of R/V SONNE. *Calliaxina* sp. nov. was identified a new species of the family Callianassidae. The new species is described and illustrated on the basis of 18 specimens. The habitat of this species was determined by zinc (Zn) poor crust in low temp vent fields. *Calliaxina* sp. nov. is characterized by broadly triangular rostrum, pointed lateral projections on carapace, laterally compressed chelipeds (first pair of legs) and third maxillipeds with the presence of exopods as found the other nominal species belonging to the genus *Calliaxina* Ngoc-Ho, 2003. However, it mainly differs by asymmetrical-sized chelipeds and absent denticules on the lower marginal side of ischium and merus in shape from congeners. In addition, three mitochondrial 16S ribosomal DNA (16S rDNA) sequences were newly determined from *Calliaxina* sp. nov. This new species show the closest relationship with *C. sakaii* (Accession No. EU882905, bootstrap value 83 % in NJ) based on 16S rDNA. This study combined morphological and molecular approach helps delineate the phylogenetic relationship within the family Callianassidae that is a complex group in decapods.





**P70**

**ESTABLISHING AN ABYSSAL ECOLOGY OBSERVATORY ON THE NEPTUNE CANADA UNDERSEA NETWORK**

**Juniper K**, Matabos M, Gervais F  
NEPTUNE Canada, University of Victoria

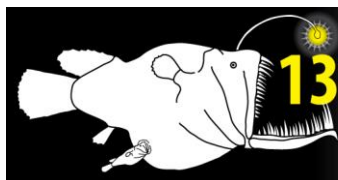
The NEPTUNE Canada undersea observatory network currently hosts sensors and cameras at 5 science nodes at depths down to 2630m in the northeast Pacific Ocean. An electro-optical backbone cable provides power and real-time communications to all seafloor and moored instruments. Since the network went live in early 2010, benthic ecology studies have been limited to an original group of interdisciplinary community experiments, at the Barkley Canyon/Upper Slope and Endeavour hydrothermal vent sites. NEPTUNE Canada's new Core Instrument program will extend a basic suite of sensors and cameras to all node locations, including the abyssal node near Ocean Drilling Program (ODP) site 1027. Research at this location is currently restricted to hydrogeology in instrumented boreholes, seismic monitoring and studies of tsunami propagation that use an array of bottom-pressure recorders. The deployment of cameras, CTD's and other instruments at ODP 1027 over the next few years will enable the study of deep-sea ecological processes. In addition to benthic communities typical of the abyssal northeast Pacific, this site hosts seep communities supported by fluid discharge around several basement edifices that emerge from the sediments. This presentation will provide an overview of the benthic environment and fauna at ODP 1027, and use examples from the Barkley Canyon/Upper Slope sites to illustrate the types of ecological studies that can be conducted with a cabled observatory.

**P71**

**DEEP-SEA TREASURES — MACROBENTHIC ASSEMBLAGES OF THE TROPICAL PACIFIC NODULE PROVINCE (CLARION-CLIPPERTON FRACTURE ZONE)**

Janssen A<sup>1</sup>, **Kaiser S**<sup>2</sup>, Albers L<sup>1</sup>, Miljutin D<sup>1</sup>, Larsen K<sup>3</sup>, Neal L<sup>4</sup>, Rogacheva A<sup>5</sup>, Menot L<sup>6</sup>, Rühlemann C<sup>7</sup>, Martínez AP<sup>1</sup>  
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Manganese nodule provinces occur across all oceans; they are of particular economical interest for the recovery of metals such as Mn, Ni, Cu and Co. One of the commercially most valuable nodule deposits is located in the North-eastern tropical Pacific, the Clarion-Clipperton Fracture Zone. This region is characterized by heterogeneous environmental conditions (e.g. differences in surface-productivity, topography and sediment characteristics), and thus comprises a great variety of (micro-) habitats. Seabed mining will have an impact on the associated fauna (e.g. regarding removal of nodules, deposition of suspended sediments). Thus, prior to mining-related exploitation, there is a need to obtain baseline data on the diversity, abundance and distribution of the nodule fauna in order to assess and predict potential responses to changing environmental conditions. During the BIONOD expedition in 2012, ten epibenthic sledge samples were taken in the French and German license area. Here, we focus on some key taxa (polychaetes, tanaids, isopods and echinoderms) in order to investigate macrofaunal abundance, composition and higher-taxon diversity, how it varies across different (local to regional) spatial scales, bathymetry and taxonomic levels and which factors may drive variability. Overall, abundance levels, richness and composition differed greatly between the German and French area, which can be partly explained by differences in surface productivity and depth. Further analyses (to lower taxonomic resolution) as well as integration of results from molecular studies will maximize insights into diversity and range size of the nodule fauna and thus provide guidelines to minimize adverse effects on the benthic environment.



International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

P72

**THE INFLUENCE OF CHEMOSYNTHETIC ECOSYSTEMS ON NEMATODE COMMUNITY  
STRUCTURE AND BIOMASS IN THE DEEP EASTERN MEDITERRANEAN SEA**

Kalogeropoulou V<sup>1</sup>, Keklikoglou K<sup>2</sup>, Sevastou K<sup>1</sup>, Lampadariou N<sup>1</sup>

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Amsterdam and Napoli are two of the numerous mud volcanoes found along the active and passive margins of the eastern Mediterranean. Napoli, located south of Crete (1940 m depth), is dome-shaped surrounded by irregular mud flows and circular depressions. Amsterdam is located south western of Turkey and has a very rough morphology with depressions and abrupt scarps (2025 m depth). During the MEDECO cruise aboard the R/V *Pourquoi Pas?* (October 2007), 9 different microhabitats in the vicinity of the two volcanoes and a control site were sampled. For the meiobenthic community analysis the microhabitats were: on Napoli a) the Lamellibrachia, b) the *Lamellibrachia* periphery, c) the bivalve shell and d) the bivalve shell periphery and on Amsterdam a) the summit, b) the reduced sediment, c) the Lamellibrachia, d) the *Lamellibrachia* periphery and e) the bivalve shell. Total meiofaunal densities ranged from 400 to 2000 ind/10 cm<sup>2</sup>. The bivalve shell microhabitat from Napoli exhibited the lowest densities while the same habitat on Amsterdam had the highest, despite similar methane concentrations. Nematodes dominated all stations, ranging from 87 to 97% and were followed by harpacticoid copepods and polychaetes. The analysis of nematode community structure revealed 144 species belonging to 83 genera. *Sabatieria* was the most abundant genus representing more than 27% of the community and consisted of a four species complex. The second rank genus was *Aponema* (sp. 1), representing more than 10% of the entire community. Both diversity and biomass varied significantly among the different microhabitats of the two mud volcanoes, indicating a strong influence of seep ecosystems on the nematode assemblages. Among the different habitats studied, the bivalve shell microhabitat from Napoli exhibited the highest biomass values and significantly low diversity while the same habitat on Amsterdam consisted mainly of small sized nematodes and higher diversity rates. A comparison with samples collected from oxygenated sediments of similar depths revealed that the densities recorded from the bivalve shell and the *Lamellibrachia* microhabitats were unexpectedly high.

P73

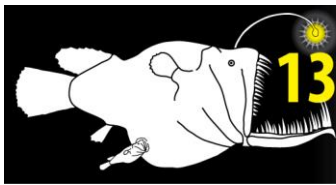
**$\alpha$  and  $\beta$  DIVERSITY OF HARPACTICOID COPEPODS AROUND THE RYUKYU AND KURIL TRENCHES, NORTH-WEST PACIFIC**

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A hadal trench (6,000–11,000 m water depth) is a narrow, elongated depression of the deep-sea floor associated with a subduction zone. The ecosystem of deep sea is remarkably modulated by food availability. The organic matter supplied from the euphotic zone drastically varies at a small spatial scale around trenches. This makes trenches an ideal area to test the effect of food availability on animal assemblages. In the present study, we investigated the genus diversity, community structure of harpacticoid copepods and their relationship with environmental factors around the Ryukyu Trench (430–7,150 m) and around the Kuril Trench (490–7,090 m). Around the Ryukyu Trench, diversity indices significantly decreased along the water depth ( $p < 0.05$ ), while they indicated the unimodal patterns with water depth, with peaks appearing at intermediate depth around the Kuril Trench. These findings would reflected the difference in food availability between two trench regions, that is, around the Ryukyu Trench, where productivity is low, only left side of the general unimodal pattern of diversity along the water depth appeared, and around the Kuril Trench, where productivity is high, the entire pattern appeared. This means the general pattern of diversity would also apply to meiofauna at all depth ranges. Significant changes in harpacticoid assemblages with water depth were detected for both trench regions. Multivariate analyses suggested that the food availability affected the harpacticoid assemblages around the Ryukyu Trench, while water depth or certain factors associated with water depth influence them around the Kuril Trench.





International

# 13<sup>th</sup> Deep-Sea Biology Symposium

Wellington, New Zealand 3 – 7 December 2012

P74

## ARE MESOZOIC SHALLOW-WATER SERPULIDS (ANNELIDA, POLYCHAETA) ANCESTORS OF THE RECENT DEEP-SEA FAUNA?

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Serpulidae are sedentary polychaetes that inhabit cylindrical calcareous tubes attached to hard substrates. A notable exception is the subtidal *Ditrupa* with characteristic unattached tusk-shaped tubes resembling shells of scaphopods. Less known are abyssal serpulids building unattached polygonal tubes. Until now, only three species were reported: *Spirodiscus grimaldii* with tetragonal spirally coiled tubes, *Bathyditrupa hovei* with quadrangular straight tubes, and *Ditrupa groenlandica* known from empty straight octagonal tubes only. These deep-sea species have morphological analogues in fossil record: both coiled tubes and tusk-shaped are very common in Jurassic and Cretaceous shallow-water environments and known as *Nogrobs*, *Tetraserpula*, and *Tetraditrupa*. To test the hypothesis that the Recent forms are “living fossils” that migrated into deep-sea refugia, we revised Recent deep-sea serpulids and compared their tube ultrastructures with those of the fossil material. The study of Recent material has revealed six species attributed to genera *Bathyditrupa*, *Bathyvermilia*, *Hyalopomatus*, *Spirodiscus*, and *Vermiliopsis*. Tube ultrastructures of fossil species have simple prismatic (SP) or homogenous granular (HG) ultrastructures, while Recent species show irregularly oriented prismatic (IOP), semi-ordered irregularly oriented prismatic (SOIOP), and spherulitic irregularly oriented prismatic (SIOP) ultrastructure. We conclude that the similarity between examined Recent and fossil serpulids is a result of convergence and the hypothesis that Recent deep-water forms are descendants of fossil shallow-water species should be rejected.

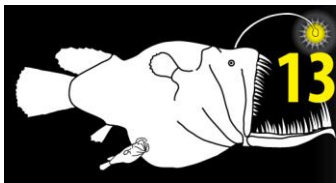
P75

## SHAKEN BUT NOT STIRRED: RESPONSE OF A DEEP-SEA NEMATODE COMMUNITY TO A ONE-OFF PHYSICAL DISTURBANCE EVENT

Leduc D<sup>1,2</sup>, Pilditch C<sup>3</sup>

<sup>1</sup> NIWA, <sup>2</sup> University of Waikato

Physical disturbance is an important factor influencing the diversity and structure of shallow benthic communities. Little is known about the impact of disturbance on deep-sea soft sediment communities due to difficulties associated with conducting experiments in this biome. We conducted a short term (9 days) laboratory experiment to determine (1) the response of a bathyal nematode community (400 m water depth) to a one-off physical disturbance event, and (2) the effect of this disturbance on sediment characteristics (granulometry, pigment concentrations) and ecosystem function (sediment community oxygen consumption). The nematode community at the study site was characterised by high species diversity, and community structure differed markedly between sediment depth layers (0–1, 1–3, 3–5 cm). Physical disturbance had little influence on sediment characteristics and ecosystem function, but led to changes in nematode species diversity and community structure 2 days after disturbance. No difference, however, was detected between the disturbed treatment and controls 9 days after disturbance, which suggests that this community is resilient to a one-off physical disturbance event. Whether this is a common feature of bathyal nematode communities remains to be investigated.



International

# 13<sup>th</sup> Deep-Sea Biology Symposium

Wellington, New Zealand 3 – 7 December 2012

**P76**

## **IN THE (SEA)BED WITH INDUSTRY: WHY DEEP-SEA BIOLOGISTS MUST ENGAGE IN INTERCOURSE (WITH THE COMMERCIAL SECTOR)**

**Levin L**

Center for Marine Biodiversity and Conservation, Scripps Institution of Oceanography

As basic research scientists we pursue problems related to species distributions, biodiversity, connectivity, recruitment, resilience, and ecological functions. We also study how physical, chemical and biological properties of the environment shape assemblages and ecosystems. As humans increase their extractive uses of the deep sea, via fishing, oil and gas drilling, and mining, they stand to alter, on both large and local scales, many of these features. Much of this is happening without regulation, relevant policy, and without the input of knowledgeable biologists capable of assessing impacts. We can choose to decry the commercial rape and pillage of the deep sea, but the non-living resources of the deep-sea are vast and exploitation is almost inevitable. In some cases this is possibly preferable to the destruction engendered by comparable resource extraction on land. I argue that our expertise is better used to work from within. We need to educate industry about how to create a baseline in a realm where the ecology is unknown and most species are undescribed, and how to apply basic conservation principles - ie ecosystem-based management and the precautionary principle. We are uniquely qualified to (i) identify potential impacts based on fundamental principles of ecology, physiology, genetics and ecotoxicology (ii) in the face of disturbance assess resilience, recovery times and trajectories, (iii) understand the implications and interactions of climate change with anthropogenic stressors and (iv) advise on 'best' (ie least damaging) practices, remediation and restoration measures and very importantly (v) implementation of deep-sea spatial planning and protection from exploitation. Where exploitation of a 'renewable resource' is completely non sustainable, we should say so (and many have). The challenges are immense, but stewardship of the deep sea demands engagement of industry.

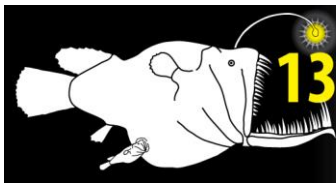
**P77**

## **AMAZING AMPHIPODA OF NEW ZEALAND'S VASTLY UNKNOWN DEEP-SEA**

**Loerz AN**

NIWA

The New Zealand marine amphipod fauna comprises nearly 400 species, more than half of which are endemic. The total diversity of the New Zealand marine amphipod fauna is likely to comprise at least five times the presently known species. A number of studies focusing on the amphipod fauna of the region have recently been published. This research includes taxonomic and phylogeographic studies, as well as ecological studies of amphipod assemblages sampled using baited traps at abyssal and hadal depths, and small meshed epibenthic sleds gear in the deep sea off New Zealand and Antarctica. Recent findings will be synthesised to provide an understanding of the evolutionary and ecological factors responsible for the distribution of amphipod species in New Zealand seas.



International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

**P78**

**BENTHIC ASSEMBLAGE STRUCTURE AND ENVIRONMENTAL DRIVERS ON MONOWAI SEAMOUNT, KERMADEC VOLCANIC ARC**

**Long N**<sup>1</sup>, Probert K, Rowden A

<sup>1</sup> University of Otago, <sup>2</sup> National Institute of Water and Atmospheric Research

The New Zealand region of the south-west Pacific includes about 800 seamounts with a vertical relief of 100 m or more. Monowai seamount lies ~1400 km NNE of New Zealand on the 2500 km long Kermadec Ridge. The Monowai complex consists of a central volcanic cone, a large caldera, and several parasitic cones. The caldera was investigated as part of the New Zealand American Submarine Ring of Fire expedition in 2005 using the ROV, *Pisces V*. Four dives were conducted on the Monowai caldera which is ~11 km wide with a maximum depth of 1500 m. Still and video footages were collected to study the benthic community composition. Analyses of still images revealed distinct vent- and non-vent communities. Communities near vent openings were dominated by vast beds of bathymodiolid mussels, swarms of alvinocaridid shrimps, zoarcid fish, anemones, and lithodid crabs. There is evidence of variability in substrate types (hard and soft) across bathymetric and horizontal gradients, in response to active and passive venting. Bedrock and mud-overlying bedrock emerge as the dominant substrate types driving species abundances and composition. Venting activity differs between the south-western and south-eastern sides of the caldera. Effect of depth, proximity to vent-openings and aspect (location on the caldera) are also examined. Plotting location and extent of communities on a topographical map, provides baseline environmental and biological data for this seamount for future comparative studies.

