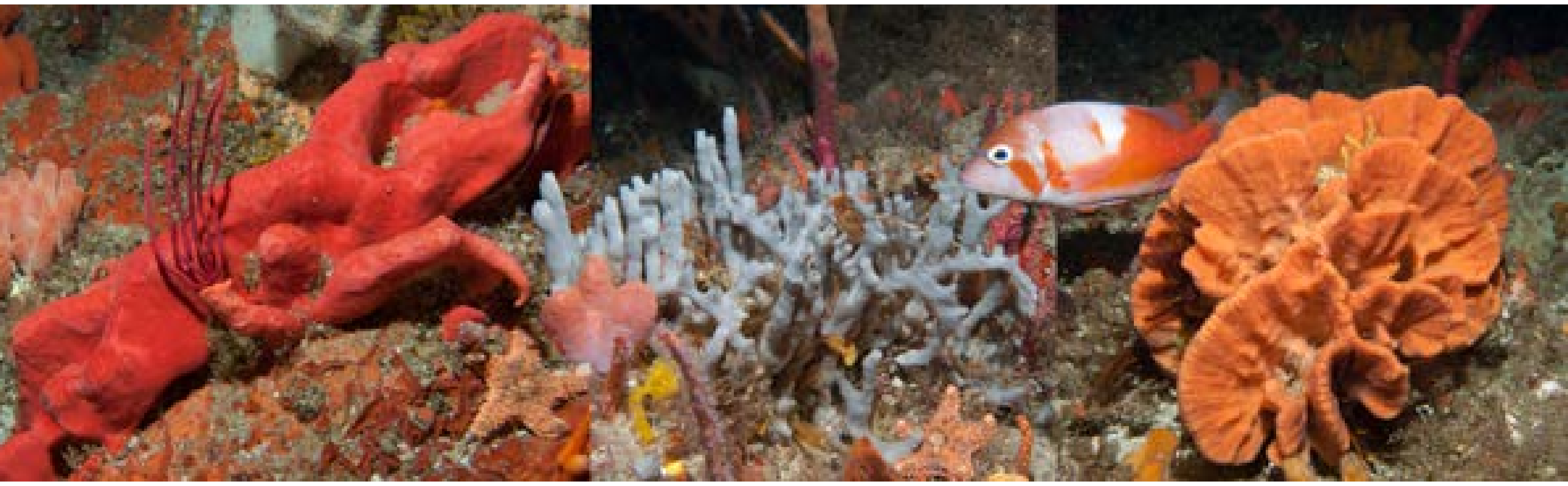
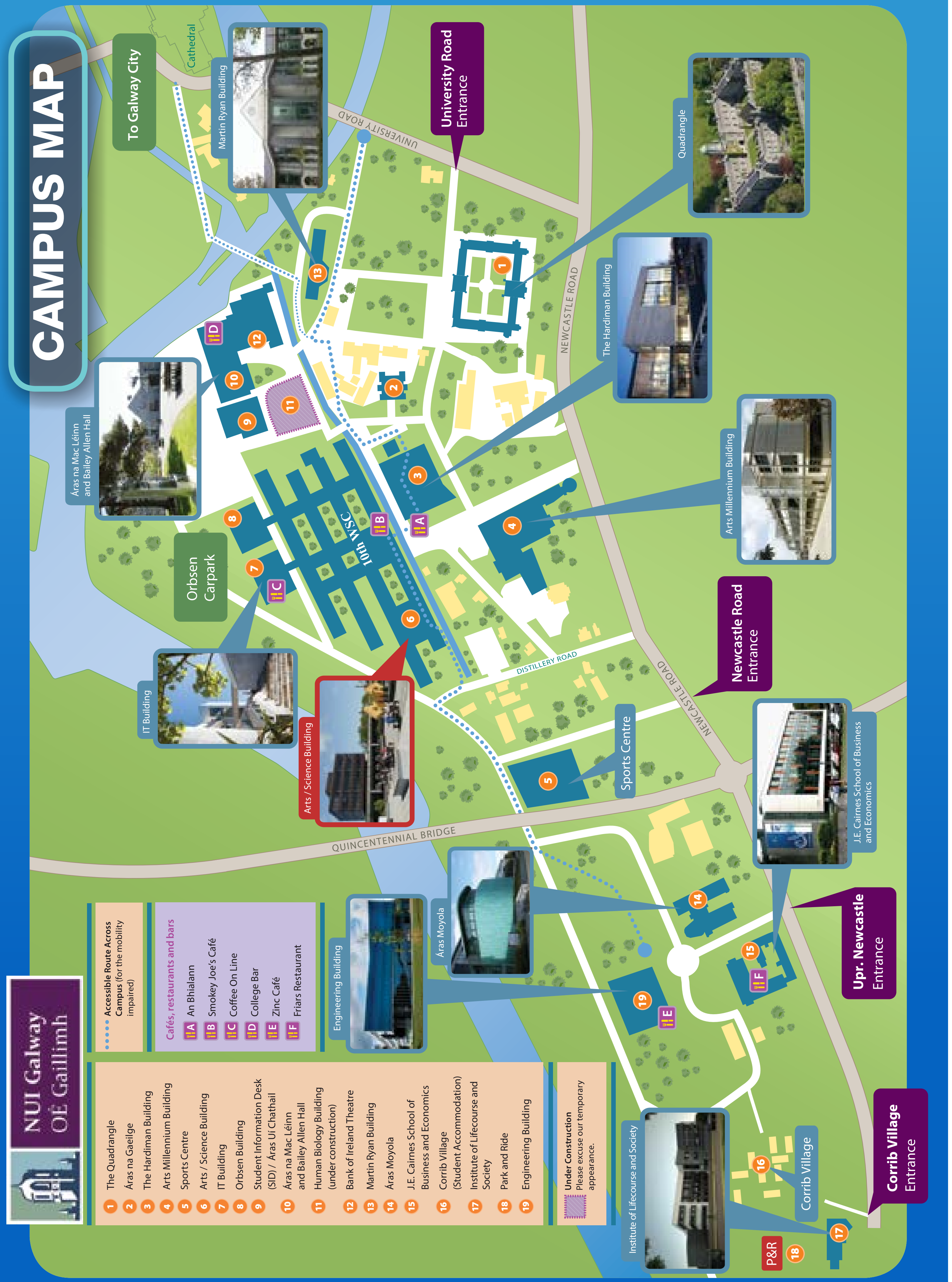
10th World Sponge Conference

NUI Galway

25-30 June 2017

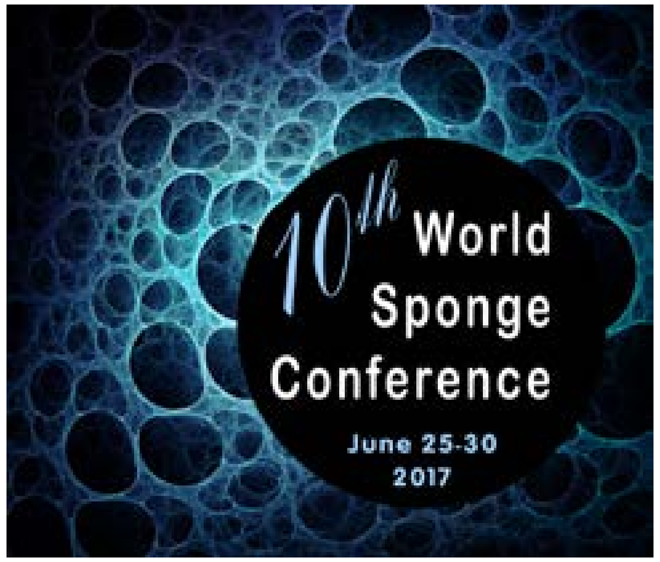




Cover photographs - Bernard Picton. South Africa, 2008.

10th World Sponge Conference
NUI Galway

June 25-30 2017



Contents

Plenary Session

Evolution

Systematics

Sponges & Microbes

Biomaterials & Biomolecules

Ecology

Cell & Molecular Biology

Sponges & their Environment

Organismal Biology

Molecular, Cell and Organismal Speed Talks

Ecosystems & Environment

Posters Evolution & Systematics

Posters Sponges and Microbes

Posters Biomaterials

Posters Ecology

Posters Molecular, Cell and Organismal Biology

Attending Delegates

Index

Poster list

Welcome to Galway

Ba mhaith liom céad mile fáilte a chur róimh chuig Cathair na Gaillimhe.

Welcome to the 10th World Sponge Conference 2017.

It gives me great pleasure to welcome you to National University Ireland, Galway. This is the first time we have hosted the sponge conference in Galway and we are delighted to welcome old and new friends to our beautiful city.

The topics of this conference reflect the main areas in which sponge biology is developing at present, as well as traditional research categories. While sponge ecology and systematics are continuing to hold sway as the most popular subject areas we see the use and development of new technologies and applications, for example exploring sponge natural products and the use of '-omic' technologies. We provide a platform for learning about future funding opportunities globally and how to go about becoming a part of new initiatives. Finally we hope to provide opportunities to socialise and network, to connect with old friends and make new ones.

The conference format is plenary session allowing full participation of the exciting programme scheduled.

I wish to thank our conference sponsors SFI, Marine Institute, Fáilte Ireland, and NUI Galway and our committee members for their contribution to the event. I hope that you benefit from your participation in the event and enjoy your visit to Galway.

Marine Institute
Foras na Mara

Fāilte Ireland
National Tourism Development Authority

Science Foundation Ireland
sfi
For what's next

SponGES

NUI Galway
OÉ Gaillimh

COMMITTEE

CHAIR

Prof. Grace McCormack, Zoology, NUI Galway

LOCAL ORGANISING COMMITTEE

Olivier Thomas (NUI Galway)
Christine Morrow (NUI Galway)
Colin Lawton (NUI Galway)
Louise Allcock (NUI Galway)
Maria Vittoria Marra (NUI Galway)
Jose Maria Aquillar Camacho (NUI Galway)
Belinda Longakit (NUI Galway)

Secretariat Assistant: Maeve Egan (Conference & Events, NUI Galway)

Book of Abstracts: Bernard Picton & Christine Morrow

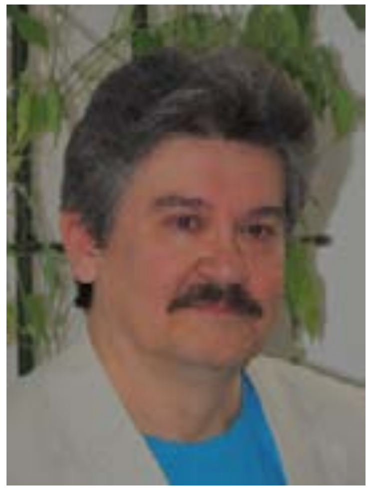
SCIENTIFIC COMMITTEE

Joseph Pawlik, University of North Carolina Wilmington, USA
James Bell, Victoria University of Wellington, NZ
John Hooper, Queensland Museum, Australia
Manuel Maldonado, Spanish National Research Council, Spain
Ute Hentschel, Geomar, Germany
Joe Lopez, Nova Southeastern University, USA
Michelle Kelly, NIWA Tiahoro Nukurangi, New Zealand
Olivier Thomas, NUI Galway, Ireland
Ana Riesgo, The Natural History Museum London, UK
Malcolm Hill, University of Richmond, USA
Kenan Matterson, Smithsonian Institution, USA
Andia Chaves, University of the Virgin Islands, USA
Shirley Sorokin, Primary Industries and Regions South Australia, Australia
Emilio Lanna, Universidade Federal da Bahia, Brazil
Shirley Pomponi, Florida Atlantic University, USA
Stephanie Archer, Fisheries and Oceans Canada
Peter Schupp, Carl-von-Ossietzky University Oldenburg, Germany
Christine Morrow, NUI Galway, Ireland
Gert Wörheide, Ludwig-Maximilians-Universität München, Germany
Grace McCormack, NUI Galway, Ireland
Lucia Pita Galán, GEOMAR

Speaker Biographies

Professor James Bell

Associate Professor James Bell is a marine biologist in the School of Biological Sciences at Victoria University of Wellington in New Zealand, and is currently the Marine Biology Programme Director. James graduated from the University of Wales, Bangor in 1998 with a first class honours degree in marine biology, and gained his PhD in 2001 from University College Cork in Ireland. James moved to New Zealand to take up a lectureship at Victoria University in 2006. His research focuses on understanding the functional roles of sponges in marine systems, the ways in which human impacts influence these roles and the subsequent ecosystem consequences of declines or increases in sponge abundance. James has published over 100 peer-reviewed journal articles and book chapters in leading international journals and has received funding from many sources to support his research including a recent Royal Society of New Zealand Marsden grant. James leads a large research group and is currently supervising 12 PhD students, most of whom are working on sponges.



Professor Hermann Erlich

Prof Hermann Ehrlich after the defense of the PhD thesis (1984) served as a postdoctoral researcher at Max-Bergmann Centre of Biomaterials and Institute of Materials Science in Dresden, Germany. After successful habilitation in 2011 at Christian-Albrechts University in Kiel he holds a W3 Heisenberg full professor position at the Institute of Experimental Physics at the TU Bergakademie Freiberg. His research is focused on marine biomaterials, biominerals, biocomposites and biomimetics. Using biochemical, cellular, molecular, and analytical approaches, he and his co-workers, for the first time, discovered and characterized chitin in marine and freshwater sponges as well as novel hydroxylated collagen in the skeletal formations of glass sponges. During last ten years, he has published over 80 peer-reviewed articles, ten book chapters, two monographs and additionally holding four patents. Being the corresponding author, Hermann Ehrlich published his papers in such high impact journals as Nature Chemistry, Scientific Reports, Chemical Reviews, Advanced Functional Materials, Chemistry of Materials etc. In recent times, together with members of his team, he published various scientific discoveries in the field of biological materials and biomimetics.

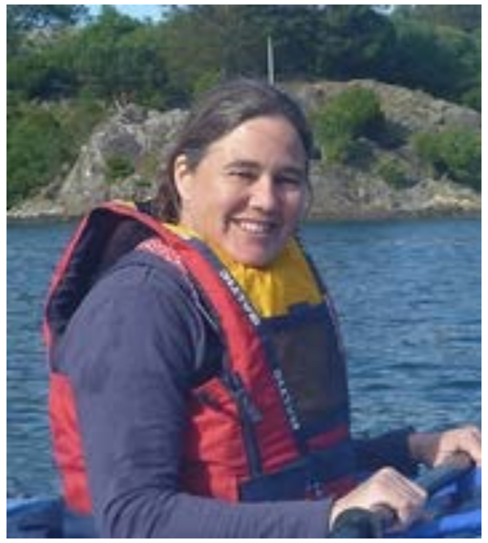
Dr. Nicole Boury-Esnault

Nicole Boury Esnault has published 140 articles on areas including Integrative taxonomy, population dynamics, population genetics, life story, systematics, phylogeny, ecology, biogeography of Porifera. She is also actively involved in the Mediterranean and Caribbean fauna for World Porifera Database checking all primary sources and is editor for Homoscleromorpha, Keratosa, Verongimorpha, Polymastiida. She pays particular attention to the precise geographical location to obtain maps with clear repartition of the species.

Professor Ute Hentschel Humeida

Ute Hentschel Humeida obtained her Ph.D. degree in Marine Biology at Scripps Institution of Oceanography, La Jolla, USA, and performed her postdoctoral research in Infection Biology both at the University of Santa Barbara, USA, and the University of Würzburg, Germany. In 2008, she became professor for Chemical Ecology at the University of Würzburg, Germany. In 2015, she returned to her academic roots and accepted the professorship for Marine Microbiology at the GEOMAR Helmholtz Institution for Ocean Research, Kiel. Her research interests focus on host-microbe interactions, with special attention on function, diversity, and biotechnological potential of marine sponges and their beneficial microbial consortia. A combination of modern molecular biology techniques, in particular the –omics repertoire, in vivo experimentation, and regular field work is employed towards this goal. Her laboratory's efforts are directed at providing a deeper understanding of the high-complexity microbial ecosystems within sponges, and at providing research strategies to a sustainable use of this natural resource. Ute has published over 150 publications and 3 patents in leading international journals.

Professor Sally Leys



Sally Leys obtained her Bachelor of Science from the University of British Columbia and PhD from the University of Victoria, British Columbia in 1996. She carried out three postdoctoral projects: at McGill University, Quebec and Barbados; Université Aix Marseille; and the University of Queensland, Australia. She held a Canada Research Chair Tier II in evolutionary and developmental biology at the University of Alberta from 2002-2012. She is currently a Professor in the Department of Biological Sciences at the University of Alberta. Her group uses a range of molecular, microscopy and physiological techniques to explore the origin of nerves, coordination, and sensory systems, using in vitro and in situ studies on sponges. They carry out fieldwork at the Bamfield Marine Sciences Centre, and as marine biologists their travel also takes them on yearly research cruises to study deep-water glass sponge reefs in coastal British Columbia, and to study sponges in Norway, Panama and the Canadian Arctic.

Professor Joe Lopez

Since 2007, Dr. Jose V. Lopez, PhD has been a biology Professor at the Guy Harvey Oceanographic Center, Halmos College of Natural Sciences and Oceanography, Nova Southeastern University. He earned a Master's degree at Florida State University (under National Academy Member J. Herbert Taylor), and his doctorate at George Mason University studying the evolution of mitochondrial DNA and its transpositions (Numt) in feline nuclear genomes under Stephen J. O'Brien. Dr Lopez then applied his molecular evolutionary training in postdoctoral appointments with Dr. Nancy Knowlton characterizing the *Orbicella* (formerly *Montastraea*) *annularis* coral sibling species complex at the Smithsonian Tropical Research Institute in Panama, and sponge genetics with Dr. Shirley Pomponi at Harbor Branch Oceanographic Institute. The latter allowed him to use submersible technology to investigate deep sea sponges and corals. Dr. Lopez's current research at the Nova Southeastern University's Guy Harvey Oceanographic Center, involves diverse projects on marine invertebrate-microbial symbiosis, genomics and metagenomics of marine habitats, gene expression of marine organisms, and marine microbiology. Dr. Lopez was on the Porifera Tree of Life team for placing marine sponges on a global Tree of Life (www.PorToL.org). He also founded and initiated the Global Invertebrate Genomics Alliance - GIGA (http://GIGA-cos.org), that will apply genome sequencing of non-model invertebrate species. Dr. Lopez is also involved with other sponge biologists in the global Earth Microbiome Project (www.earthmicrobiome.org) characterizing the diversity and abundance of various microbes.

Dr. Manuel Maldonado

Dr. Manuel Maldonado is a senior scientist at the Centre for Advanced Studies of Blanes (CEAB) in the Spanish National Research Council (CSIC). Over his career, he has sought to achieve an integrative perspective of the biology and ecology of sponges, combining studies of taxonomy, experimental and observational ecology, reproductive and larval biology, functional physiology, and cell biology. He has funded the Sponge Bio-ecology and Biotechnology (SBB) Group at the Department of Marine Ecology in the CEAB. His recent interests focus on the manipulative use of sponge reproduction for experimental and biotechnological applications, the role of sponge communities in the benthic-pelagic coupling of marine nutrient cycles, and the use of sponge silica for scientific and biotechnological applications.

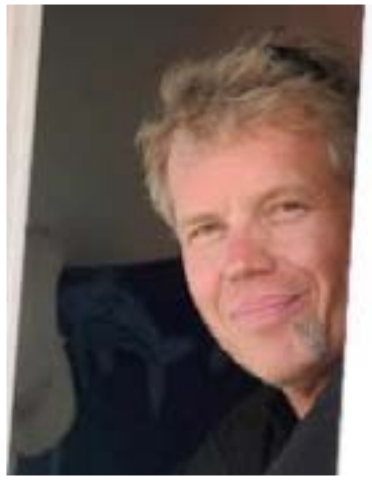
Professor Joe Pawlik

Joseph Pawlik received his undergraduate degree in 1982 from the University of Minnesota and his PhD in 1988 from Scripps Institution of Oceanography, UCSD. After postdoctoral fellowships at Friday Harbor Labs (University of Washington) and Woods Hole Oceanographic Institution, he joined the faculty at UNC Wilmington in 1991, where he teaches Invertebrate Zoology and directs a research program involving undergraduate, MS and PhD students. Dr. Pawlik has over 140 scientific publications, mostly in the areas of marine chemical ecology and the biology of sponges on Caribbean coral reefs. He also enjoys documenting his research program using underwater videos, which can be found at the YouTube channel "Pawlik Lab."

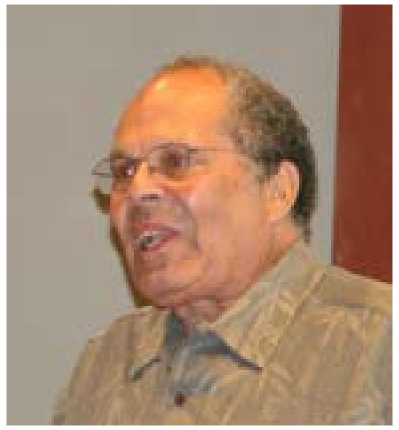
Professor Peter Schupp

Our research investigates the chemical ecology of marine invertebrates and aims to understand the ecological function of their secondary metabolites. To gain a better understanding of the ecological roles of secondary metabolites we are assessing possible antimicrobial, antifouling, allelopathic, defense functions, and also possible pharmacological activities. One goal is to combine the chemical ecology research with management-oriented studies to develop new management techniques and strategies to help preserve and manage ecosystems in temperate (e.g. Wadden Sea and North Sea) and tropical locations (e.g. Coral reefs in the Indo-Pacific region).

Professor Gert Wörheide



Professor Dr. Gert Wörheide holds the Chair for Palaeontology & Geobiology at the Ludwig-Maximilians-Universität (LMU) Munich and is Director of the Bavarian State Collections for Paleontology and Geology in Munich (Germany). Currently he is Vice-Dean Faculty of Geosciences at the LMU. He received his Dr. rer. nat. in Geobiology in early 1998 at the University of Göttingen in Germany, to where he returned as a Junior Professor for Molecular Geobiology in 2002 after a PostDoc at the Queensland Museum and the University of Queensland in Brisbane (Australia). In 2008 he took up the Professorship in Munich and since then has bulit up a large research group focussing on phylogenomics, molecular systematics, DNA barcoding, biomineralization and genomics of non-bilaterian animals, with special focus on sponges and lately octocorals. In 2013 he co-founded the international Masters Program "Geobiology & Paleobiology" at the LMU. Gert has published more than 140 peer-reviewed articles in leading international journals.



Professor Philip Crews

Professor Phillip Crews is Distinguished Research Professor of Chemistry, at the University of California, Santa Cruz. The enduring focus of his lab is to expand fundamental knowledge about the novel structures and bioactivity of marine natural products. Another goal has been to lead and participate in collaborative academic-biotech research and educational projects. Phillip has contributed to over 232 peer-reviewed papers on natural products chemistry.

General Information

Conference Venue:

The conference will be held on the Main Concourse, Arts-Science Building, NUI Galway. Driving access is through Newcastle Road entrance. Please see detailed maps included in this book for more information.

Parking on Campus:

Parking permits issued electronically is for the Orbsen Building carpark only. There are a limited number of Pay & Display spaces on campus (blue lined spaces), delegates must pay between 09.00 and 17.30 if parked in these spaces. All illegally parked vehicles, including cars not displaying a permit will be clamped.

Included in Conference Registration Fee:

Welcome BBQ, Monday 26 June
Poster Session Reception, Tuesday, 27 June
Poster Session Reception, Wednesday, 28 June
Teas/Coffees, Lunches, Monday – Friday
Note: The conference dinner and the hike to the Burren are optional extras.

Computer Access

Wi-Fi Code

Network	User ID	Password
NUIGWIFI	987600IT	htbps4729

10th World Sponge Conference, NUI Galway

Conference Programme

Venue: O'Flaherty Theatre, Main Concourse

Sunday, June 25, 2017

18.00 – 19.30 **Conference Registration, Main Concourse, NUI Galway**

Monday, June 26, 2017

08.00 Conference Registration, Main Concourse
09.00 Conference Opening
09.15 Welcome by CEO, Marine Institute, Dr Peter Heffernan
09.30 KN – 1: Keynote Speaker, Prof. Sally Keys
Sensation and the energetics of sponge filter feeding

Session 1: Evolution
Chair: Prof. Grace McCormack & Prof. Gert Wörheide

10.15 KN – 2: Keynote Speaker, Prof. Gert Wörheide
A Solution to the Conundrum of Non-Bilaterian Relationships?
10.40 OS -1: Sponges versus Ctenophora: The Evolution of Epithelial Proteins rmida Ziñiga
Dr Carole Borchiellini

10.55 OS -2: Save the best for the last: mRNA editing and multiple linear chromosomes in mitochondria of calcaronean sponges.
Dr Dennis Lavrov
11.10 Coffee Break
11.30 OS – 3: Think like a sponge: Examining neural-marker genes in context
Ms Jasmine Mah
11.45 OS – 4: Tetractinellida is a hot-spot of Group I Introns: vertical gene transfer, secondary losses and implications for DNA barcoding
Ms. Astrid Schuster
12.00 OS – 5: Evolution and Development of the Skeleton in Selected Marine Haplosclerida
Mr. Jose Maria Aguilar-Camacho
12.15 OS - 6: Molecular Diversity of Demosponges in the Indo-Pacific
Dr. Dirk Erpenbeck
12.30 OS – 7:The *Chondrilla* species complex along a N-S gradient in the tropical Western Atlantic: an integrative approach
Prof. Carla Zilberberg
12.45 ST- 2: Diversity analysis of a fossil sponge fauna (Hexactinellida and Demospongiae) from Italy (Eocene, Lessini Mts)
Dr. Viviana Frisone
12.50 ST -1: Foliose fans of the sea: The Phyllospongiinae
Dr. Muhammad Azmi Abdul Wahab
12.55 ST- 3: Biodiversity and Biogeography of Tropical Western Atlantic Calcarea (Porifera)
Dr. Fernanda Azevedo

13.00 Lunch

Session 2: Systematics 1

Chair Dr. Nicole Boury Esnault & Dr Christine Morrow

14.00 KN – 3: Keynote Speaker, Dr. Nicole Boury Esnault
The Evolution of Sponge Systematics from Aristotle (4th AC) to the 10th Sponge World Conference in Galway (21st BC)

14.25 OS – 8: The importance of cytology towards integrative taxonomy of sponges
Prof. Alexander Ereskovsky

14.40 OS - 9: Diversity of Deep-Water Lithistids of the Tropical Western Atlantic: Are They Really Isolated survivors.
Prof Andrzej Pisera

14.55 OS- 10: Variation between Giant Barrel Sponges Around the Globe
Mr Thomas Swierts

15.10 OS -11:Homoscleromorpha diversity revised through an Integrative Systematics
Mr. César Augusto Ruiz Pinzon

15.25 OS -12: Current outlook on carnivorous sponge diversity and systematics
Dr. Jon Thomassen Hestetun

15.40 OS -13: Nothing in sponge systematics makes sense - except in the light of DNA!
Dr. Christine Morrow

15.55 Coffee Break

Session 3: Systematics 2

Chair: Dr. Paco Cárdenas & Dr. Dirk Erpenbeck

16.15 OS-14: Are We There Yet? Novel Famisa and Genera Revealed Within Verongimorpha While Expanding Geographic And Habitats Explorations
Dr. Maria Cristina Diaz

16.30 OS –15: A proposal for the family level classification of Calcinea (Porifera, Calcarea)
Dr. Oliver Voigt

16.45 ST- 4: *Cinachyrella australiensis* (Cater, 1886) in the Indo-West Pacific: An Integrative Approach to Understanding a complex species complex
Dr. John Hooper

16.50 ST- 5:Taxonomy of deep-sea sponges living on polymetallic nodule fields in the Clarion-Clipperton Fracture Zone (CCFZ), East Pacific
Daniel Kersken

16.55 ST-6: Three new and four poorly known species of *Plakina* (Porifera, Homoscleromorpha)
Ms. Anaíra Lage

17.00 ST -7: Calcareous Sponges from Palau and the Great Barrier Reef, Australia
Dr. Anita Mary George

17.05 ST – 8:Divergence between molecular and morphological data in Brazilian *Arenosclera* sponges (Haplosclerida, Demospongiae)
Mr. Camille Victória Leal

17.10 ST - 9: *Cliona laticavicola* is an ecophenotype and an ontogenic life stage of the coral excavating sponge *Cliona delitrix*.
Dr. Andia Chaves Fonnegra

17.15 ST-10: A revised molecular phylogeny of the subclass Calcaronea
Ms. Adriana Alvizu

17.20 ST-11: Exploring remote islands and remote habitats: the key role of hidden cave sponges in solving systematic issues
Dr. Pierre Chevaldonné

17.25 ST- 12: Chemosystematics as a complementary tool for *Haliclona* species (Class Demospongiae, Order Haplosclerida)
Dr. Miriam Reverter

17.30 ST- 13: Integrative taxonomy reveals a high diversity of Homoscleromorpha in Cabo Frio, South-eastern Brazil (SW Atlantic)
Dr. Guilherme Muricy

17.35 ST- 14: Phenotypic Plasticity in Sponges: a case study on *Callyspongia* sp. from Northeastern Brazil
Dr.Gisele Lobo-Hajdu

17.40 ST- 15: Sponges of the genus *Agelas* from the Indo-Pacific
Dr. Merrick Ekins

17.45 ST- 16: Evolutionary transformations of choanocyte kinetid in the phylum Porifera and their significance for phylogenetic reconstructions
Mr. Igor Pozdnyakov

17.50 ST- 17: Historical overview on the Adriatic calcarean sponges.
Dr. Mirna Halasz

18.30 BBQ, Sult Bar, NUI Galway

Music by *My Fellow Sponges*

Tuesday, June 27, 2017

Session 4: Sponges & Microbes 1

Chair: Prof. Joe Lopez

09.00 KN-4: Keynote Speaker, Prof. Ute Hentschel
Exploring microbial dark matter in sponge symbioses

09.25 OS- 16: Sponge bleaching, *Symbiodinium* symbioses, and forces that shape co-evolutionary specialization.
Dr. Malcom Hill

09.40 OS -17: Molecular and metabolic interactions in sponge-microbe symbiosis
Prof. Torsten Thomas

09.55 OS -18: Genome-Informed Insights Into The Function Of A Coral Reef Sponge Holobiont
Dr. Sandie Degnan

10.10 OS-19: Sponge Symbionts – key to understanding sponge responses to climate change
Dr. Heidi Luter

10.25 OS - 20: Metagenomics and FISH-CLEM visualization of marine sponge-associated *Chloroflexi*
Dr. Kristina Bayer

10.40 OS -21: Metabolic Diversification Across Caribbean Sponges
Dr. Christopher Freeman

10.55 Coffee Break

Session 5: Sponges & Microbes 2

Chair: Prof. Ute Hentschel

11.15 KN – 5: Keynote Speaker, Prof. Joe Lopez
Function and Form: Finding the Raison d'être of Symbiotic Communities within Sponge

11.40 OS – 22: The impact of depth: sponge-associated microbes and antimicrobial activity change
Dr. Detmer Sipkema

11.55 OS -23: Dissolved organic matter cycling by the sponge holobiont
Dr. Laura Rix

12.10 OS -24: Virus: an Important Component of the Sponge Holobiont
Ms. Cecilia Pascelli

12.25 OS -25: Tide After Time: Structural Shifts and Functional Stability in the Microbiome of an Intertidal Sponge
Dr. Patrick Erwin

12.40 OS -26: Looking for barettins and barretides in north Atlantic demosponges: a case in favour of a species specific microsymbiont production?
Dr. Paco Cardenas

12.55 ST - 18: Metabolic profiles of microbiota from Antarctic sponges revealed by metagenomics.
Mr. Mario Moreno

13.00 Lunch

Session 6 Sponge and Microbes 3

Chair Dr. Lucia Pita & Dr Bob Thacker

13.45 OS -27: Do Freshwater Sponges Facilitate the Transfer of Antibiotic Resistance in Water-Borne *Enterococcus faecalis*?
Mr Joerg Arnscheidt

14.00 OS -28: The microbial and chemical affairs between haplosclerid and homosclerophorid sponge pairs of the Caribbean
Mr. Jan Vicente

14.15 OS -29: The response of sponges to microbial elicitors
Dr. Lucia Pita

14.30 OS -30: Metagenomic binning of a marine sponge microbiome reveals unity in defense but metabolic specialization
Ms. Beate Slaby

14.45 OS- 31: Multi-primers Targeting 16S rDNA Variable Regions Essential for Sponge (Porifera) Microbiome Study
Prof. Wei Zhang

15.00 ST- 19: Single-cell measurement of metabolic interactions between a bioeroding sponge and its endosymbiotic dinoflagellates using nanoscale secondary ion mass spectrometry.
Ms. Michelle Achlatis

15.05 ST -20: Temporal dynamics of sponge microbial communities
Dr. Cole Easson

15.10 ST -21: Visualization of eukaryotic-like-proteins as ring-like structures within bacteria-containing sponge cells
Mr. Giampiero Batani

15.15 ST – 22: Do symbiotic bacteria help sponges to cope with eutrophication?
Ms. Marta Turon

15.20 ST – 23: Global patterns of microbial diversity and composition among three marine host types: sponges, corals, and ascidians
Dr. Georg Steinert

15.25 ST- 24: Microbiome Comparison Suggests Differential Involvement of Bacterial Associates in the Carnivorous Sponges *Chondrocladia grandis* and *Cladorhiza oxeata*
Mr. Joost Verhoeven

15.30 ST – 25: Searching for bacterial genes involved in the symbiosis between sponges and calcifying endosymbiotic bacteria
Ms. Leire Garate

15.35 Coffee Break

Session 7 Biomaterials & Biomolecules

Chair: Prof. Olivier Thomas

16.00 KN – 6: Keynote Speaker, Prof. Philip Crews
The Potential of Biosynthetic Products from Sponges and Sponge-Derived Gram-Negative Bacteria to Open New Research Horizons

16.25 OS -32: Identification of calcareous sponge spicule matrix proteins
Ms. Benedetta Fradusco

16.40 OS -33: Poriferan Chitin as a Universal Template for Extreme Biomimetics
Dr. Marcin Wysokowski

16.55 OS -34: Five new siphonodictyals from Caribbean Sponge *Siphonodictyon coralliphagum*
Ms. Daria Firsova

17.10 ST – 26: Taxonomic Identification, immunopharmacological and toxicological study of *Haliclona (Soestella*) sp: A novel marine sponge species from Sri Lanka
Dr. Marco Bertolino

17.15 ST- 27: Deep-sea discovery – deep-sea sponges as a source of novel biologics
Dr. Mathew Upton

17.20 ST -28: Value-Added in Thai Pottery by Biological Materials from Freshwater Sponges
Dr. Nisit Ruengsawang

17.25 KN – 7: Keynote Speaker, Prof. Hermann Ehrlich
Poriferan Chitin: 10 years after discovery. Structural biology and practical applications

18.00 Poster session
Canapes & Wine

Wednesday, June 28, 2017

Session 8: Ecology 1 Population Biology

Chair: Prof Joe Pawlik

09.00 KN – 8: Keynote Speaker, Dr. James Bell
Sponge Resilience and susceptibility

09.25 OS – 35: Genomic approach to the evolutionary history and population structure of *Dendrilla antarctica* Topsent, 1905 (Porifera, Demospongiale) from southern ocean shallow waters
Mr. Carlos Leiva

09.40 OS- 36: Population connectivity of an abyssal sponge across the Clarion Clipperton Zone (Central Pacific)
Dr.Sergi Taboada

09.55 OS -37: Considering Habitat Fragmentation and Dispersal Potential: How *Pheronema carpenteri* Aggregations May Be Particularly Vulnerable Marine Ecosystems
Dr. Rebecca Ross

10.10 OS -38: Genetic structure patterns in Atlanto-Mediterranean sponges: environmental factors and biological features driving connectivity in scenarios with mass-mortalities
Dr. Ana Riesgo

10.25 OS -39: Limited connectivity promotes cryptic speciation in *Tethya* spp.
Ms. Megan Shaffer

10.40 OS -40: The environment selects?
Dr. Leontine Becking

10.55 ST- 29: Genetic Population Structure of *Ircinia campana* and *Spheciospongia vesparium* in the Greater Caribbean
Ms. Sarah Griffiths

11.00 Coffee Break

Session 9: Ecology 2: Sponge assemblages

Chair: Dr. James Bell

11.30 OS - 41: Sponges of the Marianas: Initial Observations of Newly Collected Specimens
Dr. Shirley Pomponi

11.45 OS – 42: Sponge Assemblages on the recently declared Menorca Channel Marine Protected Area (Western Mediterranean Sea)
Mr. Andreu Santin

12.00 OS -43: Deep-sea Sponge Grounds of the North Atlantic: State of the Knowledge, Recent Advances and Outlook.
Dr Joana Xavier

12.15 ST -30: Aspects of the ecology of *Pheronema carpenteri* aggregations
Dr. Kerry Howell

12.20 ST- 31: Sponge communities from the mud volcanos of the Gulf of Cadiz
Ms. Celia Sitja

12.25 ST- 32: Exploiting and conserving deep-sea genetic resources
Dr. Claire Laguionie Marchais

12.30 ST- 33: SponGES - Deep-sea Sponge Grounds Ecosystems of the North Atlantic: an integrated approach towards their preservation and sustainable exploitation
Prof. Hans Tore Rapp

12.35 Lunch
Town Hall Meeting International collaboration & funding
Venue: AC201, Main Concourse

Session 10 Ecology 3: Reefs

Chairs: Dr. Stephanie Archer & Dr. Kenan Matterson

14.00 KN – 9: Keynote Speaker, Prof. Joseph Pawlik
The "vicious circle" hypothesis: Sponges and reduced resilience of Caribbean coral reefs

14.25 OS- 44: Nutrient Fluxes and Ecological Functions of Coral Reef Sponges in a Changing Ocean
Dr. Jasper M. de Goeij

14.40 OS – 45: A decadal analysis of bioeroding sponge cover on the inshore great barrier reef
Mr. Blake Ramsby

14.55 OS - 46: Ecological interactions between photosymbionts and spongivores reveal complex interplay between bottom up and top-down controls on Caribbean sponges.
Mr. Kenan Matterson

15.10 OS – 47: Combined effects of ocean acidification and eutrophication on reef sponge bioerosion
Dr. Lennart de Nooijer

15.25 ST- 34: Better estimates of chemical and mechanical excavating rates of coral boring sponges in the Caribbean
Mr. Didier de Bakker

15.30 ST – 35: Increase of excavating sponges after coral bleaching events
Dr. Andia Chaves-Fonnegra

15.35 ST – 36: How Do Glass Sponge Reefs Get Enough Food? Feeding And Excretion By The Glass Sponge *Aphrocallistes vastus*
Dr. Amanda Kahn

15.40 ST – 37: Initial report on nine newly discovered glass sponge reefs in British Columbia, Canada
Dr. Stephanie Archer

15.45 ST -38: Defense by association: sponge-eating fishes alter the small-scale distribution of Caribbean reef sponges
Mr. Michael Wooster

15.50 Coffee Break

Session 11| Ecology 4: Speed Talks

Chair: Dr. Andia-Chaves & Dr Nicole De Voogd

16.10 ST – 39: Bleaching recovery of a phototrophic bioeroding sponge.
Mr. Joe Marlow

16.15 ST- 40: Environmental drivers of deep-sea reefs
Ms. Ulrike Hanz

16.20 ST- 41: Biogeographic and bathymetric distribution of coral-eroding sponges.
Dr. Christine Schonberg

16.25 ST – 42: Changes in Mediterranean coralligenous sponge assemblage at a pluri-milennial temporal scale
Ms Gabriele Costa

16.30 ST - 43: Coral cavities – Stable habitats with zero growth? Assessing potential growth rates and community changes in cryptic sponges
Dr. Benjamin Mueller

16.35 ST – 44: Increase in light intensity: A threat or not for calcareous sponge survival?
Ms Bárbara Ribeiro

16.40 ST – 45: Spatial and temporal adaptation of a traditional Mediterranean fishery facing regional change: combining history and ecology to study past, present and future of sponge harvesting
Mr. Maïa Fourt

16.45 ST -46: Effects of temperature on survival, pigmentation and regeneration of three Caribbean
Ms. Juliet Rugiero

16.50 ST – 47: Geographic Variability in Antibacterial Chemical Defenses Among Branching Morphotypes of Caribbean *Aplysina*
Dr. Deborah Gochfeld

16.55 ST – 48: Assessing the regional conservation status of sponges: the case of the Aegean ecoregion
Dr. Vasilis Gerovasileiou

17.00 ST – 49: Spatial variation in chemistry and microbial diversity of Philippine blue sponge, *Xestospongia* sp. in relation to some ecological factors
Ms. Geminne Manzano

17.05 ST – 50: Sponges in Space: Spiculous skeleton formation in *Ephydatia fluviatilis* under hypergravity conditions
Mr. Martijn Bart

17.10 ST – 51: Past and present scenario of the western Atlantic sponge *Clathrina aurea* (Porifera, Calcarea)
Mr. Andre Padua

17.15 ST- 52: New Species Records for Sponges of the Eastern Canadian Arctic and Subarctic
Mr. Curtis Dinn

17.20 ST- 53: Functional Redundancy in Tropical Marine Sponge Communities
Ms. Marla Valentine

18.00 Poster Session
Pizza & Beer

19.00 Workshop on Mediterranean IUCN Redlist
Venue: AC201, Main Concourse

Thursday, June 29, 2017

Session 12: Cell and Molecular Biology

Chair Dr. Malcolm Hill

09.00 OS – 48: Origin of animal cells.
Prof. Bernie Degnan

09.15 OS - 49: Sponge cell reaggregation: inter- and intraspecific variations
Mr. Andrey Lavrov

09.30 OS – 50: Toward the Development of a Marine Sponge Cell Line: a Sponge-Specific Vector for Introduction and Expression of Foreign DNA
Ms. Kylie Hesp

09.45 OS – 51: Characterisation of mucus and mucus producing cells in haplosclerid sponges.
Ms. Maria Vittoria Marra

10.00 OS – 52: Cell dynamic during ectosomal and endosomal regeneration on an organotipic culture of *Hymeniacidon heliophila*
Dr. Cristiano Coutinho

10.15 OS – 53: A novel secreted frizzeld related proteins is a downstream target of paxb and a regulator of aquiferous system development in the freshwater sponge, *Ephydatia muelleri*
Prof. April Hill

10.30 OS -54: Differential expression analysis of RNAseq data during the formation of the aquiferous system in *Halichondria panicea* (Suberitida, Demospongiae)
Dr. Nadia Santodomingo

10.45 OS -55: Expansion of oxygen-associated pathways at the dawn of animals
Dr. Warren Francis

11.00 Coffee Break

Session 13: Sponge and their environment- A Lab Approach
Chair: Dr. Manuel Maldonado

11.20 OS -56: Metabolic plasticity of HMA sponges allows them to completely oxidize all reduced sources in the water: an energetic view
Dr. Marta Ribes

11.35 OS -57: Differential gene expression analysis in the threatened sponge *Spongia officinalis* following exposure to different temperature conditions
Ms. Vasiliki Koutsouveli

11.50 OS -58: Sponges in a high C0$_2$ World: A mechanistic understanding of sponge tolerance to elevated pCO$_2$ and temperature
Ms. Holly Bennett

12.05 OS -59: Pressure-response relationships of sponges to dredge pressures – a laboratory approach
Dr. Mari-Carmen Pineda

12.20 OS – 60: Glass Sponge Pump Rates and their Role in Biogeochemical Cycles in the Weddell Sea, Antarctica
Ms. Luisa Federwisch

12.35 OS -61: Effects of copper on early development of the freshwater sponge *Radiospongilla inesi*
Mr. Ulisses Pinheiro

12.50 OS- 62: Sub-lethal stress responses of sponges to dredging pressures
Mr. Brian Strehlow

13.05 Lunch

Session 14: Organismal Biology
Chair: Dr Christine Schönberg

14.00 KN -10: Keynote Speaker, Prof. Peter Schupp
Rising of the Porifera: Are sponges becoming the dominant sessile benthic organisms in certain habitats?

14.25 OS -63: Multispecies competitive interactions among coral, sponges and macroalgae in St. Thomas, U.S. Virgin Islands
Ms. Lauren Olinger

14.40 OS – 64: Specificity of predator defenses of tropical marine sponges
Dr. Janie Wulff

14.55 OS – 65: Sponges produces a chemical seascape acting on benthic ecosystem functioning
Dr. Thierry Perez

15.10 OS – 66: Using 3D photogrammetry to model sponge morphological plasticity
Dr. Amy Scott-Murray

15.25 OS- 67: Diversity in Epibenthic Megafauna Associated with a Unique Vase Glass Sponge Ground in the Emerald Basin
Mr. Nicholas Hawkes

15.40 OT -68**:** Taxonomic, phylogenetic, microbial and ecological assessment of two coral-killing cyanobacteriosponges in the Spermonde Archipelago, Indonesia
Ms. Esther van der Ent

15.55 Coffee Break

Session 15 : Molecular, Cell and Organismal Biology Speed Talks
Chair: Prof Peter Schupp and Dr. Ana Riesgo

16.25 ST – 54: A molecular approach to understanding the resurrected order Axinellida
Dr. Jane Fromont

16.30 ST – 55: Mitochondrial basic leucine zipper (bZIP) regulatory domain from freshwater sponges conserved across animals
Dr. Bruna Plese

16.35 ST – 56: Regeneration in sponges
Prof. Alexander Ereskovsky

16.40 ST – 57: Spatially and temporally variable oxygen conditions as determinant of microbial processes in and around Irish sponges
Dr. Marie-Lise Schläppy

16.45 ST – 58: Evolution on Ice: Molecular Adaptation to Temperature in Antarctic Sponge Species
Dr. Nathan J Kenny

16.50 ST – 59: Osculum dynamics and filtration activity studied in small single-osculum demosponge (*Halichondria panicea*) explants
Mr. Lars Kumala

16.55 ST – 60: Plastic additive changes contraction patterns in *Hymeniacidon heliophila*: A change point analysis
Ms. Liv Goldstein Ascer

17.00 ST – 61: In vitro formation of chimaeric individuals after cell dissociation in a calcareous sponge
Dr. André Padua

17.05 ST – 62: Spatiotemporal Variation and the Invasibility of Mesofaunal Communities Associated with *Tedania iginis*.
Ms. Kate Hill

17.10 ST – 63: Getting started with the whole genome sequencing project of the demosponge *Geodia barretti*
Ms. Karin Steffen

17.15 ST – 64: The Mechanism underlying carbonate dissolution by excavating sponges: pH reduction and cell differentiation
Ms. Alice Webb

17.20 ST – 65: Infection with *Aplysina* Red Band Syndrome results in biochemical and bacterial community changes to the holobiont
Dr. Julie Olson

19.30 Conference Dinner in the Meyrick Hotel with Live Entertainment

Friday, June 30, 2017

Session 16: Ecology 5: Ecosystems and Environment
Chair: Dr Shirley Pomponi

09.30 KN – 11: Keynote Speaker, Dr. Manuel Maldonado
The marine silicon cycle in the light of sponge silica: a global review

09.55 OS – 69: Silica-induced fibrosis: an ancient response from the early metazoan
Prof. Marco Giovine

10.10 OS -70: Silicon consumption kinetics in demosponges
Ms. Maria Lopez-Acosta

10.25 ST- 66: Effects of dredging on benthic filter feeding
Dr. Muhammad Azmi Abdul Wahab

10.30 ST- 67: Spatiotemporal variations in stable isotope signatures (delta13C and delta15N) of sponges on the Saba Bank, Caribbean Sea
Dr Fleur van Duyl

10.35 ST- 68: What Dictates Sponge Distribution Patterns?: Use Of Freshwater Sponges To Assess Species Requirements
Dr. Karen Evans

10.40 ST- 69: Evaluating The Influence Of Abiotic Factors On The Recruitment Rate Of Calcareous Sponges (Porifera, Calcarea) In Salvador, Bahia State, Tropical Brazilian Coast.
Prof. Fernanda Cavalcanti

10.45 ST – 70: Deep-sea sponges under stress: from nutrient sources to nutrient sinks?
Dr. Christine Rooks

10.50 ST- 71: A Trophic Niche Separation May Explain the Tight Coexistence of High (HMA) and Low (LMA) Microbial-Abundance Sponges
Dr. Teresa Morganti

11.00 Coffee Break

Session 17: Sponge Conferences past, present, future
Chair: Prof Grace McCormack

11.20 OS- 71: Sponge science culture and demography
Dr. Christine Schönberg

11.45 Prizes

11.50 Next Step

12.30 Official Conference Closing

14.00 Systematics Update & Discussion

14.45 Genomics Forum

15.00 Hexactinellid Identification Workshop with Dr Henry Reiswig
Venue: Lab, MRI

Plenary Session

Sensation and the energetics of sponge filter feeding

Sally P. Leys[1]

[1]Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada T6G 2E9 sleys@ualberta.ca

Sponges are one of the earliest evolving animal lineages. They lack nerves yet have at least two well-documented sensory cells: ciliary photoreceptors for phototaxis in larvae, and primary cilia in the osculum that may trigger contractions to expel unwanted debris. In other animals, primary cilia also detect subtle changes in the environment such as pH, temperature, chemicals and fluid motion. We have been studying the evolution of sensory systems using sponges as a model and wondered whether sensory cilia might function in a similar way in sponges. Sponges are thought to take advantage of passive flow to enhance their feeding, yet given their sensory systems, is this really passive? Could sensory cilia allow a sponge to detect and respond to changes in its fluid environment?

Using flow and oxygen sensors we have studied metabolism and energetics of shallow water demosponges in temperate and tropical waters, and in glass sponges at 200m-deep sponge reefs on the continental shelf of the Pacific coast of Canada. We also used morphology to model the resistance across the filter in each of these sponges' aquiferous systems. Our results show radical adaptations to habitats and highlight the need for sponges to sense their environment to optimize metabolism. Shallow warm-water species filter large volumes of water at a high energetic cost; shallow cold-water species filter small volumes at a reduced cost; and glass sponges filter large volumes to survive in food- poor deep water, but use ambient flow to enhance filtration at reduced cost. In contrast, at least one species of deep-water demosponge with high microbial abundance does not take advantage of ambient flow, suggesting a diminished reliance on particulate carbon in exchange for nutrition derived from dissolved carbon and symbionts.

If the filter feeding seen in modern sponges was a feeding mechanism used by the earliest evolving animals, then reducing the cost of filtration would have been an effective driver of the evolution of sensory and signalling systems, and would have given rise to a diversity of sensory responses. The range of sensory systems in sponges may have allowed them to respond and adapt to conditions in early oceans; these same sensory systems may also allow them to respond to the changes in our oceans that are already taking place, or are still to come.

Financial support by the Natural Science and Engineering Research Council of Canada Discovery Grants, NSERC Strategic Grants (CHONeI and CHONeII), Department of Fisheries and Oceans, and the Norwegian Research Council, is gratefully acknowledged.

Evolution

A Solution to the Conundrum of Non-Bilaterian Relationships?

Gert Wörheide[1,2], Paul Simion[3], Michael Eitel[1], Michaël Manuel[4], Hervé Philippe[4], Davide Pisani[6]

[1] *Department of Earth- and Environmental Sciences, Paleontology and Geobiology & GeoBio-Center, Ludwig-Maximilians-Universität München. woerheide@lmu.de*

[2] *SNSB – Bayerische Staatssammlung für Paläontologie und Geologie*

[3] *Sorbonne Universités, UPMC Univ paris 06, CNRS, Evolution Paris-Seine, Institut de Biologie Paris- Seine, Paris, France*

[4] *Sorbonne Universités, UPMC Univ Paris 06, CNRS, Evolution Paris-Seine UMR7138, Institut de Biologie, Paris-Seine, Case 05, 7 quai St Bernard, 75005 Paris, France*

[5] *Centre de Théorisation et de Modélisation de la Biodiversité, Station d'Ecologie Théorique et Expérimentale, UMR CNRS 5321, Moulis 09200, France.*

[6] *School of Earth Sciences, University of Bristol, UK; [2]*

Despite many years of intense effort, the deep phylogenetic relationships of the five major animal lineages Porifera, Placozoa, Ctenophora, Cnidaria, and Bilateria remain problematic and highly controversial. Recent attempts to address this difficult phylogenetic question using large molecular datasets failed to find an agreement especially on the position of ctenophores relative to the other metazoans. Instead of resolving the problems, these studies rather fuelled old debates initiated by morphologists long ago.

Here, the current status of non-bilaterian phylogenomics will briefly be reviewed and some of the most important controversial issues highlighted to show that some of the most recent large phylogenomic datasets, partially building on recently sequenced genomes, are still sensible to systematic error. Analyses of new datasets will be presented that provide a large step towards a robust solution to the conundrum of non-bilaterian relationships – those datasets all converge on the same solution to place especially Porifera in the tree of life.

Sponges versus Ctenophora : The Evolution of Epithelial Proteins

André Le Bivic[1], Hassiba Belahbib[2], Emmanuelle Renard[3], Carole Borchiellini[3]

[1] *Institut de Biologie du Développement de Marseille, Aix-Marseille University, France*

[2] *Information Génomique et Structurale, Aix-Marseille University, France*

[3] *Institut Méditerranéen de Biodiversité et d'Ecologie, Aix-Marseille University, France. Carole.borchiellini@imbe.fr*

Bilaterian epithelia were defined by the presence of three major features: cell polarity, cell-cell junctions, presence of a basement membrane that are central to their key functions[1] : the regulation of internal/external exchanges and morphogenesis. The persistent neglect of the diversity across non-bilaterian animals prevented objective comparisons and evolutionary interpretations on epithelial structure.

Despite the absence of a basement membrane in all but one sponge class, Porifera possess bona fide functional epithelia and most of the proteins involved in cell polarity and adhesion of bilaterians. It now remains to decipher whether these conserved proteins have conserved interactions and functions in sponges. To this purpose, proteins that compose and pattern adherens junctions were carefully identified and analyzed from private and publicly available transcriptomic and genomic databases of the four classes of Porifera, two genera of Ctenophora and Placozoa : classical cadherins (E- type) and catenins, Par3/Par6/aPKC and Crumbs apical polarity complexes themselves dependent on the Scribble lateral polarity complex. In sponges, we found contrasted results in accordance with contrasted epithelial features. In addition, we found a totally unexpected lack of conservation of the epithelial toolkit in Ctenophores asking for a profound revision of our understanding of Ctenophore biology. Ancestral state or very derived character? These findings will be discussed in the context of the hot debate opposing sponge-first and ctenophore-first hypotheses.

References

1. Le Bivic, A. Evolution and cell physiology. 4. Why invent yet another protein complex to build junctions in epithelial cells? (2013) *Am J Physiol Cell Physiol*. Dec 15; 305(12):C1193-201.

Financial support by "investissement d'avenir" French Government program, A*MIDEX project (n° ANR-11-IDEX-0001-02) is gratefully acknowledged.

Save the best for the last: mRNA editing and multiple linear chromosomes in mitochondria of calcaronean sponges.

Dennis Lavrov[1]

[1] *Department of Ecology, Evolution, and Organismal Biology, Iowa State University, Ames, Iowa, USA. dlavrov@iastate.edu*

Animal mitochondrial DNA (mtDNA) is commonly described as a small, circular molecule that is conserved in size, gene content, genome organization and high rate of sequence evolution. Studies in four major classes of sponges challenged this view by revealing substantial mitochondrial diversity both among and within these groups[1]. Our recent work on mitochondrial genomes from calcaronean sponges uncovered what is arguably the most unusual mtDNA both in sponges and animals in general[2]. Not only do mt-genomes of calcaronean sponges consist of multiple small linear chromosomes, but all mt-coding sequences in this group are edited at RNA level by multiple insertions of single or double uridylate (U) (See figure below). Here I will describe the patterns and process of RNA editing in calcaronean mitochondria, its influence and interdependence with genome organization, and potential mechanisms involved.

References

1. D. Lavrov and W. Pett, Genome Biol. Evol. 8 (2010) 2896-2913.
2. D. Lavrov, M. Adamski, P. Chevaldonné, and M. Adamska, Curr. Biol. 26 (2016). 86-92.

Financial support by NSF and Iowa State University is gratefully acknowledged.

Think like a sponge: Examining neural-marker genes in context

Jasmine Mah[1] & Sally P. Leys[1]

[1] *Department of Biological Sciences, University of Alberta, Edmonton, Canada. jmah@ualberta.ca*

The assertion that Ctenophora is the most basal phylum[1] strikes dissonance with the apparent simplicity of sponges. Yet sponges harbour a surprising degree of genetic complexity[2], including the presence of neural-marker genes. Given that ctenophores possess a full nervous system, are neural-marker genes indicative of a 'proto-nervous' system, or nervous system loss in sponges? Bilaterian gene function is not necessarily conserved in non-bilaterian animals; genetic and functional context is required to interpret this data. We performed a meta-analysis of *in situ* hybridization studies in sponges to examine all current gene expression data. It revealed that while sensory structures do express neural-marker genes, so do cell types with no known sensory function. We also performed an RNA-seq experiment investigating the osculum, a sponge sensory organ.

We asked whether a particular set of genes was associated with the osculum, and whether some of these were neural-marker genes. Oscular development was examined by comparing the pre-oscular and juvenile stages of *Spongilla lacustris*, while the osculum itself was investigated by comparing the oscular and body tissue of *Aphrocallistes vastus* (Fig. 1). With few exceptions, neural-marker genes were not differentially expressed during oscular development and in the osculum itself. However, a distinct cohort of genes was upregulated in the osculum and during its development, indicating that at the molecular level the osculum is a specialized structure. This, together with a lack of evidence for neural function of neural-marker genes suggests neural-marker genes have cryptic, non-sensory functions in sponges.

References

1. J. Ryan et al. Science, 342(6164) (2013) DOI: 10.1126/science.1242592.
2. M. Srivastava et al. Nature, 466 (2010) 720-726.

Financial support from NSERC Discovery and PGM, Alberta Innovates and the Alberta Government is gratefully acknowledged.

Tetractinellida is a hot-spot of Group I Introns: vertical gene transfer, secondary losses and implications for DNA barcoding

Astrid Schuster[1], Jose V. Lopez[2], Leontine E. Becking[3, 4], Shirley A. Pomponi[5], Michelle Kelly[6], Gert Wörheide[1, 7, 8], Dirk Erpenbeck[1, 8], Paco Cárdenas[9]

1. Department of Earth- & Environmental Sciences, Palaeontology and Geobiology, Ludwig- Maximilians-Universität München, Richard-Wagner Str. 10, 80333 Munich, Germany.
a.schuster@lrz.uni-muenchen.de
2. Center of Excellence in Coral Reef Ecosystem Research, Nova Southeastern University, Dania Beach, FL 33004, USA.
3. Marine Animal Ecology, Wageningen University & Research Centre, P.O. Box 3700 AH Wageningen, The Netherlands.
4. Naturalis Biodiversity Center, Marine Zoology Department, PO Box 9517, 2300 RA Leiden, The Netherlands.
5. Harbor Branch Oceanographic Institute-Florida Atlantic University, 5600 U.S. 1 North, Ft Pierce, FL 34946, USA.
6. National Centre for Aquatic Biodiversity and Biosecurity, National Institute of Water and Atmospheric Research, P.O. Box 109-695, Newmarket, Auckland, New Zealand.
7. SNSB – Bavarian State Collections of Palaeontology and Geology, Richard-Wagner Str. 10, 80333 Munich, Germany.
8. GeoBio-CenterLMU, Ludwig-Maximilians-Universität München, Richard-Wagner Str. 10, 80333 Munich, Germany.
9. Department of Medicinal Chemistry, Division of Pharmacognosy, BioMedical Center, Uppsala University, Husargatan 3, 75123 Uppsala, Sweden.

Introns constitute "selfish" and "mobile" genetic elements that intermit coding regions of genes. In eukaryotic mitochondrial genomes they are divided into Group I and Group II introns according to their splicing mechanisms and secondary structures. In metazoans they have so far only been detected in sponges, cnidarians, placozoans and one annelid species. Within demosponges, Group I and Group II introns are present in six families. Based on their different insertion sites within the *cox1* gene and their secondary structure, four types of Group I and two types of Group II introns are known, which harbour homing endonuclease genes (HEG) of the LAGLIDADG family (Group I) and/or reverse transcriptase (Group II).

In the current study we analysed the largest dataset to date on sponge mitochondrial introns (95 taxa), encompassing 11 different sponge genera. We provide strong evidence that one LAGLIDADG encoding gene was vertically transmitted within the subtropical-tropical genus *Cinachyrella* (family Tetillidae) for which we analysed 73 samples comprising 13 species. Additionally, the extent of independent horizontal gene transfer between different demosponge groups was studied. Furthermore, we detected for the first time up to two introns in the family Scleritodermidae. Finally, our study highlights the potential biases and consequences of using standard *cox1* barcoding primers in demosponge systematics and DNA barcoding.

Evolution and Development of the Skeleton in Selective Marine Haplosclerids

Jose Maria Aguilar-Camacho[1], Liam Morrison[2] & Grace P. McCormack[1]

[1] Zoology, School of Natural Sciences and Ryan Institute, National University of Ireland Galway, University Rd., Galway, Ireland
[2] Earth and Ocean Sciences and Ryan Institute, National University of Ireland Galway, Galway, University Rd., Galway, Ireland

Marine haplosclerids are one of the most diverse groups of sponges in terms of habitat exploited and numbers of species. All haplosclerids share a simple skeleton comprised only of oxeas or strongyles as megascleres. The arrangement of the spicules in the skeleton has been used as a diagnostic feature for species identification but there is incongruence between morphological classification and molecular phylogeny based on mitochondrial and nuclear markers. Greater understanding of the evolution vs environmental influence on the skeleton using an integrated approach will inform systematics in this difficult group. In addition to employing morphological, ultrastructural and ecological approaches transcriptomes from specimens of three species dispersed across three major clades (A) *Haliclona oculata,* B) *H. simulans* and C) *H indistincta*) were sequenced, assembled and analysed. Silicateins and cathepsins-L were identified from this data and from all other available sponge transcriptomes and genomes. We identified cathepsins L in all the four major classes within Porifera but silicateins were only found in demosponges. A novel scenario in the evolution of the silicateins in sponges will be presented. We recognize silicatein types based on the aminoacid composition of the active site, 1) SHN, 2)C/SQN and 3)CHN. All demosponges have at least one copy of the first type (SHN). The second type (C/SQN) is only present in haplosclerids. The third type (CHN) was not found in all transcriptomes analysed. This latter type was found in all haplosclerids and some other demosponges but no obvious phylogenetic pattern could be determined. The SHN type can be further divided into three subtypes (α, β, γ) and while all other demosponges (bearing spicules) analysed had more than two of these copies (i.e. Poecilosclerids, astrophorids and freshwater sponges) haplosclerids only possess silicatein β. We hypothesise that the simplicity of the skeleton in marine haplosclerids maybe related to this genomic feature and differences in the skeletal architecture amongst haplosclerid species may be due to differential expression of the various silicatein copies. To explore the impact of environment on skeletal architecture a comparison of the transcriptomes of branching vs encrusting morphotypes from *Haliclona simulans* was carried out. Morphotypes found in habitats with different energy environments were found to possess different skeletal architectures. Comparative transcriptomics showed 19 differentially expressed genes between the morphotypes, however no differences in expression levels of any silicatein genes were identified. Further investigations using RT-qPCR to compare expression patterns of the silicatein genes within and between species are ongoing and some of this data will also be presented.

Molecular Diversity of Demosponges in the Indo-Pacific

Dirk Erpenbeck [1, 2], Astrid Schuster[1], Oliver Voigt[1], Kathryn Hall[3], Merrick Ekins[3], Christine Schönberg[4], Nicole J. de Voogd[5], Michelle Kelly[6], John N.A. Hooper[3, 7], Cecile Debitus[8], Gert Wörheide[1, 2, 9]

1 Department of Earth- & Environmental Sciences, Palaeontology and Geobiology, Ludwig-Maximilians-Universität München, Richard-Wagner Str. 10, 80333
Munich, Germany erpenbeck@lmu.de
2 GeoBio-CenterLMU, Ludwig-Maximilians-Universität München, Richard-Wagner Str. 10, 80333 Munich, Germany
3 Biodiversity Program, Queensland Museum, PO Box 3300, South Brisbane, QLD 4101, Australia
4 School of Earth and Environment and Oceans Institute The University of Western Australia, Crawley, WA 6009, Australia
5 Naturalis Biodiversity Center, P.O. Box 9517, 2300 RA Leiden, the Netherlands
6 National Centre for Coasts and Oceans, National Institute of Water and Atmospheric Research, Private Bag 99940, Newmarket, Auckland, 1149, New Zealand
7 Eskitis Institute, Griffith University, Nathan, QLD, Australia
8 LEMAR, IUEM Technopôle Brest-Iroise, Plouzané, France
9 SNSB - Bavarian State Collections of Palaeontology and Geology, Richard-Wagner Str. 10. 80333 Munich, Germany.

The Indo-Pacific is the world's largest marine biogeographic region, covering tropical and subtropical waters from the Red Sea to Easter Island. It is characterized by taxon specific and different degrees of biogeographic connectivity, in particular, in its marine realm. The Indo-Pacific also harbours the majority of demosponge species currently known to science. Comparisons between several regional sponge faunas have been undertaken in the past - most based on morphological features of individual putative sponge species. The Sponge Barcoding Project (www.spongebarcoding.org), in tandem with other regional molecular taxonomy campaigns, has now provided one of the largest molecular data sets from the Indo-Pacific that includes several independent molecular markers, such as mitochondrial gene sequences as well as nuclear rDNA. This data, acquired from analyses of sponges, for example, from the Red Sea, Mayotte, Mauritius, Indonesia, Thailand, Western Australia, Queensland and Polynesian Islands now provides a platform to investigate fundamental but as yet unanswered questions on the distribution, evolution, dispersal and ecology of demosponges in the Indo-Pacific. For example, the use of molecular tools has thus far rejected the presence of cosmopolitan or otherwise very widespread sponge species based on few case studies. This is consistent with the hypotheses of a higher level of endemism among marine invertebrates than previously thought. Reasons for this might be, for example, the short life-span of the sponge larvae or adaptations to special ecological niches. Therefore, we analyze with the most comprehensive data set on Indo-Pacific demosponges whether we can generally assume a high level of endemism throughout this area and provide the fundament for subsequent in-depth regional assessments of demosponge biodiversity.

Foliose fans of the sea: the Phyllospongiinae

Muhammad Azmi Abdul Wahab[1], Jane Fromont[2], Oliver Gomez[2], Nikos Andreakis[1] & Nerida Wilson[2, 3]

[1]Australian Institute of Marine Science, Indian Ocean Marine Research Centre, The University of Western Australia (MO96) 35 Stirling Hwy, Crawley WA 6009, m.abdulwahab@aims.gov.au

[2]Department of Aquatic Zoology, Western Australian Museum, Locked Bag 49, Welshpool DC, WA 6986, Western Australia, Australia

[3]Molecular Systematics Unit, Western Australian Museum, Locked Bag 49, Welshpool DC, WA 6986, Western Australia, Australia

The Phyllospongiinae are unique within the Thorectidae in having foliose, lamellate, or digitate forms and, except in one genus, the possession of tertiary fibres. Five genera are recognised within the subfamily, and are distinguished by the presence or absence of surface armour, fasciculation of primary fibres, type of patterning around the oscules, and details of the tertiary skeleton. Abdul Wahab et al. (2014) using ITS2 and morphological characteristics of tropical Australian specimens, found good support for eight clades, some of which represented well known species such as *Phyllospongia lamellosa, P. papyracea, Carteriospongia foliascens, C. flabellifera* and *Strepsichordaia lendenfeldi*. However, they also found discrepancies in generic assignments of species of *Phyllospongia* and *Carteriospongia*. Our study aims to resolve these discrepancies by utilising additional specimens and three gene regions of 28S (D1-D2, D3-D5, D6-D8) and whole 18S ribosomal subunits, as well as the Internal Transcribed Spacer 2 region and ATP Synthase 8, and by further examining morphological features. The inclusion of additional phyllospongiinid species within the genera *Candidaspongia* and *Lendenfeldia*, and a genus from the sister subfamily Thorectinae (*Cacospongia* spp.) further explores phylogenetic and morphological associations for the Thorectidae.

References

1. Abdul Wahab et al. (2014) Combining morphometrics with molecular taxonomy: How different are similar foliose keratose sponges from the Australian tropics? Mol. Phylogenet. Evol. 73: 23–29.

This work was funded by the Gorgon Project's Barrow Island Net Conservation Benefits Fund, which is administered by the Department of Parks and Wildlife, and the Western Australian Museum, Western Australia, Australia.

Diversity analysis of a fossil sponge fauna (Hexactinellida and Demospongiae) from Italy (Eocene, Lessini Mts)

Viviana Frisone [1], Andrzej Pisera [2], Nereo Preto [3] & Wolfgang Kiessling [4]

[1] Museo di Archeologia e Scienze Naturali 'G. Zannato', Montecchio Maggiore, Italy museo.scienze@comune.montecchio-maggiore.vi.it

[2] Institute of Paleobiology, Polish Academy of Science, Warsawa, Poland

[3] Università degli Studi di Padova, Dipartimento di Geoscienze, Padova, Italy

[4] GeoZentrum Nordbayern, Universität Erlangen, Erlangen, Germany

The bodily preserved sponge fauna from the middle Eocene (ca. 48 Ma) of Chiampo

Valley in north-eastern Italy shows a high diversity, with 32 species.

A systematic study by Frisone et al. (2016) identified fifteen hexactinellid species (47% of the total), among which one (3%) belongs to the order Lyssacinosida, seven to Hexactinosida (22%) and seven to Lychniscosida (22%). Seventeen species belong to the class Demospongiae (53%), of which 15 are lithistids (47%) and two (*Astrosclera* sp. and *Vaceletia progenitor* Pickett, 1982) are non-lithistids (6%). The percentage values above are based on museum material and selective sampling for well-preserved sponges and are thus unlikely to reflect true abundance patterns. To explore the rank-abundance distribution of the sponge fauna more rigorously, we performed repeated bulk sampling at the original collection site. We gathered 362 specimens that could be assigned to 23 taxonomic entities, usually species. Of the sampled individuals, 92% belong to Hexactinellida, while only 8% belong to Demospongiae. At the ordinal level, 68.1% of the specimens belong to Hexactinosida, 19.6% to Lychniscosida, 4.3% to Lyssacinosida, and 7.9% are lithistids. These numbers differ substantially from the museum-based material, which suggests that quantitative information from museum material should be treated with care. For example, non- lithistid sponges were probably not found because they are too rare to be represented in the random sampling.

Hexactinellids are strongly dominant over lithistids in the Chiampo fauna. Additional evidence supports a middle to outer carbonate ramp depositional environment of the assemblage: (1) the most common taxa dwell in rather deep water today. Examples are *Laocoetis*, *Hexactinella* and lyssacinosids; (2) the absence of shallow water "ceractinomorphs" (*sensu* Buckeridge et al. 2013) non-lithistid demosponges; and (3) sedimentological evidence and composition of the associated fauna (e.g. planktonic foraminifera and pteropods).

The presence of sponge clusters, delicate encrusting bases, and various ontogenetic stages provides evidence that the Chiampo fauna is autochthonous and was rapidly buried. The rank-abundance distribution suggests a moderately complex community with a Zipf-Mandelbrot distribution, characterised by relatively long tail of rare species.

References

1. V. Frisone, A. Pisera, N. Preto, J. Syst. Palaeontol. 14 (2016) 949-1002
2. J.S. Buckeridge, M. Kelly, D. Janussen, H.M. Reiswig, New Zeal. J. Geol. Geop. 56 (2013) 171-185

The *Chondrilla* species complex along N-S gradient in the tropical Western Atlantic: an integrative approach

Carla Zilberberg[1], C. Lazoski[2], Alexander V. Ereskovsky[3], Marinella S. Laport[4], Cristiane Hardoim[4, 5], Michelle Klautau[6], Antonio M. Solé-Cava[7] & Nicole Boury-Esnault[3]

[1]Universidade Federal do Rio de Janeiro, Departamento de Zoologia, Laboratório de Biodiversidade de Cnidaria, Rio de Janeiro, Brazil

[2]Universidade Federal do Rio de Janeiro, Departamento de Genética, Rio de Janeiro, Brazil

[3]Mediterranean Institute of Marine and Terrestrial Biodiversity and Ecology, Aix Marseille University, CNRS, IRD, Marseille, France

[4]Universidade Federal do Rio de Janeiro, Instituto de Microbiologia Paulo de Góes, Laboratório de Bacteriologia Molecular e Marinha, Rio de Janeiro, Brazil.

[5]Universidade Federal do Rio de Janeiro, Museu Nacional, Rio de Janeiro, Brazil

[6]Universidade Federal do Rio de Janeiro, Departamento de Zoologia, Laboratório de Biologia de Porifera, Rio de Janeiro, Brazil

[7]Universidade Federal do Rio de Janeiro, Departamento de Genética, Laboratório de Biodiversidade Molecular, Rio de Janeiro, Brazil

The biodiversity of *Chondrilla* species along a N-S gradient in the Tropical Western Atlantic was studied, including the Eastern Caribbean, Florida, Belize, Bahamas and several localities along the Brazilian coast. Specimens from the type locality of *Chondrilla nucula* (the Mediterranean Sea) were included in the phylogenetic analyses and *C. australiensis* was added as an outgroup. The molecular markers used were the Folmer region of the COI mtDNA, the spacer between COII and ATP6 mtDNA, and the region encompassing the ITS1, 5.8S and ITS2 rDNA. The COI mtDNA had the best resolution in the phylogenetic analyses, so this region was chosen for the haplotype network analysis. A cytological study was also done to compare the sponge cells and symbiotic microorganisms of Mediterranean *C. nucula* with those from the Eastern Caribbean and Brazilian coast. The phylogenetic and phylogeographic analyses demonstrated that in the Tropical Western Atlantic there are four species of *Chondrilla*, which are genetically different from *C. nucula*. The cytological results showed that cells with inclusions are particularly abundant and the morphology of the spherulous cells is typical of the genus *Chondrilla*. Granular cells of different types allowed discrimination between the Mediterranean and the Tropical Western Atlantic species. At least three symbiotic morphotypes were found in *Chondrilla* species: coccoid cyanobacteria, Gram-positive and Gram-negative rod shape cells. This study highlights the importance of integrative approaches to identify and describe sponge species, particularly those with one to few spicule types.

Biodiversity and biogeography of Tropical Western Atlantic Calcarea (Porifera)

Fernanda Azevedo [1], Báslavi Cóndor-Luján[1], André Padua[1], Taynara Louzada[1], Tayara Fontana[1], Raisa Rizzieri[1], Pedro Leocorny[1], Eduardo Hajdu[2], Thierry Pérez[3] & Michelle Klautau[1]

[1]Universidade Federal do Rio de Janeiro, Instituto de Biologia, Departamento de Zoologia, Av. Carlos Chagas Filho, 373. CEP 21941-902. Rio de Janeiro, Brazil. nandaporifera@gmail.com, mklautau@gmail.com

[2]Universidade Federal do Rio de Janeiro, Museu Nacional, Quinta da Boa Vista s/n, 20940-040, Rio de Janeiro, RJ, Brazil.

[3]Institut Méditerranéen de Biodiversité et d'Ecologie marine et continentale, CNRS, Aix Marseille Univ, IRD, Avignon Univ., Station Marine d'Endoume, rue de la Batterie des Lions, 13007 Marseille.

According to the Census of Marine Life, the Caribbean and the South America marine shelves are two of the most threatened regions of the world, submitted to various local anthropogenic pressures and to the Global Change (1, 2). Allied to this, taxonomic knowledge is insufficient for many marine taxa, sponges notorious among these. This context justifies biological inventories in order to feed programs for the preservation of marine natural resources and ecosystem services in this area. The International Associated Laboratory (LIA-MARRIO) was implemented in 2013 to fill in gaps of knowledge on the sponge diversity of the Tropical Western Atlantic (from Brazil to North of the Caribbean Sea). A huge collection was acquired along the Lesser Antilles and the Brazilian Coast, resulting in more than 700 specimens of the class Calcarea which is the focus of the present study. Calcareous sponges are generally neglected in scientific field surveys; consequently, their diversity is seriously underestimated worldwide. In the TWA, only 68 species were known. Therefore, the goals of this study were to determine richness, distributional, and endemism patterns of calcareous sponges, by means of an integrative taxonomic approach (morphology and rDNA) to identify species.

Preliminary results increased the number of Calcarea in the Caribbean from 24 to 42, and in the Brazilian Coast from 52 to 70 species. Both areas share 18 species, of which 15 are calcineans belonging to *Arthuria*, *Ascandra*, *Borojevia*, *Clathrina*, *Ernstia*, *Leucaltis*, *Leucetta*, and *Nicola* genera, and 3 are calcaroneans of the *Leucandra*, *Leucilla*, and *Sycon* genera. Overall, the TWA Calcarea fauna increased from 68 to 98 species. The Caribbean Province exhibits a higher provisional endemism of 59%. The Tropical Southwestern Atlantic and the Warm Temperate Southwestern Atlantic exhibited respectively 47% and 36% of endemism, as well as a variety of discontinuous patterns with unexpectedly wide distributions. Indeed, species belonging to calcinean (*Arthuria*, *Ascaltis*, *Ascandra*, *Clathrina*, *Ernstia*) and calcaronean genera (*Leucilla*, *Paraleucilla*, *Sycettusa*, *Vosmaeropsis*) also occur in Eastern South America, Eastern Atlantic, Northeastern Atlantic, Arctic, Mediterranean Sea, Western Indian Ocean and Australia. Four major patterns of endemism were recovered in the TWA, and a total of 30 new species are still awaiting completion of their detailed integrative descriptions.

References

1. M.J. Costello, M. Coll, R. Danovaro, P. Halpin, H. Ojaveer, P. Miloslavich, PLoS ONE, 5(8) (2010):e12110. doi:10.1371/journal.pone.0012110.
2. P. Miloslavich, J.M. Díaz, E. Klein, J.J. Alvarado, C. Díaz, J. Gobin, E. Escobar-Briones, J.J. Cruz-
3. Motta, E. Weil, J. Cortés, A.C. Bastidas, R. Robertson, F. Zapata, A. Martín, J. Castillo, A. Kazandjian, M. Ortiz, PLoS ONE, 5(8) (2010): e11916. doi:10.1371/journal.pone.0011916.

Financial support by CAPES, CNPq, FAPERJ, CNRS, LIA MARRIO and Fundação Grupo Boticário.

Systematics

The Evolution of Sponge Systematics from Aristotle (4th BC) to the 10th World Sponge Conference in Galway (21stAC).

Nicole Boury-Esnault

IMBE, CNRS, Aix Marseille University, Station Marine d'Endoume, 13007 Marseille, France.
E-mail : nicole.boury-esnault@orange.fr

Aristotle studied sponges in Lesbos Island (Eastern Mediterranean) where there was an important community of sponge fishermen. In his "*History of Animals*" he was able to distinguish 5 species of dictyoceratid sponges. He made observations on live sponges, noting the presence of pores and water flow, their ability to regenerate, differences in consistency, habitat and depth (Voultsiadou, 2007). Several centuries later Linnaeus (18th AC) named 9 marine and 2 freshwater sponges that he placed in Cryptogamia, as he considered sponges a group of algae. For many years, depending on the author, sponges have been considered as animals or plants. However, most scientists observing sponges in life considered them as animals.

The first major step in the study of sponges came with the application of the light microscope which permitted a more detailed description of the skeleton. Donati (1750) was the first to describe and draw the skeleton consisting of "*minutissime spine*" of a "*Tetie sferica*" in his "*Storia naturale marina dell'Adriatico*". The word "**spicula**" appeared for the first time in the work of Ellis & Solander (1786). They noted that "*the texture of them* (e.g; sponges) *is very different in different species"* and they linked these differences to the organisation of the skeleton. However, it was Grant (1826, 1833) who emphasised the "*various and remarkable form of the skeleton*". He demonstrated that the skeleton can be siliceous, calcareous or composed of a horny substance. He described the different types of spicules, and saw that "*each form is indicative of a particular species*". These observations were the basis of the classification of sponges, and it is still one of the most important characters used in sponge taxonomy.

Bowerbank (1858) proposed a very precise protocol for the description of sponge species. In addition to the nature of the sponge skeleton and the position of skeletal elements in the body of the sponge, he also described the cells, the inhalant and exhalant orifices, the aquiferous system, the movement of the cilia, the reproduction and the presence of gemmules. He also attempted to define the variety of different spicules. The necessity to have a common language for sponge descriptions was a constant preoccupation for all sponge scientists and many followed Bowerbank, giving accurate descriptions of the skeleton, aquiferous system and anatomy. The plates illustrating the works of e.g; Schulze, Sollas, Ridley & Dendy, Haeckel and Topsent are a testimony to these accurate descriptions. However the classification was mainly based on the skeleton and the tentative use of cytological or reproductive characters were mostly ignored or rejected. A good example of this was the hypothesis of Minchin & Bidder (1898) which used cytological and embryological characters to classify Calcarea, It took more than a century for this hypothesis to gain acceptance!

During the second half of the 20th century the development of transmission and scanning electron microscopy permitted a better knowledge of the anatomical and cytological diversity of sponges. However as emphasised by Lévi (1956) "*taxonomists have ignored embryology and cytology, and embryologists and cytologists have completely neglected taxonomy*." Although some progress has been made and more taxonomists take into account cytology and embryology, these characters are not "universally" adopted except for sponges without skeletons!!

An important evolution in sponge taxonomy was the introduction of cladistics by Rob Van Soest (1984-1990). Although cladistics is nowadays accepted and applied in most recent works, spongologists are still faced with a huge problem, i.e., the absence of knowledgeabout the homology and ancestral state of skeletal characters.

After a slow start of molecular phylogeny at the end of 20th century, improvements in DNA sequencing combined with better phylogenetic methods enabled huge developments in molecular systematics at the beginning of the 21st century. Whilst some of this work was based solely on molecular markers, some used a more integrative approach. As Jenner (2004) underlined "*no single data set, molecular or morphological, can reasonably be expected to be the Holy Grail of phylogenetics*." The recent progress in sponge systematics is clearly the result of an integrative approach.

The importance of cytology towards integrative taxonomy of sponges

Alexander Ereskovsky[1, 2] & Philippe Willenz[3, 4]

[1] *Institut Méditerranéen de Biodiversité et d'Ecologie marine et continentale (IMBE), Aix Marseille Université, CNRS, IRD, Marseille, France*

[2] *Saint-Petersburg State University, Faculty of Biology, Department of Embryology, Saint-Petersburg, Russia*

[3] *Royal Belgian Institute of Natural Sciences, Taxonomy and Phylogeny, Bruxelles, Belgium*

[4] *Université Libre de Bruxelles, Laboratoire de Biologie Marine, Bruxelles, Belgium*

Traditional sponge taxonomy was initially based on the comparative morphology of spicules and their organization in a framework, or the shape of a fibrous network when present. With the development of molecular methods, population genetics, embryology data or phylogenetic and biogeographic analysis, a new concept of "integrative taxonomy" has emerged in the last decade. However, other characters as cytology, associated microbionts or embryonic development are still considered as marginal in sponge taxonomy. Although ultrastructural features recently appeared more and more necessary for species differentiation in groups lacking spicules like some Homoscleromorpha or some Verongimorpha, their use is still neglected for "spiculate taxa".

Some cells are present in all species but have no distinctive characters like pinacocytes, archaeocytes or lophocytes. If choanocytes bear distinctive features, in particular the position of the nucleus or the presence of periflagellar sleeves, different mesohylar cells with inclusions appear prominently promising in sponge taxonomy by their presence vs absence, or their particular morphology: spherulous, granular, globular, vacuolar cells, etc. We show the importance to compare all stages of cell ontogenesis (ex: pocket cells in *Halisarca* or spherulous cells in *Chondrilla*) and we bring forward the taxonomical value of cytology from the level of order to genus and even species.

Diversity of Deep-Water Lithistids of the Tropical Western Atlantic: Are They Really Isolated Survivors?

Andrzej Pisera

Institute of Paleobiology, Polish Academy of Sciences, ul. Twarda 51/55, 00-818 Warszawa, Poland apis@twarda.pan.pl

Lithistid sponges, a polyphyletic group of demosponges characterized by choanosomal articulated desma skeleton, are among the most common and diversified sponges in the fossil record. They are believed to be of low diversity today, sometimes treated as "isolated survivors of a much larger fossil sponge fauna" (Van Soest *et al.* 2012). However, recent studies (Pisera and Fromont 2010, Pisera unpublished) suggest that this picture may be wrong. The present study is based on new material from the several widely distributed localities in the tropical Western Atlantic (including Bermuda). Earlier Schmidt (1870, 1879, 1880) reported about 24 species from the same region, while Van Soest and Stentoft (1988) observed 14 species solely from Barbados. The study revealed 48 lithistid species (among them 26 new) belonging to 20 genera (including one new). Lithistids are dominated by Theonellidae (both in terms of diversity and number of specimens, represented by 3 genera and 16-17 species), the next in diversity being Scleritodermidae (4 genera and 6 species), Neopeltidae (3 genera, 7 species), Corallistidae, (2 genera, 6 species). Other less common are Azoricidae (2 species), Siphonididae (2 genera, 3 species), Macandrewiidae (3 species) Vetulinidae (2 species). Families Pleromidae and Desmanthidae has one species each. This diversity, incidentally similar to that known from other oceans, for example off Western Australia in the Indian Ocean (Pisera and Fromont 2010) or the SW Pacific in the New Caledonia region (Pisera unpublished), is also comparable to the diversity of Mesozoic lithistids reported from Europe (Pisera 1999). It clearly shows that lithistid demosponges are today not isolated survivors, but simply understudied group.

References

1. Pisera, A. 1999. Postpaleozoic history of the siliceous sponges with rigid skeleton. *Memoires of the Queensland Museum* 44: 463-472.
2. Pisera, A., Fromont, J. 2010. The lithistid fauna of Western Australia: general characteristics and distribution. In: *Ancient animals new challenges*. VIII World Sponge Conference 2010. Book of Abstracts, p. 296.
3. Schmidt, O. 1870. Grundzüge einer Spongien Fauna des atlantischen Gebietes. (Engelman: Leipzig).
4. Schmidt, O. 1879. Die Spongien des Meerbusen von Mexico. I Abt. Lithistiden. I Heft. (G. Fischer: Jena).

5. Schmidt, O. 1880. Die Spongien des Meerbusen von Mexico. II Heft. (G. Fischer: Jena).
6. Soest, R.W.M. Van, Stentoft, N. 1988. Barbados deep-water sponges. *Studies on the Fauna of Curaçao and other Caribbean Islands* 70: 1-175.
7. Van Soest, R.W.M., Boury-Esnault, N., Vacelet, J.; Dohrmann, M., Erpenbeck, D., de Voogd, N.J., Santodomingo, N., Vanhoorne, B., Kelly, M., Hooper, J.N.A. 2012. Global diversity of sponges (Porifera). *PLoS ONE*, 7, e35105.

Financial support by the Polish National Science Center Grant 2016/21/B/ST10/02332, to A. Pisera

Variation between Giant Barrel Sponges Around the Globe

Thomas Swierts[1], Daniel F. Cleary[2], Katja T.C.A. Peijnenburg[1] & Nicole J. de Voogd[1]

[1] *Naturalis Biodiversity Center, Leiden, the Netherlands Thomas.Swierts@naturalis.nl*

[2] *CESAM, Universidade de Aveiro, Aveiro, Portugal*

Three giant barrel sponge species have been described so far, with species delineations mainly based on geographical distributions. *Xestospongia muta* occurs in the Tropical Atlantic, *Xestospongia testudinaria* in the Indo-Pacific from the Red Sea to Taiwan and *Xestospongia bergquistia* is thought to be confined to inshore environments in Northern Australia where it lives in sympatry with *X. testudinaria*. It is virtually impossible to assign a specimen to especially *X. muta* or *X. testudinaria* without knowledge of its origin. This gives rise to the question whether genetic and morphological differences between the two species are yet to be exposed, or if the current species delineations do not represent the genetic and morphological variation between giant barrel sponges around the globe. Here we present the results of multiple studies seeking to map the variation between giant barrel sponges around the globe using different approaches, including phylogenetics, taxonomy and microbial biology. Our efforts revealed multiple genetically isolated lineages which were sometimes confined to certain water bodies or which had a preference for certain habitats. Furthermore, we found that specimens of both *X. muta* and *X. testudinaria* can be genetically more closely related to a giant barrel sponge in another ocean basin, than to a sympatric congener on the same reef. Some of the genetically isolated lineages also showed distinct morphological features as spicule size and organization of the ectosome and choanosome. Together these genetic and morphological differences make a strong case for the existence of additional species resulting from an intricate evolutionary history.

Homoscleromorpha diversity revised through an Integrative Systematics

César Ruiz[1], Thierry Pérez[1]

[1] *Institut Méditerranéen de biodiversité et d'Ecologie Marine et Continental (IMBE), UMR CNRS 7263, IRD 237, Aix-Marseille Université, Avignon Université, Station Marine d'Endoume, Marseille, France. cesar.ruiz@imbe.fr*

Homoscleromorpha taxonomy is one of the most challenging among Porifera. Recently elevated to the rank of Class, this group, made of one Order and two families, has seen a high rate of new descriptions over the last two decades. The development of an integrative taxonomic approach and the exploration of remote marine ecosystems have revealed an hidden diversity, highlighting the importance of complementary datasets such as morphology, cytology, chemistry and genetics to clarify erroneous identifications, cases of alleged cosmopolitanism and unresolved species-complexes. Using this integrative approach, we have studied the Homoscleromorpha dwelling in submarine caves. Every new exploration has allowed to discover new species. The analysis of worldwide fauna provides new insights into Homoscleromorpha classification, challenging the present systematics and calling the revision of several non-monophyletic groups.

This work takes place in the framework of the LIA MARRIO, and was funded by the CNRS, the Total Foundation and Colciencias-Colfuturo.

Current outlook on carnivorous sponge diversity and systematics

Jon Thomassen Hestetun[1], Hans Tore Rapp[1]

[1] *Department of Biology and K.G. Jebsen Centre for Deep-Sea Research, University of Bergen, Thormøhlensgate 53A/B, N-5020 Bergen, Norway. Jon.hestetun@uib.no*

Carnivorous sponges constituting Cladorhizidae (Demospongiae, Poecilosclerida) have the ability to capture small invertebrates, representing a unique life strategy within the sponges. Prey items such as small crustaceans get entangled by filaments or other structures, and are subsequently enveloped by the sponge. Cladorhizids are more prevalent at greater depths, and carnivory is generally regarded as an evolutionary adaptation to oligotrophic deep-sea conditions, where filter feeding is less viable[1]. Currently, Cladorhizidae contains nine genera with some 150 species[2], a number that has increased significantly in the last twenty years.

Carnivorous sponges are very diverse in microsclere chela morphology, making it difficult to establish a secure systematics based only on morphological characters. Here, we present some main findings from our recent molecular phylogeny of the carnivorous sponges. Results show that all known carnivorous sponges constitute a monophyletic clade containing no known non-carnivorous sponges, strengthening the hypothesis that carnivory evolved only once within known sponges[3].

Cladorhizid collection records are scattered, and many areas worldwide remain virtually unexplored. Still, recent discoveries have added to the available information for the group, and in light of several investigations into regional cladorhizid faunas[4, 5, 6], we draw some general conclusions on current knowledge in terms of distribution patterns and diversity, as well as indicating possible directions for further research.

References

1. Vacelet, J. (2007). Diversity and evolution of deep-sea carnivorous sponges. Porifera research: biodiversity, innovation and sustainability. Série Livros, 28, 107-115.
2. van Soest R.W.M., Boury-Esnault N., Hooper J.N.A., Rützler K., de Voogd N.J., Alvarez B.d.G., Hajdu E., Pisera A.B., Manconi R., Schoenberg C., Janussen D., Tabachnick K.R., Klautau M., Picton B., Kelly M., Vacelet J., Dohrmann M., Cristina Díaz M. and Cárdenas P. (2016) World Porifera Database. Accessed 2017-02-20.
3. Hestetun J.T., Vacelet J., Boury-Esnault N., Borchiellini C., Kelly M., Ríos P., Cristobo F.J. and Rapp H.T. (2016) The systematics of carnivorous sponges. Molecular Phylogenetics and Evolution, 94, 327-345. DOI:10.1016/j.ympev.2015.08.022
4. Hestetun J.T., Pomponi S. and Rapp H.T. (2016) The cladorhizid fauna of the Caribbean and adjacent areas. Zootaxa, 4175(6), 521-538. DOI:10.11646/zootaxa.4175.6.2
5. Hestetun J.T., Rapp H.T. and Xavier J. (2016) Carnivorous sponges (Porifera, Cladorhizidae) from the Southwest Indian Ocean Ridge seamounts. Deep Sea Research Part II: Topical Studies in Oceanography, 1-24. DOI:10.1016/j.dsr2.2016.03.004
6. Hestetun J.T., Tompkins-MacDonald G. and Rapp H.T. (in press) A review of carnivorous sponges (Porifera: Cladorhizidae) from the boreal North Atlantic and Arctic. Zoological Journal of the Linnean Society.

Financial support by the Norwegian Research Council, Norwegian Biodiversity Information Centre and the European Union's Horizon 2020 research and innovation programme under grant agreement No. 679849, is gratefully acknowledged.

Nothing in sponge systematics makes sense - except in the light of DNA!

Christine Morrow[1, 2, 3], Jean Vacelet [4], Tatjana Bakran-Petricioli [5], Ulisses Pinheiro [6], Kevin Calabro [2], Olivier Thomas [2] & Grace P. McCormack [1].

[1] Zoology Department, Ryan Institute, School of Natural Sciences, NUI Galway, University Road, Galway, Ireland
[2] Marine Biodiscovery Laboratory, School of Chemistry, NUI Galway, University Road, Galway, Ireland
[3] Queen's University Marine Laboratory, 12-13 The Strand, Portaferry, Northern Ireland
[4] Station Marine d'Endoume, Chemin de la Batterie des Lions, 13007 Marseille, France
[5] Department of Biology, Faculty of Science, University of Zagreb, Rooseveltov trg 6, HR-10000 Zagreb, Croatia
[6] Departamento de Zoologia, Universidade Federal de Pernambuco, Departamento de Zoologia, Centro de Biociências, Av. Prof Moraes Rego, 1235, Cidade Universitária, Brasil

Demospongiae is by far the largest group of sponges, representing approximately 80% of all known sponges. *Systema Porifera* (2002) aimed to provide an updated classification for sponges based (almost entirely) on morphological characters. Since the early 1990's a number of molecular studies on sponges suggested that several demosponge orders and families were not monophyletic, however it was only in 2015 that the demosponge classification was revised in light of molecular data. Although this revision proposed many radical changes to the classification it stressed that the discovery of new taxa and the sequencing of additional species would likely lead to new phylogenetic hypotheses, which would require further changes to the classification.

The current study uses a combination of morphological, molecular and chemical data to investigate the taxonomic affinities of *Jaspis* Gray, 1867 (Ancorinidae: Astrophorina). This is the first study to include molecular data from the type species of *Jaspis*, *J. johnstonii* (Schmidt, 1862). Although *Jaspis* (with 37 valid species) is

the second largest genus of Ancorinidae, to date the only available DNA sequence is 18S rRNA data from *J. novaezealandiae*. In addition to obtaining sequence data from the type species, the present study has generated 18S and 28S rRNA sequences from a further 5 species of *Jaspis*.

A total analysis tree using a combination of 18S and 28S rRNA sequence data shows strong support for some *Jaspis* species clustering with *J. novaezealandiae* in Astrophorina (Tetractinellida); *J. iacuitaster* clustering closely with *Paratimea* (Stelligeridae, Axinellida), and the type taxon, *J. johnstonii* clustering with *Hemiasterella bouilloni* in a newly identified clade, separate to Astrophorina, Hemiasterellidae (Tethyida) and Stelligeridae. Chemical screening shows *H. bouilloni* contains bengamides and bengazoles that are the same as those previously described from a species of *Jaspis* from Fiji. Our analysis of CO1 barcoding fragments shows newly obtained sequences from *H. bouilloni* and *J. splendens* clustering with *Hemiasterella* sp. 2 (GenBank AY561977) and Hemiasterellidae (Sponge Barcoding Database Hemiasterellidae sequence SBD 532).

In this study we present morphological and molecular to support the transfer of *J. iacuitaster* to *Paratimea*, morphological, molecular and chemical data for the reassignment of *Hemiasterella bouilloni* to *Jaspis* and morphological and molecular data for the erection of a new order Jaspida ord. nov. The present study highlights the insights that can be gained by taking a more integrative approach to sponge systematics and incorporating morphological, molecular and chemical datasets.

Are we there yet? Novel families and genera revealed within Verongimorpha while expanding geographic and habitats explorations.

M. Cristina Díaz[1, 2], Pierre Chevaldonné[3], Maude Dubois[3], Marie Grenier[3], César Ruiz[3], Alexander Ereskovsky[3], Jean Vacelet[3], Nicole Boury-Esnault[3] & Thierry Pérez[3]

[1] HBOI-Florida Atlantic University, 5600 US1, Fort Pierce, Fl 34946, U.S.A. [2] NSU, Guy Harvey Oceanographic Cente, Dania Beach, FL, USA. [3] Institut Méditerranéen de Biodiversité et d'Ecologie marine et continentale, CNRS, Aix Marseille Univ, IRD, Avignon Univ. Station Marine d'Endoume, chemin de la Batterie des Lions, 13007 Marseille, France.

Verongimorpha includes taxa of heterogeneous morphologies, as they may possess fibers (containing chitin and/or spongin), spicules only, or no macro-skeleton at all. Current phylogenies depict three main orders within the subclass: Verongiida, Chondrosiida, and Chondrillida (see Morrow and Cardenas, 2015). Recent studies seem to indicate that genetic data and the choanocyte chamber morphology (eurypylous vs diplodal) seem to produce the most congruent phylogenies within this group.

In recent years, we have collected more than 200 specimens of Verongimorpha while exploring shallow tropical habitats, mostly from caves and other cryptic habitats, of remote areas such as the Marquesas archipelago (Western Central pacific) and 11 islands in the Lesser Antilles. The COI gene (Folmer fragment, 575 bp) was amplified, sequenced, and aligned with the Verongimorpha datasets on genetic databases. Morphological studies have been advanced on some of the taxa. The genetic affinities of taxa collected in these expeditions confirm certain concepts of Verongimorpha phylogeny, but also reveal novel clades (taxa). Some of the most important results obtained so far are the monophyly of Verongiida and its families Aplysinidae, Ianthellidae, and Pseudoceratinidae and the finding of basal novel clades within major Verongimorph groups: *i.e.* basal Verongiida and basal Pseudoceratinidae. Among the novel genera and families uncovered, are: i) a novel clade, sister to *Aiolochroia*, suggesting the need of a distinct genus, possibly within a new family of Verongiida; ii) a novel Ianthellidae clade, composed of a *Hexadella*-like species with a very distinct genetic identity; iii) a novel taxon sister to *Aplysina*, from Marquesas Islands, reinforcing the unique genetic identity of *Aplysina*; and iv) two novel clades within Chondrillida, suggesting a much greater diversity within this order, and the need to search for other anatomical and biological synapomorphies within the group.The results here presented clearly show that even within a well-known poriferan group, expanding geographic and habitats explorations show that "We are not done yet" discovering new taxa, relationships, and understanding the congruence between genetic identities and anatomical features.

This work takes place in the framework of LIA MARRIO. Sampling cruises *Pakaihi I Te Moana* and *Pacotilles* were financially supported by the "Agence des Aires Marines Protégées (AAMP)" and the "UMS Flotte Océanographique française", respectively. Post processing of the samples was achieved thanks to funding by CNRS, Aix Marseille University and the Total Foundation.

A proposal for the family level classification of Calcinea (Porifera, Calcarea)

Oliver Voigt[1], Fernanda Azevedo[2], Báslavi Cóndor-Luján[2], Hans Tore Rapp[3], Gert Wörheide[1, 4] & Michelle Klautau[2]

[1] Ludwig-Maximilans-Universität Munich, Paleontology and Geobiology, Department of Earth and Environmental Sciences, Richard-Wagner-Str. 10, 80333 Munich, Germany. oliver.voigt@lmu.de

[2] Universidade Federal do Rio de Janeiro, Instituto de Biologia, Departamento de Zoologia. Avenida Carlos Chagas Filho, 373. CEP 21941-902. Rio de Janeiro, Brazil.

[3] University of Bergen, Department of Biology and K.G. Jebsen Centre for Deep-Sea Research Thormøhlensgt. 53 A/B, Bergen, Norway

[4] GeoBio-Center, Ludwig-Maximilians-Universität München, Richard-Wagner-Str. 10, 80333 München, Germany.

Integrative approaches have more recently advanced the understanding of the taxonomy and phylogenetic relationships of calcareous sponges of the subclass Calcinea. With the help of DNA phylogenetic analyses and morphological re-interpretation of characters several genera were revised. It became obvious that several classically recognized genera such as example *Clathrina* and *Guancha* comprised species that sometimes were not particularly closely related to each other. As a result, several new genera were proposed, for example *Arthuria* Klautau, Azevedo, Cóndor-Luján, Rapp, Collins & Russo, 2013, *Borojevia* Klautau, Azevedo, Cóndor-Luján, Rapp, Collins & Russo, 2013, *Brattegardia* Klautau, Azevedo, Cóndor-Luján, Rapp, Collins & Russo, 2013 and *Nicola* Cóndor-Luján & Klautau, 2016. These revisions also led to the recognition of new synapomorphic morphological characters for the genera. Consequently, however, uncertainties about the family-level taxonomy of Calcinea exist. We analysed two nuclear DNA markers, the internal transcribed spacer region and the partial 28 ribosomal RNA gene from 18 genera of Calcinea. Based on the results of our phylogenetic analyses, we propose a revised family-level taxonomy for the subclass.