**P79**

**PHYLOGENY OF SERGESTIDAE AND ALVINOCARIDIDAE**

**Lunina A**, Vereshchaka A

P. P. Shirshov Institute of Oceanology of Russian Academy of Sciences

Phylogenetic analyses of two shrimp families, Sergestidae and Alvinocarididae, were made. The former family is primarily planktonic, distributed throughout tropical and temperate waters of all oceans. The second family is benthic, living in hot vents and cold seeps. Analyses were made on the morphological basis, although available molecular data for Alvinocarididae were used. Phylogeny features for both families are analyzed in regard to speciation in various geographical and ecological zones. Speciation of both families in various geographic areas show different pattern. Speciation of the families in different ecological zones is also different. In both families there are clades penetrating to the communities of the continental slopes and seamounts. Species of the planktonic family Sergestidae living above seamounts and continental slopes show more numerous and more prominent morphological adaptive characters than species of the benthic family Alvinocarididae. These adaptations are related to changes in trophic, behavioral, and other characteristic of the shrimps, living above seamounts and continental slopes. Sergestidae living at different depths also demonstrate much more numerous apomorphies than Alvinocarididae.

The studies were financially supported by the Ministry of Education and Science of the Russian Federation (contract No 16.512.11.2133).



**P80**  
**PREDICTING TRAJECTORIES OF DISSOLVED HYDROCARBONS IN THE DEEP-SEA USING A 3-DIMENSIONAL GENERAL CIRCULATION MODEL OF THE OCEANS**

**Main C**<sup>1</sup>, Yool A<sup>2</sup>, Popova E<sup>2</sup>

<sup>1</sup> University of Southampton, <sup>2</sup> National Oceanography Centre

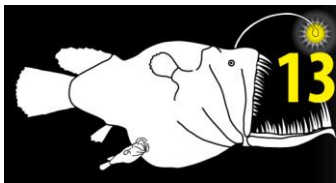
Large releases of oil in the deep-sea can allow hydrocarbons to enter and persist in deep water ecosystems. Tracking hydrocarbon plumes from a deep-sea oil release is impeded by the complex behaviour of crude oil at depth. Tools for predicting where hydrocarbons could go and their effects on ecosystem function include 3-dimensional general circulation models for the oceans (GCM). These have global coverage, so could be applied to estimate possible trajectories and effects on the ecosystem for any location where an accidental oil release might take place. Here, circulation output from a GCM, NEMO, is used with off-line Lagrangian particle-tracking, ARIANE, to simulate a hypothetical release of oil that has remained in the water column as dissolved hydrocarbons and small droplets with neutral buoyancy. Hence, the oil behaves as passive “particles” that are transported by ocean currents from the GCM. The aim of this preliminary study is to assess the role of depth of oil release on distance travelled by the particles.

**P81**  
**EXPLORING THE DEEP-WATER MEDITERRANEAN BIODIVERSITY: IN SITU OBSERVATIONS IN THE SANTA MARIA DI LEUCA COLD-WATER CORAL PROVINCE**

**Maiorano P**, Sion L, Capezzuto F, Carlucci R, Mastrototaro F, Panza MTA, D'Onghia G  
Department of Biology, University of Bari Aldo Moro

The video inspections are generally less invasive on the fragile deep-sea ecosystem than other experimental or fishing gears and they could also provide information on the habitat selection of the species and their distribution. In the context of the CoralFISH EU 7FP project, the MEMO (Marine Environment MONitoring system) baited lander has been developed with the aim to investigate the small-scale distribution of the benthopelagic fauna in the Santa Maria di Leuca (SML) cold-water coral province (Central Mediterranean, Ionian Sea). MEMO consists of a stainless steel metallic frame, two digital cameras, a multiparametric probe, an acoustic modem, and an ICT infrastructure capable of managing the entire system. The lander can work down to 1200 m depth.

Three video surveys were carried out in the SML coral province in June and November 2010, and March–April 2011. Ten deployments between 547 and 790 m were carried out for a total of about 90 hours. A total of 20 benthopelagic species (1 cephalopod, 6 decapod crustaceans, 5 cartilaginous fishes and 8 teleost fishes) were identified. The total number of individuals by species was standardised to the time of video record. The crab *Paromola cuvieri* and the fishes *Conger conger* and *Helicolenus dactylopetrus* were the most abundant species recorded during these video surveys. The blackspot seabream *Pagellus bogaraveo* and the wreckfish *Polyprion americanus* are common in the SML coral habitat; the former seems to avoid the lander, the latter seems to be attracted.



International

# 13<sup>th</sup> Deep-Sea Biology Symposium

Wellington, New Zealand 3 – 7 December 2012

**P82**

## **THE HIGHLIGHTS OF THE JOINT RUSSIAN/GERMAN DEEP-SEA EXPEDITION SOJABIO (SEA OF JAPAN BIODIVERSITY STUDIES) IN 2010**

**Malyutina M<sup>1</sup>, Brandt A<sup>2</sup>**

<sup>1</sup> Institute of Marine Biology FEB RAS, <sup>2</sup> Biocentre Grindel and Zoological Museum

The few deep-sea biological investigations in the last century characterized the deep-sea fauna of the Sea of Japan as scanty (about 30 species of invertebrates), consisting of cold-adapted eurybathic rather than true deep-sea species. This was attributed to its isolation from the oceanic abyssal and the relatively young age of the basin. The joint Russian/German expedition in the summer of 2010, SoJaBio on board of the R/V Akademik Lavrentyev studied biodiversity of the benthos of the Sea of Japan between 455–3666 m depth. More than 600 species were collected, about one third of these are new for science, more than 80 species are recorded the first time for the Sea of Japan or for the northwest Pacific. The descriptions of 3 new genera, 15 new species and redescriptions of more than 30 poorly known species of different taxa are in press for a *Deep-Sea Research II* special volume besides the analyses of the the meio- and macrofauna and a few surveys of the dominant faunal elements. The results confirm that the deep-sea fauna of the Sea of Japan consists mainly of eurybathic species. However, almost all studied taxa include few true abyssal species which already successfully colonized the young deep-sea environments of the Sea of Japan. The results will be compared with the biodiversity of an open deep-sea area of the Kurile Kamchatka Trench in future.

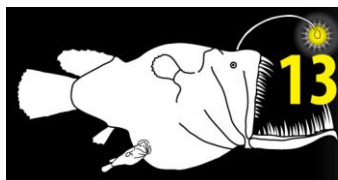
**P83**

## **EXTENDING THE WORLD'S LONGEST ECOLOGICAL TIME-SERIES OBSERVATION OF A HYDROTHERMAL VENT FIELD**

**Marsh L, Copley J, Tyler P**  
University of Southampton

The East Scotia Ridge (ESR) is the world's most isolated back-arc spreading centre. A seafloor image from February 1966 shows fauna now recognised to be associated with the E9 vent field of the ESR, making this site the location of the longest time-series observation in vent ecology. In 2009, hydrothermal activity was visually confirmed at the E9 vent field using a towed camera system, followed by a detailed survey of the vent field using a remotely operated vehicle (ROV) in 2010. This survey revealed faunal assemblages distinct from those of other vent biogeographic provinces. Fauna closest to vent sources are visibly dominated by a new species of anomuran crab, *Kiwa n. sp.*, followed by a peltospiroid gastropod, eolepedadid barnacle, and carnivorous actinostolid anemones. Peripheral fauna are not dominated by a single taxon, but include predatory and scavenger taxa such as pycnogonids and an undescribed species of stichasterid seastar. In 2011, further investigation using a towed camera system revisited several areas of the E9 vent field for a third consecutive year. These time-series observations show little variation in the location of individual stichasterids over three years. In contrast, numbers of solitary *Kiwa n. sp.* in some peripheral areas appear to have decreased over the same period. In December 2012, we are returning to the E9 vent field to investigate short-term variations in faunal distribution using timelapse photography, and to clarify patterns of interannual variation by repeating ROV surveys. Overall, however, observations spanning 45 years at the E9 vent field suggest a constancy in the taxonomic composition of vent fauna at this site on an intermediate-spreading ridge.





International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

**P84**

**DEEPFORAMS — DEEP-SEA FORAMINIFERAL STUDIES ON THE PORTUGUESE MARGIN**

Aranda da Silva A<sup>1&2</sup>, Costa A<sup>3</sup>, Matos F<sup>1&2</sup>, Ravara A<sup>1</sup>, Rodrigues C<sup>1</sup>, Gooday A<sup>4</sup>, Pawlowski J<sup>5</sup>, **Cunha MR**<sup>1</sup>

<sup>1</sup> Departamento de Biologia & CESAM, Universidade de Aveiro, Portugal, <sup>2</sup> Instituto Português do Mar e da Atmosfera, Portugal, <sup>3</sup> IGESPAR, CIBIO, Portugal, <sup>4</sup> National Oceanography centre, Southampton, United Kingdom, <sup>5</sup> Department of Genetics and Evolution, University of Geneva, Switzerland

Foraminiferans are unicellular eukaryotes (protists) characterized by an extendable granuloreticulopodial network used in feeding, locomotion and other life processes. They are ubiquitous in aquatic environments, from moist terrestrial soils to the deepest parts of the ocean. They play an important role in ecosystem functioning and biogeochemical cycling, modifying the sediment structure, providing refuges and substrates for metazoans and other protists, influencing particle depositions on the seafloor, preventing larval settlement, and in some cases out-competing metazoans for scarce resources. The Portuguese margin experiences seasonal upwelling, which contributes to an organic enrichment on the seabed, enhanced within the canyons that cross the margin. The DeepForams project (PTDC/MAR/110082/2009) aims to study deep-sea benthic foraminifera from the Portuguese margin, within the canyons and on the adjacent slopes. First, we are characterizing benthic foraminiferal communities inhabiting the Portuguese margin canyons and adjacent slopes, including the soft-shelled species. We have analysed replicate cores in order to assess patchiness, something rarely done in foraminiferal studies. Published data from HERMES and HERMIONE (EU projects) on meiofauna, macrofauna and megafauna metazoan are available, enabling us to compare protistan and metazoan responses to environmental gradients. Linking the ecology of foraminifera, which have a good fossil record, to that of metazoans, which do not, is important for understanding responses to climatic changes in the geological past. In addition to the faunal work, we are assessing the phylogeny of the most common foraminiferal species from the canyons and adjacent slope, with particular focus on the soft-shelled taxa. We will also sequence soft-shelled species from around the world, in order to refine the molecular phylogeny of foraminifera as a group within the Rhizaria.

**P85**

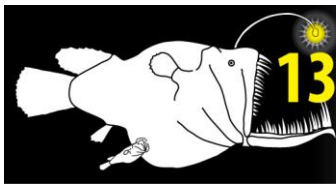
**BIONOD: A FRENCH-GERMAN CRUISE TO STUDY SPECIES DISTRIBUTION AND BIODIVERSITY PATTERNS ACROSS POLYMETALLIC NODULE FIELDS IN THE NORTH-EAST PACIFIC**

**Menot L**<sup>1</sup>, Ruehleemann C<sup>2</sup>, Galéron J<sup>1</sup>

<sup>1</sup> Ifremer, <sup>2</sup> Bundesanstalt für Geowissenschaften und Rohstoffe (BGR)

The exploration for polymetallic nodules in the Clarion-Clipperton Fracture Zone (CCFZ, NE Pacific) is experiencing a renewal of interest with two new licenses granted in 2011 and three more applications submitted to the International Seabed Authority (ISA) in 2012. Environmental concerns regarding the impact of nodule mining are also growing, though biodiversity conservation strategies are dampened by a lack of knowledge on species distribution across the CCFZ. Together with seven other contractors, Ifremer on behalf of France, and BGR on behalf of Germany, hold contracts for the exploration of polymetallic nodules in the CCFZ. Both institutes jointly organized the BIONOD cruise in April/May 2012. Beside the need to comply with mandatory environmental studies on mining claim areas, the purpose of this collaboration was to compare benthic communities and benthic processes at two spatial scales; a 1000-km scale, between two mining claims crossing a gradient in surface productivity and at a km scale according to nodule coverage within claims. The investigation of the two license areas was carried out by an interdisciplinary and multinational group of twenty-six scientists from nine research institutes and five countries. The study encompassed all benthic size classes and functional groups, from the protozoan meiofauna to the megabenthos, combining the expertise of taxonomists and molecular biologists onboard. Species distribution and biodiversity patterns at small and large spatial scales will be deciphered in the light of sediment physico-chemistry, oxygen profiles and oxygen demand.

An overview of the cruise and preliminary results will be given.



International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

**P86**

**INTERANNUAL CHANGES IN THE BENTHIC MEGAFUNAL COMMUNITY IN THE EASTERN FRAM STRAIT**

**Meyer K**<sup>1,2</sup>, Bergmann M<sup>1</sup>, Soltwedel T<sup>1</sup>

<sup>1</sup> Alfred Wegener Institute for Polar and Marine Research, <sup>2</sup> Oregon Institute for Marine Biology, University of Oregon

Interannual changes in the benthic megafaunal community at Hausgarten I, a sampling station located at 1200 m in the eastern Fram Strait, were identified. The 10-year time series included photographs from the same transect recorded in 2002, 2007 and 2012. A vertically-facing camera system was used to automatically photograph the deep-sea floor at regular intervals, and pictures were analyzed using the web-based program Biigle to identify megafauna present in each image. The faunal composition was significantly different between years, and a significant overall decrease in the density of total fauna was observed between 2002 and 2007. This decrease in fauna was paralleled by a significant decrease in the density of biotic habitat features, including stalks and tracks and burrows in the sediment. Implications of and possible reasons for these changes are discussed.

**P87**

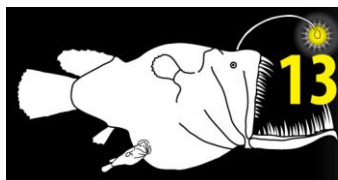
**HYDROTHERMAL AND ADJACENT DEEP-SEA FAUNAL ASSEMBLAGES AT SOUTHERN LAU BACK-ARC BASIN REVEALED BY HIGH-RESOLUTION VIDEO IMAGE**

**Min WG**<sup>1</sup>, Kim D<sup>2</sup>, Ju SJ<sup>3</sup>, Lee KY<sup>3</sup>, Won YJ<sup>4</sup>

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This study was conducted to investigate the community structure and distributional pattern of hydrothermal and adjacent deep-sea fauna at the hydrothermal vent fields of spreading axis and arc of the Lau Basin located the southern part of Tonga islands. The study area includes two seamount sites with different depths (site A: 450–600 m, site B: 800–1300 m). Visual surveys were carried out by 34 dives of ROV Magnum (RV *Araon*) and 12 dives of ROV Ropos (RV *Sonne*) using HD video camera and high-resolution digital still camera in March 2011 and February 2012. Quantitative samples were collected using the suction sampler and manipulator of ROV. Total 60 deep-sea species including 24 vent species (5 species of Cnidaria, 4 species of Mollusca, 3 species of Annelida, 4 species of Arthropoda, 2 species of Echinodermata, 1 species of Hemichordata and 5 species of Pisces) were found by analyzing high-definition photographs, video images and identifying specimens sampled by ROV at study sites. Three types of faunal assemblages defined by biogenic taxa (a provannid snail, *Avinichoncha* spp., sessile mussel, *Bathymodiolus* sp. and a brachyuran crab, *Austinograea* sp.) identified from high-definition photographs and HD video images at hydrothermal study sites. The differences observed in assemblage and substratum distribution were related to habitat characteristics. Density and diversity of vent fauna were significantly different between two sites. Although two sites are geographically very close, the hydrodynamics and vent geochemical properties of the two sites were distinctively different.