Cinachyrella australiensis (Carter, 1886) In The Indo- West Pacific: An Integrative Approach To Understanding A Complex Species Complex

Kathryn A. Hall[1], Miranda E. Vidgen[1] & John N.A. Hooper[1]

[1] Biodiversity and Geosciences Program, Queensland Museum, South Brisbane, Queensland, Australia. kathryn.hall@qm.qld.gov.au

Species of *Cinachyrella* Wilson, 1925 (Demospongiae, Tetractinellida, Tetillidae), with their distinctive ball shapes and complements of delicate triaenes protruding beyond their surfaces, are charismatic and conspicuous components of benthic marine sponge fauna. Within the large collection of sponges at Queensland Museum, several hundred specimens are identified provisionally as *Cinachyrella australiensis* (Carter, 1886), largely due to their yellow colouration and spherical habitus. Much of this material was collected by benthic trawls of locations spanning the entire length of the inter-reef seabed of the Great Barrier Reef and Torres Strait. Additional material from subtropical and temperate eastern Australia, Papua New Guinea and other western Pacific and eastern Indian Ocean localities supplements the GBR collection. The physical forces associated with the collection method, and subsequent handling of large volumes of material from the trawls, caused many sponges to be broken and fragmented, making identification using light microscopy alone extremely demanding.

Given the inadequacy of light microscopy for resolving the identities of the specimens within this large and problematic collection, it seemed the perfect candidate for an integrative taxonomy study, using DNA barcoding and detailed electron microscopy. Examinations using SEM demonstrated variation in the morphology of the specimens, suggesting that we did not have a homogenous set of samples, despite their macroscopic similarity. Although biological variation was evident, the partial COI mtDNA barcode sequences we obtained were insufficient to resolve satisfactorily any species limits within the sample. Consequently, we adopted a combined approach to the molecular examination, employing four additional markers: partial COII mtDNA, two mitochondrial intergenic spacers, and partial 28S rDNA.

Our results to date support previous studies (1), which suggest that, for tetillid sponges at least, COII and the intergenic spacers have faster rates of evolution than the COI barcoding region, and are useful for taxonomic studies. Given the very large collection housed at Queensland Museum, we are amassing a substantial database of sequences for these regions. Preliminary phylogenetic analysis indicates broad agreement among the mitochondrial and ribosomal gene trees, and further, that these trees are consistent with observed morphological variation. Given that these four additional markers are quicker and easier to amplify compared to COI (50–70% success rate, compared to 25% for COI), and have a higher information content because they are more rapidly evolving, we advocate strongly for a multilocus approach to the "barcoding" of tetillid sponges. Although the study is still in infancy, already our data show that at least 10 MOTUs hide within the *C. australiensis* species complex.

References

1. C.P.J. Rua, C. Zilberberg, A. Solé-Cava, JMBA, 91 (5) (2011) 1015–1022.

Financial support by the Australian Biological Resources Study (ABRS) is gratefully acknowledged.

Taxonomy of deep-sea sponges living on polymetallic nodule fields in the Clarion-Clipperton Fracture Zone (CCFZ), East Pacific

Daniel Kersken[1, 2,] Dorte Janussen[1] & Pedro Martínez Arbizu

[1] Senckenberg Research Institute and Nature Museum (SGN), Department of Marine Zoology, Senckenberganlage 25, D-60325 Frankfurt am Main, Germany. Daniel.kersken@senckenberg.de

[2] Senckenberg am Meer, German Centre of Marine Biodiversity Research (DZMB), Am Südstrand 44, D-26382 Wilhelmshaven, Germany.

Up-to-date knowledge on the deep-sea sponge fauna (Porifera) of the Clarion- Clipperton Fracture Zone (CCFZ) in the eastern Pacific is relatively scarce and needs to be extended, because the CCFZ is one of the worldwide biggest potential deep-sea mining areas for industrial mining of polymetallic nodules. The framework of this project is the Joint Programming Initiative Oceans (JPIO), which is focused on the ecological aspects of deep-sea mining. The project-related research expedition SO239 EcoResponse by RV *Sonne* was focused on the study of benthic deep-sea communities living in polymetallic nodule field systems. During this expedition, 68 deep-sea sponges of 18 morphotypes and 35 species were collected in depths from 1700 to 5000 m by deployment of a Remotely Operated Vehicle (Figure 1). Main objective of this project is the establishment of a picture-based species catalogue of the deep-sea sponge fauna in the CCFZ. Further main objectives are DNA-Barcoding with four genetic markers (16S, 18S, 28S and COI) and software-based annotation of video material from ROV transect dives. The presentation during this workshop includes preliminary results of the deep- sea sponge taxonomy with additional project-specific information, e.g. on species distribution within the CCFZ or potential occurrence of new deep-sea species.

Financial support by the German Bundesministerium für Bildung und Forschung (BMBF) is gratefully acknowledged.

Calcarean sponge fauna of the eastern Mediterranean Sea

Vasilis Gerovasileiou[1], Tayara Fontana[2], Fernanda Azevedo[2], Chryssanthi Antoniadou[3], Eleni Voultsiadou[3] & Michelle Klautau[2]

[1] Institute of Marine Biology, Biotechnology and Aquaculture, Hellenic Centre for Marine Research, Heraklion, Greece. vgerovas@hcmr.gr;

[2] Universidade Federal do Rio de Janeiro, Instituto de Biologia, Departamento de Zoologia, Rio de Janeiro, Brazil.

[3] Department of Zoology, School of Biology, Aristotle University of Thessaloniki, Thessaloniki, Greece.

Sponge research in the eastern Mediterranean Sea has mainly focused on demosponges. Calcareans have been scarcely studied in this area, especially when compared with the north-western Mediterranean basin and the Adriatic Sea. Recent sponge sampling in various habitat types of the Aegean Sea (e.g. shallow rocky beds, semi- and entirely submerged caves, artificial substrates), in the framework of different research projects, yielded several specimens of calcareous sponges. The examination of this material revealed 11 taxa, of which 6 species are new to science: *Amphoriscus* sp. nov., *Sycantha* sp. nov., *Sycon* sp. nov. and *Vosmaeropsis* sp. nov. 1-3. Furthermore, a detailed overview of the relevant scientific literature was performed and an updated checklist of the calcarean fauna of the eastern Mediterranean Sea was compiled. According to our results, the new records included, the up-to-date calcarean fauna of the eastern Mediterranean consists of 32 species (40% of the Mediterranean Calcarea) belonging to 16 genera, 13 families, and 4 orders. Calcaronea is the richest subclass, with 23 species, while Calcinea is represented with 9 species. The most diverse genus was Sycon (8). Most species were recorded in the Levantine Basin (17), North Aegean (12), and South Aegean Sea (6). Our review showed that most calcarean records from the eastern Mediterranean Sea were included in old publications and that the calcarean species found to date exclusively in the eastern Mediterranean make up 25% of its total calcarean fauna. This and the fact that recent research effort in the Aegean Sea yielded 6 new species indicate that further research could increase our knowledge on the calcarean diversity of the Mediterranean.

Three new and four poorly known species of *Plakina* (Porifera, Homoscleromorpha)

Anaíra Lage[1], Vasilis Gerovasileiou[2], Eleni Voultsiadou[3], Thierry Pérez[4], César Ruiz[4] & Guilherme Muricy[1]

[1] Departamento de Invertebrados, Museu Nacional, Universidade Federal do Rio de Janeiro, Brasil;

[2] Hellenic Centre for Marine Research, Greece;

[3] School of Biology, Aristotle University of Thessaloniki, Greece;

[4] Institut Méditerranéen de Biodiversité et d'Ecologie marine et continentale, CNRS, Aix Marseille Univ, IRD, Avignon Univ, Marseille, France

Plakina is among the most representative genera of the class Homoscleromorpha, with 29 valid species occurring in subtidal hard substrates, mostly ceilings and walls of dark or semi-dark habitats. The genus is widely distributed around the world, although the regions of the Mediterranean Sea (8 spp.) and Caribbean Sea (5 spp.) record the highest species richness. Two Mediterranean species, *Plakina monolopha* and *P. trilopha,* are allegedly cosmopolitan but most records from outside the Mediterranean need revision, including the Brazilian record of *P. trilopha* (Muricy *et al*., 1998, Domingos *et al.*, 2016). In the present study, we describe three new species of *Plakina* and redescribe four others from different regions (Central Pacific, Aegean Sea, Antarctic, and Southwestern Atlantic). *Plakina* sp. nov. 1 from the Marquises Island, Central Pacific, is distinguished by its lophose calthrops exclusively trilophose and with all actines terminally spined. *Plakina* sp. nov. 2 from Greece is massive, orange to red-pink with whitish borders *in vivo*, and has trilophose and tetralophose calthrops with very irregular shapes. *Plakina monolopha var. antarctica* Topsent, 1917 from Petermann Island, Antarctica, has monolophose calthrops with the basal actines bifurcated and the lophose actine ramified in a complicated 1m, 2d, ts pattern. Furthermore, its spicules are larger than those of Mediterranean *P. monolopha* (cf. Muricy *et al*., 1998). We thus propose to rename it as a new species, provisionally called *Plakina* sp. nov. 3. We also revised other four poorly known species of *Plakina* and added the following new characters to their descriptions: to *P. crypta*, the irregular shape and rare trilophose calthrops; to *P. weinbergi* details of spicule shape (regular and irregular, with blunt and microspined tips); to *P. bowerbanki* the presence of a marginal canal, circular oscules and basal cavities, and SEM analysis of spicules; and to *P. coerulea* the presence of a marginal canal, basal cavities and rare mono-, di- and trilophose calthrops. The geographic distribution of *P. crypta* from SW France is extended to the Aegean Sea, with its first record for Greece. The distribution of the Tropical Southwestern Atlantic species *P. coerulea* is extended from Maceió to Fernando de Noronha oceanic archipelago and to Cabo Frio, in SE Brazil. These preliminary results indicate that the genus *Plakina* is more diverse and that its species are more widely distributed than previously thought.

References

1. Domingos, C., Lage, A., Muricy, G., (2016). J Mar Biol Assoc UK 96(2), 379–389.
2. Muricy G., Boury-Esnault N., Bézac C., Vacelet J., (1998) Zool J Linn Soc 124, 169–203.
3. Topsent E., (1917). Paris: Masson et Cie., 1–97.

This research takes place in the framework of the LIA MARRIO. Financial support by CNPq, CAPES, FAPERJ, EU and Greek national funds through the Research Funding Program: Heracleitus II, Investing in knowledge society is gratefully acknowledged.

Calcareous Sponges From Palau And The Great Barrier Reef, Australia

Anita Mary George[1], Merrick Ekins[1], Sam McCormack[2] & Michelle Klautau[3]

[1]Queensland Museum, South Brisbane, Queensland, Australia anita.george@qm.qld.gov.au

[2]University of Waikato, Tauranga, New Zealand

[3]Universidade Federal do Rio de Janeiro, Brazil

Calcareous sponges are composed of calcium carbonate spicules that can be diactines, triactines, tetractines, and/or polyactines. Their aquiferous system is very diverse, being asconoid, syconoid, syllebid, leuconoid or solenoid. Currently there is a dearth of taxonomists and knowledge in calcarea taxonomy in Australia. As part of acquiring taxonomic knowledge and updating the calcareous sponge collections from Queensland Museum, a set of 21 vouchered samples from Palau and the Great Barrier Reef were examined at the first calcareous workshop conducted at the South Australian Research Development Institute (SARDI) Aquatic Sciences, Adelaide, South Australia. Four specimens were from Palau while the remaining specimens were from the Queensland coast with 12 specimens exclusively from the Great Barrier Reef. Eighteen species were identified as calcareous sponges, of which, 12 species were from the subclass Calcinea and five from Calcaronea. Order Clathrinida (Calcinea) was represented by the genera: *Arthuria*, *Ascandra, Ascoleucetta*, *Clathrina*, *Leucaltis*, *Leucetta* and *Levinella.* Whilst the subclass Calcaronea was represented by the genera *Grantia*, *Leucandra*, *Sycettusa* and *Sycon.* Of these, the widespread dominant genera were *Leucetta*, followed by *Ascoleucetta.* New species are expected from this collection for Australia and Palau.

Divergence between molecular and morphological data in Brazilian *Arenosclera* sponges (Haplosclerida, Demospongiae)

Camille V. Leal[1, 2, 3], Fernando C. Moraes[4], Adriana Froes[2], Ana Carolina Soares[2], Fabiano Thompson[2] & Eduardo Hajdu[1]

[1] Universidade Federal do Rio de Janeiro, Museu Nacional, Rio de Janeiro, Brazil camille.victoria@gmail.com

[2] Universidade Federal do Rio de Janeiro, Instituto de Biologia, Departamento de Biologia Marinha, Rio de Janeiro, Brazil

[3] Graduate Program in Genetics, Universidade Federal do Rio de Janeiro

[4] Jardim Botanico do Rio de Janeiro, Rio de Janeiro, Brasil

Arenosclera has six accepted species in the Indo-Pacific (5): Australian (3), New Caledonia (1), Red Sea (1) and West Atlantic: Brazil (1). Recent expeditions to the Amazon reefs yielded three specimens assignable to *Arenosclera*, but seemingly quite distinct from the sole species this far known from Brazil, namely *A. brasiliensis*. The rich chemistry known from *A. brasiliensis* caught our attention about relationships among these species and inspired us to perform a phylogenetic analysis to verify if *Arenosclera* is monophyletic. We integrated morphological and metagenome derived molecular analyses (28S). Morphology was studied as usual, and metagenomes were extracted according to (1), and then sequenced with Illumina MySeq technology. A 28S Genbank database was compiled with sequences ≥80% similar to the complete 28S of *A. heroni* (type species of *Arenosclera*). Metagenomes were compared with this database using BLASTN and only 28S-like sequences were saved. Following, we used CAP3 and SPADES to assemble sequences in contigs, and selected the largest contig for the phylogenetic analysis. The latter also used additional haplosclerid 28S sequences collected from Genbank. Sequences were aligned with MAFFT 7 and the Maximum likelihood phylogeny obtained with RAxML. The Amazon species feature delicate oxeas and sand in the fibers (carbonatic in one, siliciclastic in the other), with soft consistency and beige color. Additional differences between both species are the structure of their callyspongiid skeleton and morphology of the oxeas. Aside their arborescent habit, these species are very similar to other *Arenosclera* spp. However, the phylogeny retrieved shows that not only Amazon reef species, as well as *A. brasiliensis* do not form a monophyletic group with *A. heroni*. Brazilian species appear in a distinct clade, suggesting that these species represent a new genus. The confused systematics of the Haplosclerida hinders the objective classification of this new clade for now. Additional studies using other Haplosclerida and molecular markers are necessary to better define this group.

References

1. G.D. Garcia, G.B. Gregoracci, O. Santos Ede, P.M. Meirelles, G.G. Silva, R. Edwards, T. Sawabe, K. Gotoh, S. Nakamura, T. Iida, R.L. de Moura, F.L.Thompson. Metagenomic Analysis of Healthy and White Plague-Affected *Mussismilia braziliensis*

Corals. Microb. Ecol. (2013) 1076-1086.

Financial support by CAPES, CNPq, FAPERJ and LIA-MARRIO is gratefully acknowledged.

Cliona laticavicola is an ecophenotype and an ontogenic life stage of the coral excavating sponge *Cliona delitrix*

Andia Chaves-Fonnegra[1], **Angela Marulanda-Gómez**[2], **Benjamin Mueller**[3], **Jose V. Lopez**[4] **& Sven Zea**[2]

[1] *Center for Marine and Environmental Studies, University of the Virgin Islands, #2 John Brewers Bay, St Thomas, U.S.-Virgin Islands, USA. andiachaves@gmail.com*

[2]*Department of Natural Sciences and Mathematics, Pontificia Universidad Javeriana, Cali, Colombia*

[3]*Institute for Biodiversity and Ecosystem Dynamics, University of Amsterdam, The Netherlands.*

[4]*Halmos College of Natural Sciences and Oceanography, Nova Southeastern University, 8000 North Ocean Drive, Dania Beach, Florida, USA.*

[5] *Instituto de Estudios en Ciencias del Mar—CECIMAR, Universidad Nacional de Colombia, Sede Caribe, Santa Marta, Colombia.*

Excavating sponges burrow galleries and tunnels in calcareous substrata. Their epilithic portions may be papillated, encrusting or massive, and some species may pass through these stages as part of their ontogeny-growth. The red-orange excavating sponges *Cliona laticavicola* Pang, 1973 and *Cliona delitrix* Pang, 1973 were described simultaneously from the same reefs in Jamaica as separate species, the former being papillated and the latter fully encrusting. Despite similarities in spicule morphology, they appeared to be separate species due to their geographical and ecological distribution throughout the Caribbean, with papillated forms widely distributed in shallow habitats, and encrusting forms restricted to deeper settings and absent in certain localities. However, detailed observations of *C. delitrix* papillated recruits and their subsequent growth led us to question whether *C. laticavicola* and *C. delitrix* are the same species. Extensive morphological comparisons of material from different locations in the Caribbean showed that their tylostyle spicules strongly overlap in shape and size between both species wherever they co-exist. In addition, in Southern Caribbean localities (continental coast of Colombia and Panama) both species share a complement of unique spiraster spicules that are absent in other studied areas including the type locality. Genetic analyses using the mitochondrial segment from CO2 to ATP6 genes supported a monophyletic group with genetic distances between species compatible with conspecificity, confirming previous published work with nuclear ITS1 sequences, while microsatellites analyses suggest incomplete speciation or recent hybridization between species. Based on both morphological and genetic information, we herein suggest synonymizing the two species, choosing *C. delitrix* as the valid name, and *C. laticavicola* as an early ontogenetic life stage and an ecophenotype.

A revised molecular phylogeny of the subclass Calcaronea

Adriana Alvizu[1], **Mari Heggernes Eilertsen**[1], **Joana R. Xavier**[1] **& Hans Tore Rapp**[1]

[1] *Department of Biology and K.G. Jebsen Centre for Deep-Sea Research, University of Bergen, PO Box 7803, N-5020 Bergen, Norway adriana.alvizu@uib.no*

Calcareous sponges are acknowledged to be taxonomically challenging and molecular data does not support the current morphology-based classification. We sequenced a short fragment (C-region) of the 28S gene, which was recently proposed as the most phylogenetically informative marker to be used as a DNA-barcode for calcareous sponges. Our analyses, that combine newly generated sequences with those from previous studies, include a total of 125 sequences representing ca. 71 taxa across 23 (out of 56) genera and all 14 families of Calcaronea. Our results are congruent with previous studies in that the current ordinal classification within Calcaronea is artificial, and most families and genera are non-monophyletic. Our study also supports the basal position of *Leucosolenia*, however, the increased taxon sampling reveals this genus to also be polyphyletic. We further recovered a well-supported monophyletic clade that includes *Sycon*-like species with a stem collected in both shallow- and deep-water. This study highlights the need for a thorough revision of the subclass Calcaronea and provides a molecular framework for future studies.

Financial support by the Norwegian Biodiversity Information Centre (grant to HTR, project number 70184219), the Norwegian Academy of Science and Letters (grant to HTR), the Research Council of Norway (through contract number 179560), and by the European Union's Horizon 2020 research and innovation program (grant agreement No 679848) is gratefully acknowledged.

Exploring remote islands and remote habitats: the key role of hidden cave sponges in solving systematic issues

Pierre Chevaldonné[1], **Nicole Boury-Esnault**[1], **Maria Cristina Díaz**[2, 3], **Maude Dubois**[1], **Alexander Ereskovsky**[1], **César Ruiz**[1], **Marie Grenier**[1], **Jean Vacelet**[1], **Michelle Klautau**[4], **Thierry Pérez**[1]

[1] *Institut Méditerranéen de Biodiversité et d'Ecologie marine et continentale, CNRS, IRD, Aix Marseille Université, Avignon Université, Station Marine d'Endoume, rue Batterie des Lions 13007 Marseille, France*

[2] *Harbor Branch Oceanographic Institute, Florida Atlantic University, 5600 US1, Fort Pierce, FL 34946, USA*

[3] *NSU, Guy Harvey Oceanographic Center, Dania Beach, FL, USA*

[4] *Universidade Federal do Rio de Janeiro, Instituto de Biologia, Departamento de Zoologia, Rio de Janeiro, RJ, BR-21941-902, Brazil*

Some entire groups of Porifera are still phylogenetically unsettled and are commonly reorganised at the supra-generic level. Recent explorations conducted by our group, targeted remote or poorly explored islands of tropical areas, as well as habitats that are not commonly surveyed. Among such remote habitats are underwater marine caves that have been rather well studied for sponges in areas such as the Western Mediterranean, but are still reservoirs of unknown biodiversity in most other parts of the world. Their environmental peculiarities make marine caves indeed common shelters for representatives of groups otherwise uncommon at shallow depths, including some carnivorous sponges (cladorhizids), hexactinellids or lithistids. Research cruises to the Marquesas Islands (West Central Pacific) and to several islands of the Lesser Antilles (Caribbean) focussing on caves and shaded habitats have indeed allowed to gather an unprecedented collection of cave-dwelling sponges with original body plans, living strategies and/or associations with microorganisms. Our efforts have improved tremendously the scope of species diversity among two Porifera classes, the Calcarea, and Homoscleromorpha. Targeting the preferred habitat (caves) of Homoscleromorpha allowed us to recover a high proportion of new species (*ca* 20) that help understand the phylogenetic relationships within this still poorly-studied, difficult group. We have confirmed the rather common distribution of sponges with hypercalcified or hypersilicified skeletons in underwater caves. Furthermore, these preliminary investigations produced a great number of taxonomic novelties, not only at the species level, which was expected, but also at the levels of genera and most probably families. This was most striking for Verongimorpha, for which the number of new clades of high rank recovered was surprising, despite this is a rather well studied group.

This work takes place in the framework of LIA MARRIO. Sampling cruises *Pakaihi I Te Moana* and *Pacotilles* were financially supported by the "Agence des Aires Marines Protégées (AAMP)" and the "UMS Flotte Océanographique française", respectively. Post processing of the samples was achieved thanks to funding by CNRS, Aix Marseille University and the Total Foundation.

Chemosystematics as a complementary tool for *Haliclona* species (Class Demospongiae, Order Haplosclerida).

Miriam Reverter[1, 2], **Marie-Aude Tribalat**[1], **Grace P. McCormack**[3] **& Olivier P. Thomas**[1]

[1] *School of Chemistry, National University of Ireland, Galway, University Road, Galway, Ireland. mirireverter@gmail.com*

[2] *Marine Institute, Rinville West, Oranmore, Ireland.*

[3] *National University of Ireland Galway, Zoology, School of Natural Sciences, University Road, Galway, Ireland.*

The sponge Order Haplosclerida (Class Demospongiae) is one of the most diverse groups of sponges in terms of number of species and habitats. Despite Haplosclerid sponges being well defined morphologically, the systematics within this group remains challenging since molecular evidence is discrepant with the morphological indicators [1]. Gratifyingly, haplosclerids produce a high diversity of specialized metabolites, including alkaloids, polyacetylenes and terpene derivatives [2]. Chemosystematics, which is the classification of organisms based on their metabolite contents, has proven to be a valuable tool to complement morphology and molecular genetics for some sponge groups like Homoscleromorpha [3]. In this study, we have combined UHPLC- ESIqQToF and NMR metabolomics analyses of 11 *Haliclona* species from the Northeastern Atlantic and the Northwestern Mediterranean. Integration of results from both techniques through a multiple factor analysis (MFA) allowed the identification of six statistically different groups based on the sponge metabolomes, which are in accordance with the previously established *Haliclona* sub-genera. This study shows the potential of chemosystematics as a complementary tool, as well as the importance of integrating both NMR and LC-MS techniques for the study of sponge metabolomes. The perspectives and limitations of this approach will be discussed.

References

1. Redmond, N.E., Morrow, C.C., Thacker, R.W., Diaz, M.C., Boury-Esnault, N., Cardenas, P., Hajdu, E., Lôbo-Hajdu, G., Picton, B.E., Pomponi, S.A., Kayal, E., Collins, A.G. Int. Comp. Biol. 53 (2013) 388-415.
2. Tribalat, M-A., Marra, M.V., McCormack, G.P., Thomas, O.P. Planta Med. 82 (2016) 843-856.
3. Ivanisevic, J., Thomas, O.P., Lejeusne, C., Chevaldonné, P., Pérez, T. Metabolomics 7 (2011) 289-304.

Financial support by the Marine Institute (grant PBA/MB/16/01) is gratefully acknowledged.

Integrative taxonomy reveals a high diversity of Homoscleromorpha in Cabo Frio, Southeastern Brazil (SW Atlantic)

Guilherme Muricy[1], Celso Domingos[1], Anaíra Lage[1], Mirelly Balbino[1], Carolline Pequeno[1], Daniele S. Quintela[1], Emilio Lanna[2], Cristiane Hardoim[1, 3], Gabriela Puccinelli[3], Marinella Laport[3], Carla Zilberberg[4], Philippe Willenz [5], Alexander Ereskovsky[6, 7], Thierry Perez[6], Dennis Lavrov[8]

1. Departamento de Invertebrados, Museu Nacional, Universidade Federal do Rio de Janeiro, Brazil
2. Instituto de Biologia, Universidade Federal da Bahia, Salvador, Brazil
3. Instituto de Microbiologia Paulo de Góes, Universidade Federal do Rio de Janeiro (UFRJ), Brazil
4. Departamento de Zoologia, Instituto de Biologia, Universidade Federal do Rio de Janeiro, Brazil
5. Royal Belgian Institute of Natural Sciences, Taxonomy and Phylogeny, & Université Libre de Bruxelles, Belgium
6. Institut Méditerranéen de Biodiversité et d'Ecologie marine et continentale, CNRS, Aix Marseille Univ, IRD, Avignon Univ, Marseille, France
7. Department of Embryology, Faculty of Biology, Saint-Petersburg State University, Russia
8. Department of Ecology, Evolution, and Organismal Biology, Iowa State University, Ames, US

So far, the Class Homoscleromorpha was poorly represented in the Southeastern Brazil ecoregion of the Warm Temperate Southwestern Atlantic province, with only one unidentified record of *Oscarella* from Búzios, in the coast of Rio de Janeiro State (Muricy & Hajdu, 2006). An exhaustive search in the nearby city of Cabo Frio revealed a rich fauna of Homoscleromorpha with several chromotypes of *Plakina* spp. and *Oscarella* spp. living in the underside of boulders and massive corals of the subtidal zone (5-10 m depth) and of stones of a tide pool (0.1-1.0 m depth at low and high tides, respectively). The lack of useful morphological characters and the high variability of the external morphology requested to describe these species with an integrative approach including morphology, anatomy, cytology, reproduction, ecology, and sponge barcoding DNA sequences generated with two distinct phylogenetic markers (cox-1 and cit-b). We found that the different morphotypes belong to three species of *Plakina* and to between six and eight species of *Oscarella*. The genus *Plakina* includes the first record of *P. coerulea* outside its type locality and two new polychromatic species found only in a single tide pool. The different *Oscarella* species are highly polymorphic and are still under cytological and molecular investigations. This integrative approach applied to the species from Cabo Frio, combined with extensive searches directed to Homoscleromorpha in cryptic habitats, showed that the diversity of the class is significantly higher than previously known.

References

1. G. Muricy, E. Hajdu, Porifera Brasilis, Eclesiarte (2006) 1–104.

This research takes place in the framework of the LIA MARRIO. Financial support by CNPq, CAPES, FAPERJ and FNRS is gratefully acknowledged.

Phenotypic Plasticity in Sponges: a case study on *Callyspongia* sp. from Northeastern Brazil

Gisele Lôbo-Hajdu, Mariana Ventura Alves, Thomáz Vieiralves & Thiago Silva de Paula

Department of Genetics, Universidade do Estado do Rio de Janeiro, Rua São Francisco Xavier, 524, PHLC, sala 205, 20550-013, Rio de Janeiro, Brazil. lobohajdu.uerj@gmail.com

Classically, phenotypic plasticity promotes diversification because the developmental pathway which determines the phenotypes induced by the environment consists of multiple genes, responsive to the action of natural selection. However, environmental changes can induce disparity in the expression of genes, by modifying the DNA without changing the allelic frequencies. Sessile organisms activate different genetic programs in response to environmental changes by large scale DNA methylation control and chromatin modification. One modified route can be fixed if the environment is stabilized, and the selected phenotype can be expressed this way as long as the environment is kept unchanged. This expressed phenotype can, and is, inherited, as long as the selective pressure continues. This expression level of phenotypic plasticity in sponges has been a source of impairing for both species identification and delimitation. Changes in the morphology of the sponges have been correlated with the action of the waves, currents, sedimentation, temperature, bioavailability of minerals, and several biotics factors, such as predation. In Northeastern Brazil, four colour morphotypes of *Callyspongia* sp. are observed, blueish, greenish, redish, and yellowish; which may regard to interspecific differences. A total of 55 samples of *Callyspongia* sp. collected in Salvador, were examined: 15 blueish, 22 greenish, 06 redish, and 12 yellowish. All phylogenetic reconstructions, whether if using ITS, 16S or cox1, shown that individuals of *Callyspongia* sp. comprise the same clade, regardless of colour. Besides genetically identical, specimens of *Callyspongia* sp. were also morphologically indistinguishable. Their skeleton are strongly stratified, and show the double integrated net of spogin fibres, typical of the genus. The primary fibres have about 40 micrometers (µ m) and secondary fibres, about 30 µm. The endosome is constituted by primary fibres of 47- 59, 81-66 µ m, secondary 23-33, 14-38 µm and tertiary 5-10, 62-18 µm. Spongin fibres are filled by the megascleres oxeas, measuring 48-121 µm long and 2 - 8 µm wide. Toxa are the only microscleres observed type, ranging from 8 to 19 µm in length. No difference was found among colour morphotypes of *Callyspongia* sp. either in their external or internal morphology. Although these results evidence that colour variation in *Callyspongia* sp. is not a case of diversification, the underlying causes for such plasticity in this species are still to be demonstrated.

References

1. E.J. Duncan, P.D. Gluckman, P.K. Dearden, J. Exp. Zool. (Mol. Dev. Evol.) 322B (2014) 208–220.
2. K.N. Laland, T. Uller, M.W. Feldman, K. Sterelny, G.B. Müller, A. Moczek, E. Jablonka, J. Odling-Smee, Proc. R. Soc. B 282 (2015) doi: 10.1098/rspb.2015.1019.

Financial support by Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES), Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq) and Fundação Carlos Chagas Filho de Amparo à Pesquisa do Estado do Rio de Janeiro (FAPERJ).

Sponges of the genus *Agelas* from the Indo-Pacific

Merrick Ekins

Queensland Museum Po Box 4400, South Brisbane, 4101

The genus *Agelas* is one that has caused a great deal of confusion over the past hundred years or so. It has confused taxonomists by its deceptively seductive verticillated acanthostyles. However despite it's obvious bright orange colour, specimens have been classified rather haphazardly, not because of incompetence but rather due to the combination of poor descriptions, type specimens that were either destroyed during the second world war, lost, badly preserved, or too small a fragment to examine. Revision of the Indo-Pacific *Agelas* species involved examination of all available type specimens. The revision includes molecular data as well as photographs of the specimens, spicules, skeletons and additional specimens to show the variation that occurs within each species, and descriptions of new species. This should provide a useful resource for identification of *Agelas* species around the world.

Evolutionary transformations of choanocyte kinetid in the phylum Porifera and their significance for phylogenetic reconstructions

Igor Pozdnyakov[1], Agniya Sokolova[2], Sergey Karpov[1, 3], Alexander Ereskovsky[4, 5]

1. St. Petersburg State University, Department of Invertebrate Zoology, Biological Faculty, Saint-Petersburg, Russia
2. A. N. Severtzov Institute of Ecology and Evolution, Moscow, RU
3. Zoological Institute RAS, St. Petersburg, Russia.
4. InstitutMéditerranéen de Biodiversitéetd'Ecologie marine et continentale (IMBE), Aix Marseille Université, CNRS, IRD, Marseille, France
5. Dept. Embryology, Saint-Petersburg State University, Saint-Petersburg, Russia

Sponges were traditionally considered as the most primitive multicellular animals because of their general simplicity and similarity between choanocytes and choanoflagellates. Recent molecular data confirmed the hypothesis of common ancestor for choanoflagellates and sponges. One could expect the presence of common characters in cytoskeleton in both groups. It is well known that the kinetid structure of eukaryotes is a good phylogenetic marker for the analysis of macroevolutionary processes and relationships among organisms through time. Kinetid of sponge choanocyte might possesses some characters of choanoflagellates, or even deeper lineages of opisthokonts.

Using transmission electron microscopy we obtained original data on the choanocyte kinetid structure from three main branches of Porifera: Demospongiae, Calcarea, and Homoscleromorpha.Based on the analysis of kinetid diversity and known molecular phylogeny of Porifera we reconstructed the ancestral type of choanocyte kinetid for each of these branches. Kinetids of Demospongiae differ from each other by presence/absence of accessory centriole and the connection with nucleus as well as by the arrangement of MTOCs around the kinetosome. Subclasses Keratosa and Verongimorpha apparently have one kinetid type. In subclass Heteroscleromorpha representatives of different monophyletic groups have different kinetid types. The tendencies of kinetid evolution in Demospongiae appear to be the reduction of centriole and transformation of kinetid-associated MTOCs pattern. In Calcarea the choanocyte kinetids of subclasses Calcinea and Calcaronea differ by the presence/absence of kinetosome-nucleus connection, which corresponds to nuclear position in the choanocyte. In Homoscleromorpha all the Plakinidae and few species of *Oscarella* (Oscarellidae) with apical nucleus in choanocyte have the kinetid connected to the nucleus, but the *Oscarella* species with basal nucleus have different kinetid type. Each evolutionary choanocyte kinetid transformation occurs within certain branch of sponges, but the kinetid transformation does not occur in every sponge lineage. In different subdivisions of Porifera the changes of kinetid structure are confined to the taxa of different levels. The nuclear-kinetid disconnection and nuclear migration from apical to basal position in choanocyte is a common evolutionary tendency that was observed in all three classes of Porifera. On the base of comparative morphological analysis we reconstructed the ancestral type of choanocyte kinetid for Porifera that differs essentially from the kinetid type of choanoflagellates. Thus, these data contradict to hypothesis of the direct origin of the choanocytes from choanoflagellates and does not support an opinion that choanoflagellates were ancestors of Metazoa.

Financial support by Russian Foundation for Basic Research (project No 15-04-03324), and RC of Molecular and Cell Technologies of Saint-Petersburg State University are gratefully acknowledged.

Historical overview on the Adriatic calcarean sponges

Mirna Halasz[1], Helena Ćetković[1], Michelle Klautau[2]

[1] *Ruđer Bošković Institute, Division for Molecular Biology, Bijenička cesta 54, 10002 Zagreb, Croatia.*

[2] *Universidade Federal do Rio de Janeiro, Instituto de Biologia, Departamento de Zoologia, Av. Carlos Chagas Filho 373, Cidade Universitária, 21941-902 Rio de Janeiro (RJ), Brazil.*

The Adriatic Sea represents one of the seven eco-regions of the Mediterranean. It is situated in the northernmost part of the Mediterranean and can be subdivided into three ecologically distinct areas: Northern, Central and Southern Adriatic. Some of the first sponge studies have been carried out in the Adriatic, starting a long time ago with Aristotle dissecting an Adriatic sponge in 300 BC. Since then, many scientists have been investigating this area and the Adriatic Sea is known today as the type locality of many sponge species. Calcarean sponges in the Adriatic were most intensively investigated in the 19th century, primarily by Schmidt, who had

described in details the localities he had visited back then, in some of his most famous works[1]. Ten years later, in his extensive monograph[2], Haeckel finds and describes some of the Adriatic calcarean species, and also revises Schmidt's species along the way. After Lendenfeld's work[3] on the Adriatic calcareans in the end of the 19th century, calcarean sponge taxonomy of this region has been rather neglected. Only in recent years, the interest in calcarean sponges and in their type species and localities has grown wider, so in the 21st century a few papers e.g.[4, 5] revived this subject. We here present a historical overview of calcarean species records in the Adriatic Sea, comparing chronologically since Schmidt till nowadays the presence/absence of recorded species and their localities.

References

1. Schmidt O. 1862. Die Spongien des Adriatischen Meeres, enthaltenddie Histologie und systematiche Ergänzungen. Wilhelm Engelmann, Leipzig.
2. Haeckel E. 1872. Die Kalkschwämme, eine Monographie. Vols 1–3. Reimer, Berlin.
3. Lendenfeld R. von 1891. Die Spongien der Adria. I. Die Kalkschwämme. Wilhelm Engelmann, Leipzig.
4. Pansini M. & Longo C. 2008. Porifera. In: Relini G. (ed.) Checklist della Flora e della Fauna dei Mari Italiani (Parte I). Biologia Marina Mediterranea 15 suppl.(1); 42–66.
5. Klautau M, Imešek M, Azevedo F, Pleše B, Nikolić V, Ćetković H (2016) Adriatic calcarean sponges (Porifera, Calcarea) with description of six new species and richness analysis. European Journal of Taxonomy 178; 1-52.

Sponges & Microbes

Exploring microbial dark matter in sponge symbioses

Ute Hentschel Humeida[1]

RD3 Marine Microbiology, GEOMAR Helmholtz Centre for Ocean Research Kiel, Germany. uhentschel@geomar.de

The term "holobiont" (syn. "metaorganism") was coined in recognition of the fact that in the environment, all multicellular hosts (animals, plants) associate with microorganisms[1]. The concept has profound impacts on our understanding of ecology which seeks to understand the interactions between organisms and between organisms and their environment. There is a growing awareness that such microbial communities may fulfil many essential functions, from nutrition to development and defense against pathogens. Sponges are excellent examples of such holobionts[2], because many species harbor enormously dense and diverse communities of symbiotic microorganisms in their tissues. Up to 41 bacterial phyla and candidate phyla as well as two archaeal lineages representing thousands of symbiont lineages per sponge individual have been recorded[3]. This diverse array of microbial communities has received considerable research attention, yet much remains unknown about the mechanisms of interactions with the sponge host and their in situ ecological function(s). The presentation will focus on recent insights into the HMA LMA dichotomy obtained by machine learning[4] as well as summarize our current understanding of the genomic adaptations of sponge symbionts to a lifestyle within sponges.

References

1. McFall-Ngai, M., Hadfield, M., Bosch, T., Carey, H., Domazet-Loso, T., Douglas, A., Dubilier, N., Eberl, G., Fukami, T., Gilbert, S., Hentschel, U., King, N., Kjelleberg, S., Knol, A.H., Kremer, N., Mazmanian, S., Metcalf, J., Nealson, K., Pierce, N., Rawls, J., Reid, A., Ruby, E., Rumpho, M., Sanders, J., Tautz, D., Wernegreen J (2013) Animals in a bacterial world: a new imperative for the life sciences. Proc Natl Acad Sci 110(9): 3229-3236
2. Pita, L., Fraune, S., Hentschel, U. (2016) Emerging sponge models of animal-microbe symbioses. Frontiers in Microbiol: 7:2102.
3. Thomas, T., Moitinho-Silva, L., Lurgi , M., Björk, J.R., Easson, C., Astudillo, C., Olson, J.B., Erwin, P.M., López-Legentil, S., Luter, H., Chaves-Fonnegra, A., Costa, R., Schupp, P., Steindler, L., Erpenbeck, D., Gilbert, J., Knight, R., Ackerman, G., Lopez, J.V., Taylor, M.W., Thacker, R.W., Montoya, J.M., Hentschel, U., Webster, N. (2016) Global Sponge Microbiome: Diversity, structure and convergent evolution of symbiont communities across the phylum Porifera. Nature Communications, 7:11870.
4. Moitinho-Silva, L., Steinert, G., Nielsen S., Hardoim C.P., Wu Y.C., McCormack G.P., López-Legentil S., Marchant R.,Webster N.,Thomas T., Ute Hentschel U (2017). Predicting the HMA-LMA status in marine sponges by machine learning. Front Microbiol. 2017; 8: 752.

Financial support by the "DFG-CRC1182 Origin and Function of Metaorganisms" and the EU project "SponGES" is gratefully acknowledged.

Sponge Bleaching, *Symbiodinium* Symbioses, and forces that shape Coevolutionary Specialization.

Malcolm Hill, Garrett Fundakowski, Tyler Heist[1], Connor Hughes[2], Nasheya Rahman, Shiv Toolsidass, Tongu Wang, Paul Kwam, April Hill, John Wesley Cain[3], Barry Lawson

University of Richmond, Richmond, VA mhill2@richmond.edu

[1] *Present address: Lewis-Sigler Institute, Princeton University, Princeton, NJ*

[2] *Present address: School of Medicine, University of Colorado, Boulder, CO*

[3] *Present address: Department of Mathematics, Harvard University, Cambridge, MA*

Cliona varians harbors dense intracellular populations of Clade G *Symbiodinium*. These symbioses are typically unaffected by environmental stressors that induce coral bleaching. However, widespread sponge bleaching was observed during a mass coral bleaching event in October 2015 on shallow reefs in the Florida Keys, and community- wide consequences of disrupting this sponge symbiosis are unknown. The shallow water form of *C. varians* did not bleach in 2015 despite experiencing maximum temperatures >41°C. To better understand the basic biology of the symbiosis, and the role of the sponge and its symbionts in reef ecology, we are empirically and theoretically exploring sponge:algal partnership from an interdisciplinary perspective at multiple spatial and temporal scales. Sponges offer unique opportunities to study the evolutionary processes that produce mutualistic interactions. We are exploring dynamics of photosynthate translocation and mechanisms by which symbionts co-opt host cellular machinery to avoid detection and maintain residency within the host. We will present work that contrasts findings from shallow (<1 m) and deep (>10 m) populations of *C. varians* in terms of feeding efficiency, symbiont densities, and general aspects of trophic ecology. We will also present results from two models designed to evaluate factors that promote symbiont persistence *in hospite*. The first is an agent based model constructed to explore the role of energy budgets in the dynamics of host:symbiont partnerships. The second is a Lotka-Volterra-type model designed to examine how two symbiont species might compete for access to a single host. Empirical work testing aspects of these models (e.g., how novel and native symbionts navigate host cellular responses) will be presented.

Financial support from National Science Foundation awards 1617255 & 1555440 is gratefully acknowledged.

Molecular and metabolic interactions in sponge-microbe symbiosis

Torsten Thomas, Lucas Moitinho e Silva, Giampiero Batani, Ana I.S. Esteves, Mary Nguyen, David Reynolds, Cristina Diez-Vives, Rajesh Thangamani, Lu Fan

Centre for Marine Bio-Innovation, University of New South Wales, Sydney

Sponges host complex communities of symbiotic microorganisms, but how this symbiosis is mediated remains poorly understood. Our recent studies based on –omics approaches have provided new insights into how the uncultured, microbial symbionts interact with their sponge host.

Firstly, we discovered the presence and abundance of genes encoding for eukaryotic-like proteins (ELPs) in microbial symbionts. Phylogenetic analyses indicate that these ELPs have been horizontally transferred from sponges and other eukaryotes into symbiont lineages. Meta-transciptomic analyses showed that a large array of different ELPs is expressed under natural settings, indicating their functional role in symbiosis. Through recombinant approaches we also showed that ELPs can inhibit eukaryotic phagocytosis, which is a relevant phenotype for a symbiont to avoid being consumed by sponge amoebocytes. Some ELPs could also specifically bind to sponge proteins involved in bacterial recognition and degradation. These findings suggest that microbial symbionts have acquired eukaryotic host genes that have subsequently evolved to function as molecular mediators of symbiotic interactions.

Secondly, we used genome-centered meta-transcriptomics to develop a model for the integrated metabolism in the sponge *Cymbastela concentrica*. Transcriptional analysis indicated that diatoms and sponge likely provide dissolved organic carbon and organic nitrogen compounds, such as creatine, creatinine, urea, and cyanate, to bacterial and archaeal community members. This fuelled both heterotrophic and chemolithoautotrophic processes that retained and recycled biochemical resources within the sponge holobiont. These findings provide an unprecedented view of the metabolic interactions within sponge-microbe symbiosis, bridging the gap between cell- and community-level knowledge.

Financial support by Australian Research Council and the Betty and Gordon Moore Foundation is gratefully acknowledged.

Genome-informed insights into the function of a coral reef sponge holobiont

Rebecca Fieth[1], Jabin Watson[1], Benedict Yuen[1], Maely Gauthier[1] & Sandie Degnan[1]

[1] *School of Biological Sciences, University of Queensland, Brisbane QLD, Australia s.degnan@uq.edu.au*

The critical ecosystem engineering roles of marine sponges are achieved in large part due to the symbiotic bacteria with which they associate. Working with the coral reef sponge *Amphimedon queenslandica* and its low complexity bacterial symbiont community, we are exploring how intimate interactions between the partners shape the biological function of the holobiont. Genomic, transcriptomic, microbiomic and cellular analyses together provide strong support for a high fidelity relationship of all partners that begins with vertical transmission of core symbionts and is complemented at larval settlement by selective horizontal transmission [1]. The result is an adult microbiome dominated by a sulphur-oxidising bacterial symbiont (order Chromatiales) that assists the holobiont to function in its low energy, high deposition intertidal reef flat environment [2].

The gene content of both host and symbiont genomes, and a draft mixed-species genome-scale metabolic model built from these, suggests that amino acids traded in both directions between the partners are critical to holobiont development and ecology. As further evidence of the intimacy of this relationship, we see different transcriptional responses by the host to symbiont versus non-symbiont bacteria, with an initial discrimination between the two appearing to involve conserved animal innate immune pathways. The emerging picture from our multi-facted approach is that the *A. queenslandica* holobiont has evolved a diverse set of molecular interactions that underlie a strong and stable alliance. Ongoing study of specific interactions highlighted in this presentation will help us to further understand how sponges cooperate with their bacterial symbionts to produce biomass while living in a seasonally variable, oligotrophic, reef environment.

References

1. Fieth RA, Gauthier MA, Bayes J, Green KM, Degnan SM. 2016. Frontiers in Marine Science 3, 228.
2. Gauthier MA, Watson JR, Degnan SM. 2016. Frontiers in Marine Science 3, 196.

Financial support by the Australian Research Council is gratefully acknowledged.

Sponge Symbionts – key to understanding sponge responses to climate change

Heidi Luter [1, 2], **Holly Bennett**[1, 2], **James Bell**[1], **Nicole Webster**[2]

[1] *School of Biological Sciences, Victoria University of Wellington, Wellington, New Zealand. h.luter@vuw.ac.nz*

[2] *Australian Institute of Marine Science, Townsville, Australia*

Coral reefs worldwide are facing increasing pressures due to ocean warming (OW) and ocean acidification (OA). Given that Intergovernmental Panel on Climate Change (IPCC) scenarios are predicting further increases in both OW and OA, we are likely to see significant loss of coral cover in the future. However, non-calcifying organisms like sponges may not be affected in the same way, with a recent study revealing that sponges can tolerate IPCC projections for 2100 under CO_2 Representative Concentration Pathway (RCP) 6.0[1]. While we are beginning to understand sensitivity thresholds of sponges exposed to OW and OA, much less is known about the mechanisms that enable them to cope with environmental pressures. In this study, we used aquarium-based experiments to examine the effects of OW and OA on microbial symbiont function in two phototrophic (*Carteriospongia foliascens* and *Cymbastela coralliophila*) and two heterotrophic (*Rhopaloeides odorabile* and *Stylissa flabellformis*) species. Sponges were exposed to OW and OA conditions predicted for 2100 under two CO_2 RCPs. Principle component analysis (PCO) of the Clusters of Orthologous Groups of proteins (COGs) revealed distinct symbiont functional profiles for each species, with the two phototrophic species being most similar (Fig.1). In both phototrophic species, the functional potential of the symbionts was not significantly affected by OW or OA. In both heterotrophic species, the functional gene profiles were not significantly affected by OA but were significantly disrupted by OW. In particular, sponge microbial communities at ambient temperature (28.5°C) were enriched in symbiont functions including substrate utilization, defense and repair, and membrane transport, whereas these functions were underrepresented in sponges exposed to 31.5°C. Decreases in these functions likely indicate a breakdown in the sponge-microbe symbiosis in heterotrophic species in response to temperature stress.

References

1. H. Bennett, C. Altenrath, L. Woods, S.K. Davy, N.S. Webster, J.J. Bell, Glob. Change Biol. (2016) DOI: 10.1111/gcb.13474

Metagenomics and FISH-CLEM visualization of marine sponge-associated *Chloroflexi*

Kristina Bayer, Beate Slaby, Martin T. Jahn, Lucas M. Silva & Ute Hentschel

Geomar Helmhotz Centre For Ocean Research, Geomar Helmhotz Centre For Ocean Research, Marine Microbiologie, Düsternbrooker Weg 20 24105 Kiel, Germany

Marine sponges harbor an exceptional microbial diversity with up > 10.000 different operational taxonomic units (OTUs), the vast majority of which remains uncultivated. Members of the phylum *Chloroflexi* can dominate the microbiome of the high microbial abundan ce (HMA) sponges. In order to elucidate the diversity and function of Chloroflexi symbionts within marine sponges, we combined amplicon sequencing with metagenomics and single cell genomic analysis, as well as microscopy (FISH-CLEM). A total of five metagenomics bins and 13 single amplified genomes of the classes Caldilineae, Anaerolineae and SAR 202 group were recovered from the sponge metagenomes; the six most complete genomes were then analyzed in more detail. Besides shared genomic features with respect to carbon and nitrogen metabolism, carbon degradation, and respiration, the analyzed Anaerolineae genomes were depleted in the number of CRISPR systems and secondary metabolism gene clusters compared to their cultivated relative *A. thermophila* and also compared to the other *Chloroflexi* symbionts. We posit that the Caldilineae and SAR 202 type symbionts are responsible for bacterial defenses, while the Anaerolineae may benefit from this protection. Furthermore, the newly established method FISH-CLEM was applied, to our knowledge for the first time, to visualize *Chloroflexi* symbionts within the sponge extracellular matrix at ultrastructural resolution. This study contributes to our understanding of the basis of marine sponge-microbe interactions.

Metabolic Diversification Across Caribbean Sponges

Christopher J. Freeman[1], **Cole G. Easson**[2], **Kenan O. Matterson**[3], **Robert W. Thacker**[4], **David M. Baker**[5] **& Valerie Paul**[1]

[1] *Smithsonian Marine Station, Fort Pierce, Florida, USA. freemanc@si.edu*

[2] *Halmos College of Natural Sciences and Oceanography, Nova Southeastern University, Dania Beach, Florida, USA*

[3] *Smithsonian Institution, National Museum of Natural History, Washington, D.C., USA*

[4] *Department of Ecology and Evolution, Stony Brook University, Stony Brook, New York, USA*

[5] *The Swire Institute of Marine Science, School of Biological Sciences, University of Hong Kong, Hong Kong, PR China*

Microbial symbionts expand the ecological niche of host sponges by allowing for the exploitation of novel sources of carbon and nitrogen. Striking host-specificity in these interactions, however, suggests that there is strong evolutionary selection for divergent microbial communities across coexisting sponge species. If associating with unique microbial taxa alters how sponge hosts acquire resources, these interactions may also promote niche partitioning in crowded, oligotrophic ecosystems. To investigate trophic niche specialization and partitioning across common sponge species in the Caribbean, we measured the isotope values ($\delta^{13}C$ and $\delta^{15}N$) of sponges from twelve sites spanning four geographic regions across a latitudinal gradient from tropical Panama to the subtropical Florida Keys. In total, 21 species of sponges were collected. Host species varied in their utilization and processing of resources within sites, with host identity accounting for between 75-90 % of the variation in $\delta^{13}C$ and $\delta^{15}N$ values across individual sponges within a site. Isotopic niche overlap between species within a site was low (mean of 12% [+/- SE of 0.96]), suggesting that individual species are filling unique functional trophic niches. Interestingly, while $\delta^{13}C$ values varied widely and independent of host phylogeny, $\delta^{15}N$ values were highly conserved across host phylogeny, with a strong phylogenetic signal indicative of evolutionary legacies that condition resource use and isotope dynamics. Trends in $\delta^{13}C$ values may be driven by high levels of organic matter in the Caribbean leading to relaxed selection pressure for physiological constraints in carbon metabolism. In contrast, divergence in nitrogen metabolism is likely microbially mediated, with depleted $\delta^{15}N$ values in some lineages suggestive of biological nitrogen fixation and the recycling and assimilation of inorganic nitrogen. In conclusion, nitrogen limitation may have helped to shape the evolution of microbial symbioses across Caribbean sponges, leading to niche divergence and specificity in nitrogen metabolism across host species and broad scale trends in microbial symbiont community diversity.

Function and Form: Finding the Raison d’être of Symbiotic Communities within Sponges

Jose V. Lopez[1]

[1]*Halmos College of Natural Sciences and Oceanography, Nova Southeastern University,*
8000 North Ocean Drive, Dania Beach, Florida, USA

Characterizations of the identity and diversity of microbial symbiotic communities (“microbiomes”) within different sponges have advanced considerably over the last two decades. Thousands of microbial, mostly uncultivable, operational taxonomic units (OTUs) have been identified through the advances of high-throughput DNA sequencing. However, in spite of compelling data pointing to actual symbioses between many microbes and the sponge host, determination of microbial symbiont functions remains equivocal in most instances. Here, I will review current approaches towards addressing the potential *function* of microbiomes and symbionts found in marine sponges. A basic hindrance to effective study of microbial functions, stems from the uncultivability of most symbionts apart from their host. As one solution, sequencing the entire sponge holobiont (host and microbiome) as a “metagenome” can illuminate. For example, computational tools provide algorithms for inferring function from (16S rRNA) sequence data. Microbes also significantly contribute to elemental cycling and catabolism. Another likely role for symbionts is the biosynthesis of unique secondary metabolites and vitamins, exhibited in many sponge species. These can be used as defensive or communication factors benefiting the holobiont. Newer combinations of older, sophisticated technologies such as fluorescence in situ hybridization-correlative light/electron microscopy (FISH-CLEM) and nanoscale secondary ion mass spectrometry (NanoSIMS) now promise to reveal more potential symbiont functions. Other pervasive questions on the origins and co-evolution of specific symbiont-host partners, and how relevant microbiome function is to holobiont fitness and speciation will also be discussed.

The impact of depth: sponge-associated microbes and antimicrobial activity change

Detmer Sipkema[1], Anak Agung Gede Indraningrat[1, 2], Georg Steinert[1, 5], Michael W. Taylor[6], Peter J. Schupp[5], Leontine E. Becking[3, 4] & Hauke Smidt[1]

1. Laboratory of Microbiology, Wageningen University, The Netherlands.
2. Department of Biology, Faculty of Mathematics and Science Education, Institut Keguruan dan Ilmu Pendidikan Persatuan Guru Republik Indonesia (IKIP PGRI) Bali, Indonesia.
3. Marine Animal Ecology, Wageningen University, The Netherlands.
4. Naturalis Biodiversity Center, Leiden, The Netherlands
5. Institute for Chemistry and Biology of the Marine Environment, Carl von Ossietzky Universität Oldenburg, Wilhelmshaven, Germany
6. Biology Sciences, The University of Auckland, New Zealand

Some sponge species are found both in shallow and deeper waters, however, the majority of sponges seems to prefer either shallow or deeper waters. It is currently unknown whether sponge-associated microorganisms play a role in the ability of their host to cover a larger depth range. Whereas the microbiota associated with shallow water sponges has been extensively studied during the past decade, microbial communities associated with sponges that chose habitats out of reach of SCUBA divers are still largely a ‘blue hole’.

To address this knowledge gap, we selected four sponge species that are found both in shallow water (0-30 m) and in deeper waters (60-90 m). Two of these species were sampled in the Pacific (*Callyspongia* sp. and *Rhabdastrella globostellata*) and two in the Caribbean (*Xestospongia muta* and *Agelas sventres*). Next generation sequencing of PCR-amplified 16S rRNA gene fragments was applied to characterize microbial diversity in these sponges. In addition, antimicrobial activity is being determined from extracts and bacterial isolates obtained from Caribbean sponges sampled from different depths.

The first results for the Pacific sponge species and the seawater show depth-related stratification of the microbial communities. Perhaps not surprisingly, bacteria that were most important for the divide between shallow and deep individuals from the same species were cyanobacteria. However, the divide was not entirely explained by the disappearance of cyanobacteria in the deeper sponges. The highly reduced relative abundance of cyanobacterial species in the deeper sponges was accompanied by increased relative abundance of other cyanobacterial species suggesting that certain cyanobacteria are better adjusted to environmental conditions in the deeper waters. In addition, preliminary results of antimicrobial activity tests of organic extracts from the Caribbean sponges indicate that extracts from the shallow-water sponges are more active against Gram+ bacteria than extracts from their deeper counterparts. No depth-related differences in antimicrobial activity against Gram- bacteria were observed.

Dissolved organic matter cycling by the sponge holobiont

Laura Rix[1], Malik S. Naumann[2], Jasper M. de Goeij[3], Dick van Oevelen[4], Marta Ribes[5], Rafel Coma[6], Ulrich Struck[7], Fuad Al-Horani[8], Christian Wild[9], Ute Hentschel[1]

[1] *GEOMAR Helmholtz Centre for Ocean Research, Kiel, Germany lrix@geomar.de*
[2] *Coral Reef Ecology Group (CORE), Leibniz Center for Tropical Marine Research (ZMT), Bremen, Germany*
[3] *Department of Aquatic Environmental Ecology, University of Amsterdam, the Netherlands*
[4] *Department of Estuarine and Delta Systems, Royal Netherlands Institute for Sea Research (NIOZ-Yerseke), and Utrecht University, Yerseke the Netherlands*
[5] *Institut de Ciències del Mar, ICM-CSIC, Barcelona, Catalunya, Spain*
[6] *Centre d’Estudis Avançats de Blanes, Girona, Catalonia, Spain*
[7] *Museum für Naturkunde, Leibniz Institute for Evolution and Biodiversity Science, Berlin, Germany*
[8] *The University of Jordan, Marine Science Station, Aqaba, Jordan*
[9] *Faculty of Biology and Chemistry (FB 2), University of Bremen, Germany*

Sponges are increasingly recognized as important ecosystem engineers due not only to their ability to provide and modify habitat for other benthic organisms, but also their ability to influence the cycling of key nutrients like carbon and nitrogen (*1, 2*). In particular, sponges have recently been shown to play a role in the recycling of dissolved organic matter (DOM) via the sponge loop (*3, 4*). DOM is a major carbon source for a variety of sponges (*5-7*), and it is hypothesized that the abundant communities of microbes harboured by sponges play a role in its uptake (*2, 8, 9*). However, the importance of these microbes for DOM uptake and the influence of DOM quality on processing by the sponge holobiont (i.e. the sponge host and its associated microbes) are still unknown. Here we used stable isotope tracer experiments to compare the processing of different DOM sources by high-microbial (HMA) and low-microbial abundance (LMA) sponges from the Mediterranean and Red Sea. All sponges examined assimilated DOM, but significant differences in the processing of the various DOM sources demonstrated that DOM quality affects its uptake by the sponge holobiont. Phospholipid-derived fatty acid analyses further indicated that the sponge host and its associated microbes may preferentially utilize certain types of DOM, suggesting there may be resource partitioning within the holobiont. Microbes also appeared to be more active in the processing of DOM in HMA compared with LMA sponges, but similar uptake rates suggest HMA and LMA sponges may utilize different strategies to take up DOM. Finally, we found evidence for the transfer of bacterial-assimilated DOM to the sponge host, providing new insights into the metabolic interactions between sponges and their associated-microbes.

References

1. J. J. Bell, *Estuar. Coastal Shelf Sci.* **79**, 341-353 (2008).
2. M. Maldonado, M. Ribes, F. C. van Duyl, *Adv. Mar. Biol.* **62**, 113-182 (2012).
3. J. M. de Goeij *et al.*, *Science* **342**, 108-110 (2013).
4. L. Rix *et al.*, *Sci. Rep.* **6**, 18715 (2016).
5. G. Yahel, J. Sharp, D. Marie, C. Hase, A. Genin, *Limnol. Oceanogr.* **48**, 141-149 (2003).
6. B. Mueller *et al.*, *Plos One* **9**, (2014).
7. S. E. McMurray, Z. I. Johnson, D. E. Hunt, J. R. Pawlik, C. M. Finelli, *Limnol. Oceanogr.* **61**, 1271–1286 (2016).
8. H. M. Reiswig, *J. Exp. Mar. Biol. Ecol.* **14**, 231-249 (1974).
9. J. B. Weisz, N. Lindquist, C. S. Martens, *Oecologia* **155**, 367-376 (2008).

Virus: an Important Component of the Sponge Holobiont

Cecília Pascelli[1,2,3], Patrick Laffy[2], Marija Kupresanin[4], Emmanuelle Botte [2], Timothy Ravasi[4] & Nicole Webster[2]

[1] *AIMS@JCU, Townsville, Australia. C.Pascelli@aims.gov.au*

[2] *Australian Institute of Marine Science, Townsville, Australia.*

[3] *James Cook University, Townsville, Australia.*

[4] *Division of Biological and Environmental Sciences & Engineering King Abdullah University of Science and Technology, Thuwal, Kingdom of Saudi Arabia*

Sponges are extraordinary holobionts since they host a diverse array of macro and micro symbionts. This high symbiont complexity makes them an ideal model for studying host- viral interactions. Viruses are ubiquitous biological entities that regulate diverse biological processes[1]. However, despite their abundance, we have limited knowledge about how viruses interact with marine sponges. Morphological and molecular approaches were used to describe the diversity and function of viruses in some of the most representative coral reef sponge species from the Great Barrier Reef (GBR) and the Red Sea (RS). Sponge viruses were isolated from their hosts, viral metagenomes were sequenced and taxonomic composition and function were assessed using a customized bioinformatic pipeline designed specifically for analysis of holobiont metaviromes. In addition, Transmission Electron Microscopy (TEM) was used to morphologically characterize the viral particles and resolve their spatial location within the holobiont. Molecular analyses indicate that sponges host a wide diversity of bacterial and eukaryotic viruses including abundant Caudovirales and representatives of Mimiviridae, Phycodnaviridae and Iridoviridae. Functional annotation revealed the presence of viral accessory genes, as Nylon degradation and heavy metal resistance, indicating that virus can potentially contribute for sponge environmental acclimation. TEM analysis further revealed tailed bacteriophages (Caudovirales), non-tailed icosahedral, dumble-ear, geminated and filamentous virus-like particles (VLP) in the sponge mesohyle matrix, mucus or associated with their microbial symbiont. Multivariate analysis demonstrated that the viral community are mostly consistent within the same sponge specie, although it varies among species. Similarities in the viral community from sponge species that co- occur in the GBR and the RS reinforce the host specificity in the sponge-viral association. This study highlights viruses as a diverse and important component of the sponge holobiont.

References

1 R. Danovaro, C. Corinaldesi, A. Dell'anno, J.A.Fuhrman, J.J. Middelburg, R.T. Noble, C.A.Suttle, Marine viruses and global climate change. FEMS Microbiol Rev. 35 (2011) 993-1034.

Financial support by AIMS@JCU is gratefully acknowledged.

Tide After Time: Structural Shifts and Functional Stability in the Microbiome of an Intertidal Sponge

Patrick M. Erwin[1], Brooke L. Weigel[1, 2]

[1] *Department of Biology and Marine Biology, Center for Marine Science, University of North Carolina Wilmington, Wilmington, NC. erwinp@uncw.edu*

[2] *Current address: Committee on Evolutionary Biology, University of Chicago, Chicago, IL.*

Marine sponges host complex bacterial and archaeal communities (microbiomes) that exhibit a high degree of host-specificity among different sponge species. However, the factors controlling variation in the microbiome among conspecific sponge individuals are poorly characterized, yet provide critical insight into the stability of sponge-microbe associations. The contrast between intertidal and subtidal habitats, with large environmental variation over a small spatial scale, provides an ideal system to assess the effects of environmental variation on sponge-microbe symbioses. Here, we investigated intraspecific variation in the microbiome of the intertidal sponge *Hymeniacidon heliophila* from oyster reefs in North Carolina (USA). First, we characterized the microbial communities of intertidal and subtidal *H. heliophila* sponges, ambient seawater, and sediment [1]. *H. heliophila* samples yielded clearly distinct microbial communities from those found in sediment and seawater. Further, significant differences in the diversity, structure, and composition of microbiomes were detected between subtidal and intertidal sponges, despite their close proximity (<10 m). These differences were driven by changes in the relative abundance of a few dominant microbial symbiont taxa, as well as the presence or absence of numerous rare symbionts. Second, we conducted a 70-day reciprocal transplant experiment to directly test the effects of tidal exposure on the microbiome of *H. heliophila* [2]. Sponges transplanted between habitats displayed shifts in microbial communities, however, temporal variation was the dominant factor affecting microbiome composition. We identified core symbionts that persisted across these spatio-temporal scales and used a metagenomic approach to show that these stable members of the microbiome in *H. heliophila* represent nitrogen cycling taxa that have the potential to contribute to a diverse array of nitrogen transformations in the sponge holobiont. Together, these results indicate that (1) extreme abiotic fluctuations, such as periodic air exposure in intertidal habitats, can drive intraspecific differences in complex sponge-microbe symbioses, and (2) despite these spatio-temporal shifts in symbiont composition, core symbiont functions (e.g. nitrogen cycling) can be maintained in sponge microbiomes through functional redundancy.

References

1. B. L. Weigel, P. M. Erwin, Appl. Environ. Microbiol. 82 (2016) 650-658.
2. B. L. Weigel, P. M. Erwin, Sci. Reports 7 (2017) 43247.

Looking for barettins and barretides in north Atlantic demosponges: a case in favour of a species specific microsymbiont production?

Paco Cárdenas[1], Erik Jacobsson[1], Stefanie Schempp[1], Gabrielle Tompkins-MacDonald[2], Ulf Göransson[1] & Lars Bohlin[1]

[1]*Department of Medicinal Chemistry, Division of Pharmacognosy, BioMedical Center, Husargatan 3, Uppsala University, 751 23 Uppsala, Sweden. paco.cardenas@fkog.uu.se*

[2]*Bedford Institute of Oceanography, Department of Fisheries and Oceans, Dartmouth, Nova Scotia, Canada.*

Barettins[1] are brominated diketopiperazines with many acknowledged bioactivities: antifouling, anti-inflammatory, anti-coagulant and antioxidant activities. Barettides[2] are disulfide-containing peptides with antifouling activities. These compounds were all originally isolated from the deep-sea boreal north Atlantic demosponge *Geodia barretti*[3]. Barettins have so far only been reported from *G. barretti* and *G. macandrewii*. Barettides have never been reported elsewhere. We therefore wonder whether they may be present in other species of *Geodia*, or even other species of demosponges. In other words, could these compounds be used in sponge systematics as synapomorphies of the genus *Geodia*, the family Geodiidae, or the suborder Astrophorina? The distribution of barettins and barrettides may also help our understanding of their biological function and their origin (sponge vs. symbionts).

We looked for presence/absence of barettins and barrettides in extractions of specialized metabolites from several north Atlantic demosponges, including 35 specimens of *G. barretti* (from different populations), 11 species of north Atlantic *Geodia* and 15 other demosponge species. Metabolic profiles were produced using a Liquid Chromatography-Mass Spectrometry (UPLC-MS) system.

Our results show that only barettin and 8, 9-dihydrobarettin were occasionally found in other north Atlantic demosponges, most of the time in very small amounts. Bromobenzisoxalone barettin was never found in other species than *G. barretti*. Likewise, barrettides A and B were never found in other species than *G. barretti*. More surprising, we found *G. barretti* intra-specific variation in the presence/absence and amounts of the barettins and barrettides. Furthermore, these variations reflected major changes in the metabolic profiles from different populations. We conclude by suggesting that i) barettins are produced by a species specific microsymbiont and that ii) depth explains the *G. barretti* metabolic variations.

References

1. Hedner E, Sjögren M, Hodzic S, Andersson R, Göransson U, Jonsson PR, Bohlin L (2008) Antifouling Activity of a Dibrominated Cyclopeptide from the Marine Sponge *Geodia barretti*. J Nat Prod 71 (3):330-333
2. Carstens BB, Rosengren KJ, Gunasekera S, Schempp S, Bohlin L, Dahlström M, Clark RJ, Göransson U (2015) Isolation, Characterization, and Synthesis of the Barrettides: Disulfide-Containing Peptides from the Marine Sponge *Geodia barretti*. J Nat Prod 78 (8):1886–1893
3. Cárdenas P, Rapp HT, Klitgaard AB, Best M, Thollesson M, Tendal OS (2013) Taxonomy, biogeography and DNA barcodes of *Geodia* species (Porifera, Demospongiae, Tetractinellida) in the Atlantic boreo-arctic region. Zool J Linn Soc 169:251-311

Financial support from the EU FP7 through the Bluegenics project (grant agreement No. 311848) and from the

EU Horizon 2020 programme SponGES under grant agreement No. 679849.

Metabolic profiles of microbiota from Antarctic sponges revealed by metagenomics

Mario Moreno Pino[1], **Mariela Guajardo**[1] **& Nicole Trefault** [1]

[1] *Center for Genomics and Bioinformatics, Faculty of Sciences, Universidad Mayor, Camino La Pirámide 5750, Santiago, Chile.*
mario.moreno@mayor.cl

Marine sponges harbour diverse and abundant microorganisms which play key metabolic roles in biogeochemical cycles[1]. Whereas most of the general observations of sponge microbiomes have focused in temperate and tropical environments, the functional roles of sponge symbionts from Polar Regions remain largely unknown.

Our study aims to characterize the functional potential of microorganisms associated to Antarctic sponges. Two sponge species, *Myxilla* sp. and *Leucetta antarctica,* were collected from Fildes Bay (King George Island, South Shetlands) to perform, shotgun metagenomic sequencing.

Community composition of microorganisms associated to *Myxilla* sp. and *L. antarctica* showed a high predominance of sequences assigned to the Bacteria domain and differences between the two sponge species, consistently with previously reported data[2]. Profiles of general functions were homogeneous in the two sponges (Fig 1A), with a high proportion of genes related to amino acid transport and metabolism, replication, recombination and repair. The presence of genes involved in the nitrogen cycle like *narCGH, nirK, qnor, nosZ (*denitrification), and *amoA* (ammonia oxidization) was detected, as well as genes implied in carbon cycle like *pgi*, *rbcs, tkt* (Calvin-Benson cycle), and sulphur cycle like *cysD*, *cysC, cysH* and *papsR* (sulfur assimilation). As evidenced in sponge-associated microbial communities from other environments, genes implicated in (i) Vitamin synthesis, (ii) Eukaryotic like proteins and (iii) CRISPR associated (CAS), were also identified in both sponges (Fig 1B). To our best knowledge, this work is the first insight into the functional potential of sponge- associated microbial communities from the Antarctic environment, and reveals a similar metabolic profile in both sponges.

References

1. M.W. Taylor, R. Radax, D. Steger, M. Wagner. MMBR (2007)71(2):295-347.
2. S. Rodríguez-Marconi, R. De la Iglesia, B. Díez, C.A. Fonseca, E. Hajdu, N. Trefault. PLoS One (2015);10(9):e0138837. doi:10.1371/journal.pone.0138837.

Do Freshwater Sponges Facilitate the Transfer of Antibiotic Resistance inWater-Borne *Enterococcus faecalis*?

Allison Cartwright[1], **Michael Conwell**[2], **Joerg Arnscheidt**[1], **James Dooley**[2], **Patrick Naughton**[2], **Chris McGonigle**[1]

[1] *School of Environmental Sciences, Ulster University, Cromore Road, Coleraine, BT52 1SA*

[2] *School of Biomedical Sciences, Ulster University, Cromore Road, Coleraine, BT52 1SA*
Corresponding authors email address: Cartwright-A4@email.ulster.ac.uk

The rise in antibiotic resistance among bacteria is currently a major healthcare concern (Berendonk et al. 2005). Opportunistic pathogens which have acquired high levels of antibiotic resistance include *Enterococcus faecalis* (Berendonk et al. 2015; Zhang et al. 2015). *E. faecalis* is regularly found in aquatic ecosystems polluted with faecal matter where it has the opportunity to interact with other bacterial species and aquatic organisms (Harwood et al. 2014). Freshwater sponges have been shown to concentrate bacteria through the process of filtration (Kefalas et al., 2003), and could, therefore, facilitate the transfer of antibiotic resistance genes in bacteria.

Laboratory experiments for the horizontal transfer of Vancomycin resistance in *E. faecalis* as indicated by cultivation on antibiotic-selective plates were tested using live and dead *Ephydatia fluviatilis* and *Spongilla lacustris*. We found that sponges facilitated gene transfer of vancomycin resistance among our selected strains of *E. faecalis* (Cartwright et al. in prep). The facilitation of gene transfer was similar in both species of sponges. Gene transfer occurred in both live and dead sponges. There was no significant difference in the number of bacteria with successful gene transfer between the live and dead sponges or between either sponge species.

This provides experimental evidence for facilitation of antimicrobial resistance transfer by an aquatic invertebrate. Sponges can provide a substrate for the gene transfer whether they are alive or dead. Future work is needed to address which bacterial interactions with sponges facilitate the gene transfer and where exactly in the sponge it occurs.

References

1. Berendonk, T.U., et al., (2015). Tackling antibiotic resistance: the environmental framework. *Nature Rev. Microbiol*, 13, 310-317.
2. Harwood, V.J. et al., (2014). Microbial source tracking markers for detection of fecal contamination in environmental waters: Relationships between pathogens and human health outcomes. *FEMS Microbiol Rev*, 38(1), 1–40.
3. Kefalas, E., et al., (2003). Bacteria associated with the sponge Spongia officinalis as indicators of contamination. *Ecol. Indic*., 2(4), 339–343.
4. Lucey, J. & Cocchiglia, L., (2014). Distribution of Sponges (Porifera: Spongillidae) in Southern Irish Rivers and Streams. *Biol Environ*, 114(2), 89–100.
5. Zhang, R. et al., (2015). Antibacterial and residual antimicrobial activities against *Enterococcus faecalis* biofilm: A comparison between EDTA, chlorhexidine, cetrimide, MTAD and QMix. *Scientific Reports*, 5, 1–5

Financial support provided by Department of Employment and Learning is gratefully acknowledged

The microbial and chemical affairs between haplosclerid and homosclerophorid sponge pairs of the Caribbean

Jan Vicente[1], **Lucas Moitinho-Silva**[2], **Micah J. Marty**[3], **Sven Zea**[4], **Russell T. Hill**[5]

[1]*Hawaii Institute of Marine Biology, University of Hawaii at Mānoa, Kaneohe, HI 96744, USA. janv@hawaii.edu*

[2]*The University of New South Whales, Sydney, New South Wales 2052, Australia*

[3]*Center for Marine Science, University of North Carolina Wilmington, Wilmington, NC 28403 USA*

[4]*Centro de Estudios en Ciencias del Mar, Universidad Nacional de Colombia, Santa Marta, Colombia*

[5]*Institute of Marine and Environmental Technology, University of Maryland Center for Environmental*
Science Baltimore, MD 21202, USA

Most marine sponges have evolved free-living lifestyles, with specific chemical and microbiological adaptations that help compensate for any ecological limitations. In a microbiological context sponge species have evolved by either selecting a low microbial abundance (LMA), an intermediate abundance, or a high microbial abundance (HMA) of bacteria. In a chemical ecological context sponge species are either chemically defended, variably defended or palatable. These specific lifestyles are therefore restricted to a particular trait and are necessary for adaptation to ecological pressures. In this study, we describe four new sponge pairs which consist of two haplosclerid sponges associating with two homosclerophorid sponges in the Caribbean and determine whether these sponge pairs associate to offset the limitations of a free-living lifestyle. Bacterial and sponge cell counts revealed that haplosclerid sponges are LMA sponges that live epibiotically on basibiont, HMA, homosclerophorid sponges. Characterization of the microbial community using next-generation sequencing of the 16S rRNA gene showed higher diversity indices of microbial symbionts in basibiont sponges than epibiont sponges for three geographic locations of the Caribbean.

Free-living individuals of the haplosclerid sponge *Xestospongia deweerdtae* were also analyzed and the microbial community in free-living individuals showed less diversity than found in associated individuals. Relative abundance of microbial phyla in associated cases of *X. deweerdtae* also showed microbial OTUs belonging to phyla found in the basibiont, homosclerophorid sponge *Plakortis* spp., suggesting that epibionts could be acquiring symbionts from the basibiont sponge through horizontal transmission. Fish feeding assays using crude extracts from both sponge species on two Caribbean fish species (generalist and spongivore) revealed that basibiont homosclerophorids are strongly chemically defended, *X. deweerdtae* is variably defended in their free- living state but always defended when associated to its homosclerophorid pair. In addition, diode-array HPLC coupled with high resolution mass spectrometry (LC-MS/IT-TOF) of crude extracts from each pair showed that plakinic acids I and K are main compounds of the basibiont sponge, while trace amounts were detected in the epibiont *X. deweerdtae*; potentially contributing to the consistent deterrence observed in the associated lifestyle of the epibiont. Comprehensively, these results show how the two sponge species in a pair with disparate lifestyles are likely associating opportunistically to access advantageous traits from their counterpart.

The response of sponges to microbial elicitors

Lucía Pita[1], Marc Höppner[2], Marta Ribes[3] and Ute Hentschel Humeida[1, 4]

[1]GEOMAR Helmholtz Centre for Ocean Research, Kiel, Düsternbrooker Weg 20, 24105 Kiel, Germany. lpita@geomar.de

[2 4]ChristianAlbrechtsUniversity Kiel, Institute of Clinical Molecular Biology, Kiel, Germany

[3]Institute of Marine Science CSIC, Passeig Marítim de la Barceloneta 37-49, 08003 Barcelona, Spain

[4]ChristianAlbrechtsUniversity Kiel, ChristianAlbrechtsPlatz 4, 24118 Kiel

Diverse invertebrate and vertebrate models of symbiosis suggest that host immunity is involved in the maintenance of symbiosis [1]. In sponges, recent analysis of genomes and transcriptomes revealed potential receptors for recognition of microorganisms [2, 3] and the presence of complete innate immune signalling pathways [4]. The functional evidence of the receptors and effectors in sponge immunity is still scarce [5]. Here, we adopted an experimental approach followed by RNA-seq and differential gene expression in order to identify and characterize receptors and effectors involved in the sponges' microbial pattern recognition. We focused on two Mediterranean species, *Aplysina aerophoba* and *Dysidea avara*, as representatives of high microbial abundance (HMA) and low microbial abundance (LMA) sponges, respectively. To study the short-term response, sponges were exposed to a "cocktail" of microbial elicitors (i.e. LPS and peptidoglycan) or sterile artificial seawater (control) and tissue samples were collected at three different time points. We identified differentially expressed genes in treatment *vs* control. We further compared the reference transcriptomes to published data of other sponge species. By exploring the gene repertoire in an experimental approach, our data provide evidence for candidate genes that might mediate the response of sponges to microorganisms.

References

1. Chu, H. & Mazmanian, S. K. Innate immune recognition of the microbiota promotes host-microbial symbiosis. *Nat. Immunol.* **14,** 668–75 (2013).
2. Hentschel, U., Piel, J., Degnan, S. M. & Taylor, M. W. Genomic insights into the marine sponge microbiome. *Nat. Rev. Microbiol.* **10,** 641–54 (2012).
3. Ryu, T. *et al.* Hologenome analysis of two marine sponges with different microbiomes. *BMC Genomics* **17,** 158 (2016).
4. Riesgo, A., Farrar, N., Windsor, P. J., Giribet, G. & Leys, S. P. The analysis of eight transcriptomes from all Poriferan classes reveals surprising genetic complexity in sponges. *Mol. Biol. Evol.* **31,** 1102–1120 (2014).
5. Pita, L., Fraune, S. & Hentschel, U. Emerging sponge models of animal-microbe symbioses. *Front. Microbiol.* **7,** (2016).

U.H.H. received financial support from the DFG (CRC1182-TPB1) and L.P. was awarded a postdoctoral fellowship from Alexander von Humboldt Foundation, which was sponsored by The Future Ocean Cluster.

Metagenomic binning of a marine sponge microbiome reveals unity in defense but metabolic specialization

Beate M. Slaby[1, 2], Thomas Hackl[3], Hannes Horn[1, 2], Kristina Bayer[1], Ute Hentschel[1, 4*]

[1]RD3 Marine Microbiology, GEOMAR Helmholtz Centre for Ocean Research Kiel, Germany. bslaby@geomar.de

[2] Dept. of Botany II, Julius-von-Sachs Institute for Biological Science, University of Würzburg, Germany

[3]Dept. of Civil and Environmental Engineering, Massachusetts Institute of Technology, Cambridge, MA, USA

[4]Christian-Albrechts University of Kiel, Germany

Marine sponges are ancient metazoans that are populated by distinct and highly diverse microbial communities. In order to obtain deeper insights into the functional gene repertoire of the Mediterranean sponge *Aplysina aerophoba*, we combined Illumina short-read and PacBio long-read sequencing followed by un-targeted metagenomic binning. We identified a total of 37 high-quality bins representing 11 bacterial phyla and 2 candidate phyla. Statistical comparison of symbiont genomes with selected reference genomes revealed a significant enrichment of genes related to bacterial defense (restriction-modification systems, toxin-antitoxin systems) as well as genes involved in host colonization and extracellular matrix utilization in sponge symbionts. A within-symbionts genome comparison revealed a nutritional specialization of at least two symbiont guilds, where one appears to metabolize carnitine and the other sulfated polysaccharides, both of which are abundant molecules in the sponge extracellular matrix. A third guild of symbionts may be viewed as nutritional generalists that perform largely the same metabolic pathways but lack such extraordinary numbers of the relevant genes. This study characterizes the genomic repertoire of sponge symbionts at an unprecedented resolution and it provides greater insights into the molecular mechanisms underlying microbial-sponge symbiosis.

Financial support by DOE JGI, by the European Commission, and by the German Excellence Initiative with a grant to the Graduate School of Life Sciences of the University of Würzburg is gratefully acknowledged.

Multi-primers Targeting 16S rDNA Variable Regions Essential for Sponge (Porifera) Microbiome Study

Wei Zhang[1,2], Qi Yang[1, 2], Christopher M.M. Franco[1, 2]

1 Centre for Marine Bioproducts Development, and 2 Department of Medical Biotechnology, School of Medicine, Flinders University, Adelaide, South Australia, SA 5042, Australia
Wei.Zhang@flinders.edu.au

PCR-based amplification and sequencing of 16S rRNA gene is the cornerstone molecular approach for microbiome survey of many environmental samples, which contributes greatly to our understanding of the microbial world. Amplicon-based study of sponge microbiome using Illumina platform has become the method of choice, however exclusively sequenced only one specific 16S rDNA variable region, even with well-recognised primer bias problem. We demonstrated that different primers targeting different variable regions revealed vastly different parts of the microbiome, and the combination of multi-primers is essential and improves unprecedentedly the microbiome coverage. This new multi-primer approach represents a philosophical, but simple change of conventional single primer amplicon -based microbiome study that will uncover many black-holes and enhance greatly our understanding of the microbial world.

References

1. Caporaso, J. G. *et al.* Ultra-high-throughput microbial community analysis on the Illumina HiSeq and MiSeq platforms, *ISME J*, **6(8),** 1621-1624 (2012).
2. Claesson, M. J. *et al.* Comparison of two next-generation sequencing technologies for resolving highly complex microbiota composition using tandem variable 16S rRNA gene regions, *Nucleic Acids Res.*, **38(22)**, e200 (2010).
3. Engelbrektson, A. *et al*. Experimental factors affecting PCR-based estimates of microbial species richness and evenness. *ISME J.*, **4**, 642–647 (2010).
4. Shin, J. *et al.* Analysis of the mouse gut microbiome using full-length 16S rRNA amplicon sequencing. *Sci. Rep.* **6**, 29681; doi: 10.1038/srep29681 (2016).
5. Thomas, T. *et al.* Diversity, structure and convergent evolution of the global sponge microbiome. *Nat. Commun*. **7**, 11870 doi: 10.1038/ncomms11870 (2016).
6. Wang, Y. and Qian, P.Y. Conservative fragments in bacterial 16S rRNA genes and primer design for 16S ribosomal DNA amplicons in metagenomic studies. *PLoS ONE*, **4**, e7401 (2009).

The authors would like to thank Dr. Jason Tanner and his team in South Australian Research and Development Institute for the collection of the sponge specimens, Ms Shirley Sorokin for sponge identification; Dr. Nicola Angel in the Australian Centre for Ecogenomics of the University of Queensland for data processing and consultation. This study was funded by Flinders University, the Centre for Marine Bioproducts Development. This work was supported by a Chinese Scholarship Council-Ph.D. Scholarship and Flinders University-CSC Fund for Qi Yang. Wei Zhang also acknowledges the support by the National Natural Science Foundation of China (Grant No. 41428602).

Single-cell measurement of metabolic interactions between a bioeroding sponge and its endosymbiotic dinoflagellates using nanoscale secondary ion mass spectrometry.

Michelle Achlatis[1], Mathieu Pernice[3], Kathryn Green[4], Ove Hoegh-Guldberg[1, 2] & Sophie Dove[1, 2]

[1] *Coral Reef Ecosystems Laboratory, School of Biological Sciences, University of Queensland, Brisbane, QLD, Australia, m.achlatis@uq.edu.au*

[2] *Australian Research Council Centre of Excellence for Coral Reef Studies, University of Queensland, Brisbane, QLD, Australia*

[3] *Plant Functional Biology and Climate Change Cluster (C3), Faculty of Science, University of Technology, Sydney, NSW, Australia*

[4] *Centre for Microscopy and Microanalysis, University of Queensland, Brisbane, QLD, Australia*

Sponges of the genus *Cliona* are common bioeroders that have an important ecological role in shaping reef habitats and influencing seawater carbonate cycling. Some of the most aggressive clionaid species host intracellular dinoflagellates of the genus *Symbiodinium*, which purportedly fuel the sponge with autotrophic energy, thereby indirectly promoting bioerosion. In contrast to cnidarian symbioses, little is known about the metabolic partnership between sponges and *Symbiodinium* dinoflagellates. Traditional studies have been hampered by the difficulty of separating the two partners in a metabolically meaningful timeframe and without cross-contamination. Here, we report on the use of a novel technology to study nutrient assimilation and transfer in the intact symbiosis between the Indo-pacific bioeroding sponge *Cliona orientalis* and its endosymbiotic alga. Combining transmission electron microscopy (TEM) with nanoscale secondary ion mass spectrometry (NanoSIMS), we were able to visualize and measure isotopic signatures at the individual cell level, allowing us to track the fate of ^{13}C- bicarbonate and ^{15}N-ammonium within this symbiosis. We found strong uptake of both inorganic sources by the symbiont cells and rapid assimilation especially of the carbon tracer. Labelled nutrients were translocated from the symbionts to the hosting archaeocyte cells within 6 hours, and to other host cells within 3 days. Our findings strongly support hypotheses of metabolic interaction between the two partners, shedding light on the ecological advantage that photosymbiotic bioeroding sponges have in marine habitats.

Financial support by the Australian Research Council (ARC), the ARC Centre of Excellence for Coral Reef Studies, the Australian Government Research Training Program Scholarship and the Holsworth Wildlife Research Endowment by Equity Trustees Charitable Foundation is gratefully acknowledged.

Temporal dynamics of sponge microbial communities

Cole G. Easson[1], Robert W. Thacker[2], Xavier Turon[3], Patrick Erwin[4], Susanna Lopez-Legentil[4]

[1] *Nova Southeastern Halmos College of Natural Sciences and Oceanography, Dania Beach, FL. ceasson@nova.edu*

[2] *Department of Ecology and Evolution, Stony Brook University, Stony Brook, NY*

[3] *Center for Advanced Studies of Blanes (CEAB-CSIC), Blanes Girona, Spain*

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

Sponges host diverse symbiont communities with compositions that are largely species- specific and structured by host evolutionary history. However, little is known about how these communities vary over time and whether this variability is linked to the community dynamics of ambient bacterioplankton. To address this question, we sampled individuals of three closely related species of Irciniidae and ambient seawater each month for 15 (*Ircinia oros*) and 18 (*Sarcotragus. fasciculatus, I. variabilis*) months. We characterized symbiotic and ambient microbial communities as part of the Earth Microbiome Project using Illumina sequencing of the 16S ribosomal subunit V4 region. Microbial taxa were grouped according to their occurrence frequency (transient vs. core) and abundance (rare vs. dominant) within individual hosts over time. Our analysis revealed that sponge microbial communities are stable compared to the highly dynamic bacterioplankton community in the surrounding seawater. Temporal shifts in the microbial symbiont community were largely driven by gains and losses of rare taxa, and decoupled from broad shifts in bacterioplankton diversity and composition. A lesser portion of temporal variability was also driven by shifts in persistent taxa abundance. Overall, these data indicate that sponge-associated microbial communities are mostly stable over time, with minor shifts in core taxa abundance and transient, rare taxa occurrence, and are minimally affected by variability in ambient bacterioplankton communities.

Visualization of eukaryotic-like-proteins as ring-like structures within bacteria-containing sponge cells

Giampiero Batani[1], Lucas Moitinho-Silva[1], Martin T. Jahn[2], Kristina Bayer[2], Ute Hentschel[2], Torsten Thomas[1]

[1]*Centre for Marine Bio-Innovation and School of Biological, Earth and Environmental Sciences, The University of New South Wales, Sydney, New South Wales 2052, Australia g.batani@student.unsw.edu.au*

[2]*Marine Microbiology, GEOMAR Helmholtz Centre for Ocean Research, Kiel, 24105, Germany*

Sponges (Porifera) are known to establish and maintain stable symbiotic associations with dense and highly diverse microbial communities (Erwin *et al.*, 2015; Pita *et al.*, 2016). However, it is not well understood how the microbial symbionts are controlled on a molecular and cellular level and how they escape from being digested like any other food particle. Eukaryotic-like-proteins (ELPs) were recently discovered in high abundance and expression levels in the bacterial communities of sponge (Fan *et al.*, 2012, Díez-Vives *et al.* 2016) and they were subsequently been found to influence phagocytosis behavior of eukaryotic cells (Nguyen *et al.*, 2013; Reynolds & Thomas, 2016). Therefore, we aimed to localize ELPs inside sponge tissues to shed light on the poorly understood cellular mechanisms in which these proteins are involved. We studied here the cellular localization of a particular ELP (SSA4) of the ankyrin-class from an uncultured gamma-proteobacterial symbiont of the marine sponge *Cymbastela concentrica.* Using a combination of fluorescence *in situ* hybridization (FISH) and immunohistochemistry (IHC) on ultra-thin sponge tissue sections we obtained a picture of SSA4 localization. This shows that SSA4 is present in ring-like structures around bacterial cells that reside within sponge cells. Such localization would be consistent with the secretion of SSA4 from engulfed bacterial cells and highlights the possibility that ELPs might directly interfere with structures and processes involved in phagocytosis. This information could provide new insights into the ELPs function and the molecular and cellular processes underlying bacteria-sponge symbiosis.

References

1. P.M. Erwin, R. Coma, P. López-Sendino, E. Serrano, M. Ribes, *FEMS Microbiology Ecology*, 91.10 (2015): fiv115.
2. L. Pita, S. Fraune, U. Hentschel, *Frontiers in Microbiology*, 7 (2016).
3. L. Fan, D. Reynolds, M. Liu, M. Stark, S. Kjelleberg, N.S. Webster, T. Thomas, *Proceedings of the National Academy of Sciences*, 109. 27 (2012): E1878-E1887.
4. C. Díez-Vives, L. Moitinho-Silva, S. Nielsen, D. Reynolds, T. Thomas, *Molecular Ecology* (2016).
5. M. THD Nguyen, M. Liu, T. Thomas, *Molecular Ecology*, 23.6 (2014): 1635-1645.
6. D. Reynolds, T. Thomas, *Molecular Ecology*, 25.20 (2016): 5242-5253.

Do symbiotic bacteria help sponges to cope with eutrophication?

Marta Turon[1], Leire Garate[1], Xavier Triadó-Margarit[1], Joan Cáliz[1] & Maria J.Uriz[1]

[1] *Centre d'Estudis Avançats de Blanes, CEAB-CSIC, Accés Cala St.Francesc 14, Blanes, Girona, 17300, Spain. mturon@ceab.csic.es*

Microbes have been intimate partners of sponges since the Pre-Cambrian and can represent up to 50% in volume of the microbial-sponge holobiont. However, little is known about the role (if any) that symbiotic bacteria may play in shaping the ecological distribution of sponge species. To address this issue, we analyzed the associated microbiomes of the most common sponges found in Nha Trang Bay (central Vietnam), which offered at short geographical distances contrasting areas such as well-preserved coral reefs within a marine protected area and eutrophic zones highly impacted by mariculture (Tkachenko K.S. et al 2016). Collection of the specimens was performed by SCUBA diving along 25 m long transects, randomly placed in the two targeted habitats. The microbiome from the 20 most abundant sponge species was analyzed by throughput 16S-tag sequencing. After analysis, we obtained a total of 12733 bacterial OTUs (97% identity) corresponding to 39 bacterial phyla, with *Proteobacteria* (64.4%), *Chloroflexi* (5.1%), *Acidobacteria* (4.6%) and *Actinobacteria* (4.1%) being the most abundant taxa. The structure of sponge-associated bacterial communities was closely related to host- species regardless of the environment. The microbiome of the most dominant sponges in well-preserved habitats (*Aaptos suberitioides* and *Neofibularia hartmani*) showed significantly higher Shannon diversity indices than those of the dominant ones (*Amphimedon sp* and *Clathria reinwardti*) in the eutrophic environment (Fig1). Members of the Rhodobactereacea family and *Shewanella* genus, which play important roles in the sulfur and carbon cycling, weresignificantly (Indicador Value: 0.7) associated to those sponge species dominating in the eutrophic habitat. Indeed, some genus of these groups have been proposed for bioremediation in polluted environments due to their ability to oxidize toxic compounds that thrive in such habitats (Fredickson 2008, Zhang 2013). The particular abundance of these bacteria in sponges adapted to live in eutrophic habitats points to the sponge microbiomes as drivers of sponge adaptation to get over eutrophication (or other) environmental pressures.

References

1. Tkachenko K.S. et al. (2016) Influence of anthropogenic pressure and seasonal upwelling on coral reefs in Nha Trang Bay (Central Vietnam)
2. Fredickson J.K. et al (2008) Towards environmental systems biology of *Shewanella.* Nature reviews 6: 592-603
3. Zhang B. et al (2013) Identification of removal principles and involved bacteria in microbial fuel cells for sulfide removal and electricity generation. Int J Hydrogen Energ 38: 14348-14355

Financial support by he Spanish Ministry of Science and Innovation through the project MarSymbiOmics (CTM2013-43287-P) is gratefully acknowledged.

Global patterns of microbial diversity and composition among three marine host types: sponges, corals, and ascidians

Andrea Aldas-Vargas[1], Detmer Sipkema[1], Hauke Smidt[1] & Georg Steinert[1]

[1] Laboratory of Microbiology, Wageningen University, The Netherlands georg.steinert@wur.nl

Marine sponges, corals, and ascidians constitute three taxonomically different holobiont groups, which are well-known to host dense and diverse microbial communities. All three groups are acknowledged sources of bioactive natural products, some of which are potentially of microbial origin. While these animals are phylogenetically vastly different, often they share the same habitats along with similar lifestyle traits, such as filter feeding or being sessile. However, normally the majority of studies investigating patterns of host-associated microbial community diversity and composition solely focus on one of the three holobiont groups. This inevitably leaves a great number of available independent 16S rRNA gene amplicon datasets that encompass in theory a much larger common history of host-symbiont evolution.

Here we present, for the first time, an integrative processing and analysis approach across these three groups of marine holobionts to tackle this so far untouched potential of individual datasets from multiple studies, comprising different host taxonomies, geographic locations, sequencing technologies, and primer regions. Prokaryotic host- associated communities were analysed using 16S rRNA gene amplicon datasets from 41 publications, accounting for 492 samples almost evenly distributed among various sponge, coral, and ascidian taxa. The general aim was to investigate the global prokaryotic diversity and composition distribution among those three holobiont groups. For instance, with 56 associated prokaryotic phyla sponges represent an intriguing host- taxon that harbours many marine bacteria and archaea, while at the genus level, corals exhibited the most host-specific taxa among those three host groups (Figure 1). At the class level several Proteobacteria differentially dominated the three host types, with Alphaproteobacteria highly abundant in ascidians and Gammaproteobacteria mainly present in corals. Sponges, in turn, exhibited also very abundant assemblages of Chloroflexi members. Furthermore, *Synechococcus* spp., *Ruegeria* spp., and *Endozoicomonas* spp. were the most abundant genera associated with sponges, corals, and ascidians, respectively.

Additionally, the variance in prokaryotic community composition was analysed by fourfactors: (1) host type (i.e., sponge, coral, or ascidian), (2) host taxonomy (at host-genus level) (3) amplicon region, (4) publication. It was shown that the most influential factor regarding the microbial distribution was the host taxonomy, while the weakest correlation was observed for the host type. This indicates that marine prokaryotic host- symbiont interactions may be highly specific to individual host taxa regardless of higher evolutionary relationships.

Financial support by the People Programme (Marie Curie Actions) of the European Union's Seventh Framework Programme FP7/2007-2013/ under REA grant agreement n° 607786 (BluePharmTrain) is gratefully acknowledged.

Microbiome Comparison Suggests Differential Involvement of Bacterial Associates in the Carnivorous Sponges *Chondrocladia grandis* and *Cladorhiza oxeata*

Joost Verhoeven[1] & Suzanne C. Dufour[1]

[1] Department of Biology, Memorial University of Newfoundland, St. John's, Canada. jverhoeven@mun.ca

In deep-sea and arctic environments, carnivorous sponges feeding on mesoplanktonic prey could fulfill important ecological functions, some of which may be mediated by associated microbial communities. In this study, we used Illumina based high-throughput sequencing of the 16S rRNA gene to investigate the bacterial community structure (microbiome) of the carnivorous sponge *Chondrocladia grandis*, collected off the coast of Baffin Island (N=3) and within the Gulf of Maine (N=4), and *Cladorhiza oxeata* (N=2) from Baffin Island. Subsampling of sponges was performed to allow separate, inter- and intra-specimen analyses of anatomical regions with predicted involvement in prey capture (sphere), support (primary and secondary axis) and benthic substrate attachment (root, base axis).

At phylum level, operational taxonomic units (OTU) were distributed amongst 33 bacterial phyla, with the vast majority of OTUs assigned to either the Proteobacteria or Bacteroidetes. A diverse bacterial community (Chao1: 356) was observed within *C. grandis,* including the most abundant Flavobacteriaceae (23%) along with other families such as the Rhodobacteraceae, Halieaceae, Colwelliaceae and Hyphomonadaceae, with minor differences within the two geographic locations. Within *C. oxeata*, a significantly lower diversity was detected (Chao1: 229), mainly dominated by Flavobacteriaceae (~62% relative abundance).

Sediment-associated anatomical regions in *C. grandis* generally showed a high diversity (Chao1: 262), whereas other regions displayed a more restricted, lower diversity community (Chao1: 47 - 144). No large scale difference in diversity were seen amongst regions within *C. oxeata*. Within *C. grandis,* enrichment of specific bacterial genera within root and sphere regions was detected. Notably, significant increases of the chitin hydrolysis enabling *Colwellia* and *Reichenbachiella* (log2 fold-change of 2.5 and 6.8) within trapping spheres could indicate a dependency on bacteria to degrade prey exoskeleton-associated chitin. Furthermore, enrichment of the genera *Robiginitomaculum* and *Mycobacterium* (log2 fold-change of 2.1 and 4.9) in root samples could indicate that *C. grandis* supplements its carnivorous diet with the bacterial degradation of environmental hydrocarbons. This hypothesis was corroborated by the observation of a significant decrease in δ^{13}C isotope ratios within *C. grandis* specimens sampled in areas with suspected hydrocarbon presence (Gulf of Maine). No significant bacterial taxon enrichments were detected in different anatomical regions of *C. oxeata,* possibly indicating a divergent carnivorous strategy with less reliance on bacterial symbionts.

This study highlights the remarkable microbiome diversity of two carnivorous sponge genera, and the potential for these sponges to be intrinsically involved in deep-sea food webs through microbiome specialization.

This project was funded by ArcticNet, the Natural Sciences and Engineering Research Council of Canada, and the National Oceanographic and Atmospheric Administration.