International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

**P88**

**MEIOBENTHOS COMMUNITY IN HYDROTHERMAL VENT AND ADJACENT DEEP-SEA BED ON THE SOUTHERN LAU BACK-ARC BASIN**

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This study was conducted to investigate the community structure and distributional pattern of hydrothermal and adjacent deep-sea meiobenthos at the hydrothermal vent field sites of spreading axis and arc of the Lau Basin located southern part of Tonga islands. Qualitative Sampling were carried out by 3 dives of ROVs Magnum (RV *Araon*) and Ropos (RV *Sonne*) using the suction sampler and TV grab (RV *Sonne*) at 7 stations of study sites in March 2011 and February 2012. Quantitative samples were collected using the multiple corer (11 stations) and push corer of ROV (2 stations). Sediment subsamples by acryl cores (diameter 3.4 cm) for quantitative analysis of meiobenthos were sliced 0.25–1 cm thick from the surface to 10 cm deep to analysis of vertical distribution in the sediment of study area. In all, 10 meiofauna taxa (3–7 taxa at each station) were found. Nematodes were the most abundant taxon (14–96%). Harpacticoid copepods (3–57%), crustacean nauplius (3–29%) were also dominant groups at all sites. The total meiobenthos density varied from 7 to 191 ind.10 cm<sup>-2</sup> and biomass were 5–188 µg.10 cm<sup>-2</sup> at each station. The sediments beneath the chimney mound of active hydrothermal vents contain up to 30 harpacticoid copepods per 10 cm<sup>2</sup> of sediment. In inactive ridge sediments, the abundance of harpacticoid copepods never exceeded 15 ind.10 cm<sup>-2</sup>. The distribution of meiobenthos in the adjacent deep seafloor showed high densities at the stations within the caldera of seamount. Vertical distribution of meiobenthic animals showed the highest individual numbers in the surface sediment layers of 0–1 cm depth and more steep decreasing trend as sediment gets deeper on the chimney mound sediment in a active hydrothermal vent area than another adjacent non-hydrothermal deep-sea area.

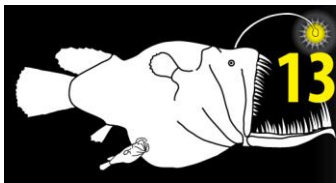
**P89**

**COMMUNITY STRUCTURES OF MEIOBENTHOS AND DISTRIBUTIONAL PATTERNS OF NEMATODE ASSEMBLAGE ON THE DEEP SEAFLOOR OF KODOS AREA IN THE CLARION-CLIPPERTON FRACTURE ZONE (NE PACIFIC)**

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This study was conducted to investigate the community structure and distributional pattern of meiobenthos associated with future deep-sea mining in the KODOS (Korea Deep Ocean Study) area present at the Clarion-Clipperton Fracture Zone (CCFZ) located in the southeastern part of the North Pacific Ocean. This study was carried out as part of baseline environmental study of KODOS long term project in the proposed mining areas for the environmental impact assessment that is comparable to future mining and whose effects are monitored over a period of time. Samples for meiobenthic study were collected at 14 stations (water depth: 4860–5021 m) in KR5 blocks of KODOS area during the cruise of R/V *Onnuri* (July 2010) and R/V *KOK* (July 2011). Sediment samples were collected using MC (multiple corer) and acryl subcorers (diameter 3.6 cm). 10 meiobenthic taxa (3–8 taxa at each station) were found. Nematodes were the most abundant taxon (60–86%). Harpacticoid copepods (5–26%), benthic foraminiferans (1–12%) were also dominant groups at all sites. Total meiobenthic density varied from 9 to 59 ind.10 cm<sup>-2</sup> (nematodes: 7–25 ind.10 cm<sup>-2</sup>) and biomass were 9–66 µg.10cm<sup>-2</sup> at each station. A total of 171 nematode individuals were sorted into 20 families, 50 genera and 73 species in the study area. The diversity index of the nematode community was 2.04–3.20 (H': 0.50–1.01 at meiobenthic higher-group level). The study area is characterized by oligotrophic waters with low nutrients and chl-a concentration below 1g/l. In such an oligotrophic environment, low food supply may limit meiobenthic abundance, biomass and effect their low heterogeneity at each station.



International

# 13<sup>th</sup> Deep-Sea Biology Symposium

Wellington, New Zealand 3 – 7 December 2012

P90

## COMMUNITY STRUCTURES AND DISTRIBUTIONAL PATTERNS OF MEIOBENTHOS ON THE DEEP SEAFLOOR AND CONTINENTAL SLOPE OF EAST SEA (SEA OF JAPAN)

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The East Sea is a semi-enclosed and mid-latitude marginal sea (total area:  $1.01 \times 10^6$  km<sup>2</sup>, average depth: 1684 m), surrounded by Korea, Japan and Russia. It is divided into the 4000 m deep Japan Basin in the northern half, the Ulleung Basin in the southwest and the Yamato Basin in the southeast, each about 2200 m deep. In this study, we report on the community structure and distributional pattern of deep-sea meiobenthos on the deep basin and continental slope of the Ulleung Basin in the southwestern part of East Sea. In this area, there is no published data of meiobenthic standing stocks and community structure. Samples for meiobenthic study were collected at 21 stations (water depth: 143–2155 m) in the center and slope area of the Ulleung Basin during the cruise of R/V *Onnuri* (June 2011) and R/V *Eardo* (June 2006). Sediment samples were collected using BC (Box corer) and acryl subcorer (diameter 3.6 cm). Altogether, 15 meiobenthic taxa (2–9 taxa at each station) were found. Nematodes were the most abundant taxon (53–80 %). Benthic foraminiferans (7–39 %) were the next dominant groups at the most sites. Total meiobenthos density varied from 42 to 3,697 ind.10 cm<sup>-2</sup> (nematodes: 29–3,320 ind.10 cm<sup>-2</sup>) and biomass was 11–1,671 µg.10 cm<sup>-2</sup> at each station. Distribution of meiobenthic animals in the Ulleung Basin of East Sea showed high densities at the stations within the southern slope part of the Ulleung Basin. In several stations in southern slope area of Ulleung Basin, very high standing stocks of meiobenthic animal ( 2000 ind.10 cm<sup>-2</sup>, 1000 µg.10 cm<sup>-2</sup>) were found. This hot spot is located in a dumping site of organic waste with high TOC concentration. In such eutrophic environment, high organic food supply may promote meiobenthic abundance and biomass.

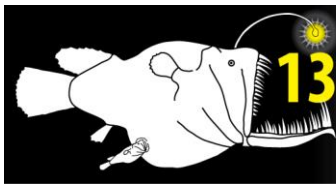
P91

## METAZOAN MEIOFAUNA FROM THE NORTH-WESTERN SLOPE OF THE SEA OF JAPAN

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Far Eastern Federal University

This study was conducted to investigate the community structure and distributional patterns of meiofauna of the north-western slope of the Sea of Japan. Sediment samples were collected during Russian-German expedition SoJaBio (Sea of Japan Biodiversity Studies) cruise of R.V. *Akademik Lavrentyev* in July 2010. In total, 20 quantitative samples at 7 stations were collected using an 8-tube multicorer with an inner tube diameter of 10 cm. The sampling stations were located in the depth range of 515 to 3367 m. Nematoda and Harpacticoid copepods were the most abundant taxa. The values of abundance of meiofauna were range of 45 ind./10cm<sup>2</sup> (water depth 3367 m) to 1620 ind.10 cm<sup>-2</sup> (water depth 515 m). Composition and structure of the nematode community obviously changed with depths. Possible relation between habitat conditions and meiofaunal community structure and distribution is discussed.



International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

**P92**

**THE ENIGMATIC NECKER RIDGE: INSIGHTS INTO FAUNA AND COMPARISON TO THE HAWAIIAN ARCHIPELAGO**

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<sup>1</sup> Florida State University, <sup>2</sup> Florida State University

In shallow water the Hawaiian Archipelago is one of the most isolated archipelagos in the world, but at depth it may be connected to the vastly understudied seamount-rich region of the central and western Pacific by the Necker Ridge, an elongated seamount which runs NE–SW perpendicular to the Hawaiian Ridge. We hypothesize that if Necker Ridge has acted as a conduit for larval dispersal between the Hawaiian Archipelago and the Mid-Pacific Mountains, then similar fauna should be found on Necker as in Hawaii. To address this hypothesis, we conducted exploratory surveys of Necker Ridge using the Pisces IV submersible in 2011, HD video transects were taken and samples were collected for morphological identifications and genetic determination of species identifications. The Ridge was characterized by hard substrates and strong currents and was dominated by suspension feeders, including corals, sponges, and crinoids. From field observations, the dominance of these three groups varied between the locations sampled on the Ridge and appeared to be related to percent sediment cover. Preliminary analyses of species composition and genetic data will be presented. These so far suggest that Necker Ridge does not have similar community structure to the Hawaiian Archipelago.

**P93**

**WHAT HAPPENED TO THE GOOSE BARNACLES?**

**Narayanaswamy B**<sup>1</sup>, Lamont P<sup>1</sup>, Chivers A<sup>1</sup>, Serpetti N<sup>1</sup>, Turnewitsch Robert<sup>1</sup>, Rogers A<sup>2</sup>, Paterson G<sup>3</sup>

<sup>1</sup> Scottish Association for Marine Science, <sup>2</sup> University of Oxford, <sup>3</sup> Natural History Museum, London

During a cruise to Senghor seamount in the North Atlantic and a second cruise to Coral and Middle of What seamounts in the South West Indian Ocean, vast quantities of goose barnacle plates were observed on the eastern sides of the seamounts. Somewhat surprisingly, no live goose barnacles were seen on the seamounts themselves, however goose barnacles were seen on the nearby hydrothermal vents in the South West Indian Ocean. Goose barnacle plates are widespread throughout the Cretaceous and Cenozoic sediments, however, the plates that were collected on these cruises were all found lying on the surface of the seamounts. We are currently investigating when the barnacles died, did they die at the same in both the North Atlantic and South West Indian Ocean? Was it a catastrophic event that killed them or was it just a natural event? By using radiocarbon dating we are aiming to determine the age of these barnacles and when they died.



P94

#### SEAMOUNT CARBONATE COMMUNITIES

Narayanaswamy B, Lamont P, Chivers A, Turnewitsch R  
Scottish Association for Marine Science

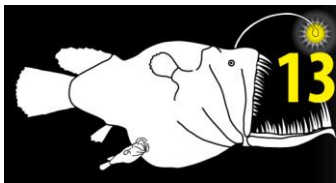
Little is known regarding the fauna living within carbonate structures, whether it is on seamounts, seeps or in other deep-sea environments. The research that has been undertaken has tended to focus on the fauna living on/within the sediment or the animals living on hard substrates such as exposed bedrock/carbonates. Carbonate samples were sometimes collected as a by-product when attempting to sample soft-sediment on Senghor and Ampere seamounts in the North Atlantic, and Erathostenes seamount in the eastern Mediterranean. On several occasions when sampling the summit plateau of Ampere seamount, large pieces of carbonate were snagged when using long line hooks. Some of the carbonate pieces were broken up on board ship whilst others have been bought back to the lab before extraction of animals was undertaken. In the laboratory we are now investigating individual carbonate pieces. One 310 g piece of carbonate material has so far been examined. Initially all visible fauna were removed from the outside of the structure, this was then followed by the carbonate being crushed in a vice and the resulting fauna following this procedure removed (0.37 g biomass and ~144 polychaetes). Finally the remaining pieces of carbonate were placed into acetic acid to dissolve the remaining carbonate structure and thus allowing for the remaining fauna to be extracted (0.03 g biomass and a further ~112 polychaetes). The number of additional polychaetes removed following acidification was really surprising.

P95

#### GAS FLUXES THROUGH CHEMOSYNTHETIC ECOSYSTEM LIVING IN THREE AREAS OF THE GULF OF GUINEA (EQUATORIAL ATLANTIC OCEAN)

Khripounoff A, Caprais JC, Decker C, Essirard M, Le Bruchec J, Olu K  
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Cold-seep areas on continental margins are characterised by biogeochemical processes that lead to the development of chemosynthetic ecosystems on the seabed. The anaerobic oxidation of methane coupled with the reduction of sulphate generates high concentrations of interstitial  $H_2S$ , sustaining microbial mats and invertebrates associated in thiotrophic symbioses, such as the widespread bivalve family Vesicomidae. In order to assess fluxes at the water/sediment interface in Vesicomidae aggregates, benthic chambers (CALMAR) measuring oxygen, sulphides, methane, total  $CO_2$  and ammonia were deployed using ROV Victor at three different areas of cold seeps in the Gulf of Guinea. The first zone, is the giant pockmark Regab, of 800 m diameter, located at 3200 m depth along the Congo margin. It is characterised by high habitat heterogeneity and is colonised by two species of Vesicomidae. The second zone called Guinness gathered several small, less active pockmarks at 700 m depth along the Gabon margin, is colonised by sparse aggregates of two other species of Vesicomidae. The third zone is the distal lobe complex of the Congo deep-sea fan, at 5000 m depth, receiving huge organic inputs from the Congo canyon/channel system. Several dense aggregates of Vesicomidae were observed, sharing one species with the Regab pockmark. Very high oxygen consumptions ( $172-434 \text{ mmol m}^{-2} \text{ d}^{-1}$ ) were measured under the benthic chambers and conversely, a high production of  $CO_2$  ( $37-1857 \text{ mmol m}^{-2} \text{ d}^{-1}$ ). The consequence of this is a strong variation of the respiratory coefficient from 0.8 to 5.2. The dissolution of the carbonates could explain the  $CO_2$  flux. The positive flux of ammonia ( $2.9-71.8 \text{ } \mu\text{mol m}^{-2} \text{ d}^{-1}$ ) is associated to the nitrogen excretion of the bivalves. The methane fluxes vary from 1.8 to 139  $\text{mmol m}^{-2} \text{ d}^{-1}$  and a sulphide flux was only evidenced at the shallower station ( $156 \text{ mmol m}^{-2} \text{ d}^{-1}$ ).



International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

P96

**NEW DATA ON SABLEFISH *ANOPLOPOMA FIMBRIA* POPULATION STRUCTURE IN THE RUSSIAN WATERS BASED ON GENETIC RESEARCH USING DNA-MARKERS**

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<sup>1</sup> Russian Federal Research Institute of Fisheries and Oceanography, <sup>2</sup> Vavilov Institute of General Genetics of the Russian Academy of Sciences

The sablefish *Anoplopoma fimbria* is a deep-water species having in the North Pacific continuous range from southern California and Mexico on the American coast to the central Honshu on the Asian coast including the Bering Sea and the Sea of Okhotsk. On the one hand, sablefish in Russian waters is prospective target of trawl, longline and trap fisheries. On the other hand, its stocks are susceptible to impact of fisheries since sablefish is long-lived species with low reproductive potential. The lack of the knowledge of sablefish population structure is one of the reasons that hamper the beginning of commercial fishing of this species in Russia. Currently, there are three hypotheses of sablefish population structure within Russian waters: 1) sablefish periodically appears in Russian waters during the periods of its high abundance in the northeastern Pacific; 2) within Russian waters sablefish from time to time forms dependent populations replenished by fish from the northeastern Pacific during periods of high abundance; 3) sablefish is permanent resident of Russian waters and forms here independent populations. During the experimental deep-water trap fishery in 2011 sablefish samples were collected from 4 different areas of the Russian waters (western Bering Sea, underwater Shirshov ridge, southeastern Kamchatka, and Commander Islands) aimed for genetic research of its population structure with the use of two types of DNA-markers: highly polymorphic microsatellite loci and mitochondrial DNA. Results of this analysis allow to obtain preliminary conception about sablefish population structure in Russian waters (to be specified in process of accumulation of new data) and to evaluate genetic affinity with sablefish populations of the northeastern Pacific.

P97

**DISTRIBUTION AND BIOLOGY OF DEMERSAL FISHES BASED ON RESULTS OF DEEP-WATER EXPLORATORY TRAP FISHERY IN THE RUSSIAN NORTHWESTERN PACIFIC**

Orlov A, Afanasiev P

Russian Federal Research Institute of Fisheries and Oceanography

The expedition that investigated possibility of deep-water trap fishing in Russian northwestern Pacific was conducted June to September 2011. During this expedition four areas of the northwestern Pacific within the depth range 315 to 1200 m were surveyed: southeastern coast of Kamchatka peninsula, western Bering Sea from Cape Olyutorsky to the border between Russian and United States EEZs, underwater Shirshov ridge, and seamounts off the Commander Islands. The study was conducted with the use of conical traps of the "Canadian" and "Korean" types. In total, there were 138 strings with about 15,000 traps deployed. About 50 fish species were registered in the catches, of which giant grenadier *Albatrossia pectoralis*, sablefish *Anoplopoma fimbria*, Greenland halibut *Reinhardtius hippoglossoides*, shortraker rockfish *Sebastes borealis*, shortspine thornyhead *Sebastolobus alascanus*, Kamchatka flounder *Atheresthes evermanni*, arrowtooth flounder *Atheresthes stomias*, and Matsubara skate *Bathyraja matsubarai* occurred most frequently. The data on spatial and vertical distributions, biological condition, catch rates of the main target species, and selectivity of different trap types were obtained. The study showed principal possibility of deep-water fish trapping in the Russian waters of the northwestern Pacific.





P98

#### FORMALDEHYDE UTILIZATION BY DEEP-SEA BACTERIA AND ITS IMPLICATION IN CHEMOSYNTHESIS

Das A<sup>1</sup>, Biche SU<sup>2</sup>, Naik SS.<sup>3</sup>, Sujith PP<sup>4</sup>, Khedekar VD<sup>5</sup>, Loka Bharathi PA<sup>6</sup>

<sup>1</sup> National Institute of Oceanography, <sup>2</sup> National Institute of Oceanography, <sup>3</sup> National Institute of Oceanography, <sup>4</sup> National Institute of Oceanography, <sup>5</sup> National Institute of Oceanography, <sup>6</sup> National Institute of Oceanography

Formaldehyde is generally used as a preservative for bacteria at  $\geq 2$  % concentration. However, it is also known to be an intermediate in many metabolic reactions. Therefore bacteria have been known to tolerate the compound at low concentrations. Nevertheless, in the course of our routine investigations for total bacterial counts in Central Indian Basin (CIB) sediments, we were surprised to find that 12/22 cores (48/140 samples) showed the presence of formaldehyde tolerant bacteria ranging from nearly 1–50 % of TC. The expression of sluggish tumbling motility in acridine orange stained cells enabled their enumeration under epifluorescence microscopy. It was interesting to note that their abundance was generally restricted to changing interfaces in the deeper parts of cores. Experiments with 11 deep sea isolates from CIB confirmed their ability to use and grow on this compound. The experiment shows the disappearance of the substrate and increase in cell numbers over 264 to 336 hours at  $4^\circ \pm 2^\circ$  C. Some of these could fix  $\text{NaH}^{14}\text{CO}_3$  while still others could express RuBisCO. More importantly, these rates were better at  $4^\circ \pm 2^\circ$  C than at  $25 \pm 2^\circ$  C. These studies suggest that the propensities for autotrophic growth or growth on C-1 compounds could help regulate hydrothermally/ biologically produced  $\text{CH}_4$  and  $\text{CO}_2$  concentrations in the deep sea.

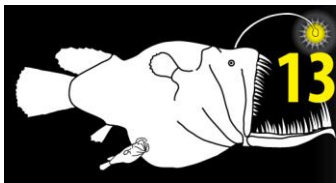
P99

#### PROGRESS ON TAXONOMIC KNOWLEDGE OF SOME DOMINANT POLYCHAETE SPECIES FROM PORCUPINE ABYSSAL PLAIN SUSTAINED OBSERVATORY (PAPSO), NE ATLANTIC OCEAN

Soto E<sup>1</sup>, Paterson G<sup>2</sup>, Neal L<sup>2</sup>, Billett D<sup>3</sup>, Hawkins L<sup>3</sup>

<sup>1</sup> Universidad de Valparaiso Chile, <sup>2</sup> Zoology Department, The Natural History Museum, London, UK, <sup>3</sup> National Oceanography Centre, European Way, Southampton SO14 3ZH, UK

A taxonomic study at species level was carried out from Porcupine Abyssal Plain, NE Atlantic Ocean for the two most abundant polychaete families. 15 different morphotypes of Cirratulidae and 13 of Spionidae were recognized and described. For Cirratulidae eight morphotypes belonged to *Chaetozone*, there were six species of *Aphelochaeta* and one of *Tharyx*. Two morphotypes of *Aphelochaeta* (*Aphelochaeta* sp. 13A and *Aphelochaeta* sp. 647D) and two morphotypes of *Chaetozone* (*Chaetozone* sp. 55A and *Chaetozone* sp. 1), possibly new species, are described. A novel approach using a complete set of taxonomic characters was used with the prostomium and thorax shape, buccal region length, branchial scars position and presence of 'bottle brush' chaetae as the most relevant. For Spionidae two morphotypes belonged to *Minuspio*, two to *Prionospio*, two to *Aurospio*, two to *Laonice* and two to *Spiophanes*. For the *Prionospio* complex three new species are described *Aurospio abranchiata* sp. nov., *Aurospio tribranchiata* sp. nov. and *Prionospio porcupinensis* sp. nov. The most important taxonomic characters considered were of kind and start of branchiae, hooded hooks, start of sabre chaetae and start of dorsal crests. The revision of whole set of morphological taxonomic characters plus the use of SEM techniques improve the diversity knowledge of the abyssal polychaete fauna.



International

# 13<sup>th</sup> Deep-Sea Biology Symposium

Wellington, New Zealand 3 – 7 December 2012

**P100**

## **REVISION OF TAXONOMIC CHARACTERS ON ABYSSAL BITENTACULATE CIRRATULIDS (POLYCHAETA: CIRRATULIDAE)**

Soto E<sup>5</sup>, Doner S<sup>1</sup>, Paterson G<sup>2</sup>, Blake J<sup>1</sup>, Chambers S<sup>3</sup>, Dean H<sup>4</sup>

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A major revision of all taxonomic characters on abyssal bitentaculate cirratulids was undertaken in two scientific workshops held in 2007 at The Natural History Museum, London, United Kingdom and at ENSR Marine & Coastal Center, Woods Hole, MA, USA. The aim of these workshops was to discuss strategies to overcome the “taxonomic impediment” in the study of abyssal (> 3000 m) polychaetes as well as to undertake trial taxonomic synthesis studies. Taxonomists and abyssal samples from multiple geographic regions were brought together to produce guidelines for a future larger study. The Cirratulidae are highly diverse in abyssal sediments with large numbers of undescribed species, consequently they were one of the families chosen for special attention. Bitentaculate cirratulid characters required for comparison of widely separated abyssal locations were compiled from data collected from the Pacific, Atlantic, and Antarctic abyssal plains and basins. The computer program DELTA (DEscription Language for TAXonomy) was selected as a means of compiling morphological data. A set of 81 morphological characters and states were established and entered into DELTA together with illustrations of these to ensure a common language among the taxonomists involved. Once this database is populated, specimens from various projects and localities will be compared in order to determine similarities and differences.

**P101**

## **ECOLOGICAL FUNCTION OF THE MID-ATLANTIC RIDGE**

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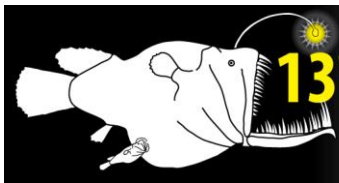
<sup>1</sup> Oceanlab, University of Aberdeen, <sup>2</sup> Institute of Marine Research, Norway, <sup>3</sup> Plymouth Marine Laboratory, UK, <sup>4</sup> Smithsonian, National Museum of Natural History, Washington, DC USA, <sup>5</sup> Shirshov Institute of Oceanology, Moscow, Russia, <sup>6</sup> National Oceanography Centre, Southampton UK, <sup>7</sup> Scottish Association for Marine Science, Oban, UK

There is an urgent need for scientific information on the ecology of mid-ridge systems to provide sound advice for international management of resources and to protect vulnerable habitats. As part of the Census of Marine Life MAR-ECO programme [www.mar-eco.no](http://www.mar-eco.no) “Patterns and Processes of the Northern Mid-Atlantic” a series of expeditions visited the Mid-Atlantic ridge (MAR) between the Azores and Iceland during 2002 and 2010 to investigate the biomass and biodiversity of photosynthesis-dependent life from the surface to the sea floor. Three main questions were addressed.

1. Surface and upper water column. Are primary production, pelagic biomass and downward export flux elevated compared with adjacent waters?
2. Sea floor. Is benthic biomass higher than in surrounding regions: Does presence of MAR influence biomass?
3. Biodiversity. How unique is the species composition?

Satellite remote sensing and sediment trap data showed that primary production over MAR and export flux from the surface are not greater than in adjacent oceanic waters. Whilst aggregation of biomass can occur on the MAR there is no enhanced production. The benthic biomass on the MAR is elevated compared with a hypothetical ocean basin with no ridge but the increase is equal to the pelagic biomass displaced by the MAR. The overall effect of the MAR on mid ocean biomass is neutral. Most species populating the MAR are typical North Atlantic lower bathyal species known from the ocean margins with greater similarity to the eastern rather than the western Atlantic.





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# 13<sup>th</sup> Deep-Sea Biology Symposium

Wellington, New Zealand 3 – 7 December 2012

P102

## OBSERVATIONS ON TORQUARATORID ACORN WORMS (HEMICHORDATA, ENTEROPNEUSTA) FROM THE NORTHERN MID-ATLANTIC RIDGE WITH DESCRIPTIONS OF A NEW GENUS AND THREE NEW SPECIES

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Enteropneusts in the family Torquaratoridae were imaged in the deep North Atlantic and collected by the ROV Isis at ca. 2500 m depth on the Mid-Atlantic Ridge. From this material, we describe *Yoda purpurata* n. gen. n. sp., *Tergivelum cinnabarinum* n. sp., and *Allapasus isidis* n. sp. The first two species browse completely exposed on the sea floor leaving characteristic faecal traces, whereas the single specimen of *A. isidis* was encountered floating approximately 1 m above the sea floor. Living specimens of *Y. purpurata* (12–19 cm long) have a dark reddish-purple proboscis, collar, and genital wings (folded dorsally over the anterior region of the trunk). Individuals of *Y. purpurata* are hermaphrodites (the first ever discovered in the phylum Hemichordata) with numerous separate testes and ovaries in the genital wings. Living specimens of *T. cinnabarinum* (12–26 cm long) have a cinnabar colored proboscis, collar, and back veils (arising from the anterior region of the trunk); sexes are separate, and the body shape and internal morphology closely resemble those of its brown congener, *T. baldwinae*, from the Eastern Pacific. The only specimen of *A. isidis* collected was a male 13 cm long and pale yellow when alive. Its body shape is proportionally shorter and broader than that of its orange congener, *T. aurantiacus*, from the Eastern Pacific, but internally the two species are virtually identical. *T. cinnabarinum* predominates north of the Charlie Gibbs Fracture Zone beneath cold waters north of the sub polar front whereas *Y. purpurata* occurs mainly to the south.

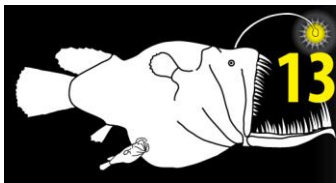
P103

## REDISCOVERED SPECIES AND NEW BATHYMETRICAL RANGES OF BATHIAL ECHINODERMS IN THE WESTERN MEDITERRANEAN SEA

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Information of bathyal echinoderms is scarce in the Mediterranean Sea, especially in submarine canyons. The present study reports new data about Mediterranean bathyal echinoderms. Samples were collected from 134 trawls conducted in the Catalan margin (north-western Mediterranean), on the open slope and Blanes, La Fonera and Cap de Creus canyons, between 850 and 3000 m depth using an otter-trawl and an Agassiz dredge. Three rare species were found: *Hedingia mediterranea* (Bartolini Baldelli, 1914), *Penilpidia ludwigi* (von Marenzeller, 1893) and *Gracilechinus alexandri* (Danielssen & Koren, 1883). All three species were observed more than twice, suggesting a higher presence than expected. Two of these species were endemic holothurians from the Mediterranean, *Hedingia mediterranea*, previously dredged only one time in 1914 on Tyrrhenian Sea, and *Penilpidia ludwigi*, previously collected only one time in the Western Mediterranean on La Fonera Canyon sediment traps. The third species was the Atlantic echinoid *Gracilechinus alexandri* (Danielssen & Koren, 1883) previously reported in the Mediterranean Sea only one time on the Valencia Trough, near the Balearic Islands in 1987 (Alvà 1987). Additionally new Mediterranean bathymetrical ranges were reported in four species: the asteroidea *Ceramaster grenadensis* (Perrier, 1881) extended down to 2843 m; the echinoid *Brissopsis lyrifera* (Forbes, 1841) extended down to 2250 m; the holothurians *Hedingia mediterranea* extended down to 1200 m and, finally, the shallower *Holothuria (Panningothuria) forskali* Delle Chiaje, 1823, extended down to 850 m in the Blanes Canyon. An absence of the classes Ophiuroidea and Crinoidea was observed. Results are discussed in relation to the distribution and ecology of the species in the open slope and submarine canyons.



International

# 13<sup>th</sup> Deep-Sea Biology Symposium

Wellington, New Zealand 3 – 7 December 2012

**P104**

## **DAY-NIGHT AND INTERNAL-TIDAL ACTIVITY RHYTHMS IN DEEP-SEA BLACK COD (*ANOPOLOPOMA FIMBRIA*) AND HAGFISH (*EPTATRETUS SP.*) BY NEPTUNE VIDEO-MONITORING AT BARKLEY CANYON (CANADA)**

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Deep-Sea remain largely faunistically unexplored for the limitation of repeating trawling and ROV video-surveys at larger temporal scales. The recent advancements in multiparametric cabled observatory technology bearing video-cameras, is now permitting a faunal monitoring over unlimited period of time, avoiding the biases in population and biodiversity assessments, due to behavioral rhythms (i.e. which can occur as massive population displacements). In this study, we tested by video-monitoring, the interplay between day-night and internal tidal cycles in regulating the behavior of the Canadian Black cod (*Anoplopoma fimbria*), hagfish (*Eptatretus sp.*) and crabs. We counted the number of animals in 50 s footages taken at 30 min frequency with 3 NEPTUNE cameras at Barkley canyon: one in the axis (984 m depth), and two at the mid wall of the canyon (896.1 m and 892 m depth, respectively). Data of pressure and current speed at the bottom were also gathered at corresponding time. Visual counts were summed for the three cameras together. The Lomb-Scargle periodogram showed weaker but significant ( $p < 0.001$ ) 24-h increments of animals in all species, along with a non significant tidal signal. Waveform analysis identified a nocturnal increment for these species. In waveforms, we related these increments with current speed (also analyzed by waveform analysis). Black cod decrement occurred at water speed increases. Conversely, hagfish and crabs seem to increment their counts with currents. These results are discussed considering a potential model of rhythmic behavior in these species.