Searching for bacterial genes involved in the symbiosis between sponges and calcifying endosymbiotic bacteria

Leire Garate[1], Rüdiger Ortiz-Álvarez[1] & Maria J. Uriz[1]

[1] Department of Marine Ecology, Centre d'Estudis Avançats de Blanes (CEAB-CSIC), Girona, Spain lgarate@ceab.csic.es

Uriz et al.[1] reported that the calcareous spherules observed in *Hemimycale columella* were produced or mediated by calcifying bacteria (calcibacteria). Later, pyrosequencing analyses revealed that they belonged to Alpha-proteobacteria class, the most abundant bacteria in *H. columella* tissues[2]. Recently, this type of endosymbiotic calcifying bacteria was identified in several sponge species, geographically apart, as well as in seawater and cnidarians[3]. It has also been reported that calcifying bacteria are actively transported to the sponge periphery by sponge cells and accumulated at the sponge periphery[3] forming a kind of rudimentary exoskeleton. The several calcibacteria found form a monophyletic clade within the SAR116. However, the metabolic patterns of calcibacteria and the potential mechanisms ending in bacteria calcification remained unexplored. To gather understanding on the symbiosis functioning we investigate the bacteria genome and thus their main metabolic pathways. We sequenced the genome of a single calcibacterium isolated from *H. columella* using whole genome amplification and sequencing techniques, and compare the results with the genomes of three SAR116 bacteria from the IMG/M. Preliminary results showed a high abundance of genes coding for calcium-related proteins. Comparisons with the other SAR116 genomes revealed significant differences in metabolic patterns between the calcibacterium (L11) and the other SAR116 representatives (Fig. 1), which make the calcibacterium metabolically singular. Current research attempts to go deeper on the unknown metabolisms, which appear particularly characteristic of calcibacteria, with a particular focus on identification of metabolic paths potentially related with calcification processes.

References

1. MJ. Uriz, G. Agell, A. Blanquer, X. Turon, EO. Casamayor. Evolution 66 (2012) 2993–2999.
2. A. Blanquer, MJ. Uriz, PE. Galand. Environ. Microbiol. 15 (2013) 3008–3019.
3. L. Garate, J. Sureda, G. Agell, MJ. Uriz. Sci. Rep. (2017) in press.

Financial support by MARSYMBIOMICS project (Spanish MINECO, CTM2013 43287-P), BluePharmTrain (FP7 People-INT, Ref. 2013- 667786) and Grup Consolidat SGR-120, to MJU is gratefully acknowledged.

Biomaterials & Biomolecules

The Potential of Biosynthetic Products from Sponges and Sponge-derived Gram-negative Bacteria to Open New Research Horizons

Phillip Crews and Co-workers

Department of Chemistry & Biochemistry, University of California at Santa Cruz, USA

The marine natural products program begun at UC Santa Cruz (UCSC) many decades ago has a rich history and continued promise for future significant discoveries. Our repository contains approximately 4,000 extracts from tropical marine sponges, more than 500 strains of marine Gram-negative derived bacteria, plus more than 1,100 purified natural product compounds. The goal to obtain unique molecules from sponge biota derived by investigating biodiverse regions of Oceania has been rewarding. It continues to be the driving force for all of the ongoing projects in the field and in the laboratory. Our continuing collaboration with Indonesian Scientists constitutes another cornerstone for the various ongoing projects.

My lecture will begin with a brief summary of past achievements involving the bengamides, which are dual marine sponge – microbial products. This prelude will underscore the continuing value and challenge of developing sponge natural products as therapeutic leads. Of wide interest is the goal to obtain and culture marine-derived microorganisms that are able to produce, during sustained culture, compounds that have been repeatedly isolated from sponges. A status report of work in this area will be discussed. Contemporary strategies employing NMR and MS data provide the key to crisp approaches for structure elucidations and rapid compound dereplications. We will provide examples of these results involving: (a) NMR, focused on the so called “Crews Rule,” pertaining to compounds with H/C<1, and (b) MS, using the emerging Dorrestein – Alexandrov GNPS informatics strategy. Finally, results from our collaboration with Prof. F. Valeriote (Ford Cancer Center) will be highlighted, which involve PANC-1 selective nM cytotoxins obtained from sponge samples housed in our repository.

Identification of calcareous sponge spicule matrix proteins

Benedetta Fradusco [1], Sofia Fortunato [2], Maja Adamska [3], David J Miller [2], Marcin Adamski [3] & Oliver Voigt [1]

1 Ludwig-Maximilans-Universität Munich, Paleontology and Geobiology, Department of Earth and Environmental Sciences, Richard-Wagner-Str. 10, 80333 Munich, Germany. b.fradusco@lrz.uni-muenchen.de

2 ARC Centre of Excellence for Coral Reef Studies, James Cook University, Townsville, Qld 4811, Australia.

3 Research School of Biology, ANU College of Medicine, Biology and Environment, The Australian National University, Canberra, 46 Sullivans Creek Road, Acton ACT 2601, Australia

How animals influence the formation and shape of their skeletal elements is not well understood. In eukaryotes, the biologically controlled deposition of calcium carbonate minerals is always associated with an organic matrix. This organic matrix plays essential roles in the nucleation, morphology, growth rate and local inhibition of mineral crystal deposition within the matrix, but its composition remains unclear. A number of proteins rich in aspartic acid and/or asparagine have been previously identified as components of the organic matrix of calcareous sponge spicules, and influenced the crystallographic properties of precipitating calcite *in vitro*. Recent work in our laboratory has led to the identification of a number of acidic matrix proteins that are produced only during specific stages of spicule formation, but until now the full complement of spicule matrix proteins has remained unknown. The study presented here combined transcriptomic and proteomic approaches with the aim of comprehensively characterizing the spicular matrix composition of calcareous sponges. The ultimate goal of this work is to understand the general rules of biomineralization that apply across the Metazoa.

Financial support by the German Research Foundation (DFG, Project VO 2238/1-1) is gratefully acknowledged.

Poriferan Chitin as a Universal Template for Extreme Biomimetics

Marcin Wysokowski[1]-Iaroslav Petrenko[2], Teofil Jesionowski[1] & Hermann Ehrlich[2]

[1] *Institute of Chemical Technology and Engineering, Poznan University of Technology, Poznan, Poland.*
Conference presenter: marcin.wysokowski@put.poznan.pl

[2] *Institute of Experimental Physics, TU Bergakademie Freiberg, Germany*

Biomimetic approaches with respect to inorganic and biological macromolecules are a driving force in development of novel advanced composite materials which exhibit unique structural, electronic, photonic, and catalytic properties. In particular, the 2D and 3D architectures that incorporate nanoorganized biocomposites are of fundamental interest for applications in nanotechnology and bio-inspired materials science. Crucial step in biomimetic synthesis is selection of proper biomacromolecules that will permit for controlled synthesis of various bioinspired architectures. Recently, we promoted new scientific direction termed *Extreme Biomimetics.* This is new vibrant area of science based on mineralization and metallization of selected biopolymers under hydrothermal conditions *in vitro*. These extreme conditions mimic natural biomineralization that occurs in submarine hydrothermal vents, and allows insight into the principles that govern this phenomenon. The key to Extreme Biomimetics is utilization of specific bio- macromolecules with high thermal and chemical stability. Practically all representatives of extremophile fauna contain chitin as the main structural component of their skeletons. This aminopolysaccharide is stable, even up to 400 °C and this property pave the way for utilization of this biopolymer as structural organic template for hydrothermal deposition of various metal oxides. The unique evolutionarily optimized 3D morphology of chitin isolated from marine sponges makes an opportunity for creation of 3D chitin-based inorganic organic composites attractive for various applications.

Here utilization of poriferan chitin in Extreme Biomimetic creation of nanostructured bioinspired materials is presented. Our experimental results show with strong evidence that selected chitinous scaffolds of poriferan origin might be used as highly structured biological templates in a broad variety of hydrothermal *synthesis in vitro*. Here, we represent several novel approaches for the design of ZrO_2-, SiO_2-, GeO_2-, ZnO-, and Fe_2O_3-based and chitin-containing biocomposites under specific hydrothermal conditions. By detailed characterization of these composite materials using a variety of advanced analytical techniques (FT-IR, Raman spectroscopy, XPS, NEXAFS, HR-TEM with SAED and FFT) we prove that Extreme Biomimetics is on the rise as a powerful approach for the design of a new generation of advanced 3D nanostructured inorganic–organic materials with complex morphology and unique physicochemical

References

1. H. Ehrlich, Extreme Biomimetics, Springer International Publishing (2017) Cham, Stitzerland.
2. M. Wysokowski, I. Petrenko, A.L. Stelling, D. Stawski, T. Jesionowski, H. Ehrlich Polymers 7 (2015) 235-265.

Financial support by PUT research grant 03/32/DSPB/0706/2017 is gratefully acknowledged.

Five new siphonodictyals from Caribbean Sponge *Siphonodictyon coralliphagum*

Daria Firsova, [1] Kevin Calabro, [1] Grégory Genta-Jouve, [2] Thierry Pérez, [3] & Olivier P. Thomas[1]

[1] *School of Chemistry, National University of Ireland, Galway, University Road, Galway, Ireland. D.firsova1@nuigalway.ie*

[2] *Université Paris Descartes, équipe C-TAC, COMETE UMR 8638 CNRS, 4 avenue de l'observatoire, 75006 Paris, France.*

[3] *Institut Méditerranéen de Biodiversité et d'Ecologie marine et continentale, IMBE UMR 7263 CNRS / IRD / Aix Marseille Université / Avignon Université. Station Marine d'Endoume, rue de la Batterie des Lions, 13007 Marseille, France.*

The sponge *Siphonodictyon coralliphagum* is a common sponge of the Caribbean region and it is most often found burrowing living coral while only an oscule part of the sponge is protruding from it (Fig. 1). Due to its interesting ecological behaviour and relative ease of access *S. coralliphagum* has been previously chemically studied leading to the discovery of new sesquiterpenes named siphonodictyals among others.[1] Herein we report the isolation and structure elucidation of five new siphonodictyal derivatives (Fig. 1). All isolated compounds contain one tetra- or pentasubstituted benzaldehyde moiety linked to the sesquiterpene. Interestingly the connection with the terpene parts is observed at the different positions of the aldehyde and the terpene cores are highly diverse. Absolute configurations were determined by comparison between experimental and theoretical data of ^{13}C NMR and Circular Dichroism.

References

1. Sullivan, B.; Djura, P.; McIntyre, D. E.; Faulkner, D. J., Antimicrobial constituents of the sponge siphonodictyon coralliphagum. *Tetrahedron* **1981,** *37* (5), 979-982.

Taxonomic Identification, immunopharmacological and toxicological study of *Haliclona (Soestella) sp*: A novel marine sponge species from Sri Lanka

V.K. Gunathilake [1,] M. Bertolino [1], G. Bavestrello [1], W.D. Ratnasooriya [1], D. de Silva [3] & P.V. Udagama [1]

[1] *Department of Zoology and Environment Sciences, University of Colombo, Sri Lanka,*

[2] *Department of Earth Sciences of the Environment and Life, University of Genoa, Corso Europa, 26, 16132, Genoa Italy*

[3] *Department of Chemistry, University of Colombo, Sri Lanka*

Marine organisms are a remarkable source of secondary metabolites that are biologically active molecules with potential therapeutic usage. The present study investigated the taxonomic identification and comprehensive immunopharmacological and toxicological study on *Haliclona (Soestella)* sp, presumably a novel marine sponge species from Sri Lankan marine waters.

Sponge material was harvested from Unawatuna, Galle, Sri Lanka, identified as *Haliclona (Soestella)* sp. These were extracted with methanol/dichloromethane, filtered and rota-vapoured to obtain *Haliclona (Soestella)* sp sponge crude extract (HSCE). Appropriate doses were prepared by diluting HSCE in 5% ethanol. *In vivo and ex vivo* immunomodulatory tests of HSCE were carried out using adult male Wistar rat and adult male ICR mice models. Antioxidant activity of the HSCE was tested by in *vitro* assays using DPPH, SO, NO and ABTS radicals and *in vivo* NO radical scavenging assay. *In vitro* cancer chemo preventive activity was assessed using human laryngeal (Hep-2) carcinoma cell line followed by a toxicological evaluation including *in vivo* general, haemo, hepato, renal toxicity and stress parameters. Chemical characterization of the active compounds present in HSCE was also evaluated.

The HSCE possesses immunosuppressive, immunostimulant and acute anti-inflammatory properties in Wistar rat and ICR mice models. Immunosupression was evident in the following tested parameters: *in vivo* WBC, WBC DC, platelet, bone marrow cell and splenocyte counts, *ex vivo* immune cell proliferation and cytokine production. Nonetheless, the HSCE showed immunostimulation with respect to *in vitro* phagocytic capacity of rat peritoneal macrophages. The HSCE showed potent anti-inflammatory activity against acute phase oedema as revealed by the Carrageenan induced paw oedema and suppression of pro inflammatory cytokine production. Both anti- radical activity on quenching DPPH radicals and *in vivo* NO scavenging activity of the HSCE established its antioxidant properties. Toxicological evaluation confirmed that the HSCE was devoid of general toxicity, and hepato and reno- toxic effects. Conversely, the HSCE was moderately haematotoxic and stressogenic. The HSCE showed marked cytotoxic effect by inhibition of proliferation of Hep-2 cell line, at an IC_{50} value of 19.63 µg/mL. The chloroform fraction of the HSCE also showed anti proliferative activity of Hep-2 at IC_{50} value of 29.52 µg/mL.

In conclusion, *Haliclona (Soestella)* sp., demonstrated immunosuppressant, immunostimulant, acute anti inflammatory, antioxidant and anti cancer properties with associated moderate haematotoxic and stressogenic effects.

Financial support by Higher Education for the Twenty first Centaury (HETC) project, (SJP/O-AS/N1) and the National Science Foundation, Sri Lanka is acknowledged.

Deep-sea discovery – deep-sea sponges as a source of novel biologics

Mathew Upton [1], Arif Felek[1], Garry Farnham[1], Kerry L. Howell[2]

[1] *School of Biomedical & Healthcare Sciences, Plymouth University Peninsula Schools of Medicine and Dentistry, Plymouth, PL4 8AA, UK. mathew.upton@plymouth.ac.uk*

[2] *Marine Institute, Plymouth University, Drake Circus, Plymouth, PL4 8AA*

Natural product screening methods are still arguably the most efficient way to identify highly novel antibiotics, which are now an urgently needed resource. Marine invertebrates have been identified as one of the most promising natural sources for future antibiotics. Sponges are, perhaps, the most prolific source of natural products with more than 7, 000 bioactive compounds identified. Existing research has focused on shallow water species, but much of the world's biodiversity is located in deep-sea regions and the potential resource that exists within this ecosystem is largely un- explored. We investigated antimicrobial activity in cultivable bacteria from two deep sea sponge species. Hexactinellid sponges were collected from between 700 and 1400m depth in the North Atlantic Ocean (Rockall Trough). Harvested bacteria were cultured using modified Zobell Marine Agar and NH4 minimal medium at 4°C and 16°C and tested for antimicrobial activity using the simultaneous antagonism assay. Draft genome sequencing of inhibitor producing bacteria was conducted. Of the 85 bacterial colonies recovered from the sponge samples, 10 (12%) were inhibitor producers and two of these are highly novel strains. Strain EU2 (Gram positive rod) and EU4 (Gram positive spiral rod) are active against Gram positive bacteria including *Staphylococcus aureus* (EU4 only). Over 92% of the sequence reads for both strains map to unclassified species (~6% are related to the Bacillaceae family). In silico analysis of the genome sequence data combined with mass spectrometric data, will facilitate rapid identification of the potentially novel agents produced by these strains. The two new bacterial species discovered here are likely to be producing novel antimicrobials, some with activity towards clinically relevant bacteria. The sponges being examined represent a unique and potentially rich source of novel biodiversity to help address the urgent need for new antibiotics.

Financial support from the EUROFLEETS2 programme and Plymouth University is gratefully acknowledged.

Value-Added in Thai Pottery by Biological Materials from Freshwater Sponges

Nisit Ruengsawang[1], Petch Suthiporn[1], Wilailak Chuchuay[2], Narumon Sangpradub[3] & Renata Manconi[4]

[1]*Division of Biology, Rajamangala University of Technology Krungthep, Bangkok, Thailand nisit.r@rmutk.ac.th*

[2]*Division of Industrial Product Development, Rajamangala University of Technology Krungthep, Bangkok, Thailand*

[3]*Department of Biology, Khon Kaen University, Khon Kaen, Thailand*

[4]*Dipartimento di Scienze della Natura e del Territorio, Università di Sassari, Sassari, Italy*

Biodiversity surveys of freshwater sponges in Northeast Thailand shown that sponges were commonly found in cage of fish culture in rivers and reservoirs. These filter feeders clogged the nets and limited water circulation in and out the cages. After fish harvesting, cages were cleaned of freshwater sponges by air-drying for cage maintenance. Therefore, the aims of this research project were to utilize freshwater sponges from net cleaning of tilapia cage culture as biological materials for pottery production and to increase the value-added in Thai pottery. Appropriated ratio of mixture clay including clay, sand and siliceous spicules of freshwater sponges, *Corvospongilla*, were tested for shrinkage and strength of pottery. New designed products were created for value-added from traditional products. Prototype products were tested and consumer willingness to pay for sponge pottery was also examined.

References

1. R. Manconi, N. Ruengsawang, V. Vannachak, C. Hanjavanit, N. Sangpradub, R. Pronzato, J. Limno. 3320 (2013) 313-326.
2. N. Ruengsawang, N. Sangpradub, C. Hanjavanit, R. Manconi, Zootaxa. 3320 (2012) 47-55.
3. S. K. Mcintosh, K. C. MacDonald. J. Field Archaeol. 16 (1989) 489–494.

This work was financial support by Rajamangala University of Technology Krungthep.

Ecology

Sponge resilience and susceptibility to current and future anthropogenic impacts

James Bell

School of Biological Sciences, Victoria University of Wellington, Po Box 600, Wellington, New Zealand

Major changes are occurring throughout the oceans as a result of anthropogenic impacts that are altering ecosystems and changing the way that they function. Such changes are only likely to intensify as the impacts of global climate change become more widely felt. In tropical systems there continues to be a general decline in coral cover and there's increasing evidence to support major collapses of reef building coral populations in response to ocean warming and acidification. However, such coral declines may provide opportunities for other non-coral organisms, such as sponges. While individual sponge responses to environmental stressors are unsurprisingly variable, there is an increasing body of evidence showing that some sponges are more resilient than corals to specific stressors. In this talk I will begin with a review of the global conservation status of sponges, and discuss the variability in the resilience and susceptibility of sponges to environmental stress. I will then describe some of my group's recent work looking at the impacts of local scale stressors on tropical sponges including long-term changes in sponge assemblage structure. I will describe our work on a now sponge-dominated reef in Indonesia, particularly focusing on the mechanisms by which some sponges are able to tolerate conditions no longer suitable for coral. I will then focus on future coral reefs and describe how reefs might function if sponges are as tolerant to ocean warming and acidification as current experimental evidence predicts. If the current decline on coral reefs is not halted and reversed then future coral reefs will look very different and therefore it is important to explore how they might function and their potential to provide ecosystems services.

Financial support by the Royal Society of New Zealand Marsden Fund, Victoria University of Wellington, The Australian Institute of Marine Sciences, and Operation Wallacea, are gratefully acknowledged.

Genomic approach to the evolutionary history and population structure of *Dendrilla antarctica* Topsent, 1905 (Porifera, Demospongiae) from southern ocean shallow waters

Carlos Leiva[1, 2], Sergi Taboada[2], David Combosch[3], Gonzalo Giribet[3] & Ana Riesgo[2]

[1] *Department of Evolutionary Biology, Ecology, and Environmental Science, University of Barcelona, Barcelona, Spain. cleivama@gmail.com*

[2] *Department of Life Sciences, The Natural History Museum of London, London, UK*

[3] *Museum of Comparative Zoology, Department of Organismic and Evolutionary Biology, Harvard University, Cambridge, Massachusetts, USA*

References

1. A. L. Allcock, J. M. Strugnell, Trends Ecol. Evol. 29(9) (2012) 520-528.
2. A. Riesgo et al. Heredity 117(2016) 427-39.
3. A. Riesgo, S. Taboada, C. Avila. Marine Genomics 31 (2015) 23:1-3.

Financial support by Funding by DISTANTCOM project (CTM2013-42667/ANT; Ministry of Economy and Competitiveness of Spain) and internal FAS (Harvard) funds to GG is acknowledged.

Population connectivity of an abyssal sponge across the Clarion Clipperton Zone (Central Pacific)

Sergio Taboada[1], Ana Riesgo[1], Helena Wiklund[1], Gordon L.J. Paterson[1], Vasiliki Koutsouveli[1], Andrew C. Dale[2], Thomas G. Dahlgren[3,4] & Adrian G. Glover[1]

[1] *Life Sciences Department, The Natural History Museum, Cromwell Road, London, UK*
sergiotab@gmail.com

[2] *Scottish Marine Institute, The Scottish Association for Marine Science, Oban, UK*

[3] *Uni Research, Bergen, Norway*

[4] *Department of Marine Sciences, Universty of Gothenburg, Sweden*

The abyssal sponge Axinellida sp. nov. is a demosponge endemic to the Clarion- Clipperton Zone (CCZ) in the North East Pacific, a region that has recently become economically viable as a source of polymetallic nodules [1]. Axinellida sp. nov. encrusts on these nodules and is an abundant component of the ecosystem at these depths. As a sessile filter-feeding organism it thus represents an excellent potential model species to assess the impact of mining operations through the study of its population connectivity and the investigation of its biogeographic patterns (from local to large spatial scales) within the CCZ. Our aim was to describe the population connectivity and dispersal capabilities of this keystone sponge using a total of 168 individuals collected from four different areas across the CCZ, including the Area of Particular Environmental Interest- 6 (APEI-6), two sites in the adjacent mining exploration contract area UK1 (UK1-A and UK1-B), and one in the Ocean Mineral Singapore reserved area (OMS1). A total of 30 sampling stations ranging from 4, 012–4, 258 m deep were studied, with stations at APEI-6 more than 800 km apart from the exploration contract areas, while stations within the exploration areas being separated 10s to 100s km. To achieve our goal we used the mitochondrial cytochrome *c* oxydase I (*COI*) and 11 polymorphic microsatellite markers newly developed using an Illumina MiSeq sequencing approach. *COI* showed very low genetic variability with only two haplotypes observed in individuals ca. 800 km apart. Analysis based on microsatellites showed that sponges at most of the sites showed significant departure from Hardy-Weinberg Equilibrium, which appears to be common in other sponge studies as well as on many other marine benthic invertebrates [see 2]. Two genetically homogeneous clusters with no clear pattern of geographic subdivision were inferred using the program STRUCTURE. Interestingly, one of these clusters grouped together samples from APEI-6 and UK1-A, which showed greater molecular affinity amongst them than with samples collected from 10s of km apart. Discriminant Analysis of Principal Components corroborated STRUCTURE results and also indicated that OMS1, the most southernmost area, is significantly different from the other two areas studied in the UK1 mining exploration contract areas. Due to the presumed lack of physical barriers in the abyssal CCZ, we suggest that the molecular connectivity observed for Axinellida sp. nov. might be explained by oceanographic currents. In this sense, we provide and discuss near-bottom dispersal models using flow simulations from the HYCOM model. In the light of our results, we suggest future scenarios for the preservation of the genetic diversity of Axinellida sp. nov.

References

1. Wedding et al. Proc. R. Soc. Lond. 280 (2013) 20131684.
2. Riesgo et al. Heredity 117 (2016) 427-439.

Financial support by MIDAS project is gratefully acknowledged.

Considering Habitat Fragmentation and Dispersal Potential: How *Pheronema carpenteri* Aggregations May Be Particularly Vulnerable Marine Ecosystems

Rebecca E. Ross[1], Edward J.G. Wort[2], Kerry L. Howell[1]

[1] *School of Biology & Marine Science, Plymouth University, Drake Circus, Plymouth, UK.*
Rebecca.Ross@plymouth.ac.uk

[2] *Ocean & Earth Science, National Oceanography Centre Southampton, University of Southampton*
Waterfront Campus, European Way, Southampton, UK

At present UK and Irish offshore conservation efforts are identifying Vulnerable Marine Ecosystems (VMEs) for protection with a dominant focus on cold water coral reefs. While deep sponge aggregations are a 'listed' VME, and have had a couple of MPAs designated primarily for their protection, there is some evidence that these ecosystems may be especially vulnerable and worthy of greater attention. This study uses an integrated modelling approach to explore the hydrographic fragmentation of aggregations of *Pheronema carpenteri* (Wyville Thomson, 1869). A published habitat suitability model [1], supported by preliminary targeted groundtruthing, forms the basis of our understanding of habitat extent and geographic fragmentation. Although little is known of *P. carpenteri*'s reproductive methods, several simulations assuming planktonic larval dispersal offer a suite of optimistic predictions for their dispersal potential. Simulations used two different simulation methods, the connectivity modeling system (CMS) takes a semi-individual based modelling approach, while the marine geospatial ecology tools (MGET) simulates the diffusion of a cloud of larvae. The global hydrodynamic model HYCOM underpins both models but is allowed to simulate bottom tracking larvae, and passive dispersal. Simulations are run with planktonic larval durations of 1, 5, 10, 20, 30, and 50 days. Dispersal simulations suggested that after 1 day a maximum of 1.6% of the wider habitat extent could be reached, 5days 3.8%, 10 days 6.6%, 20days 14.1%, 30days 21.2% and 50days 36.2% (minimum 17.9%). However all simulations, even run over 50 days, fail to connect the known populations in the (unprotected) Porcupine Seabight to those in the (partially protected) Hatton Rockall Basin, Rosemary Bank, or the historic northern Rockall Trough 'Holtenia grounds' (unprotected). As very little of the existing international MPA network protects any of these predicted or known aggregations (~3% of the predicted habitat extent is protected), *P. carpenteri* aggregations may be especially vulnerable to disturbance. More targeted exploration is necessary to establish the true extent of these habitats, and observational searches within the footprints of different simulated dispersal clouds could improve our understanding of this VME's survival potential, particularly in areas where bottom trawling is permitted.

References

1. Ross, R.E., Howell, K.L., Divers. Distrib. 19 (2013) 433-445.

Financial support by Plymouth University is gratefully acknowledged.

Genetic structure patterns in Atlanto-Mediterranean sponges: environmental factors and biological features driving connectivity in scenarios with mass-mortalities

Ana Riesgo[1], Rocío Pérez-Portela[2], Sergio Taboada[1], Lucía Pita[3], Patrick M. Erwin[4], Paolo Melis[5], Joana R. Xavier[6], Susanna López-Legentil[4]

[1]*Department of Life Sciences, The Natural History Museum, Cromwell Road, London SW7 5BD, UK.*
A.Riesgo@nhm.ac.uk

[2]*Present address: Rosenstiel School of Marine & Atmospheric Science, University of Miami, 4600 Rickenbacker Cswy, Miami, FL 33149, USA*

[3]*GEOMAR Helmholtz Center for Ocean Research, Düsternbrooker Weg 20, D-24105 Kiel, Germany*

[4]*Department of Biology & Marine Biology, and Center for Marine Science, University of North Carolina Wilmington, 5600 Marvin K. Moss Lane, Wilmington, NC 28409, USA*

[5]*Department of Animal Biology, Faculty of Biology, University of Barcelona. Avda. Diagonal 643, 08028*
Barcelona, Spain

[6]*Department of Biology and K.G. Jebsen Centre for Deep-Sea Research, University of Bergen, PO Box 7803, N-5020 Bergen, Norway*

In the past decade, several mass mortality events, resulting from anomalously high seawater temperature, were reported in Mediterranean rocky benthic communities, particularly gorgonians and sponges. From a genetic point of view, such events may lead to a reduction in population sizes (bottleneck), and consequently to an overall reduction in genetic diversity, which may decrease species resilience to environmental stressors or perturbations and their potential for recovery [1]. In this study, we investigated the genetic diversity, structure, historical demography and connectivity of two common Mediterranean species, *Ircinia fasciculata* and *Petrosia ficiformis*, and assessed whether their biological traits have an influence on their population differentiation. We genotyped 189 individuals from 12 populations in the Mediterranean for *I. fasciculata* and 298 individuals from 19 populations across the Atlanto-Mediterranean distribution of *P. ficiformis* with 14 and 10 microsatellites, respectively. While all the populations for *I. fasciculata* were found in Hardy-Weinberg equilibrium, most of the *P. ficiformis* populations deviated from it. Significant genetic differentiation based on F_{ST} values was found between 90% of the populations of *I. fasciculata* and all populations of *P. ficiformis*. Genetic differences were not caused by isolation by geographical distance. In general, similar barriers to gene flow were detected for both sponge populations, although the Almeria-Oran front was the strongest one for *I. fasciculata*, while the Atlantic barriers in the Macaronesian archipelagos were the most important ones for *P. ficiformis*. Bottlenecks were detected only in Mediterranean populations of both species. The high levels of population differentiation and inbreeding observed for *P. ficiformis* may be driven by its crawling larva, which has less potential for dispersal than the free-swimming larva of *I. fasciculata*. Hybridization between *I. fasciculata* and *I. variabilis* enhanced recovery of genetic diversity in populations experiencing a recent bottleneck due to a mass-mortality event. Overall, our results show that the genetic structure and diversity of common Mediterranean sponges inhabiting similar habitats is shaped by different factors acting at different levels.

References

1. R. Frankham. Genetics and extinction. *Biol. Conserv.* 126(2005) 131-140.

Funding by the Spanish Government project MARSYMBIOMICS CTM2013-43287-P and the Catalan Government grant 2014SGR-336 for Consolidated Research Groups is gratefully acknowledged.

Limited connectivity promotes cryptic speciation in *Tethya* spp.

Megan R. Shaffer*, Simon K. Davy*, James J. Bell*

* *School of Biological Sciences, Victoria University of Wellington, PO Box 600, Wellington, New Zealand*
Megan.Shaffer@vuw.ac.nz

Determining patterns of connectivity in marine organisms is often difficult because hydrographical barriers to gene flow can be complex and the larval dispersal abilities of many species are poorly understood. The recent use of molecular tools, however, has allowed complicated patterns of gene flow to be better resolved. Here, we use mitochondrial and nuclear microsatellite markers to examine connectivity of golf ball sponges (*Tethya* spp.) in New Zealand, which reproduce both sexually and asexually. Sponges matching the morphological description for the genus *Tethya burtoni* were collected from locations in southern, central and northern New Zealand. Microsatellite markers revealed potential cryptic speciation within *T. burtoni*, where two genetically distinct groups were found within what was formally described as one species. For one of the genetically distinct groups, strong population structure was observed between five populations within central New Zealand, with a high occurrence of asexual clones found within populations. What was thought to be *T. burtoni*, collected from northern and southern New Zealand, failed to amplify the panel of microsatellite loci, possibly due to changes in base composition at primer sites, and suggests an even higher degree of cryptic speciation within the species. To investigate this further, phylogenetic analyses was performed on mitochondrial sequences for different *Tethya* samples from across New Zealand, which revealed more genetically distinct groups in the genus than previously recorded across New Zealand. Our findings suggest that there is restricted gene flow between populations of *T. burtoni*, where divergence may occur quickly due to high incidences of clones. The limited connectivity between populations may further promote cryptic speciation and explains the complex genetic relationships found within *Tethya* spp.

The environment selects? Using marine lakes as laboratories of ecology & evolution

Leontine Becking[1] & Marine Lakes Team[1, 2, 3, 4, 5, 6, 7, 8, 9]

[1] *Marine Animal Ecology group, Wageningen University & Research, Wageningen, the Netherlands.*
Lisa.becking@wur.nl

[2] *Computational Genomics Resource Laboratory California Institute for Quantitative Biosciences, University of California Berkeley USA*

[3] *Department of Environmental Science, Policy, and Management, University of California Berkeley, USA*

[4] *CESAM, University of Aveiro, Portugal*

[5] *Naturalis Biodiversity Center, Leiden, the Netherlands*

[6] *Department of Biology, Stanford University, Stanford, USA*

[7] *Marine Life Conservation Unit, Indonesian Institute of Sciences (LIPI), Biak, Papua, Indonesia*

[8] *Research Center for Oceanography, Indonesian Institute of Sciences (LIPI), Jakarta, Indonesia*

[9] *Marine and Fisheries Department, University of Papua (UNIPA), Manokwari, Papua, Indonesia*

Recent marine invertebrate studies in the Coral Triangle show population structure & species turnover on small spatial scales. These findings indicate that isolating mechanisms at small spatial scales may play an important role in forming the spatial patterns of both genetic diversity within species and species diversity within communities. Isolation can be due to physical barriers or distance, irrespective of environment, and due to different environmental regimes. A key issue is that environmental data is generally spatially structured at multiple scales, thereby clouding the ultimate causes of divergence and differentiation. Here we use the clearly defined spatio-temporal context of marine lakes – islands of sea - to study the nature of assembly of marine communities over ecological and evolutionary timescales. By comparing marine lakes, with comparable ages and sizes, but varying degrees of connection to the open sea and differing environmental regimes (temperature, salinity, pH), we are testing the relative contribution of selective environments versus stochastic processes in the formation of sponge biodiversity patterns.

We will present preliminary data of our international project on multiple sponge lineages across the marine lake model system in Indonesia based on 1. current species diversity within lake assemblages and adjacent seas, 2. phylogenetic community analysis, 3. population genomics (RADSeq), 4. historic species diversity since formation of the lakes (6000-10000 year before the present) using sediment cores. Preliminary results show that at larger spatial scales (<200km) stochastic mechanisms of dispersal limitation play a major role while at smaller spatial scales (30 km) varied environments can lead to rapid divergence and differentiation of sponge biodiversity. At small spatial scales, we found that environmental filtering plays a greater role in gradients of geneflow and species turnover than the degree of physical connection of the lake to the sea. Harsh environments resulted in low species diversity within communities, yet high genetic divergence in populations. At small spatial scales the formation of sponge biodiversity patterns was largely shaped by deterministic processes related to environment, though priority effects during initial colonization will be further tested using sediment cores.

Financial support by The Netherlands Organisation of Scientific Research ALW-VENI (#863.14.020), INNO-WWF Subsidy, Ecology Fund KNAW, National Geographic Explorer Grant, Rufford Foundation is gratefully acknowledged.

Sponges of the Marianas: Initial Observations of Newly Collected Specimens

Shirley A. Pomponi[1], Christopher Kelley[2], Diva Amon[2], Kasey Cantwell[3], Kelley Elliott[3], Deborah Glickson[1, 4], Patricia Fryer[2]

[1] *Harbor Branch Oceanographic Institute, Florida Atlantic University, Fort Pierce, FL USA*
spomponi@fau.edu

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

[3] *National Oceanic and Atmospheric Administration, Office of Ocean Exploration and Research, Silver Spring, Maryland USA*

[4] *National Academies of Sciences, Engineering, and Medicine, Washington, DC USA*

The Porifera fill critical ecologic niches in many marine environments, however, we still understand little about deep-water sponge taxa, particularly in remote regions. From April to July 2016, an interdisciplinary team investigated the biology and geology of the waters of Guam, the Commonwealth of the Northern Mariana Islands (CNMI) and the Marianas Trench Marine National Monument. Sponsored by the U.S. National Oceanic and Atmospheric Administration (NOAA), the telepresence-enabled NOAA ship *Okeanos Explorer* collected critical baseline information from a variety of deep-water habitats to provide a foundation of publicly available data for resource managers and the global science community. Telepresence capabilities enabled active, real-time participation from scientists worldwide, complementing and expanding the knowledge of the ship-based science leads which facilitated an improved initial characterization of dive locations. Many of the sponges observed and collected are likely to be new species or new records of occurrence, including several rare and unusual cladorhizids. This presentation will highlight the exciting sponge discoveries from the 2016 Deepwater Exploration of the Marianas expedition. In an effort to quickly disseminate new information and to catalyze future research, sponge samples have been tentatively identified and are publicly available. Specimens are archived at the Smithsonian Institution's National Museum of Natural History Research and Collections and the Bernice Pauahi Bishop Museum and are available for study. Oceanographic data and high-resolution imagery from the expedition are also publicly available through NOAA's National Center for Environmental Information.

Financial support by the NOAA Office of Ocean Exploration and Research (grant #NA14OAR432026) to the Cooperative Institute for Ocean Exploration, Research, and Technology at Harbor Branch Oceanographic Institute-Florida Atlantic University is gratefully acknowledged.

Sponge Assemblages on the recently declared Menorca Channel Marine Protected Area (Western Mediterranean Sea)

Andreu Santín[1], Jordi Grinyó[1], Stefano Ambroso[1], Iosune Uriz[2], Andrea Gori[1] & Josep-Maria Gili[1]

[1] Institut de Ciències del Mar (ICM-CSIC), Barcelona, Spain. santin@icm.csic.es

[2] Centre d'Estudis Avançats de Blanes (CEAB-CSIC), Blanes (Girona), Spain.

The existence of sponge assemblages in continental shelves and slopes has been known for centuries; however, due to sampling limitations associated to the traditional sampling systems, individual sponge species rather than assemblages were mainly reported. The current study characterizes sponge assemblages over a large geographic area and bathymetric range (40–360 m) encompassing the continental shelf and upper slope.

Quantitative analysis of 85 video-transects (corresponding to a total length of 64 km), plus collection of representative samples to confirm identifications, allowed us differentiating six assemblages, mainly segregated by substrate type, depth and species composition. On the continental shelf, a semi-sciaphilous axinellid assemblage dominated shallow rocky outcrops. Shallow maërl beds were predominantly dominated by *Haliclona mediterranea,* whereas the horny sponge *Aplysina cavernicola* and several haliclonids mostly dominated deep maërl beds and rocky substrates. Soft sediments in the shelf edge hosted a monospecific *Thenea muricata* assemblage. Incrusting, columnar and fan-shaped sponges dominated in rocky substrates of the shelf edge. Finally, the upper slope area was dominated by *Hamacantha falcula* and the hexactinellid *Tretodyctium cf. tubulosum*. Overall, sponge diversity increased towards the end of the continental shelf, with a peak at 70–90 m depth, followed by a severe plummet at the shelf break. The observed assemblages were highly diverse (> 100 identified species), and reached high density values (> 70 ind/m^2) over vast extensions.

Due to their exceptional conservation status, these sponge assemblages might give an approximate idea of how sponge grounds might have looked like in the Mediterranean Sea before decades of impacts from bottom trawling fishing.

This work was funded by the European project LIFE + INDEMARES "Inventario y designación de la red natura 2000 en áreas marinas del estado español" (LIFE07/NAT/E/000732) and the EU-*ENPI* CBC-Med project *ECOSAFIMED* (2014-15).

Deep-sea Sponge Grounds of the North Atlantic: State of the Knowledge, Recent Advances and Outlook

Joana R Xavier[1], Ellen Kenchington[2], Shirley A Pomponi[3], Hans Tore Rapp[1]

[1] Department of Biology and K.G. Jebsen Centre for Deep-Sea Research, University of Bergen, PO Box
7803, N-5020 Bergen, Norway
Joana.Xavier@uib.no

[2] Fisheries and Oceans Canada, Bedford Institute of Oceanography, Dartmouth, Nova Scotia, Canada

[3] Harbor Branch Oceanographic Institute, Florida Atlantic University, Fort Pierce, Florida, USA

Sponge-dominated habitats known as sponge grounds, aggregations, gardens and reefs are widely distributed at all depths in the World's oceans. Although increasingly recognized as ecologically and biologically important and vulnerable marine habitats, sponge grounds are still underrepresented in research and conservation agendas.

Here, we review the current knowledge of the diversity, distribution, and function of the deep-sea sponge grounds of the North Atlantic. We show that, among the deep-sea habitats, sponge grounds likely represent an unparalleled diversity in terms of their community composition, as well as geographical and bathymetric extent.

We also present a synthesis of the supporting, regulating, and provisioning goods and services (e.g. habitat and nursery, nutrient recycling, carbon sequestration) known or hypothesised to be delivered by sponge grounds and the societal and economic benefits they embody in the so-called Blue Growth era.

Despite significant advances in recent years we identify a number of knowledge gaps regarding these habitats biology and ecology, and demonstrate the potential that a closer integration of molecular, ecological and oceanographic data paired with modern analytical approaches (e.g. in the fields of genomics, ecological and oceanographic modelling) may have in filling-in of those gaps.

We further highlight the main direct and indirect impacts that established (e.g. fisheries, oil and gas exploitation) and emerging (e.g. deep-sea mining) human activities, as well as climate change, may have over such habitats and the spatial and temporal scale at which they are expected to occur. Last, but not least, we assess current conservation efforts and call for a coordinated and international effort between researchers, stakeholders, policy makers and society for the sustainable management and protection of these vulnerable deep-sea habitats.

Financial support by the European Union's Horizon 2020 research and innovation programme to the SponGES project (grant agreement 679849) is gratefully acknowledged.

Aspects of the ecology of *Pheronema carpenteri* aggregations

Kerry Howell[1], Amelia Bridges[1], Christopher Babey[1], Nils Piechaud[1]

[1] Marine Institute, Plymouth University, Drake Circus, Plymouth, UK. kerry.howell@plymouth.ac.uk

Sponge aggregations are widely recognised as an important habitat. They increase the physical heterogeneity of the local area and number of available microhabitats, support high biodiversity, act as a refuge for fish, and are a storehouse for novel chemical compounds. Yet despite this recognised importance there has been very little research conducted on deep-sea sponge aggregations. We investigated various aspects of the ecology of aggregations of *Pheronema carpernteri*. Specifically we tested the following hypotheses: 1) areas of high density of *P. carpernteri* support higher species richness, 2) communities associated with *P. carpernteri* aggregations are distinct from communities of comparable depths and substrate type, 3) populations of *P. carpernteri* are size structured with depth. Three video transects in areas of sponge aggregation presence and three transects in comparable areas of sponge aggregation absence were conducted using the ROV Holland I aboard RV Celtic Explorer in 2015. Video was analysed and all taxa counted and identified to the lowest possible taxonomic level. Community data were analysed using standard multivariate and univariate statistics. The sizes of observed individual *P. carpenteri* were measured from video data using laser scaling. In addition preliminary observations were conducted to investigate sponge pumping rates. For the epibenthic megafauna there is no statistically significant difference in community composition between sponge and non-sponge transects. The highest species richness occurs at intermediate sponge densities, but there is no statistically significant difference in species richness between sponge and comparable non-sponge sites. The highest sponge density observed is 499 sponges per 1500m^2 transect (maximum of 28 sponges m^{-2} at smaller spatial scales). The largest individuals are of ~20cm diameter, the smallest observed on video footage is 3.44cm, with mean 11cm and mode 10cm. There is a weak but statistically significant relationship between sponge size and depth, with smaller individuals found at shallower depths. Qualitative observations suggest sponge pumping rates are extremely low in comparison to shallow water species.

Financial support from the EUROFLEETS2 programme and Plymouth University is gratefully acknowledged.

Sponge communities from the mud volcanoes of the Gulf of Cadiz

Cèlia Sitjà[1], Manuel Maldonado[1], José Luis Rueda[2] & Carlos Farias[2]

[1]Centro de Estudios Avanzados de Blanes (CEAB-CSIC), Blanes, Girona, Spain. csitja@ceab.csic.es

[2]Centro Oceanográfico de Málaga, Instituto Español de Oceanografía, Fuengirola, Málaga, Spain

The Ibero-Moroccan Gulf (Eastern North Atlantic) hosts several fields of mud volcanoes. In these environments, the carbonate precipitation, derived from the microbial anaerobic metabolization of seeping hydrocarbons, provides new hard substrates that persist available for colonization once methane seeping is exhausted. Thus, mud volcano fields may be relevant areas regarding benthic fauna occurrence. The present work provides a first evaluation of the composition of the sponge fauna associated to the mud volcanoes from the Spanish margin of the deep bottoms of the Gulf of Cadiz (422 - 1138 m). A total of 84 species have been recorded at the studied mud volcanoes, mostly belonging in the Class Demospongiae and two in the Class Hexactinellida. Two of them are new (*Jaspis sinuosa* nov. sp.; *Myrmekioderma volcana* nov.sp.). Two other species are recorded for the first time from the Atlantic Ocean, being so far known from the Mediterranean Sea (*Coelosphaera* (*Histodermion*) *cryosi* and *Petrosia* (*Petrosia*) *raphida*. Another remarkable finding was an aggregation of 71 specimens of the carnivorous sponge *Lycopodina hypogea* living together on a small boulder at 495 - 483 m deep. The studied field of volcanoes, nearby the Gibraltar Strait, makes an interesting area in terms of assessing possible faunal transfers between the Atlantic and the Mediterranean. Although previous work has shown that the North Atlantic Surface Water inflow imports shallow- water species to the Alboran Sea and other zones of the Western Mediterranean, the effects of the Mediterranean Intermediate Water outflow on the Atlantic deep fauna communities have seldom been evaluated. In this study, we are examining the level at which the sponge fauna from several deep-water Mediterranean communities relates to that from seeping and non-seeping North Atlantic mud volcanoes, in an attempt to assess the effect of the Mediterranean outflow on the adjacent deep-sea North Atlantic communities.

Financial support by E.C. LIFE+INDEMARES/CHICA (LIFE07/NAT/E/000732), E.C. SponGES (679848-2) and Spanish MINECO Por-Si (CTM2012-37787) grants is gratefully acknowledged.

Exploiting And Conserving Deep-Sea Genetic Resources

Claire Laguionie Marchais[1, 2], Ryan Young[1, 2, 3], Robert Nesbitt[3], Olivier Thomas[3], Mark Johnson[1, 2], Bill Baker[3, 4], A. Louise Allcock[1, 2]

[1]Ryan Institute, NUI Galway, University Road, Galway, Ireland

[2]School of Natural Sciences, NUI Galway, University Road, Galway, Ireland claire.laguionie-maarchais@nuigalway.ie

[3]School of Chemistry, NUI Galway, University Road, Galway, Ireland

[4]Department of Chemistry and Center for Drug Discovery and Innovation, University of South Florida, Tampa, Fl., USA

Started in September 2016, the 5-year Science Foundation Ireland project "exploiting and conserving deep-sea genetic resources" focuses on biodiscovery research in Irish deep-sea Cnidaria and Porifera. The aims are three-fold. Firstly, previously and newly collected samples of these two Phyla will be analysed to characterise their chemical diversity. Crude chemical extracts will be used in various biological screenings such as antibiotic or cancer assays to identify new chemical compounds and/or new activity in known compounds with pharmacological potential. Libraries of crude extracts and isolated compounds will be built to facilitate access to the material by other screening programs. Secondly, the economic potential of deep-sea Irish waters in relation to Porifera and Cnidaria bioactive compound production will be analysed. This analysis requires the: 1) development of a method to define the bioactivity of natural products, a critical step as few natural products have been tested in a comprehensive series of bioassays, but rather too often limited to a particular group of diseases; 2) prediction on the likelihood of families and genera of Cnidaria and Porifera of producing bioactive / drug-like marine natural products knowing the bioactivity of natural products found in these phyla (MarinLit database) and phylogenetic relationships between species; 3) estimation of the economic potential of Irish Atlantic margin using the above and records of both Phyla in the North East Atlantic (OBIS database). Thirdly, predictive maps of biodiscovery potential in Irish offshore waters will be created based on georeferenced records of species obtained from ROV video annotation, predictive modelling and the above economic studies. Results will inform conservation planning software to determine biodiscovery hotspot clusters. Overall, the project will develop informed bioprospecting approaches to maximise the chance of finding pharmaceutical active natural products in difficult environments to sample such as deep-sea ecosystems.

Financial support by the Science Foundation Ireland is gratefully acknowledged.

The "vicious circle" hypothesis: Sponges and reduced resilience of Caribbean coral reefs

Joseph R. Pawlik

Department of Biology and Marine Biology and Center for Marine Science, University of North Carolina Wilmington, USA. pawlikj@uncw.edu

Coral reefs have suffered unprecedented losses of corals in the recent past. Why have Caribbean reefs in particular transitioned to coral-depleted systems and exhibited less coral resilience? A synthesis of recent research from diverse sources provides novel insights into the reciprocal interactions among sponges, seaweeds, and microbes. The **vicious circle hypothesis**[1] proposes that coral loss resulted in more abundant seaweeds that release dissolved organic carbon (DOC), which is consumed by sponges. Sponges return carbon to the reef, but also release nutrients that further enhance seaweed growth. Both seaweeds and sponges compete for space with the remaining corals, and the cycling of carbon and nutrients alters microbial activity, with negative consequences for the coral microbiome. Adding to these interactions are geographic factors that enhance nutrients and DOC on Caribbean reefs, such as river discharge and windblown dust. Relatively higher abundances of sponges and the absence of phototrophic species suggest that sponge communities on Caribbean reefs have adapted to a different nutritional environment than is present on reefs elsewhere in the tropics.

References

1. J.R. Pawlik, D.E. Burkepile, R. Vega Thurber. BioScience, 66 (2016): 470- 476 doi:10.1093/biosci/biw047

Financial support from UNCW's College of Arts and Sciences and Office of International Programs and the US National Science Foundation, Biological Oceanography Program (OCE – 1029515, 1558580) is gratefully acknowledged.

Nutrient Fluxes and Ecological Functions of Coral Reef Sponges in a Changing Ocean

Jasper M. de Goeij[1], Michael P. Lesser[2], Joseph R. Pawlik[3]

[1] Department of Freshwater and Marine Ecology, Institute for Biodiversity and Ecosystem Dynamics, University of Amsterdam, PO Box 94248, 1090 GE Amsterdam, Netherlands. j.m.degoeij@uva.nl

[2] School of Marine Science and Ocean Engineering, University of New Hampshire, Durham, NH 03824, USA

[3] Center for Marine Science and Department of Biology and Marine Biology, University of North Carolina Wilmington, Wilmington, NC 28409, USA

Coral reefs are iconic examples of biological hotspots, highly appreciated because of their ecosystem services. Yet, they are threatened by human impact and climate change, highlighting the need to develop tools and strategies to curtail changes in these ecosystems. Remarkably, ever since Darwin's descriptions of coral reefs, it has been a mystery how one of Earth's most productive and diverse ecosystems thrives in oligotrophic seas, as an oasis in a marine desert. Sponges are now increasingly recognized as key ecosystem engineers, efficiently retaining and transferring energy and nutrients on the reef. As a result, current reef food web models, lacking sponge-driven resource cycling, are incomplete and need to be redeveloped. However, mechanisms that determine the capacity of sponge 'engines', how they are fuelled, and drive communities are unknown.

Here we will discuss how sponges integrate within the novel reef food web framework. To this end, sponges will be evaluated on functional traits (morphology, associated microbes, pumping rate) in the processing of dissolved and particulate food. At the community level, we discuss to what extent these different traits are a driving force in structuring shallow- to deep-sea reef ecosystems, from fuel input (primary producers), to engine output (driving and modulating the consumer food web). Finally, as climate change causes the onset of alterations in the community structure and food web of reef ecosystems, there is evidence accumulating that certain biological pathways are triggered, such as the sponge loop and the microbial loop, that may shift reef ecosystems faster than their original stressors (e.g., warming oceans and ocean acidification). Unfortunately, these biological pathways receive much less attention at present, which seriously hampers our ability to predict future changes within reef ecosystems.

Financial support by the European Research Council (ERC-stg-715513 JM de Goeij) and the National Science Foundation (NSF OCE 1632348 ML Lesser and NSF OCE 1558580 JR Pawlik) is gratefully acknowledged.