**P105**

## **SIMULATED DEEP-SEA HYDRODYNAMIC BENTHIC REGIMES MODULATE *NEPHROPS NORVEGICUS* BURROW EMERGENCE**

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Biological rhythms of deep-sea animals are poorly known because of the difficulty and cost of in-situ observations. In the aphotic depth realms, periodic internal tides and inertial motions could play an important role synchronizing the behavior and physiology of organisms in way alternative to day-night cycles. The Norway lobster, *Nephrops norvegicus*, is a burrowing decapod distributed in the European-Atlantic and Mediterranean from upper shelves to middle slopes. Animals of deeper strata experience low light condition, hence hydrodynamic regimes could be an important cue to synchronize their behavioral rhythms being this species a putative model for studies on rhythms with deep-sea organisms. Here, we investigated the hydrodynamic entrainment of *Nephrops* in the laboratory with a new automated mini-flume actographic system. 4 tanks with independent channels and burrows are separately connected with pumps generating periodical water flow motions. The activity of 32 animals was tested in constant darkness with time-lapse photography (i.e. acquiring images at 10 s frequency) in order to obtain burrow emergence rhythms under water flow (i.e 10 cm/s) cycles of 12.4 and 18-h periodicity (as representative of tidal and inertial water motions). Preliminary results indicate that water flow inhibit the burrow emergence, with a stronger effect when it overlaps with the phase of maximum activity. We found an exogenous effect of the tidal component (12.4h), while the inertial component (18h) showed signs of entrainment.



**P106**

**IMPEDIMENT BE RESOURCE: SEXUAL DIMORPHISMS IN DEEP-SEA ISOPOD CRUSTACEANS**

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University of Hamburg, Zoological Museum

Sexual dimorphisms impose difficulties for allocating conspecifics in many groups of animals, for example in deep-sea isopods. Here, adult males are often characterized by pronounced morphological differences after the final moult. This phenomenon is potentially related to precopulatory dispersal and/or search for mating partners. In several isopod families, females tend to show great interspecific morphological similarity making species differentiation difficult. The males, on the contrary, bear aberrant, sexually dimorphic character states which makes these easy to differentiate but hard to allocate to their conspecific females. Consequently, sexual dimorphism is regarded to be amongst the relevant explanations for why for example in the isopod family Macrostylidae for 50 % of the described species only one sex is known. Misidentifications caused by sexual dimorphism may thus lead to overestimation of faunal diversity. Thanks to DNA barcoding and other molecular evidence, this impediment can be overcome and turned into valuable information for taxonomy, systematics and phylogeny. A characterization of sexual-dimorphisms in the understudied Macrostylidae is presented. Their potential application for phylogenetic analyses is evaluated.

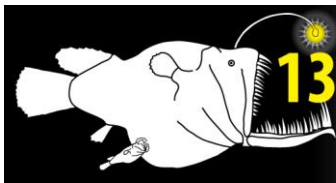
**P107**

**MEGAFUNA DIVERSITY IN THE CLARION-CLIPPERTON FRACTURE ZONE: PRELIMINARY DATA OF THE BIONOD PROJECT**

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Studies of biodiversity are a major priority in high seas areas where commercial mining is proposed. Megafaunal diversity was estimated based on extended series of deep-sea images taken with the SCAMPI photo and video sledge in the Clarion-Clipperton Fracture Zone (CCFZ) area, a manganese nodule region in the equatorial NE Pacific. Images were obtained in the German license area for the exploration of polymetallic nodules during the joint Franco-German cruise BIONOD onboard RV *L'Atalante* (Genavir, France) in March-May, 2012. In total, 3024 images were taken at four transects covering approximately 14,500 m<sup>2</sup> of the seafloor. In total, 90 megafaunal species from nine phyla were recognized. The most species-rich taxa were Holothuroidea (22 species), Porifera (16 species) and Anthozoa (12 species). Only 6 species were found at all four transects. The results of the BIONOD cruise were compared with data obtained at two previous cruises to the CCFZ area: the MANGAN cruise to the German license area in 2010 and the NODINAUT cruise to the French license area in 2004. At least 28 species (~ 30 %) recorded in BIONOD were also found at one or both of the previous cruises. In total, 149 megafaunal species were recognized at these three cruises. The species accumulation curve based on species records on all the three cruises suggests that further investigations are critical.



International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

**P108**

**DEEP-SEA INVERTEBRATES OF NEW ZEALAND: DIVERSITY, TOOLS AND OPPORTUNITIES**

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A recent inventory of the New Zealand Animalia (including vertebrates) by D.P. Gordon listed a total of ~35,000 terrestrial and aquatic species. Notably, only about a third of these (just over 13,000) are marine, despite the fact that the New Zealand marine realm is 15 times larger than its land mass. This difference becomes even more striking when one considers the deep-sea environment: not even 800 invertebrate species are known from depths > 1500 m, meanwhile, these deep waters cover more than 65 % of the New Zealand Exclusive Economic Zone. Relatively little has been published about the benthic fauna of New Zealand's deep sea below 1500 m. However, samples have been taken sporadically from the deep seafloor since the HMS Challenger passed through the region in 1874. We summarise the ongoing research efforts in the New Zealand deep sea (beyond the continental shelf), highlighting some of the technological improvements that have added a wealth of information and data that in turn allow insights into deep-sea biodiversity and ecosystem functioning. While it is not surprising that the recognition of new taxa happens at a rate much faster than they can be described, some encouraging progress has been made over the last years. Nevertheless, the possibilities for discovery remain endless.

**P109**

**POLYNOID POLYCHAETE SPECIES ASSOCIATIONS WITH DEEP-SEA CORALS AND THEIR CONNECTIVITY ACROSS THE SOUTHWEST INDIAN OCEAN RIDGE**

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Two contrasting opinions have been developed about the role of seamounts in species connectivity and dispersal in the deep sea. The earliest view was that they represented stepping points for faunal populations, facilitating dispersal between continental shelves and mid-ocean ridges and across large deep-sea basins. More recently, increasing studies underlined a high percentage of endemic species on seamounts, with up to 52 % of the benthic invertebrates found to be endemic. These results led to a more recent view that the geographic distance between seamounts and their unique topographic and hydrographic conditions stimulate genetic divergence contributing to faunal isolation. More than ten species of polynoid polychaetes associated with deep-sea corals with diverse multi-dimensional structures (scleractinians forming cold-water coral reefs and octocorals, stylasterids and antipatharians forming coral gardens) were sampled across five seamounts of the Southwest Indian Ridge that extends south westwards between South Africa and Antarctica. Previous studies showed that some of these associations are obligate commensalism with unique morphological adaptations which might require diffusible chemical releasing to promote species-specific recognition and polynoid larvae settling. In this study we analysed the habitat requirements and the level of coral-host specificity. The contiguity of these seamounts also provided us with the possibility to analyse the genetic connectivity across the Southwest Indian Ridge and evaluate the role of the host-associate co-evolution on the dispersal of these populations.



**P110**

**MEIOFAUNAL COMMUNITIES IN THE LEVANTINE BASIN (EASTERN MEDITERRANEAN): THE EFFECT OF DEPTH AND DISTANCE-TO-COAST ON DISTRIBUTION PATTERNS**

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The Mediterranean Sea is an unusually oligotrophic marine system with the eastern Levantine basin representing its extreme. Being in a land-locked sea, Mediterranean deep-sea ecosystems are not only dependent on pelagic production but are also influenced by inputs from the surrounded lands. LEVAR expedition (Levantine Basin Biodiversity Variability) carried out on board R/V *Meteor* during December 2006–February 2007 aimed at exploring biodiversity patterns and the underlying factors and processes in the Levantine basin. One of its main goals was to investigate the relationships of benthic fauna with environmental variables, in particular with depth and distance to coast. For that purpose, meiobenthic samples were collected from two areas southeast of the island of Crete: Area 1 (Ierapetra Basin) is located close to the island and is deeper than 4000 m, whereas Area 2 (Pliny Plain) is more distant but shallower (2700 m). Several multiple-corer deployments at three stations within each area and the vertical sectioning of the sediment samples allowed the detailed study of horizontal and vertical meiofaunal distribution. Data analyses indicated differences between the two studied areas and among sediment horizons when richness and community structure at major taxa level were used, but these patterns do not stand for overall metazoan meiofaunal abundance. Nevertheless, nematode and copepod standing stocks follow diversity community patterns that could even indicate differences among stations of the same area. The results of this study suggest that meiofaunal richness and community structure are rather related to depth than distance to coast, exhibiting the well-known decreasing bathymetric trend even in an enclosed, event driven system.

**P111**

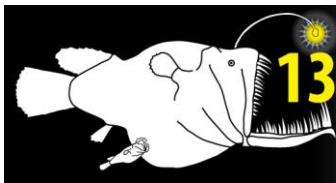
**CONTROLS ON HADAL MEGAFUNAL COMMUNITY STRUCTURE: A SYSTEMATIC EXAMINATION OF PRESSURE, FOOD SUPPLY, TOPOGRAPHY, AND EVOLUTION**

Heyl T<sup>1</sup>, Drazen J<sup>2</sup>, Yancey P<sup>3</sup>, Jamieson A<sup>4</sup>, Rowden A<sup>5</sup>, Bowen A<sup>1</sup>, Clark M<sup>5</sup>, Mayor D<sup>4</sup>, Piertney S<sup>6</sup>, Ruhl H<sup>7</sup>

<sup>1</sup> Woods Hole Oceanographic Institution, <sup>2</sup> University of Hawaii, <sup>3</sup> Whitman College, <sup>4</sup> OceanLab, University of Aberdeen, <sup>5</sup> National Institute of Water & Atmospheric Research, <sup>6</sup> University of Aberdeen, <sup>7</sup> National Oceanography Centre

The hadal zone, comprised primarily of deep ocean trenches and troughs, represents the deepest marine habitat on Earth (6000–11,000 m), accounting for the deepest 45 % of the global ocean. The geomorphological heterogeneity of these habitats has provided settings where environmental conditions (hydrostatic pressure and food supply) differ greatly from the majority of the deep sea and resulted in high levels of endemism at hadal depths. In 2012, a new initiative, the Hadal Ecosystems Studies (HADES) Program was launched to determine the composition and distribution of hadal species, the role of hadal pressures, food supply and depth/topography on community structure within deep-ocean trenches in comparison to neighboring abyssal plains using the hybrid remotely operated vehicle “Nereus” in conjunction with full-ocean depth imaging landers (Hadal-Lander). Beginning studies along the Kermadec Trench in 2013, PIs from seven institutions will examine megafaunal community structure and the relationship between POC and benthic bacterial biomass as a function of depth and location by systematic high-definition imaging and sediment/faunal sampling transects from abyssal to full trench depths. Population genomic approaches will provide levels of genetic divergence and evolutionarily independent lineages to assess the role of depth and topography in promoting the formation of species. Physiological constraints will be investigated by examining in-situ respiration of selected fauna and tissue concentrations of such protein stabilizers as trimethylamine oxide (TMAO), and the structural adaptations of macromolecules. The HADES Program will establish a comparative framework for investigating hadal and abyssal community structure throughout the global network of trench and hadal environments.





International

# 13<sup>th</sup> Deep-Sea Biology Symposium

Wellington, New Zealand 3 – 7 December 2012

**P112**

## **NEMATODE COMMUNITY STRUCTURE IN A HYDROTHERMAL VENTING FIELD IN MYOJIN KNOLL, A SEAMOUNT ON THE IZU-OGASAWARA ARC, THE WESTERN NORTH PACIFIC OCEAN**

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In contrast to the specific large benthic animals at chemosynthetic environments such as hydrothermal vents, meiofaunal communities in such habitats have been reported to show high taxonomic similarities with those in the adjacent “normal” environments. However, meiofauna have only recently been included in studies of those environments, and detailed information for them is still rare, especially in the western North Pacific Ocean, although there are many seamounts that have active vents in those calderas. We investigated nematode community structure at family and genus levels in sediments from a hydrothermal vent field in Myojin Knoll (32°06' N, 139°53' E, depth 1300 m), one of the seamounts on the Izu-Ogasawara Arc, Japan, for the first time. ANOSIM showed that the composition of nematodes in the hydrothermal field was not different significantly from that in any non-hydrothermal field in or outside of the caldera. On the other hands, when the data from the knoll were compared with those that have been reported from the other deep-sea chemosynthetic environments in the different regions (e.g. North Fiji Basin, EPR, MAR), significant differences were detected in nematode composition among the regions. Our data from the western North Pacific Ocean also suggested the absence of pelagic transport systems and local adaptations for meiofauna at hydrothermal vents.

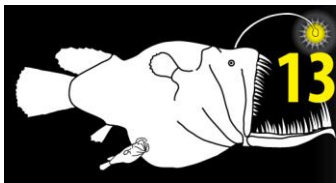
**P113**

## **NEMATODE ASSEMBLAGE FROM DEEP-SEA POLYMETALLIC NODULE AREA OF THE CENTRAL INDIAN OCEAN BASIN**

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The Central Indian Ocean Basin (CIOB) is known as a important area for potential deep-sea polymetallic nodule mining. Studies of biodiversity are a major priority before the commercial mining will start. The present study is aimed to investigate the nematode assemblages inhabiting polymetallic nodule fields in CIOB. Samples were collected during the 39th cruise of RV *Akademic Boris Petrov* (2009) from the nodule poor and nodules rich areas using a box corer. The results of preliminary analysis (8 corers from 2 stations) reported mean density of nematode 7.6 inds/10 cm<sup>2</sup>. The nematodes were represented by 93 genera belonging to 28 families. Among families, Xyalidae (23 %), Chromadoridae (20 %), and Desmodoridae (10 %) were dominant. The most abundant genera were *Acantholaimus* (8 %), *Desmoscolex* (4 %), and *Daptonema* (3 %). The most species-rich genus was *Acantholaimus*. The dominant morphotype was *Thalassomonhystera* sp. 2 (4 %), followed by *Acantholaimus* sp. 4 (3 %) and *Acantholaimus* sp. 3 (3 %). The mean values of diversity indices were: H' = 4.27, J' = 0.89 d = 6.43 and ES(51) = 23.65. Several species belonging to the genera *Acantholaimus*, *Theristus*, *Caligocanna*, and *Capsula* display a broad distribution in the abyssal zone. They have been described previously from other regions and even other oceans. Present data show a big similarity with other abyssal areas in their composition of dominant genera and families and in values of diversity indices, however the nematode density was significantly lower ( $p < 0.05$ ).



International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

**P114**

**THEY ARE EVERYWHERE! ON WORLDWIDE DISTRIBUTION OF DEEP-SEA COPEPOD AND NEMATODE SPECIES**

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Meiofaunal organisms are considered to be primarily bound to the sediment and to show limited mobility, since all stages of most species dwell in the sediment and are poor swimmers. Land masses and undersea mountain ranges are therefore considered to prevent meiofauna species from dispersing. Deep-sea meiobenthic species are not able to use shallow-water facilities for their dispersal, e.g. strong near-shore currents, transportation by the way of adhering to birds or floating materials, dispersal using of ballast water from commercial vessels, etc. The analysis of geographical distributions of 793 adult females of the genus *Mesocletodes* Sars, 1909 (Copepoda, Harpacticoida, Argastidae) belonging to 61 species throughout twelve regions at abyssal depths indicated that most species are cosmopolitan. Among ca. 700 nematode species known from the deep-sea, about 60 ones (most of them belong to the genera *Acantholaimus*, *Desmoscolex*, *Quadracoma*, *Tricoma* and *Trophomera*) also show a cosmopolitan distribution. Therefore, neither the topography of the sea bottom nor long distances seem to prevent species from dispersing. It is likely that many species are cosmopolitan, and their natural habitats will be extended as new deep-sea areas of the world ocean will be studied.

**P115**

**MACROFAUNAL SPECIES DIVERSITY ALONG THE WESTERN ANTARCTIC PENINSULA DEEP CONTINENTAL SHELF AND THE IMPLICATIONS OF CLIMATE CHANGE**

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The Western Antarctic Peninsula is experiencing some of the fastest rates of regional warming in the world, resulting in significant decrease in winter sea ice extent and duration. Observed changes in sea ice may have unexpected effects on benthic ecosystems due to interactions between sea ice, primary production, and pelagic-benthic coupling. Within the framework of FOODBANCS2 program, we conducted a study of responses of Antarctic soft-bottom macrofaunal (animals < 300 µm) communities to sea-ice decrease. We sampled at five stations (AA, B, E, F, and G) spanning a latitudinal sea ice gradient from Smith Island (63° S) to Marguerite Bay (68° S) on the Antarctic Peninsula continental shelf. Average annual sea-ice duration varies from around 1 month at the northernmost end of the transect (Stn AA) to > 7 months at the southernmost part (Stn G). We found that macrofaunal community structure and diversity changed along this sea-ice gradient. The highest species richness was found on the northernmost end of the transect, station AA, and the lowest surprisingly on the station B. Station AA had a distinct community structure, species richness and evenness, possibly due to the effects of a different water mass, coming from the Weddell Sea. Strong latitudinal trend was observed in community structure, with dominance increasing southwards driven by Spionid polychaetes. Spionid dominance was driven by a single, recently described species, *Aurospio foodbancsia*, with its relative abundance highly correlated with the duration of sea-ice.





P116

**BIODIVERSITY, CONNECTIVITY AND ECOSYSTEM FUNCTION IN ORGANIC-RICH WHALEBONE AND WOOD-FALL HABITATS IN THE DEEP SEA**

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Organic-rich habitat islands support specialized communities throughout natural ecosystems and often play fundamental roles in maintaining alpha and beta diversity, thus facilitating adaptive radiation and evolutionary novelty. Whale-bone and wood falls occur widely in the deep-sea and contribute fundamentally to biodiversity and evolutionary novelty. Nonetheless, large-scale patterns of biodiversity, connectivity and ecosystem function in these organic-rich metacommunity systems remain essentially unexplored. We describe a novel comparative experimental approach, using bottom landers carrying bone and wood, to evaluate bathymetric, regional and inter-basin variations in biodiversity and connectivity, as well as interactions between biodiversity and ecosystem function, in whale-bone and wood-fall habitats at the deep-sea floor. Our experiments will test fundamental hypotheses concerning biodiversity and biogeography of resource-rich habitats in energy limited deep-sea environments, and explore the utility of whale-bone and wood falls as model experimental systems to address patterns of connectivity and decomposer function in the deep sea. Six replicate bone/wood landers will be deployed at two depths (1500 and 3000 m), 250–500 km apart, in the NE Pacific and SW Atlantic basins, with quantitative recovery of bone/wood macrofaunal assemblages 15 month later. Through molecular-genetic, taxonomic, and functional studies of macrofaunal and microbial assemblages on bone/wood substrates, we will address key hypotheses concerning connectivity, adaptive radiation, and interactions between biodiversity and ecosystem function in the NE Pacific and SW Atlantic.

P117

**DEEP-SEA URCHIN (*STRONGYLOCENTROTUS FRAGILIS*) PHYSIOLOGY AND BEHAVIOR ARE IMPAIRED BY OCEAN ACIDIFICATION AND HYPOXIA, ULTIMATELY REDUCING REPRODUCTIVE CAPACITY**

Taylor J, Lovera C, Whaling PJ, Buck KR, Barry JP  
Monterey Bay Aquarium Research Institute

Anthropogenic CO<sub>2</sub> is now reaching depths over 1000 m in the Eastern Pacific, overlapping with the Oxygen Minimum Zone (OMZ). Deep-sea animals living in this energy-limited environment have evolved in relatively stable biochemical conditions and are subject to minimal variation in water chemistry compared to shallow marine ecosystems. The deep sea urchin *Strongylocentrotus fragilis* lives at depths of 200–1200 m, at the brink of the saturation horizon for aragonite and calcite in Monterey Bay, CA, USA. We have investigated the physiology (acid-base balance, metabolism, growth, and reproductive indices) and behavior (feeding and locomotion) of *S. fragilis* on exposure to four levels of pH (7.9, 7.6, 7.2, and 6.6) and two levels of O<sub>2</sub> (surface O<sub>2</sub> of 220 ± 10 μM and approximate OMZ O<sub>2</sub> of 20 ± 5 μM O<sub>2</sub>) at 5° C, using a gas-controlled aquarium system, for up to four months. Results show *S. fragilis* has no significant acid-base compensatory ability at the levels of acidification tested. Feeding frequency and quantity were significantly reduced within three days of exposure to pH 6.6, for the duration of the experiment; feeding quantity was significantly reduced after two weeks' exposure to pH 7.2, but recovered after three months' exposure. Expectedly, high O<sub>2</sub> levels led to elevated feeding frequency and quantity. Feeding, high pH and high O<sub>2</sub> were all significantly correlated with high reproductive indices. Our results suggest *S. fragilis* is vulnerable to levels of ocean acidification and hypoxia expected during this century.



P118

**COMPARATIVE POPULATION GENETICS OF TWO HYDROTHERMAL-VENT-ENDEMIC SPECIES, *CHOROCARIS* SPP. AND *OLGASOLARIS TOLLMANNI* FROM SOUTHWEST PACIFIC BACK-ARC BASINS**

Thaler A<sup>1</sup>, Plouviez S<sup>1</sup>, Zelnio K<sup>1</sup>, Jacobson A<sup>1</sup>, Jollivet D<sup>2</sup>, Carlsson J<sup>3</sup>, Schultz T<sup>1</sup>, Van Dover C<sup>1</sup>

<sup>1</sup> Duke University Marine Lab, North Carolina, USA <sup>2</sup> Station Biologique de Roscoff, Roscoff, France <sup>3</sup> University College Cork, North Mall University College Cork, Ireland

Deep-sea hydrothermal vents are dynamic ecosystems that are spatially and temporally unstable. In the southwest Pacific, vents are distributed non-linearly throughout back-arc basin spreading centers. Among hydrothermal-vent-endemic organisms, population genetic studies have focused primarily on biomass-dominant species that host chemoautotrophic endosymbionts. This study examines the population structure and connectivity of two presumably vent-endemic species that do not host chemoautotrophic endosymbionts, namely the shrimp *Chorocaris* sp. 2 and the limpet *Olgasolaris tollmanni*. Samples were collected at multiple spatial scales, from mounds separated by a few hundred meters to oceanic basins separated by several thousand kilometres. We used a partial cytochrome-C-oxidase subunit I gene (COI) to infer population structure for both species and a set of six microsatellite loci to examine fine-scale population structure in *Chorocaris* sp. 2. Based on COI, a low-abundance cryptic species of *Chorocaris* was identified from a single site in Manus Basin (*Chorocaris* sp. 1). No evidence for genetic differentiation was detected within basins at any spatial scale for either *Chorocaris* sp. 2 or *O. tollmanni*, but a strong signal of isolation was detected for the *Chorocaris* sp. 2 between Manus and North Fiji Basin. In contrast, there was no evidence for genetic differentiation among *O. tollmanni* between samples from Manus and North Fiji, suggesting that this species is panmictic throughout the south-western Pacific.

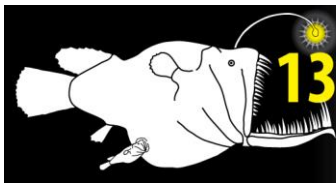
P119

**SPECIATION OF *PROVANNA* SPP. (GASTROPODA: PROVANNIDAE) IN THE DEEP-SEA CHEMOSYNTHETIC COMMUNITY AROUND JAPAN**

Tomomi O

Graduate School of Marine Science and Technology, Tokyo University of Marine Science and Technology

The gastropod genus *Provanna*, inhabiting deep-sea chemosynthetic environments, is abundant and widely distributed around the world except the Indian Ocean. The genus is highly diversified in Japanese waters, where the species colonize a variety of ecological niches (e.g. depth, substrate). They are therefore an ideal model for studying the evolutionary history of deep-sea chemosynthetic communities. Here we applied molecular genetic and morphological analyses to clarify species diversity and speciation processes in *Provanna* gastropods inhabiting the chemosynthetic community in deep-sea methane seep and hydrothermal vent fields around Japan. A total of 220 specimens were collected from methane seep sites in Sagami Bay and along the Ryukyu Trench and at hydrothermal vent sites in the Okinawa Trough. Morphological variation was assessed using morphometrical analyses of shell shapes and observations of radulae. These analyses allowed the identification of three groups. At least three specimens from each morphological group were then used for phylogenetic analysis using partial sequences of three genes (COI, 16S, 28S). Molecular phylogenetic tree was consistent with morphological grouping, but one of the three morphological groups was divided into three sublineages. Population genetics of these lineages was further analyzed using partial COI sequences from 220 specimens. All lineages have a very high genetic diversity and the lineage inhabiting the Okinawa Trough showed a complicated genetic structure. Population genetic and morphological studies with all *Provanna* species from the Western and Eastern Pacific will provide some clues to evolutionary history of the genus *Provanna* at the deep-sea chemosynthetic communities.



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**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

**P120**

**POTENTIAL EFFECTS OF OCEAN ACIDIFICATION ON HABITAT FORMING DEEP-SEA CORALS IN THE NEW ZEALAND REGION**

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<sup>1</sup> NIWA, <sup>2</sup> VUW Victoria University of Wellington

Research has been carried out to compare the carbonate mineralogy of habitat-forming deep-sea corals against water carbonate chemistry to determine which species and areas are most at risk from ocean acidification. Five common branching stony coral species (order Scleractinia) — *Goniocorella dumosa*, *Solenosmilia variabilis*, *Enallopsammia rostrata*, *Madrepora oculata* and endemic *Oculina virgosa* — have been confirmed as having aragonite skeletons. The gorgonian coral genera (order Alcyonacea) *Keratoisis* spp., *Lepidisis* spp., *Paragorgia* spp. and *Primnoa* sp., have high-magnesium (Mg) calcite in their skeletons. The spatial and depth distribution of these species have been compared with the aragonite and calcite saturation horizons (ASH and CSH), respectively. The current ASH varies between 1000 and 1300 m, while the peak in abundance of scleractinian branching forms are around 800–1000 m, with < 5 % found below 1400 m. This supports the current theory that the global distribution of habitat-forming scleractinians is controlled by the ASH. The selected Alcyonacea groups display a peak in abundance around 800–1200 m, with < 2 % below 1400 m, well above the CSH at 2800–3100 m. This may be related to the high Mg content of these calcite organisms. Carbon dioxide is taken up in the cold surface waters of the Southern Ocean and transported into the intermediate waters at 500–1500 m depth. Ocean acidification is suggested to cause the shoaling of the ASH over the next century to as shallow as 500 m in the New Zealand region. This could result in the loss of 50 % of the habitat forming scleractinians. It is likely that the high-Mg calcite gorgonian corals will also be significantly affected by this reduction in carbonate saturation states.

**P121**

**OBSERVER AND RESEARCH TRAWLS DISCOVER NEW SPECIES IN THE NEW ZEALAND REGION**

Tracey D<sup>1</sup>, Mills S<sup>1</sup>, Kelly M<sup>1</sup>, Anderson O<sup>1</sup>, Neill K<sup>1</sup>, Cairns S<sup>2</sup>, O'Hara T<sup>3</sup>

<sup>1</sup> National Institute of Water and Atmospheric Research (NIWA), Private Bag 14901, Kilbirnie, Wellington, New Zealand, <sup>2</sup> Department of Invertebrate Zoology, Smithsonian Institution, P. O. Box 37012, Washington, D. C., USA, <sup>3</sup> Museum Victoria, GPO Box 666E, Melbourne, VIC., Australia

In order to address some of the concerns about the effects of fishing, a requirement of the New Zealand Ministry for Primary Industries is the retention of unidentified bycatch benthic invertebrates unable to be identified from research trawl surveys and commercial fishing vessels. Some benthic invertebrates are able to be identified by scientist at sea or by government observers on fishing vessels, but many require expert identification. In 2011, NIWA was funded to commence a programme of taxonomic identification of these unidentifiable organisms. In the first year of this project, 620 specimen lots were authoritatively identified, 267 species from 54 surveys retained from research trawls and 73 species from 56 observer trips on commercial vessels. The specimens represent six key Phyla and several fauna identified represent undescribed and new species. Some specimens extend the known distribution of the organisms. Examples of important finds include a new species of the siliceous sponge genus *Ancorina*, which provides the southernmost world record for the genus on the Campbell Plateau, and the rarely seen, spectacularly large cidaroid sea urchin *Stereocidaris sceptriferoides*. A new undescribed tam o'shanter sea urchin in the genus *Sperosoma* was also discovered along with a species from a seastar genus in the family Goniasteridae that is new to science. A new brittlestar genus and species were also discovered in the families Ophiomyxidae and Ophiacanthidae. Only 10 primnoid sea-fan gorgonian coral species were previously known from the New Zealand region. A revision of the group by Cairns (2012), describing 18 primnoid species, 13 of which are new, comprise samples taken as by-catch on research trawl and commercial vessels. The results contribute significantly to our understanding of these invertebrate groups, expand our New Zealand's biodiversity science data, and fill knowledge gaps.



**P122**

**DEEP WATER ATLANTIC ZOOPLANKTON PASSAGE TO THE ARCTIC - STEP BY STEP TRACK.**

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Institute of Oceanology Polish Academy of Sciences (IOPAS)

Fram Strait is the only deep water passage to the Arctic Ocean. The exchanges between the North Atlantic and the Arctic Ocean are extremely important for water mass modifications and circulation in the World Ocean. So far investigations of the Atlantic Water inflow into the Arctic Ocean have been the focus of many research projects, but the northward transport of biological matter, such as zooplankton, is still unknown despite its great ecological importance. Atlantic-associated fauna expatriates north-polar regions and overlaps with Arctic-origin plankton communities. The range of such northward advection could easily be reflected by the analyses of zooplankton species composition and distribution. The Kongsfjord-Hausgarten transect was set as a particularly suitable for studies of climate impact on Arctic community structures and food webs. Here we present new results of zooplankton species composition reflecting the route of Atlantic water inflow along the northward passage (76.5° N – 79° N) through the strait followed in the step by step manner. Data was collected on transects spreading across the Fram Strait passage, in the core, east and west branches of the Atlantic inflow in 2012 summer season.