A Decadal Analysis Of Bioeroding Sponge Cover On The Inshore Great Barrier Reef

Blake D. Ramsby[1, 2, 3], Mia O. Hoogenboom[1], Steve Whalan[4], Angus Thompson[2] & Nicole S. Webster[2]

1 College of Science and Engineering, James Cook University, Townsville, Queensland, Australia
2 Australian Institute of Marine Science, Townsville, Queensland, Australia
3 AIMS@JCU, Australian Institute of Marine Science and James Cook University, Townsville, Queensland, Australia blake.ramsby@my.jcu.edu.au
4 School of Environment, Science and Engineering, Southern Cross University, Lismore, New South Wales

Decreasing coral cover on the Great Barrier Reef (GBR) may provide opportunities for rapid growth and expansion of other taxa. The bioeroding sponges *Cliona* spp. are strong competitors for space and have been hypothesized to take advantage of coral bleaching, damage, and mortality. Benthic surveys of the inshore GBR (2005-2014) revealed that the percent cover of the most abundant bioeroding sponge species, *Cliona orientalis*, has not increased. However, considerable variation in *C. orientalis* cover, and change in cover over time, was evident between survey locations. This study assessed whether the percent cover of other benthic groups, and the environmental characteristics at each location, were associated with variation in *C. orientalis* distribution and abundance. The proportion of fine particles in the sediments was negatively-associated with the presence-absence and the percent cover of *C. orientalis*, indicating that the sponge requires exposed habitat. The cover of other benthic taxa explained little variation in *C. orientalis* cover or distribution. The fastest increases in *C. orientalis* cover occurred at sites with low macroalgal cover and the lowest mean chlorophyll *a* concentration (see Figure), highlighting the importance of macroalgal competition and local environmental conditions for this bioeroding sponge. Given the observed distribution of *C. orientalis* and habitat preferences, bioeroding sponges such as *C. orientalis* likely represent site-specific – rather than regional – threats to corals and reef accretion.

We acknowledge financial support from AIMS@JCU (BDR) and an Australian Research Council Future Fellowship (NSW).

Ecological Interactions Between Photosymbionts And Spongivores Reveal Complex Interplay Between Bottom-Up And Top-Down Controls On Caribbean Sponges

Kenan O. Matterson[1] Cole G. Easson[2], Christopher J. Freeman[3], Robert W. Thacker[4],

[1] Smithsonian Institution, National Museum of Natural History, Washington, D.C., USA MattersonK@si.edu

[2] Nova Southeastern Halmos College of Natural Sciences and Oceanography, Dania Beach, Florida, USA

[3] Smithsonian Marine Station, Fort Pierce, Florida, USA.

[4] Department of Ecology and Evolution, Stony Brook University, Stony Brook, New York, USA

Sponge populations have increased in abundance in many areas of the Caribbean, generating renewed interest in the principles structuring these natural communities. Trophic factors like spongivore density and picoplankton abundance are proposed to drive patterns of sponge diversity, with experimental evidence supporting both viewpoints. However, these studies have neglected to investigate the role that microbial symbionts play in host sponge fitness, obscuring their ability to interpret the strength of these trophic mechanisms. Many dominant Caribbean sponges, for instance, utilize symbiotic cyanobacteria as a source of supplemental nutrition while also maintaining varying levels of chemical defenses. The presence of such species, with characteristics inherently linked to processes of top-down and bottom-up regulation, highlight the need for further investigations addressing the interactive effects of these processes across a greater breadth of ecologically diverse sponges. In this study, we conducted an *in situ* factorial experiment that manipulated irradiance and predator abundance over a six-week period to investigate potential interactive effects of spongivory and photosymbiont-derived nutrition on the growth of six ecologically diverse sponge species. We characterized sponge community structure on neighboring reefs and quantified spongivore abundance alongside *in situ* observations of active spongivory. Three sponge species hosting high photosymbiont densities exhibited significantly lower growth under low irradiance conditions irrespective of predator abundance, demonstrating bottom-up regulation. Alternatively, sponges lacking photosymbionts exhibited significant top-down control by predators. Interestingly, one photosymbiont-hosting species demonstrated higher growth rates under shaded conditions but only when predators were excluded, verifying the existence of interactive effects between irradiance and predation. Our results demonstrate that sponge photosymbionts serve as an alternative source of bottom-up regulation for some species, with these symbioses providing resources that are critical for host survival, especially under increased spongivory. More broadly, our results suggest that microbial symbionts likely influence sponge community structure to a greater extent than previously recognized and highlight the necessity of accounting for microbial partnerships when examining the forces that structure communities.

Combined effects of ocean acidification and eutrophication on reef sponge bioerosion

Lennart J. de Noojer, Alice E. Webb, Steven M.A.C. van Heuven, Didier M. de Bakker, Fleur C. van Duyl, Gert-Jan Reichart

The health of tropical coral reefs depends largely on the balance between constructive (calcification and cementation) and destructive forces (mechanical-chemical degradation). The ongoing gradual increase in dissolved CO_2 and the resulting decrease in carbonate ion concentration ('ocean acidification') in ocean surface water may tip the balance towards net mass loss for many reefs. Increased organic loading in surface waters ('eutrophication'), may increase the susceptibility of coral reef and near shore environments to ocean acidification (Cai et al., 2011; Cyronak et al., 2014; Yeakel et al., 2015). The negative impacts of these environmental changes on coral calcification have been recorded, however, their (separate as well as synergetic) effect on bioerosion rates by excavating sponges is poorly studied. *Cliona caribbaea*, a photosymbiont- bearing excavating sponge widely distributed in Caribbean reef habitats, was exposed to a range of CO_2 concentrations, in combination with different eutrophication levels. Results showed that chemical bioerosion rates were positively affected by both pCO_2 and eutrophication levels, but these effects did not enhance each other. The increase in organic loading made the sponges less dependend on primary production of their symbionts, which beneficiated day chemical bioerosion rates. These were found to be ~50% higher than those during the incubations at night. However, at higher pCO_2 levels, night rates of bioerosion become comparable, or even higher than day ones.

Better Estimates Of Chemical And Mechenical Excavating Rates Of Coral Boring Sponges In The Caribbean

Didier M de Bakker[1, 2], Alice E Webb[2], Steven MAC van Heuven[2], Erik HWG Meesters[1]and Fleur C van Duyl[2]

[1] Wageningen University and Marine Research, P.O. Box 57, 1780 AB Den Helder, The Netherlands

[2] NIOZ Royal Netherlands Institute for Sea Research and Utrecht University, P.O. Box 59, 1790 AB Den Burg, Texel, the Netherlands

Excavating sponges are among the most efficient bioeroders (chemical and mechanical) found on coral reefs. Multiple studies found excavating sponge biomass and activity to have increased considerably in the past decades and continue to do so under increased human impact.

Currently, the most conventional way to estimate chemical boring rates is by placing sponge infested coral cores in incubation chambers (*ex situ*) for several hours and measuring the change in alkalinity over the course of the incubation. Our preliminary results, however, indicate that sponges can remove both the particulate (e.g. bacteria) and dissolved food sources within minutes. The depletion of food and the subsequent recycling of waste water likely negatively affects the sponge metabolism when kept in a limited amount of incubation water. Indeed, we found that boring rates of sponge infested coral cores (25 cm^3) decreased by 55% as a function of time spent (2 h compared to 6 h) in the incubation chamber (500 mL).

We describe a flow-through incubation chamber that allows for continuous refreshing of the water inside the incubation chamber, therewith ensuring a continuous replenishment of food and removal of waste water. This novel incubation method combined with accurate optical alkalinity titration was used to provide better chemical erosion rate estimates for sponge species commonly found on Caribbean coral reefs (*Cliona caribbaea, C. aprica, C. delitrix, Cliona spp.* and *Siphonodictyon* spp.). In addition, we present an improved method to estimate mechanical erosion (carbonate chip removal) by these species using scanning-electron microscopy. The accurate species specific rates (combined estimates of chemical and mechanical erosion) can be used to obtain better estimates of reef erosion, e.g. within the *ReefBudget* method.

Increase Of Excavating Sponges After Coral Bleaching Events

Andia Chaves-Fonnegra[1], **Bernhard Riegl**[2], **Sven Zea**[3], **Jose V. Lopez**[2], **Tyler Smith**[1], **Marilyn Brandt**[1], **David S. Gilliam**[2]

[1] *Center for Marine and Environmental Studies, University of the Virgin Islands, #2 John Brewers Bay, St Thomas, US Virgin Islands, USA. andiachaves@gmail.com*

[2] *Halmos College of Natural Sciences, Nova Southeastern University, 8000 North Ocean Drive, Dania Beach, Florida, USA.*

[3] *Instituto de Estudios en Ciencias del Mar—CECIMAR, Universidad Nacional de Colombia, Sede Caribe, Santa Marta, Colombia.*

Subtle changes in coral-sponge interactions can alter reef balance and are important to predict trends on current algal-dominated Caribbean reefs. Although sponges are increasing on coral reefs, we lack information on how shifts from corals to bioeroding sponges occur, and how environmental factors such as anomalous seawater temperatures and consequent coral bleaching and mortality are influencing these shifts. A state transition model (Markov chain) was developed to evaluate the response of coral excavating sponges (*Cliona delitrix*) to after coral bleaching events. The model was based on observations of 217 coral colonies over 10 years (2000-2010) in Fort Lauderdale, Florida, and validated with data from 2011 to 2015. To compare and test its scalability, the model was also run with data from reef sites in St Croix, U.S. Virgin Islands (2005-2015) and Bocas del Toro, Panama (2010-2011). Projections and sensitivity analyses confirmed coral recruitment to be key for coral persistence. Excavating sponges increased in both Florida and St. Croix reefs after the bleaching event in 2005, and in Bocas del Toro after the 2010 bleaching event. The increase was more drastic in St. Croix and Bocas del Toro than in Florida, where 30% to 35% of the healthy corals that died shifted into excavating sponges. Projections over 100 years suggest successive events of moderate coral mortality could shift most live coral colonies into excavating sponges in specific reef areas. The success of excavating sponges depends of the intensity of coral bleaching and consequent coral mortality. Thus, the proportion of excavating sponges is a sensitive indicator for the intensity and frequency of recent disturbance on Caribbean coral reefs.

How Do Glass Sponge Reefs Get Enough Food? Feeding And Excretion By The Glass Sponge *Aphrocallistes vastus*

Amanda S. Kahn[1], **Sally P. Leys**[1]

[1] *Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada. kahn@ualberta.ca*

Glass sponge reefs on the continental shelf of western Canada have the highest grazing rate of any benthic suspension feeding community measured to date, consuming seven times more carbon than can be supplied by vertical flux alone. The reefs function as a sink for bacterial carbon and a source of labile nitrogen to the water column as ammonium. Glass sponges live in water that is bacteria-poor and with little dissolved organic carbon available for uptake. How then do reef sponges get enough food to sustain such high grazing rates? We studied the feeding biology of *Aphrocallistes vastus*, from particle capture to excretion. We also used stable isotope signatures of sponges and surrounding water and sediments to understand where the carbon that feeds the reefs comes from and what its fate is after digestion – whether assimilated or excreted. We found that particle uptake occurred in flagellated chambers while digestion occurs elsewhere in the tissue. Carbon-13 labeled bacteria were assimilated into and remained in tissue for at least 14 days. Following digestion, sponges released fecal pellets as aggregates that were 100 to 1000 times larger than the particles they consumed, moving microbial carbon into the benthic food web. Stable carbon and nitrogen isotope signatures showed that reef sponges relied on bacterioplankton from both terrestrial and oceanic sources. Isotope signatures also indicated that reef sponge tissues have different carbon and nitrogen isotope signatures than if feeding on bacterioplankton alone, suggesting that the sponges may also feed on bacteria and detritus resuspended from the sediments. The species that form reefs can be found elsewhere in the oceans but their efficient feeding from large volumes of water suggest that they are only able to grow into dense reefs in locations with several sources of food. By accessing bacterial carbon from the microbial loop and converting it into biomass and large fecal pellets, reef sponges also enrich their surroundings in their food-poor environment. Other deep and shallow sponges may likewise serve as oases of food energy in their ecosystems.

Financial support by NSERC Discovery and Ship Time grants to SPL is gratefully acknowledged.

Initial report on nine newly discovered glass sponge reefs in British Columbia, Canada

Stephanie K. Archer[1], **Glenn Denison**[2] **& Anya Dunham**[1]

[1] *Fisheries and Oceans Canada, Pacific Biological Station, 3190 Hammond Bay Road, Nanaimo, BC V9T 6N7, Canada*

[2] *Marine Life Sanctuaries Society of British Columbia, PO Box 54193, Lonsdale West, North Vancouver, BC V7M 3L5*
Stephanie.Archer@dfo-mpo.gc.ca

Glass sponge reefs are built by dictyonine hexactinellid sponges. These sponges are characterized by fused spicules that result in the persistence of skeletal structural integrity after the sponges' death. This property allows for reef formation as larval sponges settle on the structure provided by previous generations of sponges. Glass sponge reefs have only been documented in shelf habitats in the North East Pacific from Portland Canal to the Strait of Georgia. Recently nine small reefs in Howe Sound, British Columbia, Canada, were discovered by a citizen science group using a drop camera. Here we present the results of a survey of these nine reefs using Fisheries and Oceans Canada's ROV. A total of 19 transects (1-3 per reef) were conducted between September 29 and October 2, 2016. A forward facing high-definition video camera collected continuous video used to assess megafauna community structure. A downward facing still camera automatically took a photo every 15 seconds. The still photos were used to assess percent cover of live and standing dead sponge. These reefs, similar to others in the Strait of Georgia, are constructed by *Aphrocallistes vastus* and *Heterochone calyx*. They are the shallowest known glass sponge reefs, with some reef pinnacles as shallow as 20 m. The reefs have high live sponge cover ranging from 4 to 25%. Standing dead sponge cover was also high ranging from 5 to 42%. We documented a diverse megafaunal community associated with the reefs including several species of sponges, fish, crabs, and other crustaceans. Overall these newly discovered reefs appear healthy and represent a substantial increase in the number of known glass sponge reefs, an ecosystem that, until recently, was thought to be extinct.

Defense By Association: Sponge-Eating Fishes Alter The Small-Scale Distribution Of Caribbean Reef Sponges

Michael K. Wooster, **Micah J Marty & Joseph R. Pawlik**

Center for Marine Science and Department of Biology and Marine Biology, University of North Carolina Wilmington, 5600 Marvin K Moss Lane, Wilmington NC 28409

Sponge-eating fishes have recently been shown to control Caribbean sponge community composition through predation. Palatable sponges—in contrast to those that use secondary chemistry to deter predation (i.e., defended sponges)—are typically grazed off the reef by spongivores, but can sometimes be found in close association to sea whips, fire-corals, stony corals, and defended sponges. In the absence of sponge predators we would not expect this pattern of association with refuge organisms because palatable sponges would be relieved of top-down control and allowed to persist wherever they settle. We conducted 30m belt transect surveys of sponge abundance in relation to refuge organisms on the overfished reefs in Bocas del Toro, Panama and reefs in the Florida Keys where spongivores are common. Palatable sponge species in Panama were randomly distributed and none exhibited a significant trend of association to refuge organisms. In Florida we found the opposite trend where the palatable sponges exhibited a significant trend of association with refuge organisms. While previous studies demonstrated that predation alters sponge community structure between sites across the Caribbean, these data show that predation alters the meter-scale pattern of sponge distribution on reefs where spongivores are present.

Bleaching recovery of a phototrophic bioeroding sponge

Joe Marlow[1], Jamaluddin Jompa[2], James Bell[1]

[1] *Victoria University of Wellington, School of Biological Sciences, Wellington, 6140, New Zealand.*
Joe.marlow@vuw.ac.nz

[2] *Research and Development Centre on Marine, Coastal and Small Islands, Hasanuddin University, Makassar, Indonesia*

Despite coral reef health deteriorating globally, bioeroding sponges are thought to be a comparatively resilient group to the factors that stress and kill corals, and are increasing in abundance at many locations. Many of these bioeroding sponge species harbour endosymbiotic *Symbiodinium* dinoflagellates, an association that aids bioerosion rates and sponge growth and has been considered more resilient than in cnidarian hosts.

The El Niño event that saw corals bleach across the planet in 2015/16 also resulted in a rare mass bleaching of Indonesian *Cliona.* cf. *orientalis* and provided an opportunity to assess their ability to recovery from these events. Surveys of bleaching prevalence and severity in *C.* cf. *orientalis* were conducted six weeks apart across two Wakatobi reef sites July and August 2016, coinciding with a 2°C drop in water temperature. Over this period bleaching prevalence dropped from 73.9% (± 9.9 SE) to 25.7% (± 5.8 SE) of surveyed sponges and bleaching severity dropped from 18.3% (± 3.5 SE) to 3.1% (± 0.8 SE) of sponge tissue. An additional assessment over the same period of rates of recovery/mortality using a weekly assessment of tagged bleached sponges found a 90% drop in bleaching severity but also a 20.6% drop in overall sponge size. Our results demonstrate that this host-symbiont relationship is susceptible to breakdown under conditions of thermal stress. As this stressor diminishes, a relatively rapid recovery does occur but can incur substantial partial mortalities. Proliferation of these sponges on reefs affected by bleaching is likely dependent upon their ability to recover faster than their scleractinian competitors.

Financial support by Victoria University of Wellington and Operation Wallacea is gratefully acknowledged.

Environmental drivers of deep-sea reefs

Ulrike Hanz[1], Marc Lavaleye[1], Gerard Duineveld[1], Claudia Wienberg[3], Dierk Hebbeln[3], Christian Dullo[4], Andre Freiwald[5], Gert-Jan Reichart[1, 2,] Furu Mienis[1]

[1] *NIOZ-Royal Netherlands Institute for Sea Research, Department of Ocean Systems and Utrecht University, Den Burg, Texel, Netherlands. ulrike.hanz@nioz.nl*

[2] *Faculty of Geosciences, Earth Sciences Department, Utrecht University, Utrecht, Netherlands*

[3] *MARUM–Center for Marine Environmental Sciences, University of Bremen, Bremen, Germany*

[4] *GEOMAR Helmholtz Centre for Ocean Research, Kiel, Germany*

[5]*Department for Marine Research, Senckenberg Institute, Wilhelmshaven, Germany*

Deep-sea reefs are found worldwide in various areas. Their appearance is remarkable since the deep-sea is an in general food-limited environment where the input of particulate organic matter decreases with increasing depth. Nevertheless, deep-sea reefs feature high biodiversity and biomass. In this study, we present spatial and temporal variations of biological and physical properties in deep-sea reefs along the southwestern coast of Africa, to define the forcing factors for reef development. Characteristics of the overlying water column were measured by hydrocast transects and lander deployments in two areas on the Namibian and Angolan margin. This area is the most productive coastal upwelling system in the modern ocean, where food export to deeper waters is enhanced. The high productivity is driven by the prevailing water circulation and winds causing upwelling of nutrient rich waters, which enhance productivity, leading to an Oxygen Minimum Zone (OMZ). Even though oxygen levels in the OMZ are extremely low, rich communities of cold-water corals and sponges were found. Communities differed a lot in the two areas; The Namibia margin is characterized by fossil corals overgrown by bryozoans and sponges, while on the Angolan margin thriving cold-water coral reefs with a high diversity were found. Differences are caused by extreme low oxygen concentrations in the OMZ at the Namibian margin. In both areas we found that the expanding and retracting of the OMZ border due to internal waves define the depth distribution of the reefs, which is linked to temporary increased oxygen concentrations. Furthermore, we assume that the appearance of corals and sponges is connected to the high availability of the fresh particulate organic matter, diminishing stress on organisms caused by the oxygen limitation. The lack of living cold-water corals at the Namibian margin additionally implicates a specific ecological role of sponges in extreme environments. This could be important for future climate scenarios, since it is expected that OMZ's will be more widespread.

Biogeographic and bathymetric distribution of coral-eroding sponges

Christine H.L. Schönberg[1], James K.-H. Fang[2], José-Luis Carballo[3], Max Wisshak[4] & Lydia Beuck[4]

[1] *School of Earth and Environment and Oceans Institute, The University of Western Australia, Crawley, WA 6009, Australia.*
christine.schonberg@uwa.edu.au

[2] *Benthic Resources and Processes Research Group, Institute of Marine Research, 5005 Bergen, Norway*

[3]*Instituto de Ciencias del Mar y Limnología, Universidad Nacional Autónoma de México, Mazatlán 82040, México*

[4]*Senckenberg am Meer, Marine Research Department, 26382 Wilhelmshaven, Germany*

Environmental change is progressing at an alarming rate and leads to widespread coral demise. Bioeroding sponges have been called bioindicators of environmental change on coral reefs, they are thought to be comparatively resistant to environmental stress, and they can potentially drive reef carbonate budgets further towards net erosion. Some species of bioeroding sponges received much attention, but others have not been mentioned in the literature since their original description. This situation obstructs our progress in research. We therefore synthesized available published data across all 260 accepted and 13 presently undescribed species, generating annotated faunistic checklists per bioregion and presenting global distribution patterns (Schönberg et al. in press). We strongly suggest that 'cosmopolitan' species are usually species complexes that need to be resolved with molecular means. The best-studied area in shallow waters is the Caribbean, harbouring one fourth of all known species, but global patterns are more strongly influenced by Indo-Pacific species. We have inadequate knowledge on the species from shallow depths in the NE Indic, of the central Pacific and Japan. Along a bathymetric gradient the composition of taxa changes, favouring clionaids in depths less than 100 m, while *Spiroxya*, *Alectona, Delectona* and small species of *Siphonodictyon* become dominant at greater depth. Overall, bioeroding sponges in deep water are much less well studied (18% of the evaluated species, see below) than in shallow and warm waters (77%). At many locations bioeroding sponges have not been studied since the 1800s, and it would be desirable to conduct new surveys that involve morphological as well as molecular species identification.

Reference

C. H. L. Schönberg, J. K.-H. Fang, J.-L. Carballo. Bioeroding sponges and the future of coral reefs. In: J. J. Bell, J.-L. Carballo (eds) Climate change, ocean acidification and sponges. Springer, Berlin, Heidelberg (in press).

Changes in a Mediterranean coralligenous sponge assemblage at a pluri-millennial temporal scale

Gabriele Costa[1], Riccardo Cattaneo-Vietti[2], Maurizio Pansini[1], Simonetta Fraschetti[3] Giorgio Bavestrello[1] & Marco Bertolino[1]

[1] *DiSTAV, Università degli Studi di Genova, Corso Europa 26, 16132 Genova, Italy marco.bertolino75@gmail.com*

[2] *DiSVA, Università Politecnica delle Marche, Via Brecce Bianche, 60131 Ancona, Italy*

[3]*Department of Biological and Environmental Science and Technology, University of Salento, Provinciale Lecce-Monteroni, 73100 Lecce, Italy*

The changes occurred over a pluri-millennial span of time (6200-2000 YBP) in the sponge assemblages present in two 60 cm high coralligenous pillars, at 20 m depth in the Marine Protected Area of Porto Cesareo (Ionian Sea), have been studied. The sponge diversity has been analyzed at generic level, thanks to the study of the siliceous spicules embedded in the sediment trapped into the crevices of these bio-concretions. In total, 41 genera were identified. The actual sponge fauna of these build-ups totals 27 genera, 15 of them are shared with the ancient assemblages. The species richness during the considered span of time showed significant changes, with remarkably similar trends in both the considered pillars.

Tentatively, the observed changes in richness, may be attributed to different climatic events affecting the Mediterranean area within the considered time span. The number of genera was low 6000 YBP and increased between 5500 and 4000 YBP. During the Late Bronze Age Collapse (4000-3000 YBP), a new decrease was recorded, followed by a further increase during the Little Climate Optimum (around 2000 YBP). Afterwards, the bio-concretions stopped growing and no more siliceous spicules were trapped. The progressive increase of the spicular abundance, particularly evident in the last period of observation, was mainly due to the expansion of the boring genus *Cliona* to which one third of the recorded spicules belong. At the same time of the *Cliona* increasing, a progressive reduction of other boring genera (*Spiroxya, Dotona, Delectona, Thoosa* and *Alectona*) was evident. It is suggestive that the stop of the carbonate biodeposition coincides with the increaseg of the sponge boring activity. However, analysing the temporal trends of the spicule number for each recognized genus, a continuous decrease in terms of abundance can be observed for the most common genera (*Petrosia, Tethya, Geodia, Spirastrella, Chondrilla*).

From a biogeographic point of view, the wide presence of spiny microrhabdose microscleres belonging to the genus *Alveospongia* (Heteroxyidae), recently described from the tropical Atlantic and still unknown in the Mediterranean Sea, has to be underlined. Finally, it is remarkable that the trends recorded in the Ionian Sea match with those observed in the Ligurian Sea. In particular, in both these Mediterranean regions, the recorded loss in genus richness along the time could be related to a sharp decrease of the seawater temperature. Moreover, comparing the past periods with the present, significant changes in biodiversity have been recorded in both the areas.

Coral cavities – Stable habitats with zero growth? Assessing potential growth rates and community changes in cryptic sponges

Benjamin Mueller[1, 2], **Jasper M. de Goeij** [1, 2]

[1] *Department of Freshwater and Marine Ecology, University of Amsterdam, Amsterdam, The Netherlands muellerb@ymail.com*

[2] *Carmabi Foundation, Willemstad, Curaçao.*

Coral cavities constitute up to two-thirds of a reef's volume and the surface exceeds that of the open reef [1]. Encrusting sponges which dominate these cryptic habitats have been identified to play a key role in the energy and nutrient cycling of coral reefs [2]. Those sponges assimilate large amounts of dissolved organic matter, rapidly form new cells to rejuvenate their existing structures, and shed and expel old cells [3]. This sponge loop pathway is based on the assumption that the somatic growth of these sponges is close to zero, as newly formed cells are foremost shunted to higher trophic levels as detritus. This is in marked contrast to the majority of open reef sponges, which display substantial somatic growth. We therefore investigated the potential growth rates (specimen growing on coral rock cleared of epibionts; Fig. A) of three common Caribbean cavity sponges *Haliclona vansoesti*, *Halisarca caerulea*, and *Scopalina ruetzleri* over a period of six weeks on Curaçao. Additionally, the growth rates and community changes of cryptic sponges were followed in 11 permanent photo quadrats (50 x 50 cm; Fig. B) in an overhang at a vertical wall at a depth of 30 m for six weeks. Preliminary data suggests a potential growth rate of 1.3 ± 0.5% (mean ± SD) surface area increase per day for *H. caerulea*. Moreover, out of 175 individuals of *S. ruetzleri* followed, 94 increased in size (1.1 ± 0.8% per day), whereas 12 merged with other individuals and 42 did not change in size. Merely 27 individuals decreased in size (-0.8 ± 0.3% per day) over the six weeks. Interestingly, the potential growth rate for specimens on cleared coral rock is comparable to the observed growth of increasing individuals under natural conditions. This suggests that under favourable conditions cavity sponges exhibit considerable growth and may even increase their body size five times per year. However, for *H. caerulea* this increase in biomass only represents a minor portion of the total assimilated carbon budget (2.2%), leaving detritus production (58%), by far the largest excretion product.

References

1. C. Richter, M. Wunsch, M. Rasheed, et al., Nature 413 (2001) 726-730.
2. J.M. de Goeij, D. van Ovelen, M.J.A Vermeij, et al., Science (2013) 108-110.
3. J.M. de Goeij, A. de Kluijver, F.C. van Duyl et al. J. Exp. Biol. 212 (2009) 3892-3900.

Financial support by the Ecology Fund of the Royal Netherlands Academy of Arts and Sciences is gratefully acknowledged.

Increase in light intensity: a threat or not for calcareous sponges survival?

Bárbara Ribeiro[1], **André Rossi**[2], **Flávio da Costa**[3] **& Michelle Klautau**[1]

[1] *Universidade Federal do Rio de Janeiro, Instituto de Biologia, Rio de Janeiro, RJ, Brasil.*
Conference Presenter: barbara.pitt@gmail.com

[2] *Centro Brasileiro de Pesquisas Físicas, Rio de Janeiro, RJ, Brasil.*

[3] *Instituto de Estudos do Mar Almirante Paulo Moreira, Marinha do Brasil, Arraial do Cabo, RJ, Brasil.*

Calcareous sponges are commonly found in sciaphilous habitats, such as caves and under rocks, protected from the direct action of sunlight [1]. The preference of some sponges for this kind of environment can be explained by substrate competition, predation, and intolerance to sedimentation and light intensity [*e.g.* 2, 3, 4]. However, the real cause for this habitat preference was never tested. Thereby, our aim was to investigate if light intensity is a threat for the survival of calcareous sponges. An *in situ* experiment was done in Arraial do Cabo, Rio de Janeiro state, Brazil. Recruitment plates were placed in the seawater (~1 m depth) beside a floating mussel farm, which already had calcareous sponges attached to its structure. After four months, the species *Paraleucilla magna* Klautau *et al*., 2004 recruited under the plates (sciaphilous part) and when they achieved ~1 cm^2, the experiment started. Three plates (control replicates) were kept with the sponges in the sciaphilous side, while other three plates (treatment replicates) were turned into the light and the sponges were exposed to direct sunlight during five days (Fig. 1). Observations and photos were taken daily. By the end of the experiment, the specimens (control and treatment) were still alive and showed no changes in colour or any apparent damage. Our results suggest that light is not a threat for the survival of calcareous sponges, at least for a short period of time. As vulnerability to predators and wave action were the same in both sides of the plates (photophilous x sciaphilous), these factors do not seem to be responsible for the shaded environment preference. Comparing both shaded and light exposed sides of the plates, the major difference was the amount of macro algae, which were present principally in the photophilous side. This may suggest that the preference of calcareous sponges for shaded habitats is due competition with macro algae. Reduction of sponge populations and even their exclusion from natural habitats by competition with macro algae has already been reported for some Demospongiae [*e.g.* 5]. To confirm our hypothesis, a longer experiment will be conducted to verify if the increase of macro algae will exclude the calcareous sponges from the light exposed side of the plate.

References

1. M. Manuel *et al*., Systema Porifera (2002) 1103-1116.
2. J.L. Wulff, Can. J. Zool. 84 (2006) 146-166.
3. M. Maldonado *et al*., Marine Biology 154 (2008) 631-641.
4. P.L. Jokiel, Science 207 (1980) 1069-1071.
5. R. Baldacconi and G. Corriero, Marine Ecology 30 (2009) 337-345.

Financial support by CAPES and CNPq is gratefully acknowledged.

Sacoleve - Spatial And Temporal Adaptation Of A Traditional Mediterranean Fishery Facing Regional Change: Combining History And Ecology To Study Past, Present And Future Of Sponge Harvesting

Maïa Fourt[1], Daniel Faget[2], Thierry Pérez[1]

[1] Institut Méditerranéen de Biodiversité et d'Ecologie marine et continentale, UMR CNRS 7263 / IRD 237 / Aix Marseille Université / Université d'Avignon. Station Marine d'Endoume, rue de la batterie des lions 13007 Marseille, France

[2] Temps, Espaces, Langage, Europe Méridionale et Méditerranée, UMR CNRS 7303 / Aix Marseille Université. Maison Méditerranéenne des Sciences de l'Homme, 5 rue du Château de l'Horloge, BP 647, 13094 Aix-en-Provence Cedex 2, France

The production of Mediterranean bath sponges collapsed during the past century as it is shown by Tunisian catches which fell from 108 tons in 1920 down to 9 tons in 1988. Another example is given by the well-known sponge fishing island of Kalymnos which lost about 90% of its active fishermen population in a century between 1858 and 1967. For what reasons a Mediterranean traditional fishery once prosperous has dramatically declined? What part of the decline can be attributed to the lessening of the bath sponge stock and what to a decreasing number of fishermen? How can this sponge fishery collapse be related to changes in uses, overfishing, disease outbreaks triggered by climate events? How did sponge fishermen adapt to Regional Changes in the past? What is the future of such a fishery? What kind of guidelines can we provide for this fishery facing the on-going Regional Change? To answer these questions, SACOLEVE looks through ecological and historical windows into past evolution of the sponge fishery, chosen here as a model of traditional fishery which suffered good number of upheavals over the last three centuries. The overreaching aim of this program is to propose a management strategy for traditional fisheries that will allow attaining eco- durable practices in the current environmental, socio-economic and geopolitical contexts.

References

É. Carroll, D. Faget, HISTOSPONGIA: A database on the Mediterranean sponge (18th century). Cahiers de Biologie Marine 57 (2016) 317–321.

T. Pérez, J. Vacelet, Effect of Climatic and Anthropogenic Disturbances on Sponge Fisheries, in: The Mediterranean Sea: Its History and Present Challenges. Goffredo Stefano, Dubinsky Zvy, (2014) 577–587.

M. Valla, La pêche aux éponges: la puissance économique de Kalymnos. (Σπογγαλεία: η οικονομική δύναμη της Καλύμνου) Dodecanisiaka chronika (2012) 823-838.

H. Josupeit, Sponges: world production and markets (No. 90/8). Food and Agriculture Organisation, Rome, Italy (1990).

H.R. Bernard, Kalymnian sponge diving. Human biology (1967) 103–130. Station Océanographique de Salammbô, Tableaux statistiques des pêches maritimes en Tunisie. Année 1932. Direction générale des travaux publics. Régence de Tunis. Protectorat français, Bulletins de la Station océanographique de Salammbô 33 (1933).

Financial support by the Labex "Objectif Terre - Bassin Méditerranéen (OT-Med)", the National Center for Scientific Research through the "Mistral/Biodivmex program" and the "Projet Exploratoire Premier Soutien (PEPS) blanc 2016".

Effects of temperature stress on survival, pigmentation and regeneration of three Caribbean sponges

Juliet Rugiero[1], Marilyn Brandt[1], Andia Chaves-Fonnegra[1]

[1] Center for Marine and Environmental Studies, University of the Virgin Islands, #2 John Brewers Bay, St Thomas, USA-Virgin Islands. julietann66@gmail.com

One threat of climate change to coral reefs is the increase of ocean temperatures, which can produce coral bleaching and mortality. While coral abundances have declined, marine sponges have become abundant and are becoming increasingly important habitat-forming animals on Caribbean coral reefs. This study evaluated if anomalous water temperatures affect the survival, pigmentation and regeneration of three common Caribbean sponges. Fragments of sponges (*Aplysina cauliformis*, *Cliona delitrix* and *Desmapsama anchorata*) were collected from a reef in St. Thomas, U.S. Virgin Islands, and placed at two experimental temperatures for seven days. For control tanks, temperature was maintained at a constant similar to that of local reef conditions (27.0±0.32°C), whereas for the stress tanks two peaks of high (31.1±0.58°C) and low (26.5±0.21°C) temperatures were simulated. Our results showed that under temperature stress *D. anchorata* had higher levels of mortality and changes in pigmentation when compared to *A. cauliformis* and *C. delitrix*. However, a disease affected more fragments of *A. cauliformis* and *C. delitrix* under stress temperature. Tissue regeneration occurred for all three species under both treatments. This experimental study shows that temperature affects sponge species differently, and suggests that *C. delitrix* and *A. cauliformis* fragments better tolerate short fluctuations in seawater temperature than *D. anchorata*.

Geographic Variability in Antibacterial Chemical Defenses Among Branching Morphotypes of Caribbean *Aplysina*

Deborah Gochfeld[1, 4], Savannah Stockton[2], Claire Vickers[2], Cole Easson[3] & Marc Slattery[4]

1 National Center for Natural Products Research, University of Mississippi, Oxford, MS, USA
gochfeld@olemiss.edu
2 Sally McDonnell Barksdale Honors College, University of Mississippi, Oxford, MS, USA
3 Halmos College of Natural Sciences & Oceanography, Nova Southeastern University, Dania Beach, FL, USA
4 Department of BioMolecular Sciences, University of Mississippi, Oxford, MS USA

Sponges are susceptible to a diversity of abiotic and biotic stressors that may affect their ability to perform essential metabolic functions. Among these, the production of chemical defenses may be particularly affected. Chemical defenses provide protection against pathogens, predators and competitors, and qualitative or quantitative changes in the production of the secondary metabolites associated with these defenses may dramatically affect their efficacy and thus, the sponge's survival. Branching sponges of the genus *Aplysina* are among the most abundant sponges on Caribbean reefs, where they are susceptible to *Aplysina* Red Band Syndrome, a disease that differs in prevalence among *Aplysina* morphotypes and geographic locations, suggesting variability in resistance. This study assessed the chemical variability among healthy individuals of three distinct sponge morphotypes (*"Aplysina fulva"*, *"Aplysina cauliformis"* thick, *"Aplysina cauliformis"* thin) across geographic regions in the Caribbean, including pristine sites in the Bahamas and four sites in St. Thomas that vary in their relative exposure to human impacts. Distinct chemical profiles were observed among the three morphotypes. Within morphotypes, there was overlap in chemical profiles of sponges from the Bahamas and St. Thomas, but there were significant differences among sites within St. Thomas, indicating finer-scale geographic variability in secondary metabolite production. Site-specific differences in chemical profiles varied among the three morphotypes. To determine whether morphotype- or site-specific variability in chemical profiles was associated with variability in antibacterial activity, extracts were tested against a panel of marine and human pathogens. The extracts showed selective activity against the test strains, resulting in variability among morphotypes, sites and bacterial strains. Differences in chemical profiles were associated with variability in antimicrobial activity, which may play a role in protection from disease. This study identified clear chemotaxonomic differences associated with branching morphotypes of *Aplysina* in the Caribbean, and supports the contention that anthropogenic stressors affect the production of chemical defenses by sponges. Although *Aplysina*- specific pathogens were not tested, this study identifies potential sources of variability in disease prevalence among sponge populations.

Financial support by the National Science Foundation, National Institute of Undersea Science and Technology, and National Oceanographic and Atmospheric Administration is gratefully acknowledged.

Assessing the regional conservation status of sponges: the case of the Aegean ecoregion

Vasilis Gerovasileiou[1], Maria Sini[2], Thanos Dailianis[1], Maria del Mar Otero[3], Catherine Numa[3], Stelios Katsanevakis[2], Eleni Voultsiadou[4]

[1] Institute of Marine Biology, Biotechnology and Aquaculture, Hellenic Centre for Marine Research, Heraklion, Greece. vgerovas@hcmr.gr;

[2] Department of Marine Sciences, University of the Aegean, University Hill, Mytilene, Lesvos, Greece.

[3] IUCN-Centre for Mediterranean Cooperation, Campanillas, Málaga, Spain.

[4] Department of Zoology, School of Biology, Aristotle University of Thessaloniki, Thessaloniki, Greece.

Despite their key role in marine ecosystems, sponges are among the less studied animal groups concerning their extinction risk and conservation status. This is because of the scarce and scattered information on their species populations and their distribution, which inhibits the application of IUCN criteria. Herein, an attempt is made to provide a baseline for evaluating the regional conservation status of sponges in the Aegean ecoregion (eastern Mediterranean), one of the best studied for its sponge fauna in the Mediterranean. For this purpose, we compiled detailed distribution maps for 22 sponge species falling in three categories: i) species included in the list of endangered and threatened species (Annex II) of the Barcelona Convention, ii) species endemic in this ecoregion and iii) harvested bath sponge species. Different sources for potential data on the population trends of these species through time were examined. As a result, a total of 1551 species occurrences were collected, including unpublished observations made by the authors within the last decade (48%), data from scientific literature sources (43%), citizen science records (7%) and web sources (2%).

The most numerous occurrence data were available for the demosponge species *Sarcotragus foetidus* (436), *Aplysina aerophoba* (431) and *Axinella cannabina* (213), which are protected under the Barcelona Convention. All other species had less than 100 occurrence records with 10 endemic and rare species presenting less than 10 records. The assessment of the regional conservation status of the examined sponge species according to the IUCN Red List criteria, gave the following results: i) 10 of the examined species were assigned to the 'Least Concern (LC)' category under the broad geographical range criterion; ii) the limited information on the 8 endemic/rare species indicated their assessment status as 'Data Deficient (DD)'; iii) the 4 harvested bath sponge species were evaluated as belonging to the Threatened Category of the IUCN Red List, having suffered a massive population decline according to historical data on sponge fisheries. The present evaluation, besides providing scientific data for the regional protection and management of sponge populations, can form a basis for a wider assessment towards the conservation of Porifera.

Spatial variation in chemistry and microbial diversity of Philippine blue sponge, *Xestospongia* sp. in relation to some ecological factors

Geminne Manzano[1], Clairecynth Yu[1], Viviene Santiago[2], Lilibeth Salvador-Reyes[2], Brian Carlmichael Torres[3], Arturo O. Lluisma[3] & Porfirio Aliño[1]

[1] Community Ecology Laboratory, The Marine Science Institute, University of the Philippines, Diliman, Quezon City, Philippines 1101. geminnemanzano@msi.upd.edu.ph

[2] Marine Pharmacognosy Laboratory, Marine Science Institute, University of the Philippines, Diliman, Quezon City, Philippines 1101

[3] Marine Genomics and Molecular Genetics Laboratory, Marine Science Institute, University of the Philippines, Diliman, Quezon City, Philippines 1101

Recent studies in the Philippines focus on the potential role of sponge-associated microorganism on sponge chemistry. Yet, few studies of sponge holobiont at ecosystems level given that ecological processes may play an important role on shaping sponge microbial communities and the secondary metabolites it produces. In this study, the renieramycin-producing Philippine blue sponge, *Xestospongia* sp were used to investigate the extent of variation in sponge-associated microbial community; its secondary metabolite production in relation to some biological and environmental factors. Biological samples were collected using SCUBA, and were transported to the laboratory for morphological and molecular (CO1 sequence) identification, chemical analysis and endosymbiotic community profiling. The diversity of microbial symbionts in the blue sponge *Xestospongia* sp. were initially investigated using a 16s rRNA gene-targeted metagenomic approach. Ecological surveys were performed on two collection sites, representing two Philippine marine biogeographic regions – in Oriental Mindoro located on the West Philippine Sea (WPS) and in Zamboanga del Sur located at Celebes Sea (CS).

Ethyl acetate extracts were subjected to thin layer chromatography (TLC), high performance liquid chromatography (HPLC) and MTT-based antiproliferative assay to confirm the presence of renieramycin M. Chemical profiling using HPLC was performed to compare renieramycin M content among samples obtained from different biogeographic regions. The blue sponges were found to be more abundant on the WPS than in CS sites. Both the benthic community and the fish community in Oriental Mindoro, WPS and Zamboanga del Sur, CS sites are characterized by high species diversity and abundance and very high biomass category. Environmental factors like depth and monsoonal exposure were also compared showing that wave exposure and depth are associated with the abundance and distribution of the sponges. Initial results showed a high microbial diversity and that significant numbers of taxa are considered to be unidentified. TLC and HPLC profiles of the extracts from WPS and from CS showed differences in the amount of Renieramycin M present. Differences in the chemical components present in the extracts obtained from WPS and CS were also observed. Results in exploring the influence of ecological parameters on microbial and chemical diversity provide further impetus in pursuing studies into patterns and processes of the chemical diversity of the Philippine blue sponge, *Xestospongia* sp. and the chemical ecological significance of the coral triangle.

This research study is part of Discovery and Development of Health Products (DDHP- Marine) funded by the Department of Science and Technology – Philippine Council for Health Research and Development (DOST-PCHRD).

Sponges in Space: Spiculous skeleton formation in *Ephydatia fluviatilis* under hypergravity conditions

Martijn C. Bart[1], Sebastiaan de Vet[1], Desiderius M. de Bakker[2], Brittany E. Alexander[1], Emiel van Loon[3], Dick van Oevelen[4], Jack J.W.A van Loon[5], Jasper M. de Goeij[1]

[1] Department of Freshwater and Marine Ecology, Institute for Biodiversity and Ecosystem Dynamics, University of Amsterdam, Post Office Box 94248, 1090 GE Amsterdam, Netherlands m.c.bart@uva.nl

[2] Wageningen Marine Research, Wageningen UR, Den Helder, The Netherlands

[3] Department of Computational Geo-Ecology, Institute for Biodiversity and Ecosystem Dynamics, University of Amsterdam, Amsterdam, The Netherlands

[4] Ecosystem studies, Royal Netherlands Institute for Sea Research, Yerseke, the Netherlands

[5] Dutch Experiment Support Center (DESC), Dept. Oral Cell Biology, ACTA-Vrije Universiteit, van der Boechorststraat 7, 1081 BT Amsterdam, The Netherlands

Successful dispersal of freshwater sponges depends on the formation of degenerative sponge bodies (gemmules) in adverse conditions. This allows the sponge to overcome critical environmental conditions, for example during wintertime, and to re-establish an active sponge when conditions are more favourable in spring. A key step in the construction of a fully-developed sponge from a gemmule is the formation of the spiculous skeleton[1]. Silica spicules form the structural support for the three-dimensional filtration system the sponge uses to filter food particles from ambient water. We studied spiculous skeleton formation of both fed (i.e. providing additional ^{13}C- and ^{15}N-labeled amino acids) and non-fed developing *Ephydatia fluviatilis* exposed to environmental stress, using different hypergravity forces (1, 2.5, 5, 10, and 20 *g* for 48 h) as stressor. Results show that freshwater sponges can withstand these prolonged periods of hypergravity and successfully construct their skeleton, even up to 20 *g*. Developing sponges take up and assimilate dissolved food before forming a functional filtering system, but the gemmule's intrinsic is responsible for skeleton construction. Additionally, non-fed sponges formed active filtration systems significantly more often than fed sponges, especially under higher *g*-force, suggesting that the formation of an active filtration system might be stimulated by food deprivation in environmentally stressful conditions. These findings indicate that the process of spiculous skeleton formation is very energy-efficient and highly flexible, and demonstrate that it plays an important role in how sponges can adapt their size and shape required for indeterminate growth and successful dispersal.

References

1. F. Nakayama, S., Arima, K., Kawai, et al. Curr Biol. 25 (2015) 2549-2554.

Financial support by the ESA-ESTEC Spin Your Thesis program (ESA-DGC-DET-2014-1218) is gratefully acknowledged.

Past and present scenario of the Western Atlantic sponge *Clathrina aurea* (Porifera, Calcarea)

Pedro Leocorny[1], Báslavi Cóndor-Luján[1], André Padua[1], Thierry Pérez[2] & Michelle Klautau[1]

[1] Universidade Federal do Rio de Janeiro, Instituto de Biologia, Departamento de Zoologia. Avenida Carlos Chagas Filho, 373. CEP 21941-902. Rio de Janeiro, Brazil. pedro.leocorny@ufrj.br

[2] Institut Méditerranéen de Biodiversité et d'Ecologie marine et continentale, CNRS, Aix Marseille Univ, IRD, Avignon Univ. Station Marine d'Endoume, rue de la Batterie des Lions, 13007 Marseille.

Sponges are known for their low dispersal capability and population studies have shown high levels of genetic structure for different species in both historical (e.g. Woerheide *et al.*, 2008; DeBiasse *et al.*, 2010) and recent (e.g. Chaves-Fonnegra *et al.*, 2015; Riesgo *et al.*, 2016) time scales. Nevertheless, *Clathrina aurea* (Porifera, Calcarea) is a widespread species in the Western Tropical Atlantic with structured populations and evidence of long-distance dispersal in the Brazilian coast. Its presence in Brazil and the Caribbean turns this species into an interesting model organism to evaluate its capacity of maintaining gene flow across large distances and the role of possible barriers for dispersal in the studied region. Therefore, the present work aims to determine the structuring pattern and dispersal capability of *C. aurea* across its wide distribution range in historical (rDNA ITS) and recent (microsatellites) time scale analyses.

Studied localities included individuals from the Lesser Antilles, NE, SE and S Brazilian coast. Bayesian inferences for structure analyses using ITS marker suggested three different populations, also supported by Φst values: (i) Caribbean; (ii) Brazil, except for its south region; (iii) S Brazilian, with almost no exchange of migrants between them. Using *loci* of microsatellites, however, structure analyses revealed a strong connectivity between Caribbean and Brazilian populations with high genetic similarity between specimens from the Lesser Antilles and the NE Brazilian coast. Our results infer a strong influence of the Amazon River shaping the dynamic of connectivity among populations of *C. aurea* through time, being a permeable barrier to connectivity during periods of high sea level, as proposed by Rocha (2003). Migrant analyses show a dispersal capability for *C. aurea* much higher than what is expected to marine sponges and maintenance of gene flow between NE Brazilian coast and Lesser Antilles may occur through the sponge corridor connecting these two regions.

References

1. A. Chaves-Fonnegra, K.A Feldheim, K. Secord, J.V. Lopez. Molecular Ecology. 24 (2015) 1447–1466.
2. A. Riesgo, R. Pérez-Portela, L. Pita, G. Blasco, P.M. Erwin, S. López-Legentil. Heredity. 117 (2016) 427–439.
3. G. Woerheide, L.S. Epp, L. Macis. BMC Evolutionary Biology; 8 (2008) 24–29.
4. L.A. Rocha. Journal of Biogeography. 30 (2003) 1161–1171.
5. M.B. DeBiasse, V.P. Richards, M.S Shivji. Coral Reefs. 29 (2010) 47–55.

Financial support by CAPES, CNPq and CNRS

New Species Records for Sponges of the Eastern Canadian Arctic and Subarctic

Curtis Dinn[1], Evan Edinger[2], Bárbara de Moura Neves[2], Vonda E. Wareham[3] & Sally Leys[1]

[1] *Department of Biological Sciences, University of Alberta, Edmonton, AB, Canada. Dinn@ualberta.ca*

[2] *Memorial University of Newfoundland and Labrador, St. John's, NL, Canada*

[3] *Department of Fisheries and Oceans, Ecological Sciences Section, St. John's, NL, Canada*

The diversity of deep-water sponges in the Canadian Arctic has historically been overlooked, in part because of difficulties associated with sampling deep hard bottom environments. As part of the ArcticNet HiBio (Hidden biodiversity and vulnerability of hard-bottom environments in the Canadian Arctic) project, regions of reported coral and sponge bycatch in Baffin Bay and the North Labrador Sea were targeted for extensive sampling using remotely operated vehicle (ROV), box core, and Agassiz trawl operations aboard the CCGS *Amundsen*. During expeditions in October 2015 and July 2016, 114 sponge specimens were retrieved from depths ranging from 72 to 1148 m and encompassing latitudes 60°18N to 68°15N. Morphology-based identifications indicate the presence of at least 28 species from 19 different sponge families, several of which may be new species records for the region according to the World Porifera Database. Sponges hitherto known only from the Northeast Atlantic and higher Arctic (*Axinella arctica, Janulum spinispiculum,* and *Tetilla siberica*) are here reported for the first time from the Labrador Sea and Davis Strait. This work spans three marine bioregions, which are thought to contain few (< 35) known sponge taxa (Van Soest et al., 2017). Current results notably increase our present knowledge of sponge species richness on the Northeast Canadian shelf. Sponges are also being quantified from ROV video to give an indication of species richness and biodiversity at some of the sampled sites. Video annotation will also facilitate species identification for specimens collected during ROV surveys and quantify sponge distributions by habitat and substrate type. Additional sampling is planned near Lancaster Sound in northern Baffin Bay. This comprehensive taxonomic study has revealed wider distribution ranges and enhanced our knowledge of the richness of sponge species in the eastern Canadian Arctic.