**P123**

**OXYGEN-MINIMUM ZONE INFLUENCES CARBON FLOWS THROUGH DEEP-SEA SEDIMENT ECOSYSTEMS: A MODELLING STUDY**

Hunter WR<sup>1,3</sup>, **Van Oevelen D**<sup>2</sup>, Witte U<sup>1</sup>

<sup>1</sup> University of Aberdeen, <sup>2</sup> Royal Netherlands Institute for Sea Research (NIOZ), <sup>3</sup> Universitat Wien

The Arabian Sea OMZ (oxygen minimum zone) impinges upon the Indian continental margins at bathyal depths (150–1500 m), producing depth-dependent changes in oxygen availability that influence the structure of benthic microbial and faunal assemblages. This provides a great setting to study how changes in oxygen availability, organic matter (OM) availability and benthic ecosystem zonation affect carbon and nitrogen cycling in deep-sea sediments. Microbial and faunal processing of OM were investigated using in situ stable isotope pulse-chase experiments. 650 mg C m<sup>-2</sup> doses of <sup>13</sup>C:<sup>15</sup>N-labelled *Thalassiosira weissflogii* were deposited onto the sediment at four stations across the OMZ (540 – 1100 m; [O<sub>2</sub>] = 0.35 – 15 μM). <sup>13</sup>C and <sup>15</sup>N were traced into bacteria, foraminifera and metazoans. Linear inverse modelling (LIM) techniques provide a powerful tool to model energy flows through complex food-webs and we use biomass, and isotope tracer data to constrain models of carbon flow through food-webs in the OMZ-impacted sediments. We demonstrate how oxygen conditions affect food-web complexity, and the relative contributions of the bacteria, foraminifera and metazoa to benthic respiration. In the OMZ core, food-webs exhibited low complexity, dominated by bacteria and foraminifera only. Across the lower boundary of the OMZ, there was clear resource partitioning between bacteria and fauna, with bacteria primarily utilising refractory OM sources whilst the fauna utilised the labile algal tracer. The high taxonomic resolution of the faunal data and inclusion of megafaunal biomass data enabled construction of the first detailed food-webs quantifying carbon (and energy) flows across an OMZ-impacted continental margin.



**P124**

**COPEPODS OF THE SOUTHERN OCEAN: DO CRYPTIC SPECIES EXIST?**

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<sup>1</sup> P. P. Shirshov Institute of Oceanology of Russian Academy of Sciences, <sup>2</sup> White Sea Biological Station, Department of Biology Lomonosov Moscow State University

Most species living in the Southern Ocean are believed to occur both in the Subantarctic and Antarctic zones. Both biogeographic zones are divided by the Polar Frontal Zone (PFZ), where horizontal gradients of oceanographic characteristics are very high. The PFZ may act as a barrier, isolating the zooplankton populations. Ultimately, the species living on both sides of the PFZ may even be cryptic. To test this hypothesis, we sampled eight dominant copepod species making up about 80 % of the total mesoplankton biomass: *Calanus simillimus*, *C. propinquus*, *Calanoides acutus*, *Rhincalanus gigas*, *Ctenocalanus citer*, *Clausocalanus laticeps*, *Metridia lucens*, and *Scolecitricella minor*. Material was sampled during Russian cruises of 2010-2011 along international transects SR-1 (across the Drake Passage) and SR-2 (between Africa and Antarctica). The Folmer fragment of the mtCO1 was analyzed for all species; for *M. lucens* we additionally amplified the nuclear fragment ITS1-5.8SrDNA-ITS2. Molecular analysis revealed that 7 of the analyzed species have no genetic differences on both sides of the PFZ. The cosmopolitan copepod *M. lucens*, which is morphologically variable, proved to be a group of at least two cryptic species divided by the PFZ. Further analysis of the locus ITS1-5.8SrDNA-ITS2 indicated that both cryptic species do not breed even if they occur together in the PFZ. The studies were supported by the Ministry of Education and Science of the Russian Federation (contracts No 11.G34.31.0008 and No 16.512.11.2133)

**P125**

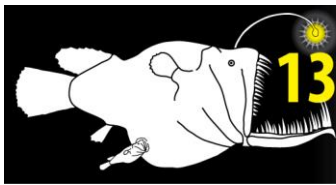
**CAN INTRA-POPULATION VARIATION IN TROPHIC ECOLOGY OF ROCKALL TROUGH DEEP-SEA FISHES BE EXPLAINED BY BODY SIZE?**

**Wigham B<sup>1</sup>**, Reid W<sup>1</sup>, Sweeting C<sup>1</sup>, Neat F<sup>2</sup>

<sup>1</sup> Newcastle University, <sup>2</sup> Marine Scotland- Science

The role of body size within a community and how this affects trophic structure has been a long-term theme in ecology and is recognised as pertinent in successful fisheries management. Intra-population increases in TP with body size are ubiquitous in shallow water fish but an understanding of size-based relationships are currently lacking in deep-sea fish. Stable carbon and nitrogen isotopes are utilised to elucidate trophodynamics, providing information on energy source (carbon) and trophic position (TP) (nitrogen). Rockall Trough (Northeast Atlantic) demersal fishes were collected along the continental slope and Rosemary Bank 1000 m contour. Stable-isotope analysis (SIA) was undertaken to examine the role of body size in intra-population trophodynamics in 11 species.  $\delta^{15}\text{N}$  increased with body size in all species, which indicated intra-population variability in TP but not all trends were linear. In some species  $\delta^{15}\text{N}$  stopped increasing at a certain body size while in others it continued to increase over the size range.  $\delta^{13}\text{C}$  increased in some species and those that increased in  $\delta^{13}\text{C}$  switched from pelagic to benthic food sources or increased in TP within the benthic-pelagic food web. Gape limitation, prey availability and competition are potential causes for the variability in body-size stable isotope trends, reflecting differences in foraging behaviour and diet among species and at different life history stages within species. SIA presents evidence that intra-population trophic roles are strongly size dependant and vary between species of deep-sea fish. The information becomes important when trying to understand community dynamics as size-spectra and predator-prey interactions change as a result of anthropogenic and climatic influences.





International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

**P126**

**THE SUCCESSFUL SCALE WORMS (APHRODITIFORMIA, POLYCHAETA) — HOW CAN THEY BE EVERYWHERE (IN THE SEA)?**

**Wiklund H<sup>1</sup>**, Neal L<sup>1</sup>, Kemp K<sup>2</sup>, Glover A<sup>1</sup>

<sup>1</sup> The Natural History Museum, Dept of Zoology, Cromwell Rd, London SW7 5BD, UK, <sup>2</sup> Zoological Society of London, Institute of Zoology, Regent's Park, London NW1 4RY, UK

The scale worm group, recognized for their dorsal elytra (scales), consists of approximately 1000 species and thus comprise a large portion of the polychaetes. The largest scale worm family, Polynoidae with around 750 species, are represented almost everywhere in the sea, occurring from shallow intertidal waters down to abyssal depths, and on soft bottoms as well as hard substrates. Furthermore, some taxa seem to have adapted to specialize on ephemeral habitats such as whale-falls and hydrothermal vents. Using molecular data from both shallow-water and deep-sea species collected in a wide range of habitats and locations, we investigate phylogenetic relationships within the scale worm group with special interest in patterns of habitat adaptations and depth distributions.

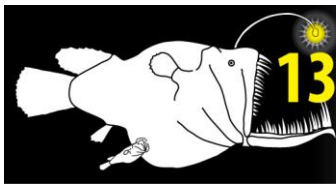
**P127**

**A UNIQUE ISOPOD CRUSTACEAN ASSEMBLAGE ASSOCIATED WITH WOOD IN THE DEEP-SEA BENTHIC ENVIRONMENT**

**Wilson GDF<sup>1</sup>**, Voight JR<sup>2</sup>

<sup>1</sup> Australian Museum, 6 College St., Sydney NSW 2010, <sup>2</sup> Field Museum of Natural History, 400 S. Lake Shore Dr, Chicago, IL, USA

Although benthic isopod crustaceans are well known from many abyssal and bathyal sedimentary habitats, data from hard substrata are scarce. Voight and colleagues made emplacements of wood substrates in the NE Pacific in the Gorda-Juan de Fuca Ridge and Cascadia Basin regions. In addition to molluscs and echinoderms, after two years, these assemblages contained numerous macrofaunal animals, including unique isopod taxa. Several wild wood-fall collections were also made in the Gulf of Mexico (GoM) and Oregon Margin. Two taxa share relationships with Antarctic genera, suggesting an abyssal biogeographic connection with the Southern Hemisphere. At least one species, *Limnoria* sp., is known to be associated with wood. Because most data came from wood emplacements on reducing sediments near hydrothermal sites, they are compared with a background sedimentary isopod assemblage from an earlier study conducted in an Eastern Tropical Pacific hydrothermal-vent field (ETP) by J.F. Grassle and colleagues. Although ETP sedimentary isopods showed a lower diversity than other abyssal Pacific locations, they were substantially more diverse than the depauperate wood assemblages. Additionally, the wood assemblages contained taxa that do not appear in sedimentary samples. Although the diversity of these wood assemblages is low, the taxa were unique from region to region, so that the global diversity for this fauna could be much greater than indicated by the observed low species richness at each site.



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# 13<sup>th</sup> Deep-Sea Biology Symposium

Wellington, New Zealand 3 – 7 December 2012

P128

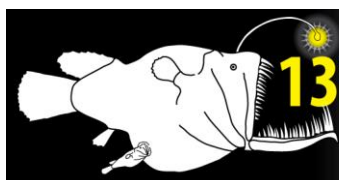
## DISTRIBUTION AND POPULATION GENETIC STRUCTURE OF VENT SHRIMPS IN THE OKINAWA TROUGH

Yahagi T<sup>1</sup>, Watanabe H<sup>2</sup>, Ishibashi JI<sup>3</sup>, Kojima S<sup>1</sup>

<sup>1</sup> Atmosphere and Ocean Research Institute, The University of Tokyo, <sup>2</sup> Japan Agency for Marine-Earth Science and Technology, <sup>3</sup> Department of Earth and Planetary Sciences, Kyushu University

Understanding connectivity among deep-sea chemosynthetic communities will help clarify how they form and develop. However, comprehensive research on connectivity of such communities are limited in the NW Pacific. Alvinocaridid shrimps are dominant macrofaunal invertebrates in vent fields in this sea area. Our research aimed to identify the factors determining the distribution and population connectivity of alvinocaridids in the Okinawa Trough, one of the western Pacific back-arc basins. Distribution and population connectivity of four alvinocaridid species collected using ROV HyperDolphin were examined by taxonomic and molecular approaches. Their geographical distributions differ — *Alvinocaris longirostris* and *Shinkaicaris leurokolos* are patchily distributed in the Okinawa Trough. In contrast, *Alvinocaris* sp. and *A. dissimilis* are distributed in single vent fields. *Alvinocaris* sp. is also distributed in the Izu-Bonin Arc, 1000 km from the Okinawa Trough. For *A. longirostris*, *Alvinocaris* sp. and *Shinkaicaris leurokolos*, population-genetic analyses based on nucleotide sequences of the partial mitochondrial COI gene showed no significant genetic deviation among vent fields, suggesting high dispersal ability in these species. The factors determining distribution of vent shrimps in the Okinawa Trough seem to be environmental, e.g. geological setting of hydrothermal-vent fields and chemical composition of vent fluids rather than dispersal ability. *Alvinocaris* sp., with the widest distribution, may have important implications for elucidating the principal factor determining the distribution of vent shrimps.

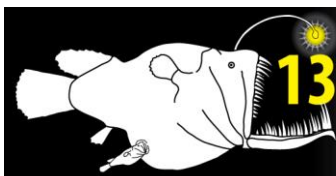




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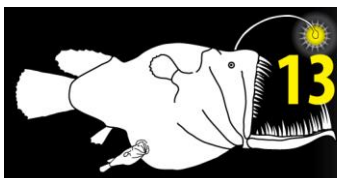
**List of Participants (as at 23<sup>rd</sup> November 2012)**

<b>Last Name</b>	<b>First Name</b>	<b>Organization</b>	<b>Country</b>
Alei	Freddie	Duke University Marine Lab	UNITED STATES
Amaro	Teresa	NIVA	NORWAY
Ardila	Nestor	Universidad de los Andes/Universidad de la Salle	COLOMBIA
Atkinson	Lara	South African Environmental Observation Network	SOUTH AFRICA
Baco-Taylor	Amy	Florida State University	USA
Baillon	Sandrine	Ocean Sciences Centre - Memorial University	CANADA
Baird	Susan Jane	National Institute of Water & Atmospheric Research	NEW ZEALAND
Baker	Maria	University of Southampton	UK
Bamber	Roger	ARTOO Marine Biology Consultants	UNITED KINGDOM
Barry	James	MBARI	USA
Basher	Zeenatul	University of Auckland	NEW ZEALAND
Beaumont	Jenny	NIWA	NZ
Becheler	Ronan	Ifremer	FRANCE
Beedessee	Girish	Mauritius Oceanography Institute	MAURITIUS
Bernardino	Angelo	Universidade Federal Do Espirito Santo	BRAZIL
Bolstad	Kat	Auckland University of Technology	NEW ZEALAND
Bors	Eleanor	Woods Hole Oceanographic Institution	USA
Boschen	Rachel	University of Southampton	UNITED KINGDOM
Bowden	David	NIWA	NEW ZEALAND
Bradford-Grieve	Janet	National Institute of Water and Atmospheric Research	NEW ZEALAND
Braid	Heather	Auckland University of Technology	NEW ZEALAND
Brandt	Angelika	Zoological Museum	GERMANY
Bromfield	Kate	Environmental Protection Authority	NEW ZEALAND
Brooke	Sandra	Oregon Institute of Marine Biology	USA
Buck	Kurt	MBARI	USA
Buhl-Mortensen	Lene	Institute of Marine Research	NORWAY
Cambon-Bonavita	Marie-Anne	Ifremer	FRANCE
Catarino	Diana	IMAR, DOP - University of the Azores	PORTUGAL
Chivers	Adam	Scottish Association for Marine Science	SCOTLAND
Choy	C. Anela	University of Hawaii, Dept. of Oceanography	USA
Christianson	Lynne	MBARI	USA
Clark	Malcolm	NIWA	NEW ZEALAND
Colaço	Ana	Larsys- Center of IMAR from the University of Azores- Department of Oceanography	PORTUGAL
Connell	Amelia	Pew Environment Group	NEW ZEALAND
Cook	April	Virginia Institute of Marine Science	USA
Cook	Adam	International Seabed Authority	JAMAICA
Cordes	Erik	Temple University	US
Crozier	Paul	WWF New Zealand	NEW ZEALAND
Cunha	Marina R.	Universidade de Aveiro - CESAM	PORTUGAL



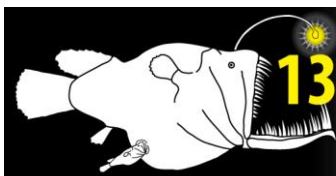
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**13<sup>th</sup> Deep-Sea Biology Symposium**  
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Currie	Bronwen	Ministry of Fisheries and marine Resources	NAMIBIA
Cuvelier	Daphne	Ifremer, Centre de Brest, Department of physical resources and deep-sea ecosystem	FRANCE
Dahlgren	Thomas	Uni Research	SWEDEN
Davey	Niki	NIWA	NEW ZEALAND
de Busserolles	Fanny	University of Western Australia	AUSTRALIA
Demopoulos	Amanda	U.S. Geological Survey	USA
Drazen	Jeffrey	University of Hawaii	UNITED STATES
		National Oceanography Centre, Southampton	UK
Duffy	Grant	NIWA	NEW ZEALAND
Dunn	Matthew	CSIRO Marine and Atmospheric Research	AUSTRALIA
Dunstan	Piers	University of Southampton	UNITED KINGDOM
Durden	Jennifer	JAMSTEC	JAPAN
Duros	Pauline	Florida State University	USA
Easton	Erin	University of Hamburg	GERMANY
Elsner	Nikolaus	Auckland University of Technology	NEW ZEALAND
Evans	Aaron		RUSSIAN FEDERATION
Fadeeva	Nataliya	Far Eastern Federal University	USA
Fisher	Charles	Penn State University	AUSTRALIA
Flynn	Adrian	Uni. Qld, CSIRO	CANADA
Forget	Nathalie	University of Victoria	JAPAN
Fujiwara	Yoshihiro	JAMSTEC	CANADA
Gale	Katie	Memorial University of Newfoundland	UNITED KINGDOM
Gates	Andrew	National Oceanography Centre	
		P.P. Shirshov Institute of Oceanology, Russian Academy of Sciences	RUSSIA
Gebruk	Andrey	Senckenberg am Meer, DZMB	GERMANY
George	Kai Horst	Whitman College	USA
Gerringer	Mackenzie	NEPTUNE Canada	CANADA
Gervais	Françoise	The Natural History Museum	UNITED KINGDOM
Glover	Adrian	NIWA	NEW ZEALAND
Gordon	Dennis	Australian Museum	AUSTRALIA
Graham	Ken	Senckenberg am Meer	GERMANY
Grimm	Maria	Japan Agency for Marine-Earth Science and Technology	JAPAN
Grossmann	Mary	Scripps Institution of Oceanography	USA
Grupe	Benjamin	University of Southampton	U.K.
Gunton	Laetitia	MBARI	USA
Haddock	Steven	Ministry for Primary Industries	NEW ZEALAND
Helson	Jeremy	MIT/WHOI	UNITED STATES
Herrera	Santiago	WHOI	USA
Heyl	Taylor	Institute for Marine and Antarctic Studies	AUSTRALIA
Hibberd	Ty	Natural History Museum	UK
Higgs	Nicholas	University of Aveiro	PORTUGAL
Hilário	Ana	University of Exeter	UK
Holland	Lyndsey	Monterey Bay Aquarium Research Institute	USA
Hoving	Henk-Jan	Plymouth University	UK
Howell	Kerry	Universidad de Chile	CHILE
Ibáñez	Christian	University of Otago	NEW ZEALAND
Ibell	Anthea	MBARI	USA
Jacobsen Stout	Nancy	University of Aberdeen	UNITED KINGDOM
Jamieson	Alan		