References

1. Van Soest, R.W.M; Boury-Esnault, N.; Hooper, J.N.A.; Rützler, K.; de Voogd, N.J.; Alvarez de Glasby, B.; Hajdu, E.; Pisera, A.B.; Manconi, R.; Schoenberg, C.; Klautau, M.; Picton, B.; Kelly, M.; Vacelet, J.; Dohrmann, M.; Díaz, M.-C.; Cárdenas, P.; Carballo, J. L. (2016). World Porifera database. Accessed at http://www.marinespecies.org/porifera/porifera.php?p=taxdetails&id=168950 on 2017-01-20]

Financial support by ArcticNet, a Network of Centres of Excellence Canada and NSERC Discovery Grant (SPL) is gratefully acknowledged.

Functional Redundancy in Tropical Marine Sponge Communities

M.M. Valentine & Mark Butler

Department of Biological Sciences, Old Dominion University, Norfolk, VA 23529

The functional diversity of marine communities is thought to influence community processes; sponge communities should, theoretically, be no exception unless functional redundancy among sponges is so great that their "ecological value" as independent species is diminished. Large expanses of hard-bottom habitat in Florida Bay, just north of the Florida Keys (USA), was once populated by a diverse community of sponges before harmful algal blooms substantially reduced their density and diversity. Given the impressive filtration rates of sponges and their role in nitrogen cycling, among other ecological processes, the effects of sponge loss on community function are potentially great. To date, most studies of the effects of sponges on water column constituents have focused on measurements of individuals in enclosures or of water entering and exiting sponges. No study has yet tested how changes in sponge community diversity and biomass affects planktonic communities and water column chemistry, in conjunction with current speed. We manipulated species composition and biomass of experimental sponge communities in flow-through mesocosms to determine the effect of water speed on sponge filtration efficiency and nutrient conversion, measured as changes in the concentrations of nutrients (nitrogen, carbon, and phosphorus), chl A, bacteria, and viruses. Sponges at high density and when exposed to low current speeds typically had the largest effect on nutrient concentrations. As the number of species increased in our mesocosms, so did the strength of ecosystem effects, peaking at four-species mixtures with an asymptote approaching 10-species. Generally, species rich sponge assemblages had a larger ecosystem effect (e.g., greater bacterial removal) than the equivalent biomass of species in monoculture. However, this varied among species and by response variables, because the filtration effects of some sponges were greater in monocultures than in high diversity combinations. These strong species-specific effects on water column properties emphasizes the importance of sponge community biodiversity in maintaining ecosystem function.

Financial support by the E.P.A. is gratefully acknowledged.

Cell & Molecular Biology

Origin of Animal Cells

Shunsuke Sogabe, William L Hatleberg, Daniel Stoupin, Kerry E Roper, Sandie M Degnan & Bernard M Degnan

School of Biological Sciences, University of Queensland, Brisbane QLD 4072, Australia b.degnan@uq.edu.au

All animal cells ultimately evolved from a single ancestral cell. It is widely held that this cell was similar to a choanoflagellate, based on the close relationship of these unicellular holozoans to animals and the putative homology of sponge choanocytes and choanoflagellates. From this ancestral cell evolved the first simple multicellular animal, a clonal hollow ball of identical flagellated cells. In this scenario, cell differentiation evolved later. In this presentation, we place this enduring view of animal origins in the context of recent insights into the molecular cell biology of non-eumetazoan basal animals - with a particular emphasis on sponges - and holozoan protists.

Financial support by the Australian Research Council is gratefully acknowledged.

Sponge cell reaggregation: inter-and intraspecific variations

Andrey Lavrov [1, 2], Igor Kosevich[1]

[1] *Dept. Invertebrate Zoology, Biological Faculty, Lomonosov Moscow State University, Russia, Moscow*

[2] *Koltzov Institute of Developmental Biology of Russian Academy of Sciences, Russia, Moscow*

Despite overall simple body organization sponges possess unique features in their organization not found in other multicellular animals. The plasticity of sponge body both at anatomical and cellular levels is one of such features. Virtually all cells in sponge body constantly moving and the majority of them have ability for transdifferentiation. Continuous tissue reorganization allows adjusting the aquiferous system to certain hydrodynamic conditions, reconstructing somatic tissue after degradation during sexual reproduction, asexual reproduction and movement.

Plasticity of sponge tissues and cells is the most evident during the process of sponge cell reaggregation after tissue dissociation. In the course of reaggregation multicellular aggregates differing in structure form, ending in certain cases in the reconstruction of intact sponge.

We studied cell reaggregation of three demosponge (*Halisarca dujardinii*, *Halichondria panicea*, *Haliclona aquaeductus*) and one calcarean *(Leucosolenia complicata*) species. Cell reaggregation of *H. dujardinii* and *H. panicea* was studied at the different stages of sexual reproduction cycles of these species.

In general the cell reaggregation of all studied species have the same common pattern. During this process multicellular aggregates pass the same developmental stages:

1) primary multicellular aggregates, 2) early primmorphs, 3) primmorphs, 4) progressively developing primmorphs, 5) reconstructed sponge. Nevertheless, each species shows some species-specific features of cell reaggregation which appear as differences in rate and final stage of the process. *Halisarca dujardinii* cell reaggregation proceeds much quicker comparing to other species and always ends with the reconstruction of intact sponge. Cell reaggregation of other species ends at early primmorph or primmorph stages.

Studies of *H. dujardinii* and *H. panicea* cell reaggregation at the different stages of sexual reproduction cycles shows intraspecific variations of the process. In both species, cell reaggregation is most successful in cultures obtained from non-reproducing individuals. After beginning of sexual reproduction and appearance of gametes and/or embryos in the sponge tissues the rate of cell reaggregation decrease and the development of multicellular aggregates stops at earlier stages. The probable reason is an alteration of the physiological condition of somatic tissue of sponge at the different stages of sexual reproduction cycle.

Collected data allow to propose the upgraded general scheme of sponge cell reaggregation considering both inter- and intraspecific variation of this process.

The study was supported by the Russian Foundation of Basic Research (project no. 16-34-00145).

Toward the Development of a Marine Sponge Cell Line: a Sponge- Specific Vector for Introduction and Expression of Foreign DNA

Kylie Hesp[1], Dirk E. Martens[1], Rene H. Wijffels[1] & Shirley A. Pomponi[1, 2]

[1] *Department of Bioprocess Engineering, Wageningen University, Wageningen, Droevendaalsesteeg, Wageningen, the Netherlands. kylie.hesp@wur.nl*

[2] *Harbor Branch Oceanographic Institute, Florida Atlantic University, Fort Pierce, Florida, United States of America.*

Since marine sponge-derived chemicals with pharmaceutical and commercial potential were discovered, many attempts have been made to create a stable or immortalized marine sponge cell line to produce these compounds. New opportunities to tackle this bottleneck are enabled by molecular tools that allow precise control over genes and their expression. However, many of these techniques require introduction and expression of foreign DNA. Expression is dependent upon many factors, including promoter recognition, ribosome binding, transcription termination and codon usage. In this study, all these factors were taken into account to develop an expression vector specifically for sponges. This vector is currently being assayed for its capability to express a fluorescent marker gene in cells of the Caribbean sponge *Dysidea etheria*. Preliminary results indicate that some sponge cells express the marker gene; research is in progress to optimize expression and increase transfection efficiency. The presence of the gene product is confirmed using fluorescence microscopy.

Financial support by the EU Horizon 2020 SponGES project is gratefully acknowledged.

Characterisation of mucus and mucus producing cells in haplosclerid sponges.

Maria Vittoria Marra [1], Caroline Ridley [2], Pierce Lalor [3], Shirley Hanley [4], Peter Owens [3], David J. Thornton [2] & Grace P. McCormack [1]

[1] *Molecular Evolution and Systematics Laboratory, Zoology Department, Martin Ryan Institute, National University of Ireland Galway, Galway, Ireland, m.marra1@nuigalway.ie*

[2] *Wellcome Trust Centre for Cell-Matrix Research, Faculty of Biology, Medicine and Health, University of Manchester, Manchester, United Kingdom*

[3] *Centre for Microscopy and Imaging, Anatomy Department, National University of Ireland Galway, Galway, Ireland*

[4] *Flow Cytometry Core Facility, National Centre for Biomedical Engineering Science, National University of Ireland Galway, Galway, Ireland*

Sponge species from the Order Haplosclerida produce mucus with different physical properties; some species produce a thick sticky form, others a slimy stringy mucus and yet other species appear to produce little or no mucus. Members of this group of sponges also produce a large array of bioactive compounds including those with antimicrobial properties. Focusing on species currently placed in the genus *Haliclona* Grant, 1841 we are investigating the nature of the mucus produced and relating it both to bioactivity potential and to microbial diversity in the same sponges. In *H. indistincta*, *H. viscosa* and *H. sarai* we identified a novel sponge cell type with inclusions that has a similar morphology to mucus producing cells in other animals. The three sponge species produce a similar ‘tacky’ mucus and for *H. sarai* the bioactive compounds produced by the sponge have already been shown to be present in the mucus. Conversely, *H. cinerea* produces a ‘slimy’ mucus clearly visible as mucus strands when the sponge is pulled apart and no putative mucous cells have yet been observed by TEM (transmission electron microscopy) analysis of this species. We are currently characterising the molecules responsible for the physical properties of the mucus from these different sponges. The four species also show a variable level of association with bacteria, which we have investigated using microscopy and microbiome approaches. Understanding the composition of mucus is of great interest for sponge biology in order to understand if mucus is involved in defence and/or symbiotic interactions with microbes. Using an integrative approach that involves transmission electron microscopy, flow cytometry, histochemistry, immunohistochemistry, mass spectrometry and transcriptomics, here we present data on the differences between mucus produced by *H. indistincta* and *H. cinerea* including insight into their microbial diversity and bioactivity potential in an evolutionary framework. Furthermore, for the first time in sponge biology, we describe the mucus producing cells in *H. indistincta* and their ultrastructure.

Keywords: *Haliclona* sponges, mucus, mucous cells, antimicrobial properties, integrative approach.

Cell dynamic during ectosomal and endosomal regeneration on an organotipic culture of *Hymeniacidon heliophila*.

<u>Cristiano Carvalho Coutinho</u>[1], Ivone de Andrade Rosa[1], John Douglas de Oliveira Teixeira[1], Leonardo Rodrigues Andrade[1], Manoel Luis Costa[1] & Claudia Mermelstein[1]

[1] *Instituto de Ciências Biomédicas, Universidade Federal do Rio de Janeiro, Rio de Janeiro, Ilha do Fundão, Av. Brg. Trompowski, s/n, ccoutinho@histo.ufrj.br*

Sponges have high capacity for regeneration, with extreme ability to generate adult individual from dissociated cells. Sponge ectosomal regeneration after superficial ablation has been currently investigated (Borisenko et al., 2015). The authors suggested migration, epithelial conversion and blastea formation as the initial step before epithelization and complete recovery. In the present study, we analyzed the endossomal and ectossomal regeneration dynamic of *Hymeniacidon heliophila* sponge cells into a new whole organism by video microscopy, bright field, confocal microscopy and scanning electron microscopy. The coordination of distinct cell processes during *H. heliophila* regeneration was investigated to address basic knowledge on sponge tissue formation in vitro. We focused on the first 20 hours regeneration with blastea formation and epithelium initialization. An innovative organotypic culture of the endosome was recorded under confocal video microscopy, with or without cell transplantation and vital staining. Three types of migration over the basoephitelial layer were observed, and cell density is likely to be determinant: I) at low density, when filopodia rich mesenchymal cells are dispersed, initial stochastic migration was followed by migration to the nearest cell cluster; II) small group of cells flowing, including basopinachocytes, toward the nearby more dense tissue; III) all sponge cell mass from a tissue specific region undergo entire tissue displacement toward a specific direction, like a blastea movement, with filopodia guiding cells at the front, like cytonemes, and predominance of oriented fusiform cells, spicules and collagen bundles. Cell-cell interaction and cell density was here shown affecting morphogenesis, such as epithelial/mesenchymal and mesenchymal/epithelial conversions. Extracellular matrix was organized according the morphogenetic process observed, with evidences for cell signaling instructions and remodeling. The present data and the here-described method of organotypic culture will further support the development of viable sponge biomass production to solve the supply problem. The identification of signaling mechanisms promoting tissue growth is now under investigation.

References

1. I.E. Borisenko, M. Adamska, D.B. Tokina, A.V. Ereskovsky. PeerJ 3: e1211 (2015) 1–23.

Financial support by Brazilian grants from Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq) and Fundação Carlos Chagas Filho de Apoio à Pesquisa do Estado do Rio de Janeiro (FAPERJ).

A novel secreted frizzled related protein is a downstream target of PAXB and a regulator of aquiferous system development in the freshwater sponge, *Ephydatia muelleri*

<u>April Hill</u>[1], Chelsea Hall[1], Dora Posfai[3], Eric Wictor[2], Melanie Rodriguez[1], Rachel Dumez[1], Josephine Garcia[1], Aheema Gazi[1], Rachel Dumez[1] & Ajna Rivera[2]

[1] *Department of Biology, University of Richmond, Richmond, Virginia. Ahill2@richmond.edu*

[2] *Biological Sciences, University of the Pacific, Stockton, California*

[3] *Molecular Genetics and Microbiology, Duke University School of Medicine, Durham, North Carolina*

The Wnt Signaling pathway and the Pax/Six gene network both play important roles in establishing the freshwater sponge body plan and aquiferous system [1-3]. Using computational approaches to identify transcription factor binding motifs in sponge genomes, we located putative PaxB binding sites upstream of a novel Secreted Frizzled Related Protein (SFRP) gene in *Ephydatia muelleri*. The EmSFRP contains a Frizzled domain with predicted glycosylation site as well as a Netrin domain. EmSFRP is expressed throughout development, but with highest levels in juvenile sponges. In situ hybridization and antibody staining show expression of EmSFRP in the basal pinacoderm in archeocytes with filipodia. Knockdown of EmPaxB expression results in decreased expression of EmSFRP, supporting that PaxB directly or indirectly regulates SFRP in sponges. Interestingly, knockdown of EmSFRP leads to ectopic oscula formation during development, as has been reported when GSK3 is inhibited in this species [1]. These data supports a hypothesis that EmSFRP may act as an antagonist of Wnt signaling in *E. muelleri* and that the regulation of the Wnt pathway by the Pax/Six network as well as the role of Wnt signaling in body plan morphogenesis was established before sponges diverged from the rest of the metazoans.

References

1. P.J. Windor, S.P. Leys, Evol Dev. 12 (2010) 484-493.
2. A. Rivera, I. Winters, A. Rued, S. Ding, D. Posfai, B. Cieniewicz, K. Cameron, L. Gentile, A. Hill, Evol Dev. 15 (2014)186-196.
3. Q. Schenkelaars, O. Quintero, C. Hall, L. Fierro-Constain, E. Renard, C. Borchiellini, A.L. Hill, Dev Bio. 412 (2016) 298-310.

Financial support by HHMI and NSF is gratefully acknowledged.

Differential expression analysis of RNAseq data during the formation of the aquiferous system in *Halichondria panicea* (Suberitida, Demospongiae)

<u>Nadia Santodomingo</u>[1], Vasiliki Koutsouveli[1], Sergio Taboada[1], Nathan J. Kenny[1], Lars Kumala[2, 3, 4], Peter Funch[5] & Ana Riesgo[1]

[1] *Department of Life Sciences, The Natural History Museum of London, Cromwell Road, SW7 5BD, London, UK*

[2] *Max-Planck Odense Center on the Biodemography of Aging, Department of Biology, University of Southern Denmark, 5230 Odense M, Denmark*

[3] *Max Planck Institute for Demographic Research, 18057 Rostock, Germany*

[4] *Nordic Center for Earth Evolution, University of Southern Denmark, 5230 Odense M, Denmark*

[5] *Department of Bioscience, Aarhus University, Ny Munkegade 116, DK-8000 Aarhus C - Denmark*

Most sponges rely on a complex aquiferous system that enables their pumping and filter-feeding activities for food capture, oxygen supply, excretion, etc. The formation of the aquiferous system begins a few hours after larval settlement hatching of the gemmule, or within the first week in primmorphs and explants [1]. Although previous studies have found several genes to be expressed during canal formation [e.g., 2-6], the complete expression profile during formation of the aquiferous system remains unknown. Here, we constructed RNA-seq libraries using four samples of explants without pumping activity (= *no-filter feeding*) and four samples of explants with pumping activity (= *filter feeding*) and pooled them to build a reference transcriptome. Then, they were mapped and aligned to the reference transcriptome to perform a differential expression analysis with DESeq2. We found genes differentially expressed between *no-filter-feeding* vs. *filter-feeding* (most upregulated in *no-filter- feeding*) mostly involved in formation of choanocytes (e.g., *tubulins, dyneins, outer dense fiber 3, rootletin*), extracellular matrix (e.g., *mucin-4, several creatine kinases*), cation channels (e.g., *adenylate cyclase, cation channel sperm-associated 1, HCN- gated cation channels*), and maintenance of totipotency (*piwi*). Interestingly, the gene *MOB kinase activator 1B*, which was upregulated in the condition *no-filter-feeding*, plays a pivotal role in restricting proliferation and promoting apoptosis. Similarly, genes upregulated in the *filter-feeding* samples were related to apoptosis (e.g., *caspase-8*), cell growth (e.g., *abl interactor 2*), and the development of the immune system (e.g., *TNF receptor-associated factor 3*). Our results indicate that the main activities carried out during the formation of the aquiferous system are the assembly of choanocytes for pumping, the arrangement of the extracellular matrix necessary for the establishment of the body plan, and the development of cation channels to coordinate cellular responses. In addition, we corroborate the concomitant occurrence of cell proliferation and apoptosis during aquiferous system development reported in primmorphs [2, 7] and provide a comprehensive resource for future investigations.

References

1. D. Sipkema et al. *J. Biotech. 100*(2003) 127-139.
2. A. Krasko et al. J. Biol. Chem. 274(1999) 31524-30.
3. S. Perović et al. *Evol. & Dev. 5* (2003) 240-250.
4. W.E. Müller et al. *J. Cell. Sci.* 117(2004) 2579-90.
5. P. Lapébie et al. PLoS One. 4(2009) e5823.
6. P.J. Windsor, S.P. Leys. *Evol. & Dev.* 12(2010) 484-93.
7. C. Koziol et al. Mechanisms Ageing Dev. 100(1998) 107-20.

Financial support from the Villum Foundation and the Max Planck Institute for Demographic Research is gratefully acknowledged.

Expansion of oxygen-associated pathways at the dawn of animals

Warren R. Francis [1], Sergio Vargas [1], Michael Eitel [1], Dirk Erpenbeck [1], Stefan Krebs [2], Helmut Blum [2], Marcin Adamski [3], Steven H.D. Haddock [4] & Gert Wörheide [1, 5]

[1] *Department of Earth and Environmental Sciences, Palaeontology and Geobiology, Ludwig- Maximilians-Universität München, Munich, Germany*
wrf@lrz.uni-muenchen.de

[2] *Laboratory for Functional Genome Analysis (LAFUGA), Gene Center, Ludwig-Maximilians-Universität München, Munich, Germany*

[3] *Research School of Biology, College of Medicine, Australian National University, Canberra, Australia*

[4] *Monterey Bay Aquarium Research Institute, Moss Landing, CA, USA*

[5] *Bavarian State Collection for Palaeontology and Geology, Munich, Germany*

Animals are thought to have evolved during the neoproterozoic in an environment of relatively low oxygen. Precisely how and when this occurred is unknown, but information about the metabolism of extant animals would give insight into the gene set and capabilities of the last common ancestor of all animals. Here we present the 125- megabase draft genome of the contractile laboratory demosponge, *Tethya wilhelma*, sequenced to almost 150x coverage. We examined pathways involved in sponge contraction behaviour, oxygen regulation and utilization, neural-related receptors, and neurotransmitter biosynthesis across all early-branching phyla of metazoans, all of which show lineage-specific gene family expansions. Sponges and ctenophores lack true orthologs in the HIFa oxygen-sensing pathway and other related proteins involved in circadian rhythms, suggesting these proteins became specialized following a duplication that occurred after separation of both sponges and ctenophores from the rest animals. Other key proteins involved in both oxygen sensing and circadian rhythms are absent in sponges and ctenophores but found in all other animals, indicating that sponges and ctenophores must detect oxygen through other mechanisms, possibly involving sulfide. The absence of these pathways is consistent with the view that these two phyla are the earliest-branching metazoan lineages and provide additional support for the proposed parahoxazoa clade.

This work was supported by a LMUexcellent grant (Project MODELSPONGE) to G.W. as part of the German Excellence Initiative.

Sponges & their Environment

Metabolic plasticity of HMA sponges allows them to completely oxidize all reduced sources in the water: an energetic view

Marta Ribes[1], Rafel Coma[2], Sally P. Leys[3], Teresa Morganti[1, 2], Gitai Yahel[4]

[1] *Institut de Ciències del Mar, ICM-CSIC, Barcelona, Catalonia, Spain*

[2] *Centre d'Estudis Avançats de Blanes, CEAB-CSIC Girona, Catalonia, Spain*

[3] *University of Alberta, Edmonton, Alberta, Canada,*

[4] *The School of Marine Sciences, Ruppin Academic Center, Michmoret, Israel mribes@icm.csic.es*

The contribution of DOM to sponge feeding is now well documented[1, 2] and uptake of labile DOC occurs in both high (HMA) and low (LMA) microbial abundance sponge[3]. In contrast, considerable DON uptake and nitrate excretion are observed only in HMA species. We used *in situ* and laboratory techniques to measure the dissolved and particulate nitrogen fluxes mediated by HMA and LMA sponges and constructed a partial nitrogen budget for 14 sponges species from four different oceanic areas: North-East Pacific, North Sea, North-West Mediterranean Sea, and the Red-Sea. Regardless of the oceanographic settings, HMA sponges exhibited high plasticity in their ability to use the available dissolved nitrogen compounds. Under normal oxygenated conditions, NH_4^+ levels are low and most of nitrate excreted by HMA sponges is derived from full oxidation of DON; when NH_4^+ concentrations are high, its uptake represent an addition to the nitrification rates. The ubiquity of nitrification among the different geographical zones and the high rates of nitrate production associated with HMA sponges suggest that it represents a relevant process for energy income and potentially microbial production within these sponges. We discuss the energetic consequences of these results considering the contribution of full oxidation of the organic matter for the sponge holobionts and the consequences for nutrient cycling. Our data suggest that the HMA sponges are unique among the metazoans in their nutritional plasticity and their ability to take advantage of the entire range of reduced compounds available in the water, provide them with a relevant additional energy source.

References

[1] Rix, L., de Goeij, J. M., van Oevelen, D., Struck, U., Al-Horani, F. A., Wild, C. and Naumann, M. S. (2016), Differential recycling of coral and algal dissolved organic matter via the sponge loop. Funct Ecol. doi:10.1111/1365-2435.12758

[2] Maldonado, M., M. Ribes, and F. C. van Duyl. 2012. Nutrient fluxes through sponges: Biology, budgets, and ecological implications. Advances in Marine Biology **62**:113-182.

[3] de Goeij, J.M., Moodley, L., Houtekamer, M., Caballeira, N.M., and van Duyl, F.C. 2008. Tracing 13C-enriched dissolved and particulate organic carbon in the bacteria-containing oral reef sponge *Halisarca caerulea*: Evidence for DOM feeding. Limnology and Oceanography **53**:1376-1386.

This work was supported by the Spanish Government project CGL2013-43106-R and the Marine Biogeochemistry and Global Change research group funded by the Catalan Government [2014SGR1029]

Differential gene expression analysis in the threatened sponge *Spongia officinalis* following exposure to different temperature conditions

Vasiliki Koutsouveli[1, 2], Tereza Manousaki[1], Jacques Lagnel[1], Spyros Kollias[3], Costas Tsigenopoulos[1], Christos Arvanitidis[1], Costas Dounas[1], Antonios Magoulas[1] Ana Riesgo[2] & Thanos Dailianis[1]

[1] *Institute of Marine Biology, Biotechnology & Aquaculture, Hellenic Centre for Marine Research, Heraklion, Greece*

[2] *Life Sciences Department, Natural History Museum of London V.Koutsouveli@nhm.ac.uk.*

[3] *Centre for Ecological and Evolutionary Synthesis, University of Oslo, Norway*

During the past decades *Spongia officinalis*, the common Mediterranean bath sponge, is being threatened due to intensive unregulated harvesting and outbreaks of mass mortality events. Temperature was shown to be a limiting factor for the survival of this and other species in the western Mediterranean [1] and other oceans, but the molecular responses of sponges to thermal stress have been rarely studied [2]. In our experiment, we tested the effect of three phases of temperature increase (gradual increase, acute heat shock and long-term heat shock) on the molecular response of *Spongia officinalis*.

The trial experiment was conducted in treatment tanks, in which the temperature was gradually increased from 24^{o}C to 27^{o}C for 3 days (27^{o}C+3d) and then immediately raised to 30^{o}C (30^{o}C+2hr) and maintained constant for 2 more days (30^{o}C+2d). A control tank maintained a constant temperature of 24^{o}C during the entire experiment. *De novo* transcriptome assembly was performed on data produced by Illumina HiSeq next- generation sequencing platform (see Manousaki et al., this volume) and differential expression analysis was conducted among the different experimental conditions. Interestingly, we found that mild thermal changes (27^{o}C+3d) produced major shifts in the gene expression profile compared to the control, although this temperature is within the natural range of the habitat of *S. officinalis*, including the upregulation of genes related with the activation of the immune system and apoptotic signaling. Following the acute heat-shock (30^{o}C+2hr), genes related to the inflammatory response, negative regulation of cell proliferation, heat shock (*HSP90*) and other stress responses were overexpressed. Finally, prolonged exposure of *S. officinalis* to a higher temperature (30^{o}C+2d) triggered the differential expression of genes related to the activation of the inflammasome polymeric complex, which is naturally formatted in response to pathogens and other damage-associated signals and genes linked with lipid metabolism and calcium signaling, while genes connected with heat acclimation were downregulated in this last condition.

Our study provides the first approach to understand the response and tolerance to changing temperatures of the economically and ecologically important sponge *Spongia officinalis* using transcriptome analysis.

References

1. J. Garrabou, R. Coma, N. Bensoussan, et al., Glob. Chang. Biol. 15 (2009) 1090-1103.
2. C. Guzman, C. Conaco. PLoS One 11 (2016) e0165368.

This work has been financially supported by the LifeWatchGreece Research Infrastructure (MIS 384676) and the Action «Proposals for Development of Research Bodies-KRIPIS», both funded by the Greek Government under the General Secretariat of Research and Technology (GSRT) and the National Strategic Reference Framework (NSRF).

Sponges in a high CO$_2$ world: a mechanistic understanding of sponge tolerance to elevated pCO$_2$ and temperature.

<u>Holly Bennett</u>[1,3], David Francis[2], Simon K. Davy[1], Nicole Webster[3], James Bell[1]

[1] *Victoria University of Wellington, Wellington 6140, New Zealand*

[2] *Deakin University, Warrnambool, VIC 2180, Australia*

[3] *Australian Institute of Marine Science, Townsville 4810, Queensland, Australia*

As atmospheric CO$_2$ concentrations rise, associated ocean warming (OW) and ocean acidification (OA) are predicted to cause declines in reef-building corals globally, shifting reefs from coral-dominated systems to those dominated by less sensitive species. Sponges are important structural and functional components of coral reef ecosystems, but despite increasing field-based evidence that sponges may be 'winners' in response to environmental degradation, our understanding of how they respond to the combined effects of OW and OA is limited. To address such gaps in our knowledge we explored the response of four Great Barrier Reef sponge species experimentally exposed to OW and OA levels predicted for 2100, under two CO$_2$ Representative Concentration Pathways (RCPs). The response of the sponge holobiont to these conditions was examined over multiple scales, from survival to sponge function, in which physiological processes including growth and metabolism were measured. Biochemical responses were also assessed to determine the effect of these stressors on sponge energy stores and membrane functioning, with the aim to understand mechanisms that underpin sponge tolerance to OW and OA.

All species were generally unaffected by conditions predicted under RCP6.0, although environmental conditions projected under RCP8.5 caused significant adverse effects: with elevated temperature decreasing the survival of all species, increasing levels of tissue necrosis and bleaching, elevating respiration rates and decreasing photosynthetic rates. OA alone had little adverse effect, even under RCP8.5 concentrations. Importantly, the interactive effect of OW and OA varied between species with different nutritional modes, with elevated pCO$_2$ exacerbating temperature stress in heterotrophic species but mitigating temperature stress in phototrophic species. Lipid class and fatty acid (FA) analysis revealed that additional energy available under OA, due to the stimulatory effect of CO$_2$, may facilitate this resistance of phototrophic sponges to OW through increased membrane lipid and FA biosynthesis. Additional innate tolerance mechanisms were also revealed whereby sponges with a higher proportion of phospholipids, sterols, and polyunsaturated FA, the main constituents of the cell membrane lipid bilayer, are more resistant to OW and OA. These lipids are likely to contribute to the ability of these sponges to maintain appropriate membrane function and subsequent cell homeostasis in the face of environmental change. Overall this research gives a holistic view of OW and OA impacts on tropical sponges and provides the basis from which to explore the potential for a sponge-coral regime shift in a high CO$_2$ world.

Pressure-response relationships of sponges to dredge pressures – a laboratory approach

<u>Mari-Carmen Pineda</u>[1, 2], Brian Strehlow[3], Alan Duckworth[1, 2], Ross Jones[1, 2,] Miriam Sternel[4], Jasmine Kamp[5] & Nicole S. Webster[1, 2]

[1] *Australian Institute of Marine Science, Townsville, Australia mcarmen.pineda@gmail.com*

[2] *Western Australian Marine Science Institution, Perth, Australia*

[3] *Centre for Microscopy Characterisation and Analysis, School of Plant Biology and Ocean Institute, University of Western Australia, Crawley, Australia*

[4] *University of Bremen, Bremen, Germany*

[5] *James Cook University, Townsville, Australia*

Dredging activity poses an environmental risk to filter feeders as sediments may smother the animal surface, clog the aquiferous system or reduce light penetration required for photosynthesizing symbionts. Despite the abundance and ecological importance of sponges, our understanding of how they respond to dredging pressures is limited. To address this knowledge gap, we undertook experimental research in the National Sea Simulator at the Australian Institute of Marine Science to test pressure: response relationships and determine thresholds for sponges and their microbial symbionts. Experiments incorporated a selection of representative sponge species, comprising different morphologies and nutritional strategies (phototrophs vs. heterotrophs). A suite of response variables were assessed, with a particular focus on sponge health (i.e. growth, bleaching, mortality), feeding strategies (i.e. respiration, energetic reserves) and changes in microbial symbiosis (i.e. maximum quantum yields, chlorophyll concentrations, composition of the microbial community).

Independent cause/effect experiments teased apart the effects of light reduction, elevated suspended sediments and sedimentation associated with dredging activity, and a final experiment assessed the effect of combined stressors using simulated dredging scenarios. Results revealed that i) light attenuation can adversely impact phototrophic species, with low light levels (<0.8 mol photons m^{-2} d^{-1} for >7 d) causing irreversible damage to *Carteriospongia foliascens*, ii) high suspended sediment concentrations (SSCs) can adversely impact the filter-feeding mode of nutrition, compromising energy stores in the long term, although SSCs of <10 mg L^{-1} could be easily tolerated by most species, and iii) sediment smothering for up to 30 d does not affect adult sponge holobionts as most species possess active and/or passive self-cleaning strategies that enable them to continue feeding. However, the response of some species to the combined effects of all three dredging-related pressures was more immediate and severe than when stressors were applied in isolation. Our results indicate that, although sponges have mechanisms or adaptations to cope with dredging-related pressures in the short term, sponge health can be negatively affected by realistic moderate to high turbidity scenarios (≥10 mg L^{-1}, ≤0.8 mol photons m^{-2} d^{-1}). The sub-lethal stress and mortality thresholds derived from this research will assist regulators and environmental managers in reducing risks from dredging development for this ecologically important group of filter-feeders.

Glass Sponge Pump Rates and their Role in Biogeochemical Cycles in the Weddell Sea, Antarctica

Luisa Federwisch[1, 2], Moritz Holtappels[1], Emil Andersson[3], Roger Johansson[3] & Claudio Richter[1, 2]

[1] *Alfred-Wegener-Institut, Helmholtz-Zentrum für Polar- und Meeresforschung, Bremerhaven, Germany luisa.federwisch@awi.de*

[2] *University of Bremen, Bremen, Germany*

[3] *Sven Lovén Centre for Marine Infrastructure, University of Gothenburg, Gothenburg, Sweden*

Glass sponges (Porifera, Hexactinellida) are an important part of epibenthic communities in the shelf areas of Antarctica. They can grow to considerable sizes of up to 2 m height and form vast sponge beds which provide habitat for various other animals. Despite continuous research on Antarctic benthic community structure and distribution and the obvious dominance of glass sponges in some shelf communities, very little is known about their physiology and their role in biogeochemical cycles. While past studies hypothesized that they have a significant impact on carbon and silicon cycling, this had so far not been investigated in Antarctic glass sponges in situ. During a recent expedition with RV Polarstern to the south-eastern Weddell Sea in 2015/16, we conducted a first in-situ study of pump rates and metabolism in Antarctic hexactinellids. Using a remotely operated vehicle (ROV), we investigated 27 sponges of various sizes (15-65 cm height) belonging to several common species (*Rossella sp.* and *Anoxycalyx joubini*) at four stations between 210 m and 420 m water depth.

We applied a fluorescent dye at the outside wall of the sponges to measure their pump rates. 63% of the sponges were found to be actively pumping. Furthermore, we sampled the exhalant current and the corresponding ambient water of 22 individuals with a new custom-made water sampling system. The samples were analysed for dissolved silicon, ammonium and picoplankton and the differences between ambient water and exhalant current were calculated for each sponge. In addition to that, we measured oxygen consumption in 10 sponges using an oxygen optode. Here, we relate the measured pump rates to sponge size, and present biomass-specific fluxes of carbon, nitrogen, and silicon, as well as clearance and respiration rates for these important foundation species. Extrapolation of our findings to larger spatial scales will help to better estimate the role of Antarctic glass sponges on carbon and silicon cycling.

Effects of copper on early development of the freshwater sponge *Radiospongilla inesi*

Ludimila Calheira[1], Emilio Lanna[2], Paulo Sérgio Martins de Carvalho[1] & Ulisses Pinheiro[1]

[1] *Universidade Federal de Pernambuco, Departamento de Zoologia, Recife, Brazil. uspinheiro@hotmail.com*

[2] *Universidade Federal da Bahia, Departamento de Biologia Geral, Salvador, Brazil.*

Aquatic environments have long been used as disposal areas for domestic and industrial wastes contaminated by metals, which produce harmful effects in aquatics organisms due to their bioaccumulation and toxicity (Cebrian & Uriz 2007). Sponges are possibly vulnerable to waterborne metals due their high filtering capacity (Hansen *et al*., 1995), and there is little information about the effects of pollutants on freshwater sponges. Mysing-Gubala & Poirrier (1981) verified that cadmium and mercury could cause malformations on spicules of *Ephydatia fluviatilis* (Linnaeus, I759), and to our knowledge there is no information about the sensitivity of early stages of development of freshwater sponges to metals. The purpose of this study was to test the effects of waterborne copper in hatchability and early development of *Radiospongilla inesi* gemmules. Gemmules were manually separated from adult sponges and exposed to copper in six concentrations (1 µg/L, 10 µg/L, 50 µg/L, 100 µg/L, 500 µg/L and 1000 µg/L) plus controls in 24 well plates. For each treatment, three replicates with eight gemmules were used. The gemmules were observed daily during 30 days to evaluate death or hatching and early development until osculum formation. No hatching was detected at the highest concentration (1000 µg/L), while the percent of hatched gemmules decreased at concentrations 50 µg/L, 100 µg/L, 500 µg/L (Anova, $p < 0.001$). Regarding sponge development, there was a decrease in the percent of individuals and forming an osculum in all concentrations (Anova, $p < 0.05$). These results show that copper exposure can affect not only hatching, but also the development of fundamental structures in early stages of juvenile *Radiospongilla inesi* sponges, and subsequent colonization of new habitats.

References

1. E. Cebrian, M.J. Uriz. Contrasting Effects of Heavy Metals on Sponge Cell Behavior. Arch Environ Contam Toxicol 53 (2007) 552–558.
2. I.V. Hansen, J.M. Weeks, M.H. Depledge. Accumulation of copper, zinc, cadmium and chromium by the marine sponge *Halichondria panicea* Pallas and the implications for biomonitoring. Mar Pollut Bull 31 (1995) 133–138.
3. M. Mysing-Gubala, M.A. Poirrier. The effects of cadmium and mercury on gemmule formation and gemmosclere morphology in *Ephydatia fluviatilis* (Porifera: Spongillidae). Hydrobiologia 76 (1981) 145–148.

Financial support by FACEPE (Fundação de Âmparo a Ciência e Tecnologia de Pernambuco) and CNPq (National Counsel of Technological and Scientific Development) is gratefully acknowledged.

Sub-lethal stress responses of sponges to dredging pressures

Brian Strehlow[1, 2, 3, 4], Mari-Carmen Pineda[3, 4], Alan Duckworth[3, 4], Peta Clode[2] & Nicole Webster[3, 4]

[1]*School of Plant Biology, University of Western Australia, Crawley, Western Australia, Australia brian.strehlow@research.uwa.edu.au*

[2]*Centre for Microscopy Characterisation and Analysis and Oceans Institute, University of Western Australia, Crawley, Western Australia, Australia*

[3]*Western Australian Marine Science Institution, Perth, Western Australia, Australia*

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

Dredging of the seafloor could affect sponges by raising suspended sediment concentrations (SSC), reducing light intensity, and smothering sponges with sediment. Experimental sediment exposures, using six abundant and broadly distributed Indo- Pacific sponge species, revealed that stress responses are highly species specific. To gain insights into sub-lethal sediment stress we developed X-ray microscopy (microCT) protocols to visualise and quantify internal sediment management strategies in 3 dimensions, as well as thermistor flowmeters, integrated with time-lapse cameras, to measure changes in sponge pumping rates and osculum behaviour. *Ianthella basta* explants were treated with acute (48 h) exposure to high SSC and chronic (4 w) exposure to SSC, light attenuation and sediment deposition, and examined by microCT. In acute treatments, *I. basta* accumulated high concentrations of sediments in its aquiferous system, and sediment concentrations decreased after dosing ceased, with all sediment eliminated within 72 h (Figure 1A). In chronic treatments, *I. basta* accumulated sediment internally, but the majority of sediment was expelled from the aquiferous system within two weeks of recovery. The flowmeter was used to assess pumping activity and osculum contraction in *Cliona orientalis*. Short-term elevation of SSC decreased pumping rates by up to 90%, ultimately resulting in closure of the oscula (Figure 1B) and cessation of pumping (Figure 1C). These experiments provide essential information to better understand and predict the effects of dredging stressors on sponges.

Organismal Biology

Rising of the Porifera: Are sponges becoming the dominant sessile benthic organisms in certain habitats?

Schupp, P.J.

Institute for Chemistry and Biology of the Marine Environment (ICBM), Schleusenstr. 1, 26382 Wilhelmshaven, Germany

In recent years there has been an increasing number of reports that sponges are becoming more abundant and in some regions the dominating benthic organisms on coral reefs. Some locations in the Caribbean provide increasing evidence that coral reefs are shifting from coral dominated to sponge dominated reefs[1]. For the Indo-Pacific there are also a number of reports which suggest that sponge biomass and abundance are increasingly correlating with a decline in coral cover caused by anthropogenic effects, such as overfishing, sedimentation, eutrophication as well as climate change[2]. To assess if sponges are indeed becoming the dominant benthic organisms we conducted a meta-analysis of available benthic monitoring data from various biogeographic regions. Preliminary results will be presented.

One possible mechanism why sponges are successful competitors is the production of bioactive compounds. It has been well established that sponges use secondary metabolites to defend themselves against predatory fish and invertebrate predators. Studies on sponge allelopathic compounds are however largely lacking. We investigated crude extracts from 10 sponges collected from Bawe Island, Zanzibar, Tanzania to study the anti-predatory effects of the sponges and tested also if sponges produced alleopathic compounds to overcome coral competitors. In addition to evaluating various reef sponges in Zanzibar, we investigated in detail the chemical ecology of a particularly dominating sponge (*Pseudoceratina* sp.), which we first sighted at Koh Phangan in the Gulf of Thailand. This sponge was covering large areas of the benthic substrate and overgrew various other invertebrate species including corals. Results from both the feeding and allelopathic experiments will be presented.

Peter J Schupp acknowledges funding of the SUTAS project by the German Leibniz Association (WGL).

References

[1] Pawlik, J.R., 2011. The chemical ecology of sponges on Caribbean reefs: natural products shape natural systems. BioScience 61: 888- 898.

[2] Bell, J. J. & D. Smith, 2004. Ecology of sponge assemblages (Porifera) in the Wakatobi Region, south-east Sulawesi, Indonesia: richness and abundance. Journal of the Marine Biological Associaion of the United Kingdom 84: 581- 591

Multispecies competitive interactions among coral, sponges and macroalgae in St. Thomas, U.S. Virgin Islands

Lauren Olinger[1], Andia Chaves-Fonnegra[1], Ian Enochs[2], Marilyn Brandt[1]

[1] University of the Virgin Islands, St. Thomas, Virgin Islands, USA
lauren.olinger@students.uvi.edu

[2] University of Miami/CIMAS-NOAA/AOML

Competition is an important structuring process on coral reefs, yet most studies focus only on two-way competition between corals and either algae or sponges. Better understanding multispecies interactions among these groups, which dominate the reef benthos, may help disentangle the drivers of benthic community change in nearshore Caribbean ecosystems. The objective of this study was to examine coral-sponge- macroalgae competition across local and community scales. Interactions between individual corals (*Porites asteroides),* macroalgae (*Lobophora variegata)*, and sponges (*Desmapsamma anchorata* and *Aplysina cauliformis*) were examined *in situ* on two reefs located south of St. Thomas, US Virgin Islands. Overgrowth and standoff interactions were surveyed to evaluate the most frequent outcomes among competing pairs of each target species. Additionally, an experiment was designed to compare each competitor's growth under simulated direct competition with a combination of other competitors. Close-range photogrammetry was used to evaluate the three-dimensional growth of each competitor during a three-month period, and two-dimensional growth was monitored for an additional five months. Preliminary data from the surveys and experiment suggest the competitive system is hierarchical across both local and community scales, contrary to the hypothesis that non-hierarchical competition exists and promotes coexistence between the three groups. Moreover, experimental results suggest that *D. anchorata* may grow more rapidly when directly competing with *L. variegata* and *P. asteroides,* compared to when it is only competing with *P. asteroides*. Contact with algae may confer a competitive edge to the sponge, allowing it to more rapidly overtake living corals. Data on growth of each competitor will be used to generate transition matrices to demonstrate how corals may change size classes when competing with different combinations of sponges and macroalgae. The results of this research may shed light on the fate of corals in the presence of growing populations of aggressive macroalgae and sponge competitors.

Specificity of predator defenses of tropical marine sponges

Janie Wulff

Department of Biological Science, Florida State University, Tallahassee, Florida, USA
wulff@bio, fsu.edu

Specificity of prey defenses against predators influences prey species diversity and habitat distribution patterns, and can illuminate evolutionary arms races and canalization of biochemical pathways. A strong phylogenetic signal in specificity of defenses against consumers might be predicted in sponges and other sessile animals, as that is the consistent pattern for defenses of terrestrial plants and marine algae. But the lack of sufficiently comprehensive data sets has impeded testing of this prediction, and it is not known if theories built on evidence from well-studied plant-herbivore and algae-herbivore systems are generally applicable. Recent compilations of data on sponge defenses, from a variety of sources, have made possible the disentangling of patterns in defense specificity that are due to history from those correlated with ecological circumstances, with surprising results.

Specificity is asymmetric for predators and their sponge prey, and predictions about specificity of defenses that are based on habitat are more reliable than those based on history. One ecological result of this pattern is that strict habitat boundaries are enforced by predation for many sponge species. Apparent trade-offs in defenses against predators vs. defenses against competitors maintain divergent species diversity patterns among habitats, specifically mangrove prop roots, seagrass meadows, and coral reefs.

Financial support by the National Science Foundation, the Caribbean Coral Reef Ecosystems Program, and the Smithsonian Tropical Reseach Institute is gratefully acknowledged.

Sponges produces a chemical seascape acting on benthic ecosystem functioning

Thierry Pérez [1], Mathieu Santonja [1, 2], Stéphane Greff [1], Olivier P. Thomas [3]

[1] Institut Méditerranéen de Biodiversité et d'Ecologie marine et continentale, CNRS, Aix Marseille Univ, IRD, Avignon Univ. Station Marine d'Endoume, chemin de la Batterie des Lions, 13007 Marseille, France.

[2] Université Rennes 1 - UMR CNRS 6553 ECOBIO, Avenue du Général Leclerc, Campus de Beaulieu, 35042 Rennes, France.

[3] Marine Biodiscovery, National University of Ireland Galway, School of chemistry, college of science, University road, Galway, Ireland.

Sponges are benthic organisms, dominant in several ecosystems, and known to produce a high chemical diversity. The release of some specialized metabolites in the surrounding seawater has been demonstrated in some rare cases. The occurrence of such molecules into the seawater might constitute a true chemical seascape influencing the behaviour of various mobile organisms and therefore contributing to benthic ecosystem structuring and functioning. In this case study, underwater Mediterranean caves were chosen as models as they are characterized by stable environmental conditions and sessile species assemblages dominated by sponges.

A two-choice tests system was developed to assess the response of two cave-dwelling crustaceans, (*Hemimysis margalefi* and *Palaemon serratus*) against two other species living in shallow water environments, (*Leptomysis* sp. and *Palaemon elegans*) to the surrounding seawater of four Mediterranean sponges commonly found at the entrance of underwater cave: *Aplysina cavernicola, Haliclona fulva, Oscarella tuberculata and Spongia officinalis*. We experienced the swimming behaviour of these crustacean species subjected to control seawater vs. (i) seawater conditioned with the community of sponges or (ii) seawater containing chemical extracts of this community.

Both cave-dwelling crustaceans were significantly attracted by the seawater conditioned with the sponge community, while *Leptomysis* sp. spent more time in the control seawater and *P. elegans* exhibited indifferent responses. In addition, the attractive effect was affected by the daytime. With the aim to decipher the metabolite composition of the conditioned seawaters, a metabolomics fingerprinting approach revealed the presence of chemical markers likely belonging to the oxylipin family.

This work takes place in the framework of the LIA MARRIO, and is funded by the CNRS and the TOTAL Foundation.

Using 3D photogrammetry to model sponge morphological plasticity

Amy Scott-Murray[1], Marie-Lise Schläppy[2]

1. Natural History Museum, London SW7 5BD

2. University of the Highlands and Islands, Thurso KW14 7EE

Sponges (Porifera) modify their morphology in response to environmental changes and in response to injury. Existing methods for assessing morphological change do not address changes in volume or do so only crudely. Plasticity behaviour of sponges has therefore been very difficult to measure and hence is poorly understood at present. In this study, the acquisition of digital sponge models using 3D photogrammetry is described and a novel technique is showcased for extracting high resolution quantitative data describing morphological plasticity over time. This method permits surface displacements of <1mm to be mapped across the organism's surface, and visualised clearly. The techniques described here provide an accessible method for studying sponge morphological plasticity and ability to heal after damage, and is anticipated to permit great benefits to sponge research.

Diversity in Epibenthic Megafauna Associated with a Unique Vase Glass Sponge Ground in the Emerald Basin

Nickolas J. Hawkes[1], Michelle Korabik[2], Hans Tore Rapp[1, 3], Joana R Xavier[1], Ellen Kenchington[2] & Lindsay Beazley[2]

[1]*Department of Biology and KG Jebsen Centre for Deep-Sea Research, University of Bergen, PO Box 7803, N-5020 Bergen, Norway*

[2]*Department of Fisheries and Oceans Canada, Bedford Institute of Oceanography, 1 Challenger Drive, Dartmouth B2Y 4A2, Canada*

[3]*Uni Environment, Thormøhlensgate 49B, N-5006 Bergen, Norway*

Deep-sea sponge-dominated communities, often referred to as sponge grounds are ecologically important in several ways: In bentho-pelagic coupling, in structuring adjacent substrate, and not least, in the provision of habitat for associated fauna. The slow growth and low recovery potential of some deep-sea sponges, combined with fragile morphologies, contributes to the vulnerability of sponges to fishing gear, particularly to bottom trawling. Sponges of the Class Hexactinellida, more commonly known as "glass sponges", form sponge grounds worldwide, and damage from fishing gear has been found in several grounds. A unique population of *Vazella pourtalesi*, also known as the "Russian Hat" was recently found in the Emerald Basin, off the Scotian shelf, between 75-275 m depth and extending over 8, 500 km^2. In this study, 5 transects containing more than 450 photos have been analysed to (i) describe and compare the epibenthic megafauna in areas with and without *Vazella* pourtalesi; and, (ii) to test if the condition (live, dead, damaged or mixed) of *Vazella pourtalesi* assemblages affects the composition of the epibenthic megafaunal communities. Preliminary results suggest that communities outside of sponge grounds have significantly lower average species richness and Shannon (H') diversity, and consist mostly of *Meganyctiphanes norvegica,* one zoanthid species, pandalid shrimps, actiniarian species and serpulids; whilst communities within sponge grounds are significantly higher in average species richness and Shannon (H') diversity, featuring the organisms previously mentioned as well as encrusting sponges (e.g. Hymedesmiidae), a bryozoan species, and various encrusting organisms. A deeper understanding of the drivers and patterns of these sponge grounds will help establish a scientific basis for their importance to local biodiversity, and in turn, aid policy-makers in future conservation efforts.

Funding: This study is part of the SponGES project funded by the European Union's Horizon 2020 research and innovation programme (grant agreement 679849).