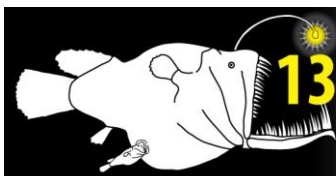
International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

Jeffreys	Rachel	University of Liverpool	UNITED KINGDOM
Johnson	Shannon	Monterey Bay Aquarium Research Institute	USA
Jones	Daniel	National Oceanography Centre	UK
Jones	Matthew	Auckland University of Technology	NEW ZEALAND
Judge	Jenna	University of California Berkeley	USA
Juniper	Kim	NEPTUNE Canada, University of Victoria	CANADA
Kaiser	Stefanie	National Institute of Water & Atmospheric Research	NEW ZEALAND
		P.P.Shirshov Institute of Oceanology	
		Russian Academy of Sciences Nakhimovsky pr.	RUSSIA
Kamenskaya	Olga		
		Korea Institute of Ocean Science & Technology (KIOST)	KOREA
Kim	Se-Joo		
		Atmosphere and Ocean Research Institute, the University of Tokyo	JAPAN
Kitahashi	Tomo		
		Japan Agency for Marine-Earth Science and Technology	JAPAN
Kitazato	Hiroshi		
Knox	Matt	University of Waikato	NEW ZEALAND
Knudby	Anders	Simon Fraser University	CANADA
Koberstein	Paul	Cascadia times	USA
Krylova	Elena	P.P.Shirshov Institute of Oceanology RAS	RUSSIA
Kuhar	Anton	The University of Western Australia	AUSTRALIA
Kupriyanova	Elena	The Australian Museum	AUSTRALIA
Lacey	Nichola	University of Aberdeen	UK
		National Oceanographic Center of Soutampton & Natural History Museum of London	UNITED KINGDOM
Laguionie-Marchais	Claire		
Laming	Sven	Université Pierre et Marie Curie	FRANCE
Leduc	Daniel	NIWA	NEW ZEALAND
Lejzerowicz	Franck	University of Geneva	SWITZERLAND
		Japan Agency for Marine-Earth Science and Technology (JAMSTEC)	JAPAN
Lindsay	Dhugal		
Lins	Lidia	Ghent University	BELGIUM
Loerz	Anne-Nina	NIWA	NEW ZEALAND
Long	Niharika	University of Otago	NEW ZEALAND
Maclsaac	Kevin	Fisheries and Oceans Canada	CANADA
Mackenzie	Melanie	Museum Victoria	AUSTRALIA
Main	Charlotte	National Oceanography Centre	USA
Maiorano	Porzia	University of Bari	ITALY
Malyutina	Marina	Institute of Marine Biology FEB RAS	RUSSIA
Matabos	Marjolaine	NEPTUNE Canada - University of Victoria	CANADA
Matsumoto	George	MBARI	JAPAN
		Institute of Biological and Environmental Sciences, Oceanlab, University of Aber	UK
Mayor	Daniel		
Mazurek	Robert	Pew Environment Group	USA
McCallum	Anna	Museum Victoria	AUSTRALIA
McClain	Craig	National Evolutionary Synthesis Center	UNITED STATES
Menot	Lenaick	Ifremer	FRANCE
Meyer	Kirstin	Oregon Institute of Marine Biology	UNITED STATES
Miller	Karen	IMAS	AUSTRALIA
Milligan	Rosanna	University of Glasgow	UK



International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
 Wellington, New Zealand 3 – 7 December 2012

Min	Won-Gi	Korea Institute of Ocean Science & Technology (KIOST)	REPUBLIC OF KOREA
Miyamoto	Norio	JAMSTEC	JAPAN
Morato	Telmo	IMAR University of the Azores	PORTUGAL
Mordukhovich	Vladimir	Far Eastern Federal University	RUSSIAN FEDERATION
Morgan	Nicole	Florida State University	UNITED STATES
Morrongiello	John	CSIRO Marine and Atmospheric Research	AUSTRALIA
Munro	Catriona	WHOI	
Nagano	Yuriko	JAMSTEC	JAPAN
Nakamura	Masako	Okinawa Institute of Science and Technology	JAPAN
Narayanaswamy	Bhavani	Scottish Association for Marine Science	UNITED KINGDOM
Nedoncelle	Karine	Sorbonne Université – Pierre et Marie Curie	FRANCE
Nodder	Scott	NIWA	NEW ZEALAND
Nomaki	Hidetaka	JAMSTEC	JAPAN
Nunes-Jorge	Amandine	Max Planck Institute for Marine Microbiology	GERMANY
Nye	Verity	University of Southampton	UK
O'Hara	Tim	Museum Victoria	AUSTRALIA
Olu	Karine	Ifremer	FRANCE
Pasulka	Alexis	Scripps Institution of Oceanography	USA
Paterson	Gordon	Natural History Museum	UK
Patrick	Mike	MERMAN Ltd	NEW ZEALAND
Pawson	Doris	Smithsonian Institution, Washington DC, USA	USA
Pilditch	Conrad	University of Waikato	NEW ZEALAND
Plouviez	Sophie	Duke University	USA
PP	Sujith	National Institute of Oceanography	INDIA
Priede	Monty	Oceanlab University of Aberdeen	UNITED KINGDOM
Probert	Keith	University of Otago	NEW ZEALAND
Ramirez-Llodra	Eva	Institut Ciències Marines, CSIC	SPAIN
Reeve	Vicky	Ministry for Primary Industries	NEW ZEALAND
Reisenbichler	Kim	MBARI	USA
Ridley	Geoff	Environmental Risk Authority	NEW ZEALAND
Riehl	Torben	University of Hamburg, Zoological Museum	GERMANY
Robert	Katleen	National Oceanography Center, Southampton	UK
Robison	Bruce	Monterey Bay Aquarium Research Institute	USA
Rodrigues	Clara	Universidade de Aveiro	PORTUGAL
Rogacheva	Antonina	P. P. Shirshov Institute of Oceanology, Russian Academy of Sciences	RUSSIA
Rosli	Norliana	University of Otago	NEW ZEALAND
Ross	Rebecca	Plymouth University	UK
Ross	Steve	Univ. of North Carolina at Wilmington	USA
Ross	Elizabeth	NOCS	UNITED KINGDOM
Rowden	Ashley	NIWA	NEW ZEALAND
Sarrazin	Jozée	Ifremer	FRANCE
Schnabel	Kareen	NIWA	NEW ZEALAND
Schnurr	Sarah	German Centre for Marine Biodiversity Research (DZMB), Senckenberg Research Inst	GERMANY



International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
 Wellington, New Zealand 3 – 7 December 2012

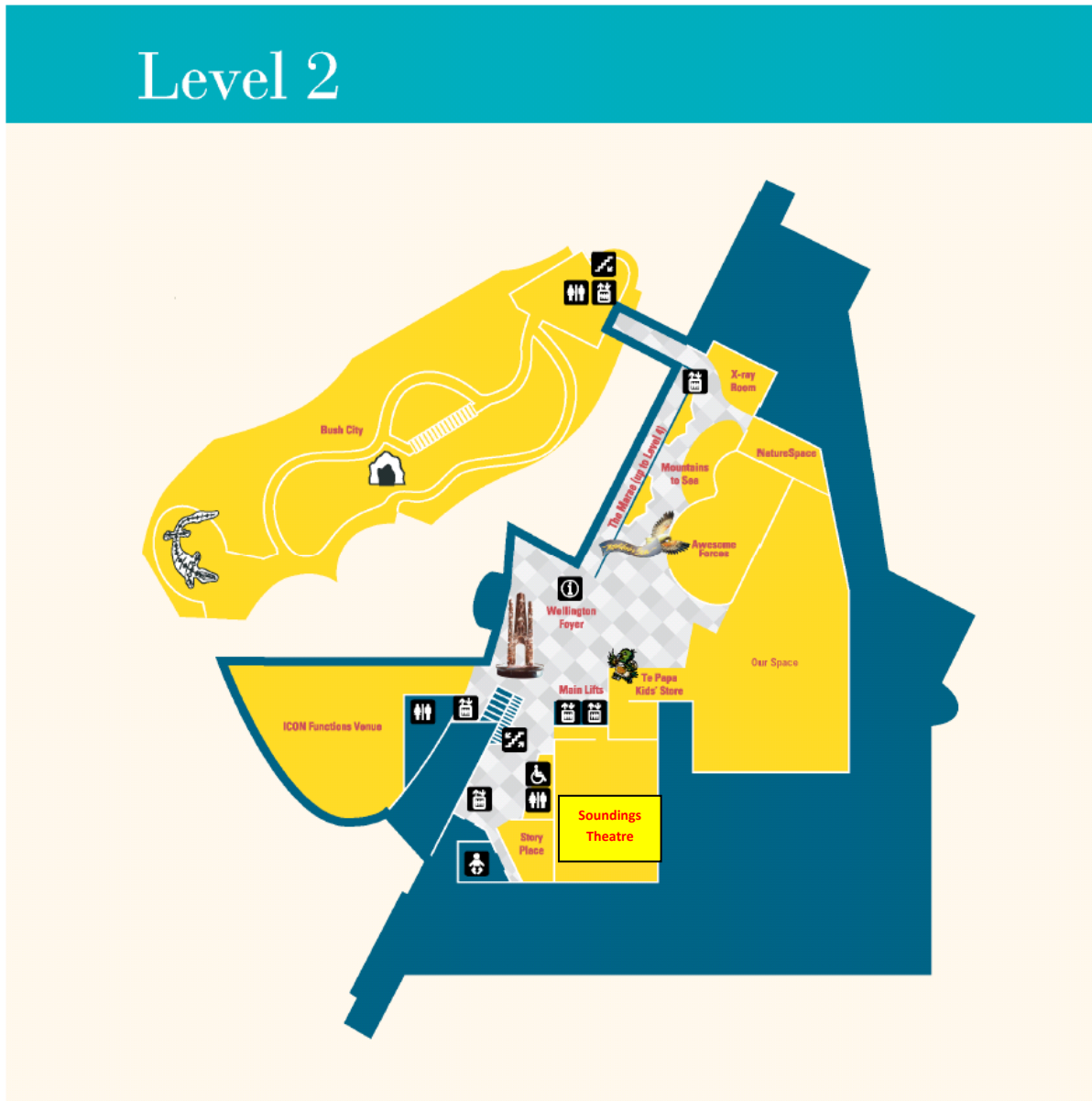
Schoening	Timm	Biodata Mining Group, Bielefeld University Atmosphere and Ocean Research Institute,	GERMANY
Seike	Koji	University of Tokyo	JAPAN
Serpetti	Natalia	Scottish Association for Marine Science	UNITED KINGDOM
Setoguchi	Yuka	Kumamoto University	JAPAN
Shank	Timothy	Woods Hole Oceanographic Institution	USA
Sherman	Alana	MBARI	USA
Shimanaga	Motohiro	Kumamoto University	JAPAN
Singh	Ravail	Deutsches Zentrum Marine Biodiversitätsforschung	GERMANY
Sinniger	Frederic	Japan Agency for Marine-Earth Science and Technology	JAPAN
Smith	Craig	University of Hawaii at Manoa	USA
Stein	David	Oregon State University	USA
Stevenson	Angela	TCD	IRELAND
Sutton	Tracey	Virginia Institute of Marine Science	UNITED STATES
Sweetman	Andrew	Norwegian Institute for Water Research (NIVA)	NORWAY
Taei	Sue	Conservation International	SAMOA
Taylor	Josi	Monterey Bay Aquarium Research Institute	USA
Teixeira	Sara	CCMAR and IFREMER	PORTUGAL
Thaler	Andrew	Duke University Marine Lab	UNITED STATES
Thistle	David	Florida State University	USA
Thresher	Ronald	CSIRO Wealth from Oceans Flagship	AUSTRALIA
Thurber	Andrew	Oregon State University	USA
Tittensor	Derek	Dalhousie University / UNEP-WCMC	CANADA
Tomomi	Ogura	Tokyo University of Marine Science and Technology	JAPAN
Tracey	Dianne	NIWA	NEW ZEALAND
van Oevelen	Dick	Royal Netherlands Institute for Sea Research (NIOZ-Yerseke)	NETHERLANDS
Vanreusel	Ann	University Ghent	BELGIUM
Voight	Janet	Field Museum of Natural History	USA
Wagner	Jamie	Duke University	USA
Wagstaff	Martine	University of Massachusetts	USA
Watanabe	Hiromi	Japan Agency for Marine-Earth Science and Technology	JAPAN
Watson	Charlotte	Museum & Art Gallery Northern Territory	AUSTRALIA
Wigham	Ben	Newcastle University	UK
Wilson	George D.	Australian Museum	AUSTRALIA
Wolff	F.	University of Liverpool	UK
Woodall	George	Natural History Museum, London	UK
Woolley	Lucy	Museum Victoria	AUSTRALIA
Yahagi	Skipton	Atmosphere and Ocean Research Institute, The University of Tokyo	JAPAN
Yancey	Takuya	Whitman College	USA
Yasuhara	Paul	University of Hong Kong	HONG KONG
Yesson	Moriaki	Zoological Society of London	UNITED KINGDOM
Young	Christopher	Oregon Institute of Marine Biology, Univ. of Oregon	U.S.A.

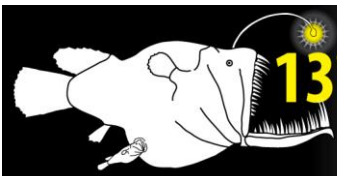


Te Papa Map

Level 2

Soundings Theatre – Main Plenary & Breakout Room





International  
**13<sup>th</sup> Deep-Sea Biology Symposium**  
Wellington, New Zealand 3 – 7 December 2012

Te Papa Map

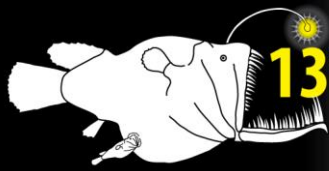
Level 3

Oceania – Registration, Catering and Poster Displays

Rangimarie 1 – Breakout Room







# International 13<sup>th</sup> Deep-Sea Biology Symposium

Wellington, New Zealand 3 – 7 December 2012



<b>Te Papa</b>	Conference Venue
<b>Macs Bar</b>	Icebreaker Venue (2 <sup>nd</sup> Dec)
<b>The Boatshed</b>	Conference Dinner Venue (5 <sup>th</sup> Dec)