Taxonomic, phylogenetic, microbial and ecological assessment of two coral-killing cyanobacteriosponges in the Spermonde Archipelago, Indonesia

Esther van der Ent[1], Nicole J. de Voogd[1]

[1] *Naturalis Biodiversity Center, Leiden, The Netherlands. esther.vanderent@naturalis.nl*

Sponges are very successful competitors for space on coral reefs, and some species present a significant threat to corals. The encrusting 'cyanobacteriosponge' *Terpios hoshinota* is notorious in Indo-pacific reefs as it occasionally undergoes massive outbreaks, actively overgrowing and smothering live corals. This sponge is aided by unusually high numbers of cyanobacteria in an endosymbiotic relationship. Once it invades a new area it can occupy substrates for several years, preventing coral larvae settlement and hindering reef recovery, and remain in the region permanently (Reimer *et al.*, 2011). We report on two other encrusting coral-killing sponges in the Spermonde Archipelago, Indonesia, which also host high abundances of endosymbiotic cyanobacteria. These species are easily misidentified as *T. hoshinota*, because they share some distinct morphological characteristics. There are similarities in coloration, shape and most notably in their aggressive growth strategy. It is therefore possible that some *T. hoshinota* recordings are actually one of these species, which could lead to an overestimation of the expansion of *T. hoshinota* in the Pacific. We present a taxonomic, phylogenetic, microbial and ecologic assessment of the cyanobacteriosponges *Haliclona* sp. nov. and *Chalinula milnei*. In addition to presenting classical morphological characters, we present data from two partitions of a mitochondrial marker (CO1), which are also used by the Sponge Barcoding Project. Both species were widely distributed throughout the Spermonde Archipelago, and their abundances were vastly higher than the recorded abundance of *T. hoshinota* in this region (Van der Ent *et al.*, 2016). *Haliclona* sp. nov. and *C. milnei* were most abundant on intermediate reefs, respectively covering up to max. 41.56 (0.42%) and 143.82 (1.44%) cm^2 per m^2 reef surface. Both species were not recorded on the most turbid inner reefs, within 7 km of the coast. Also, they were rarely observed on the outer reefs, which have pronounced oceanic influences. Interestingly, our results showed that *Haliclona* sp. nov. has a substrate preference for live branching coral, similar to *T. hoshinota* (Elliott *et al.*, 2016), while *C. milnei* showed a preference for live encrusting and massive corals. For *C. milnei*, preliminary results suggest its dominant endosymbiont is *Oscillatoria spongeliae* (relative abundance 50.8%). This presentation will contribute to the knowledge on these morphologically similar aggressive cyanobacteriosponges and prevent future misidentification of the notorious *T. hoshinota*.

References

J.D. Reimer, M. Mizuyama, M. Nakano, T. FUJII, E. Hirose (2011). Current status of the distribution of the coral-encrusting cyanobacteriosponge *Terpios hoshinota* in southern Japan. Galaxea, Journal of Coral Reef Studies, 13(1), 35-44.

E. van der Ent, B.W. Hoeksema, N.J. de Voogd (2016). Abundance and genetic variation of the coral- killing cyanobacteriosponge *Terpios hoshinota* in the Spermonde Archipelago, SW Sulawesi, Indonesia. Journal of the Marine Biological Association of the United Kingdom, 96(02), 453-463.

J. Elliott, M. Patterson, N. Summers, C. Miternique, E. Montocchio, E. Vitry (2016). How does the proliferation of the coral-killing sponge *Terpios hoshinota* affect benthic community structure on coral reefs?. Coral Reefs, 35(3), 1083-1095.

Molecular, Cell and Organismal Speed Talks

A molecular approach to understanding the resurrected order Axinellida

Jane Fromont[1], Belinda Alvarez[1], Oliver Gomez[1], Nerida Wilson [1, 2]

[1]Department of Aquatic Zoology, Western Australian Museum, Locked Bag 49, Welshpool DC, WA 6986, Western Australia, Australia. jane.fromont@museum.wa.gov.au

[2] Molecular Systematics Unit, Western Australian Museum, Locked Bag 49, Welshpool DC, WA 6986, Western Australia, Australia.

The axinellids have a dynamic taxonomy, historically located in various orders and subclasses. Most recently, the order Axinellida Levi 1953 was resurrected (Morrow and Cardenas, 2015) based on molecular data (COl and 28S), since the type species of the genus, *Axinella polypoides,* clusters in this group. In addition, the Raspailidae, previously assigned to Poecilosclerida, are now also located in this order according to molecular results (Morrow and Cardenas, 2015). This reassignment of taxa is now accepted in the World Porifera Database (van Soest et al. 2016). However, relationships among the higher taxa in Axinellida are not yet completely stable, and have not been fully explored with broad taxon sampling. Our study includes a range of tropical Australian sponges in the Axinellida, and uses a molecular phylogenetic approach to test the recently proposed relationships. We utilise three fragments of the nuclear 28S gene, as well as 18S, ITS2, and mitochondrial Cytochrome Oxidase I and ATP Synthase 8, to build a phylogeny. We discuss our results in light of some of the challenges facing sponge taxonomists.

References

1. Morrow, C and Cardenas, P. (2015). Proposal for a revised classification of the Demospongiae (Porifera). Frontiers in Zoology 12:7
2. Van Soest, R.W.M; Boury-Esnault, N.; Hooper, J.N.A.; Riitzler, K.; de Voogd, N.J.; Alvarez de Glasby, B.; Hajdu, E.; Pisera, A.B.; Manconi, R.; Schoenberg, C.; Klautau, M.; Picton, B.; Kelly, M.; Vacelet, J.; Dohrmann, M.; Diaz, M.-C.; Cardenas, P.; Carballo, J. L. (2016). World Porifera database. Accessed at http://www.marinespecies.org/porifera on 2016-11-29

This work is funded by Gorgon Project's Barrow Island Net Conservation Benefits Fund, which is administered by the Department of Parks and Wildlife.

Mitochondrial basic leucine zipper (bZIP) regulatory domain from freshwater sponges conserved across animals

Pleše Bruna[1], Dorić Semir[2], Ćetković Helena[1], Lukić-Bilela Lada[3]

[1]Division of Molecular Biology, Ruđer Bošković Institute, Bijenička cesta 54, 10002 Zagreb, Croatia bplese@irb.hr

[2]Institute for Genetic Engineering and Biotechnology (INGEB), University of Sarajevo, Zmaja od Bosne 8 Kampus, 71 000 Sarajevo, Bosnia and Herzegovina

[3]Department of Biology, Faculty of Science, University of Sarajevo, Zmaja od Bosne 33-35, 71 000 Sarajevo, Bosnia and Herzegovina

Mitochondria contain their own genome, mitochondrial DNA, which carries genes needed for oxidative phosphorylation. Mitochondrial DNA has an established place in studing the genetic variability and evolutionary relationships. Though biological functions of mitochondrial genes are well known, our knowledge of their gene regulatory networks is scarce. The majority of research is focused on human mitochondria where a single major non-coding region contains the main regulatory sequences for transcription and replication initiation. In sponges no such regulatory region has been found. To gain insights into gene regulatory networks we identified the Basic Leucine Zipper Domain (bZIP) in mitochondrial DNA of freshwater sponges. The bZIP family is a set of transcription factors involved in gene expression in the nucleus and mitochondria. Here we report the bZIP binding domain in the mitochondrial Nad4Lprotein. Protein modelling and protein-protein interactions provided *in silico* evidence of biological function. A comprehensive phylogenetic analysis revealed that the bZIP domain found in Nad4L is highly conserved, with orthologues identified in species ranging from sponges to humans. Further experimental studies are necessary in order to confirm these *in silico* results.

Financial support by the Federal Ministry of Education and Science (Bosnia and Herzegovina) grant 04-14-3684-7-1/08 and the Croatian National Science Foundation (Project No. 6400) are gratefully acknowledged.

Regeneration in sponges

Alexander Ereskovsky[1, 2], Borisenko Ilya[2], Andrey Lavrov[3], Maja Adamska[4]

[1] Institut Méditerranéen de Biodiversité et d'Ecologie marine et continentale (IMBE), Aix Marseille Université, CNRS, IRD, Marseille, France

[2] Dept. Embryology, Saint-Petersburg State University, Saint-Petersburg, Russia

[3] Dept. Invertebrate Zoology, Biological Faculty, Lomonosov Moscow State University, Russia, Moscow

[4] Research School of Biology, Australian National University, Canberra, Australia

The ability to regenerate is widespread in the animal kingdom, but the regenerative capacities and mechanisms vary widely. Sponges are known to possess remarkable reconstitutive and regenerative abilities ranging from wound healing or body part regeneration to the impressive re-building of a functional body from dissociated cells. Sponges, as an ancient animal lineage, are important models in studies aimed at understanding of the evolutionary history of animal regeneration mechanisms, including relationships between regeneration and development. Because of diversity of developmental mechanisms found among sponges, we have combined several microscopy techniques to study cellular mechanisms of reparative regeneration in four sponge species from different clades: *Oscarella lobularis* (Homoscleromorpha), *Halisarca dujardini* (Demospongiae), *Sycon ciliatum* and *Leucosolenia complicata* (Calcarea).

Wound healing followed by complete restoration of lost body parts have been observed in all four species, although the cellular mechanisms varied. Epithelial morphogenesis, mainly spreading (flattening) and fusion of epithelial sheets was found to be the key morphogenetic process during regeneration for *O. lobularis, S. ciliatum* and *L. complicata*; while mesenchymal morphogenesis by mesenchymal-epithelial transformations is the main mechanism active during *H. dujardini* regeneration. In addition, formation of blastema (accumulation of pluripotent cells and the dedifferentiated cells - choanocytes, pinacocytes beneath the wound surface) was observed in this species. Notably, transdifferentiation of choanocytes to pinacocytes accompanied the regeneration in all investigated sponges.

Altogether, we demonstrate that regeneration in sponges involves a variety of processes utilized during regeneration in other animals (e.g., cell migration, dedifferentiation, blastema formation) and points to the particular importance of transdifferentiation in this process. While further studies will be needed to uncover the molecular mechanisms governing regeneration in sponges, Wnt and Tgf-beta pathways appear to play important roles in this process as they do in other metazoans.

Financial support by RFBR n° 16-04-00084 is gratefully acknowledged.

Spatially and temporally variable oxygen conditions as determinant of microbial processes in and around Irish sponges

Marie-Lise Schläppy[1]

[1] Environmental Research Institute, University of the Highlands and Islands – marie-lise.schlappy@uhi.ac.uk

Sponges are an ubiquitous component of marine communities and make pelagic nitrogen available to other benthic community organisms through the "sponge loop". The fate of sponge-produced ammonium will depend on the activity of sponge-associated microbes[1]. Under well-aerated conditions sponge-associated microbes have been shown to produce nitrogen through nitrification. Under anoxic conditions within the sponge, sponge-associated microbes have been shown, in some species, to produce N2 gas, through anammox thereby creating a loss of nitrogen for that system. The level of oxygenation in and around sponges can also determine the level of sulfate reduction, a microbial process that happens in oxygen-depleted conditions. In corals, sediments residing on the coral surface were shown to lead to an decrease in oxygen at the coral surface, which led to subsequent sulfate reduction between the sediment layer and the coral tissue, and ultimately to tissue lesions.[2]

To investigate oxygen concentrations as precursor of microbial processes in 2 species of Irish sponges (*Dysidea fragilis* and *Pachymatisma johnstonii*) oxygen micro-electrodes were used in laboratory conditions to measure oxygen concentrations in and around sponges covered with or devoid of sediments. Oxygen concentrations varied strongly spatially and temporally. Oxygen depletion was a common occurrence and occurred more readily at the surface of sediment-covered sponges than of those devoid of sediments. Sulfate reduction was below detection level when measured with a microsensor and no sponge tissue lesions were noted in sponges exposed to sediments naturally present in the unfiltered aquarium system for 3 weeks. The highly variable oxygen concentrations within and around *Dysidea fragilis* and *Pachymatisma johnstonii* indicate that microbial processes occurring under oxic and oxygen depletion are possible, (e.g. nitrification, anammox, sulphate reduction) and that they are likely to be driven by sponge oxygenation. Further investigations using an alternative method to H2S microsensors is necessary to determine the presence/level of sulfate reduction at the surface of sponges that have been exposed to natural levels of sediments for several weeks.

Acknowledgements

The staff of the Carna research station of the Martin Ryan Institute, NUI-Galway is recognized for its significant contribution to the logistical aspects of this project.

References

1 Schläppy M-L; Schöttner, S; Hoffmann F.; Lavik, G.; de Beer, D. 2010. Microbial abundances and processes in three Mediterranean sponges. Marine Biology, 157:593-602

2. M. Weber, D. de Beer, C. Lott, L. Polerecky, K. Kohls, R.M.M. Abed, T. Ferdelman, K. Fabricius (2012) Mechanism of damage to corals by sedimentation. PNAS, (109) 24

Evolution on Ice: Molecular Adaptation to Temperature in Antarctic Sponge Species

Nathan J Kenny[1], Vasiliki Koutsouveli[1], Carlos Leiva[1, 2], Nadia Santodomingo[1], Sergio Taboada[1] & Ana Riesgo[1]

[1] *Life Sciences Department, The Natural History Museum, Cromwell Road, London SW7 5BD, UK*
n.kenny@nhm.ac.uk

[2] *Department of Evolutionary Biology, Ecology, and Environmental Science, University of Barcelona, Barcelona, Spain*

Animals in the Antarctic seas have adapted to some of the most challenging conditions found anywhere on Earth. Temperatures generally ranging between 0 and -1.8°C and a food supply which fluctuates widely from summer to winter render their survival difficult. Nevertheless, sponge species have found the means to live and thrive in such conditions. We aim to find the molecular mechanisms that have evolved to allow this, utilising next generation sequencing and comparative analyses.

Sponges of the genera *Axinella*, *Mycale* and *Phorbas* have been selected as model systems, due to their wide distribution and prevalence in these habitats (1). We have generated a range of genomic and transcriptomic resources from warm and cold water- derived samples, and are using comparative techniques to investigate molecular adaptation in these, building on previous physiological and structural work in sponges (e.g. 2, 3). These are deep and well assembled (e.g. *Phorbas areolatus* transcriptome*,* 146, 359 contigs, N50 1, 050 bp, 93, 500, 065 total bp, *Phorbas* sp. nov. transcriptome 148, 693/988 bp/93, 330, 104 bp), and as such represent an excellent basis for future work in all these species.

These novel genomic resources will be of wide utility to the sponge community in a range of contexts. Further, a number of specific pathways have been targeted for investigation, including those related to energy metabolism/storage, vitellogenesis and skeletal synthesis, which have been implicated as adaptive in a range of organisms (2, 4). We have also begun to use hypothesis-free methods to assay for gene duplication, upregulation and signatures of positive selection to identify novel genes with a potential role in cold adaptation.

This work will allow us to understand the mechanisms by which sponge species can adapt to vastly different climatic conditions. By comparing the molecular repertoire of several species of demosponge we will be able to determine exact mechanisms of evolution to these conditions, and discern whether the adaptive strategies of these species to cold conditions are convergent, are based on ancestrally shared traits, or differ widely, allowing us to speculate more broadly about the evolution of cold- dwelling species.

References

1. P. Dayton, G. Robilliard, R. Paine, L. Dayton, Ecol. Monogr. 44 (1974) 105-128.

2. A. Riesgo, S. Taboada, L. Sánchez-Vila, J. Solà, A. Bertran, C. Avila, PLoS One. 10 (2015) e0118805.

3. S. Morley, J. Berman, D. Barnes, C. de Juan Carbonell, R. Downey, L. Peck, Front. Ecol. Evol. 3 (2016) 157.

4. P. Hu, M. Liu, Y. Liu, J. Wang, D. Zhang, H. Niu, S. Jiang, J. Wang, D. Zhang, B. Han, Q. Xu. Sci Rep. 6 (2016) 28952.

Financial support from the Natural History Museum of London (DIF SDF14032 to AR) and the Horizon 2020 program (MSCA IF to NJK) is gratefully acknowledged.

Osculum dynamics and filtration activity studied in small single-osculum demosponge (*Halichondria panicea*) explants

Lars Kumala[1, 2, 3, 4*], Hans Ulrik Riisgård[1] & Donald Eugene Canfield[4]

[1] *Marine Biological Research Centre, University of Southern Denmark, Kerteminde, Denmark*

[2] *Max-Planck Odense Center on the Biodemography of Aging & Department of Biology, University of Southern Denmark, Odense, Denmark*

[3] *Max Planck Institute for Demographic Research, Rostock, Germany*

[4] *Nordic Center for Earth Evolution, Department of Biology, University of Southern Denmark, Odense, Denmark*
[*] *E-mail: kumala@biology.sdu.dk*

Contraction-inflation behavior, including the closing and opening of the exhalant opening (osculum), is common among sponges. This behavior may temporally affect filtration activity, making it difficult to study and understand sponge feeding biology. To examine the interplay between osculum dynamics and filtration activity small (18 mm^3) single-osculum explants of the demosponge *Halichondria panicea* were studied. Time-lapse video stereo-microscope recordings of the osculum cross-sectional area (*OSA*) were made simultaneously with measurements of the filtration rate (~15 ºC, ~20 PSU) using the clearance method. Osculum dynamics, as expressed in temporal variation in *OSA,* including osculum contraction and expansion, correlated with variability in explant filtration rate and no water pumping was observed during periods of osculum closure. A linear relationship between filtration rate (*F*) and *OSA* revealed a constant exhalant jet velocity: F (mL s^{-1}) = 2.3 ± $CI_{95\%}$ 0.13 (cm s^{-1}) × OSA (cm^2). The mean filtration rate of explants was 0.28 ± $CI_{95\%}$ 0.06 mL min^{-1}, corresponding to a volume-specific filtration rate of 15 mL min^{-1} (cm^3 sponge)$^{-1}$, which is 2 to 3 times higher than reported for larger *H. panicea* sponges with multiple oscula. This is the first demonstration of a direct relationship between filter-feeding and osculum dynamics in a sponge.

This work was supported by a research grant (9278) from VILLUM FONDEN and a scholarship from the Max Planck Institute for Demographic Research is gratefully acknowledged.

Plastic additive changes contraction patterns in *Hymeniacidon heliophila*: a changepoint analysis.

Liv Goldstein Ascer[1], Márcio Reis Custódio[1, 2]

[1] *Department of Physiology, Institute of Biosciences, University of São Paulo, São Paulo (SP), Brazil.*

[2] *NP-BioMar,* University of São Paulo, São Sebastião (SP), Brazil. liv.ascer@gmail.com

Microplastics are a well-known threat to the environment. For years, the lack of policies and inadequate waste management allowed these particles to end in the oceans, leading researchers to estimate that there will be more microplastic than fishes in the sea by 2050(1). Not only they are a physical threat to organisms, but plastics contain additives such as phthalates which are not physically bounded to the polymer and can be transferred (leached) to seawater or to organisms after the particles are ingested(2). Di(2- ethylhexyl) phthalate (DEHP) is the most common compound used as plasticizers, classified as a High Production Volume Chemical and known as an ubiquitous environmental pollutant. Marine invertebrates have been widely used as bioindicators of water contamination. Among them, sponges are the most abundant benthic organisms colonizing rocking shores in tropical areas(3). Their highly efficient filtration process and their ability to ingest micro-particles (<50µm) make them excellent indicators of water quality. Our work aimed to identify possible DEHP effects in sponges, using the contraction patterns as parameter. To do so, we registered the contractions of *Hymeniacidon heliophila*, a common sponge from polluted areas of the Brazilian coast before and after the introduction of DEHP (80 µg.L in seawater), and analyzed their rhythm during 24 hours. Data were analyzed by the R package Changepoint(4) to identify statistically changes in contraction patterns. The results showed that sponges change their contraction rhythm shortly after DEHP introduction in the aquarium, maintaining their aquiferous system functional. Just before 24 hours of exposure they seem to start recovering the normal pattern, with a new visible changepoint at the end of the experiment. Control organisms received the same volume of seawater without DEHP and maintained a constant pattern, without changepoints. Cellular and molecular responses for the DEHP introduction and a possible full recovery of contractions are being investigated, as well as other effects of microplastics in the organisms.

References

1. World Economic Forum, Ellen MacArthur Foundation and McKinsey & Company, The New Plastics Economy – Rethinking the future of plastics (2016), www.ellenmacarthurfoundation.org/publications
2. Agency for Toxic Substances and Disease Registry (ATSDR). 2002. Toxicological profile for Di(2- ethylhexyl)phthalate (DEHP). Atlanta, GA: U.S. Department of Health and Human Services, Public Health Service
3. Diaz, M.C.; Rützler, K. 2001. Sponges: an essential component of Caribbean coral reefs. Bull Mar Sci 69(2): 535-546
4. Killick, R., & Eckley, I. (2014). Changepoint: An R package for changepoint analysis. J Stat Software 58(3), 1-19

Financial support by CAPES and FAPESP is gratefully acknowledged.

In vitro formation of chimaeric individuals after cell dissociation in a calcareous sponge

André Padua[1], Bernard M. Degnan[2], Márcio R. Custódio[3] & Michelle Klautau[1]

[1]Universidade Federal do Rio de Janeiro, Instituto de Biologia, Rio de Janeiro, Brazil.

[2]The University of Queensland, School of Biological Sciences, Brisbane, Australia.

[3] Universidade de São Paulo, Instituto de Biociências, São Paulo, Brazil.

One of the most striking characteristics of sponges is their capacity to re-aggregate isolated cells after dissociation, reconstituting a complete and functional individual *in vitro*. Such process is highly specific in both species and individual levels, usually with an initial mixture followed by sorting and specific aggregation of cell lineages (1). Previous studies observed strong cytotoxic reactions in allogeneic (different individuals of the same species) cell mixtures followed by death of both lineages in Demospongiae (2; 3), evidencing an allorecognition system in adult sponges even after total cell dissociation and body structures disorganization. In the class Calcarea there are few allorecognition studies with adults (4; 5), and scarce observations concerning this issue with dissociated cells (6). In the present work we investigated the allorecognition capacity of dissociated cells in the calcareous sponge *Paraleucilla magna*, using specific microsatellite *loci* for individual genotypic identity and two fluorescent dyes for cell labelling. Isogeneic labelled and unlabelled cell mixtures were undertaken as controls, and all developed into functional sponges *in vitro*. In allogeneic experiments, early cell aggregates and primmorphs originated from two genetically different individuals were observed within 24 hours. Chimaeric primmorphs of *P. magna* were able to built spicules and successfully adhere to the substrate initiating its body reorganization. The formation of choanocyte chambers and the initial organization of the skeleton were observed, but adhered individuals never reached the state of fully functional sponges, which terminates in the formation of the oscule. Such results suggest that, after dissociation, cells of *P. magna* may turn into an undifferentiated state, losing their capacity of self-recognition, resulting in chimaeric primmorphs, but that do not turn into completely viable individuals. Future studies will allow the understanding of the cellular and molecular mechanisms underlying the recognition system in the class Calcarea.

References

1. AI. Lavrov, I.A. Kosevich, Rus. J. Develop. Biol. 45 (2014) 205-233.
2. I.S. Johnston, New perspectives in sponge biology (1990) 91-95
3. C. Yin, T. Humphreys, Biol. Bull. 191 (1996) 159-167.
4. S. Amano, Biol. Bull. 179 (1990) 272-278.
5. A. Padua, P. Leocorny, M.R. Custódio, M. Klautau, J. Exp. Zool A 325 (2016) 294-303.
6. M. Sarà, L. Liaci, N. Melone, Nature 210 (1966) 1167-1168.

Financial support by FAPERJ and FAPESPis gratefully acknowledged.

Spatiotemporal Variation and the Invasibility of Mesofaunal Communities Associated with *Tedania ignis*

Kate Hill

Department of Biological Science, Florida State University, Tallahassee, Florida, USA
kmhill@bio.fsu.edu

Tedania ignis is the iconic sponge of Caribbean mangrove root communities and it hosts a wide array of mesofauna including polychaetes, crustaceans, and brittle stars. *T. ignis* is a massive sponge that is abundant with respect to percent cover and total sponge volume and, as a result, it is a valuable host for mesofaunal communities by providing food, shelter, and a refuge for reproductive individuals. In the Florida Keys, *T. ignis* is abundant in both mangroves and seagrass. I investigated the spatiotemporal variation of mesofaunal community composition by sampling *T. ignis* from mangroves and seagrass in June 2014, March 2015, and March 2016. I found that mesofaunal community composition is strongly influenced by habitat and that community composition varies temporally, such that mesofaunal community composition from a previous year cannot predict mesofaunal community composition in the current year.

I investigated the invasibility of mesofaunal communities by performing a reciprocal transplant of *T. ignis* between mangroves and seagrass in 2014, 2015, and 2016. I found that both the native site and the transplant site influenced mesofaunal community composition. Mesofaunal species that were lost from the sponge following the transplant were often replaced by taxonomically similar species that inhabit a similar location in the sponge host. Furthermore, mesofauna that are sensitive to environmental factors (e.g. brittle stars) were lost when transplanted to a novel habitat (seagrass) or gained when transplanted to a native habitat (mangroves). The reciprocal transplant also revealed that *T. ignis* had an extremely high mortality rate (75%) when moved from seagrass to mangroves, but a much lower mortality rate (10%) when moved from mangroves to seagrass. This difference in mortality suggests there may be subpopulations of *T. ignis* in the Florida Keys, and that not all *T. ignis* hosts are of equal value to their associated mesofauna. Theories of the evolution of mutualism suggest that mutualisms are more likely to evolve in long-lived and reliable hosts; therefore, if *T. ignis* from seagrass populations are ephemeral hosts that offer an unreliable source of food and protection, we may expect exploitative relationships to evolve between the seagrass *T. ignis* subpopulation and its mesofauna.

Financial support by Florida State University, the Jack Winn Gramling Endowed Scholarship, and the Horace Loftin Endowment Scholarship is gratefully acknowledged.

Getting started with the whole genome sequencing project of the demosponge *Geodia barretti*

Karin Steffen[1], NGI-Uppsala[2] & Paco Cárdenas[1]

[1]Division of Pharmacognosy, Department of Medicinal Chemistry, Uppsala University, Sweden. Karin.steffen@fkog.uu.se
[2]National Genomics Infrastructure hosted by SciLifeLab, Uppsala, Sweden.

In theory, that is from an economical and technological point of view, whole genome *de novo* sequencing projects are feasible for an ever-increasing number of organisms. However, one of the key difficulties when working with non-model organisms is obtaining high-quality DNA. Long-read sequencing technology requires large amounts of pure/contaminant-free high molecular weight DNA as library input. The use of readymade kits to extract this DNA presents a static solution amenable for many standard tissues and model organisms but allows for little to no adaptation for systems containing degrading enzymes, inhibitory chemical compounds or particularly fragile DNA.

Revisiting the early extraction protocols and techniques allows for individual assessment, adaptation and optimization of DNA extraction and storage. Here, we use a pre-treatment of frozen tissue with EDTA to inactivate DNA degrading enzymes, centrifugation to roughly separate host and bacterial cells followed by a traditional Chloroform fractionation to obtain high quality genomic host DNA. Thereby, we present a strategy for isolating selected, chemically pure, high-molecular weight DNA from the deep-sea north Atlantic sponge *Geodia barretti*. The procedure yields DNA conforming to high-quality standards required for long-read sequencing (library input >20 ng; purity, measured by absorbance 260/280: 1, 8–2, 0; 260/230: 2, 0–2, 2; DNA fragment size > 40 kb) enabling *de novo* whole genome sequencing in the marine animal. Individual adaptation of classical DNA extraction protocols thus yields high-quality DNA for organisms posing challenges in the molecular genetics workflow.

References

1. Cárdenas, P. et al. Taxonomy, biogeography and DNA barcodes of Geodia species (Porifera, Demospongiae, Tetractinellida) in the Atlantic boreo-arctic region. Zool. J. Linn. Soc. 169, 251–311 (2013).
2. Green, M. R. & Sambrook, J. Molecular Cloning A laboratory manual. 3, (CHS Press, 2012).
3. Gordon, D. et al. Long-read sequence assembly of the gorilla genome. Science 352, aae0344 (2016).

Financial support by EU Horizon 2020 programme SponGES under grant agreement No. 679849 is gratefully acknowledged.

The mechanisms underlying carbonate dissolution by excavating sponges: pH reduction and cell differentiation

Alice E. Webb[1], Shirley A. Pomponi[2], Gert-Jan Reichart[1], Lennart J. de Nooijer[1]

[1] *NIOZ Royal Netherlands Institute for Sea Research and Utrecht University, P.O. Box 59, 1790 AB Den Burg, Texel, the Netherlands*

[2] *Harbor Branch Oceanographic Institution, Inc., Division of Biomedical Marine Research, 5600 US 1 North, Fort Pierce, FL 34946, USA*

Excavating sponges bore and grow into calcium carbonate substrates. In coral reef environments, their activity leads to significant loss of reef structures and can tip the balance between production and erosion in favour of the latter. Despite their ecological relevance, the underlying mechanisms adopted by these sponges to dissolve aragonite remains essentially unknown.

Erosion by excavating sponges is achieved by a combination of chemical dissolution and mechanical chip removal. It is hypothesised that specialised cells are able to lower the pH at the sponge-coral interface to promote controlled aragonite dissolution. Since this interface is not directly accessible, it remains to be investigated what the exact chemical conditions are during aragonite dissolution. Recent results showed that boring rates increase with increasing $p\mathrm{CO}_2$, suggesting that reduced ambient saturation state directly lowers the energetic costs for the sponge to lower the saturation state in which the aragonite skeleton is dissolved.

Using fluorescent confocal microscopy and the sponges *Cliona delitrix* (Pang, 1973) and *C. varians* (Duchassaing & Michelotti, 1864) grown on calcite (Icelandic spar), we show that extracellular pH is reduced at etching sites compared to ambient seawater and the sponge's tissue. This suggests that protons are actively transported into this microenvironment to lower the saturation state and hence promote CaCO_3 dissolution. Our observations also show fusiform cells forming fibre-like pathways localised at the interface between calcite and sponge and may indicate that the excess in Ca^{2+} resulting from the dissolution of CaCO_3 is used by sponges to contract a conductive pathway. Together, these results show insight in the potential role excavating sponges will play on coral reefs in the face of ongoing global climate change.

Infection with *Aplysina* Red Band Syndrome results in biochemical and bacterial community changes to the holobiont

Julie B. Olson[1], Deborah J. Gochfeld[2], Cole G. Easson[3]

[1] *Department of Biological Sciences, University of Alabama, Tuscaloosa, AL, USA*
jolson@ua.edu

[2] *National Center for Natural Products Research, University of Mississippi, Oxford, MS, USA*

[3] *Halmos College of Natural Sciences and Oceanography, Nova Southeastern University, Dania Beach, FL, USA*

Sponges are essential ecological components of coral reefs, and like corals, sponge diseases have been reported with increasing frequency worldwide. *Aplysina* Red Band Syndrome (ARBS) is a disease that affects *Aplysina cauliformis,* one of the most common members of the Caribbean sponge community. ARBS is characterized by expanding red lesions with necrotic centers that causes significant impacts on sponge physiology, and ultimately impacts sponge growth, survival and population dynamics. Due to the transmissible nature of ARBS via sponge-to-sponge contact, biochemical and bacterial community changes can be identified with infection.

During 9-day contact experiments with healthy-diseased and healthy-healthy control treatments conducted in the Bahamas in January and July, we compared individual sponges sampled initially and at successive time points to characterize short-term temporal changes in concentrations of chlorophyll *a* (associated with the loss of cyanobacterial symbionts), total protein, heat shock protein 70, and major secondary metabolites, as well as bacterial assemblages. All healthy sponges in contact with diseased sponges developed ARBS by day 9 in January and by day 6 in July, suggesting that observed changes correspond with the development of ARBS. Several major secondary metabolites, chlorophyll *a* and heat shock protein 70 concentrations changed significantly, as did the composition of the associated bacterial community in initially healthy sponges that became diseased, while total protein concentrations were unchanged during these short-term experiments. These results suggest that infection with ARBS elicits responses by the sponge holobiont, providing a model system in which to investigate immune responses in an early metazoan.

Financial support by the National Science Foundation is gratefully acknowledged.

Ecosystems & Environment

The marine silicon cycle in the light of sponge silica: a global review

Manuel Maldonado[1], Maria López-Acosta[1], Marta García-Puig[1], Cèlia Sitjà[1] Gemma Ercilla[2]

[1] *Department of Marine Ecology, Centre for Advanced Studies of Blanes (CEAB), Spanish National Research Council (CSIC), Blanes, Girona, Spain. maldonado@ceab.csic.es*

[2] *Department of Marine Geology, Institute of Marine Sciences (ICM) Spanish National Research Council (CSIC), Barcelona, Spain.*

The cycling of silicon (Si) in the ocean interacts with many relevant chemical, biological and ecological processes, including control of primary production[1] and removal of atmospheric CO_2. It also intertwines with the cycling of other relevant elements, such as carbon (C), nitrogen, phosphorus, iron, etc. Because of this importance, there is wide interest in quantifying the "journey of Si" through the world's oceans. The classical biogeochemical model proposed to this aim rests on two major assumptions: 1) Si circulates in the ocean under the biological control of planktonic diatoms that use it to elaborate their skeletons of biogenic silica (BSi), with other Si- using organisms (sponges, radiolarians, silicoflagellates, choanoflagellates, etc) making negligible contributions to the global fluxes; and 2) the marine Si cycle is under steady state, being the Si annually leaving the ocean —by burial of BSi in sediments— compensated by an equivalent Si flux entering the ocean in the form of dissolved silica (DSi). However, these two basic assumptions of the cycle have recently been challenged, with evidence suggesting that the equilibrium between Si inputs and outputs in the current cycle model is lost and that Si users other than diatoms could be responsible for such a situation. Our study reveals that the classical view of a Si cycle revolving exclusively around diatoms and their biological features has led to an oversimplification of the biological circuitry, failing to notice a secondary - but relevant - circuit fueled by siliceous sponges. The accommodation of the sponge circuit into the global marine Si cycle causes a major disruption of its classical diatom-biased conceptual frame. Unlike diatoms, sponges occur only in the benthic compartment, have life spans that extend from decades to centuries or even millennia, produce BSi skeletons without connection to the phototrophic production of organic C, and their BSi dissolves at much slower rates than that of diatoms. As a consequence, sponges slow down current diatom-based estimates of Si recycling rates and residence times, favor Si burial, and decouple predicted connections between the Si and C cycles. Importantly, the quantified deposition rate of sponge spicules to the marine sediments and their subsequent burial increase the Si outflux from the ocean up to a value in which the equilibrium between Si inputs and outputs in the global ocean budget is restituted, a steadiness broken if the global model accommodates exclusively diatom-based fluxes.

Financial support by the Spanish Ministry of Economy and Competitiveness through two research grants (CTM2015-67221-R; CTM2012-37787) to MM is gratefully acknowledged.

Silica-induced fibrosis: an ancient response from the early metazoan

Marina Pozzolini[1], Sonia Scarfi[1], Lorenzo Gallus[1], Carlo Cerrano[2] & Marco Giovine[1]

[1]*Department of Earth, Environment and Life Sciences (DiSTAV), University of Genova, Genova, Italy*

[2]*Department of Life and Environment Sciences (DiSVA), Marche Polytechnic University, Ancona, Italy*

Exposure to fine crystalline silica particles (quartz) causes silicosis, an occupational disease leading to an overproduction of collagen in the lung. The first step of this pathology is characterized by the release of inflammatory mediators. Tumor necrosis factor (TNF) is a pro-inflammatory cytokine directly involved in quartz- induced pulmonary fibrosis. On the other hand, in the Invertebrate world, the marine demosponge *Chondrosia reniformis* is able to incorporate and partially dissolve crystalline silica grains without toxic effects [1]. To investigate a possible connection between the physiological behavior of quartz incorporation in *C. reniformis* marine sponge and the pathological outcome of quartz inhalation in Mammals, sponge tissue explants (fragmorphs) were treated with fine quartz dusts and the expression level of fibrogenic genes were assayed by quantitative PCR. Both prolyl-4-hydroxylase (P4H), an enzyme involved in collagen maturation, as well as a fibrillar and a non fibrillar collagen gene (F- and NF-collagen, respectively) were upregulated in quartz-treated fragmorphs compared to controls. P4H and NF-collagen resulted early upregulated (18-48 h) while F-collagen increase was detected at longer times (48 h-7 days) from the quartz stimulation. Hence, in order to investigate the role of *C. reniformis* TNF in the quartz-induced collagen biosynthesis, the expression level of this cytokine was quantified in quartz-treated fragmorphs too, and by means of specific inhibitors, its involvement in the upregulation of the fibrogenic genes, was assessed as well. Indeed, sponge TNF resulted early upregulated after quartz dust fragmorph treatment respect to controls (18 h) and more importantly, the use of two specific TNF inhibitors pointed out that both the P4H and the NF-collagen overexpression in quartz-treated fragmorphs depended on TNF signaling. These results suggest that in *C. reniformis* TNF is important in the initial phase of the quartz erosion process, especially upregulating the two genes, P4H and NF-collagen, that seem involved in the first stages of collagen deposition.

In conclusion, quartz engulfment and erosion in *C. reniformis* seems to stimulate a physiological process of collagen deposition probably due to the necessity of this sponge to strengthen the body structure since the animal does not produce spicules by itself. We speculate that this primitive process could be the cause of the subsequent abnormal, pathological response to quartz in higher Metazoa, namely Mammals, which retain the ability to interact and engulf the quartz particles through macrophage activation but have lost the ability to dissolve them. This unresolved process leads then to a chronic inflammation which finally causes the development of silicosis.

Research supported by EU (FP7 grant agreement n: 266033 SPonge Enzyme End Cell for Innovative AppLication-SPECIAL).

References

1. Bavestrello G, Arillo A, Benatti U, Cerrano C, Cattaneo-Vietti R, Cortesogno L, Gaggero L, Giovine M, Tonetti M Sarà M (1995). Nature 378: 374-376.

Silicon consumption kinetics in demosponges

María López-Acosta[1], Aude Leynaert[2], Manuel Maldonado[1]

[1] *Department of Marine Ecology, Centro de Estudios Avanzados de Blanes (CEAB-CSIC), Girona, Blanes, Spain. lopezacosta@ceab.csic.es*

[2] *Laboratoire des Sciences de l'Environnement Marin, UMR CNRS 6539, Institut Universitaire Européen de la Mer, Technopôle Brest-Iroise, Plouzané, France*

The silicic acid (DSi) is a key marine nutrient modulating ocean primary productivity. Despite marine siliceous sponges being organisms with potential to impact on the local and regional biogeochemical balances of DSi, little is known about their DSi consumption kinetics, with information available for only two sponge genera. That scarcity of experimental data makes complicate to derive reliable estimates of field DSi demands from sponge communities. Herein we present DSi consumption kinetics of four demosponges from different families, *Hymeniacidon perlevis*, *Tethya citrina*, *Haliclona simulans*, and *Suberites ficus*, attempting to both reveal common trends and identify major sources of variability in this physiological variable. A shared trait is that silicon consumption increases with increasing DSi availability following a Michaelis- Menten kinetics. Likewise, all studied species attain saturation at DSi concentrations one order of magnitude higher than DSi availability at their natural habitats. Regarding variability, important between-species differences have been noticed in the rate of maximum DSi consumption and the saturating DSi concentration, for species that occur sharing habitat. Within species, there is also substantial between-individual and seasonal variability in the DSi consumption dynamics. All these natural sources of variability make complicate to obtain an accurate estimate of the DSi consumption by the global sponge standing stock.

This research was funded by two grants of the Spanish Ministry of Economy and Competitiveness (CTM2012-37787 and CTM2015-67221) awarded to MM and an associated FPI fellowship to ML-A.

Effects of dredging on benthic filter feeding communities

Muhammad Azmi Abdul Wahab [1, 2], **Jane Fromont**[2, 3], **Oliver Gomez**[2, 3], **Rebecca Fisher**[1], **Ross Jones**[1, 2]

[1] *Australian Institute of Marine Science, Indian Ocean Marine Research Centre, The University of Western Australia (MO96) 35 Stirling Hwy, Crawley WA 6009, Australia m.abdulwahab@aims.gov.au*

[2] *Western Australian Marine Science Institution, Entrance 2 Brockway Road, Floreat, WA 6014, Australia*

[3] *Department of Aquatic Zoology, Western Australian Museum, Locked Bag 49, Welshpool DC, WA 6986, Australia*

Changes in turbidity, sedimentation and light over a two year large scale capital dredging program at Onslow, northwestern Australia, were quantified to assess their effects on filter feeder communities, in particular sponges. Community functional morphological composition was quantified using towed video surveys, while dive surveys allowed for assessments of species composition and chlorophyll content. Onslow is relatively diverse recording 150 sponge species. The area was naturally turbid (1.1 mean P_{80} NTU), with inshore sites recording 6.5× higher turbidity than offshore localities, likely influenced by the Ashburton River discharge. Turbidity and sedimentation increased by up to 146% and 240% through dredging respectively, with corresponding decreases in light levels. The effects of dredging was variable, and despite existing caveats (i.e. bleaching event and passing of a cyclone), the persistence of sponges and the absence of a pronounced negative response post-dredging suggest environmental filtering (i.e. selective survival of species having stress-tolerant traits) or passive adaptation acquired pre-dredging may have benefited these communities.

This research was funded by the Western Australian Marine Science Institution (WAMSI) as part of a Dredging Science Program, and made possible through investment from Chevron Australia, Woodside Energy Limited and BHP Billiton as environmental offsets, and by co-investment from WAMSI Joint Venture partners. This research was also enabled by data and information provided by Chevron Australia. The commercial entities had no role in data analysis, decision to publish, or preparation of the presentation. The views expressed herein are those of the authors and not necessarily those of WAMSI.

Spatiotemporal variations in stable isotope signatures (δ^{13}C and δ^{15}N) of sponges on the Saba Bank, Caribbean Sea

Fleur C. van Duyl[1], **Benjamin Mueller**[2, 3], **Erik H. Meesters**[4]

[1]*Department of Marine Microbiology and Biogeochemistry, NIOZ Royal Netherlands Institute for Sea Research and Utrecht University, Texel, The Netherlands. Fleur.van.Duyl@nioz.nl*

[2]*Institute for Biodiversity and Ecosystem Dynamics, University of Amsterdam, The Netherlands*

[3]*Carmabi Foundation, Piscaderbaai z/n., Willemstad, Curaçao*

[4]*Wageningen Marine Research, Den Helder, The Netherlands*

Sponges are ubiquitous on coral reefs, mostly long-lived and therefore adaptive to changing environmental conditions. They feed on organic matter withdrawn from the passing water and they derive food from their endosymbionts. Diet and stable isotope (SI) fractionation determine the SI signature of the sponge holobiont. We investigated the SI signatures of δ^{13}C and δ^{15}N of seven commonly occurring sponge species and potential food sources at up to 11 stations between 15 and 32 m depth on coral reefs along the S-SE and E-NE side of the Saba Bank in October 2011 and October 2013. SI signatures differed significantly between sponge species, both in mean values and in variation, indicating different food preferences and/or fractionation. Interestingly, significant differences in the δ^{13}C signatures of sponges were found between stations at the E-NE side and the S-SE side of the bank. It shows that the nutrition differed in SI composition between sides. Consistently elevated nitrate concentrations and δ^{15}N enriched particulate organic nitrogen in reef bottom water, and a relative increase in δ^{15}N in sponges with depth at the S-SE side compared to the E-NE side, suggest that the S-SE side is more frequently exposed to upwelling than the E-NE side. Moreover, the species-specific effect on δ^{13}C and δ^{15}N and the spatial effect on the δ^{13}C in sponges differed between years indicating inter-annual variability. From 2011 to 2013 the δ^{13}C ratio in six of seven sponge species and in the plankton dropped. This drop is likely related to the anthropogenic input of radiocarbon-dead, ^{13}C depleted CO_2 from fossil fuel combustion, which entered surface waters and is reflected in the food web. We show that SI signatures of tropical sponges on the Saba Bank reflect environmental variability in time and space.

What dictates sponge distribution patterns: use of freshwater sponges to assess species requirements

Karen L. Evans[1] **& David J.S. Montagnes**[1]

Institute of Integrative Biology, University of Liverpool, Liverpool, UK. kevans@liverpool.ac.uk

Establishing patterns of sponge biodiversity assists in both quantifying this ecologically important phylum, and in recognising species' habitat requirements. The use of freshwater sponge taxa provides an opportunity to assess the influences of habitat parameters on biodiversity, and reveals important principles that can also apply to marine environments. Problems resulting from fragmentary records of freshwater species were resolved following rigorous sampling across a range of U.K. habitats, and were supplemented with data from additional sources. Species richness was established using both morphological identification and by sequencing the D3 domain of 28S subunit. We noted the first record of *Trochospongilla horrida*, and established distributions of *Spongilla lacustris*, *Ephydatia fluviatilis*, *E. mülleri*, *Eunapius fragilis*, and *Racekiela ryderii*. Widely distributed, *Ephydatia fluviatilis* and *S. lacustris* were the most common species; while *R. ryderii* and *T. horrida* were rare. *Eunapius fragilis* and *Ephydatia mülleri* most frequently co-existed, and exhibited a patchy distribution.

To assess factors governing distribution patterns, we considered the hypothesis that these species are generalists, and examined sponge presence with similar classic factors to Minna Jewell. Our data support the prediction that sponge distributions are driven by environmental tolerance ranges. For instance, sponge colonies tended to be located at sites with lower salinity (= 0.15 ppt, S.E. ± 0.02), and displayed interspecific differences linked with positive/negative oxidation reduction potential. We conclude that species display morphological and genetic differences; and increased biodiversity may occur due to both invasive European species, and from past inabilities to recognise taxa. Critically, we provide baseline information on sponge distribution that is a prerequisite for future monitoring, and go onto discuss current work identifying drivers of abundance. With our guidance, studies may now explore how the distribution of sponge species is regulated by environmental parameters.

Evaluating the influence of abiotic factors on the recruitment rate of Calcareous Sponges (Porifera, Calcarea) in Salvador, Bahia State, Tropical Brazilian Coast.

Cleslei Chagas & Fernanda F. Cavalcanti

Instituto de Biologia, Universidade Federal da Bahia. Barão de Jeremoabo s/n, Campus de Ondina, Salvador – Bahia, Brazil. 40170-115. fernanda.cavalcanti@ufba.br

The recruitment of sessile invertebrates is an important process that provides a better comprehension on the population dynamics and community structure. Although sponges are commonly found among the most abundant benthic organisms, there are several gaps on knowledge about their recruitment patterns and on the factors regulating recruitment rates. In the present work, we analyzed the temporal recruitment of calcareous sponges in a tropical portion of the Brazilian coast, and checked if it was influenced by seawater temperature and precipitation. The study was developed in Salvador, Bahia State, Northeastern Brazil, from August 2015 to October 2016. Fragments of nautical cables were kept together by cables ties, forming plates with 150 cm^2. They were submerged at one meter depth and substituted each two months by new plates (10 replicates). In the laboratory, calcareous sponges were removed from the plates and standard protocols were applied for the taxonomic identification. For the abiotic factors, seawater temperature was measured using a datalogger close to the recruitment plates. Data on the precipitation were obtained from the CPTEC/National Institute for Space Research website. A total of 510 specimens were found, belonging to the following species: *Sycon* sp. nov. 1, *Sycon* sp. nov. 2, *Sycon* sp., *Leucilla* sp. nov., *Leucilla* sp., *Heteropia* sp. nov. and *Leucandra serrata*. The former species was rare along the experiment, while *Sycon* sp. nov. 2 was the most frequent and abundant. Recruitment rates of this Calcarea assemblage varied along the year, with a significant difference between December 2015 – February 2016/ February 2016 – April 2016 (higher number of recruits) and August 2015 – October 2015/ October 2015 – December 2015/ August 2015 – October 2015 (fewer number of recruits on the plates) (F = 5.750; P = 0.0001). In addition, a significant and positive correlation was observed between seawater temperature and larval recruitment rates (r^2= 0.9076; $P<0.05$), although analysis including precipitation data was not significant (r^2= 0.0128; $P> 0.05$). The correlation between temperature and the number of recruits may be possibly due to the reproductive cycle of the species found on the plates, as increasing seawater temperature commonly triggers the beginning of reproduction in several species of calcareous sponges. Patterns observed by the present work corroborate those found by Zea[1]. In that work, demosponges from the Colombian Caribbean was studied and their recruitment rates varied according to seawater temperature fluctuations. It suggests that recruitment of sponges from both Demospongiae and Calcarea classes may follow the same pattern when occurring in tropical areas around the world.

References
1. S. Zea, Mar. Ecol. 14(1) (1993) 1-21.

Financial supports by FAPESB, CNPq, PRODOC-PROPCI/ UFBA are gratefully acknowledged.

Deep-sea sponges under stress: from nutrient sources to nutrient sinks?

Christine Rooks[1], James Fang[2], Pål Tore Mørkved[1], Rui Zhao[1], Friederike Hoffmann[1], Hans Tore Rapp[1] & Raymond Bannister[2]

[1] Centre of Geobiology, Department of Biology, University of Bergen, PO Box 7803, 5020 Bergen, Norway. Christine.Rooks@uib.no

[2] Institute of Marine Research, PO Box 1870, 5817 Bergen, Norway.

Sponges are considered major sources of bio-available nitrogen (ammonium, nitrate and nitrite) in marine ecosystems. Under exposure to high sediment loads, however, we found that boreal sponges from Norwegian Fjord ecosystems, serve as sinks rather than sources of bio-available nitrogen. Sponges cease pumping in response to environmental stressors such as sedimentation. In turn, this reduces oxygen availability within the sponge tissue, enabling microbially mediated denitrification which transfers bio- available nitrogen into di-nitrogen gas.

Our first experiments with sponges from the North Atlantic open ocean deep-sea ecosystems (June 2016), indicate that these sponges also perform denitrification – releasing di-nitrogen gas rather than bio-available nitrogen when no oxygen is available. Our studies show that environmental stressors may dramatically change the quality of goods and services provided by deep-sea sponge communities.

This work was carried out within the EU project SponGES and SedEx Sponge, funded by the Norwegian Research Council.

A trophic niche separation may explain the tight coexistence of high (HMA) and low (LMA) microbial-abundance sponges

Teresa Maria Morganti[1, 2], Rafel Coma[1], Gitai Yahel[3], Marta Ribes[2]

[1] Department of Marine Ecology, Centre d'Estudis Avançats de Blanes (CEAB-CSIC), Blanes, Spain. tmorganti@icm.csic.es

[2] Department of Marine Biology and Oceanography, Institut de Ciències del Mar (ICM-CSIC), Barcelona, Spain

[3] The School of Marine Sciences, Ruppin Academic Center, Michmoret, Israel

Sponges are commonly divided into High (HMA) and Low (LMA) Microbial-Abundance species according to the bacterial biomass in their tissue. These two groups reflect distinct aquiferous structures and feeding strategies. In the NW Mediterranean coralligenous community HMA and LMA sponges are often packed in dense, multispecies assemblages that cover many pinnacles and overhangs. This dense packing together with a developed concentration boundary layer with near-bottom plankton depletion suggests that competition for space and access to unfiltered water should be intense among these closely related suspension feeders. We investigated the metabolism of three HMA (*Chondrosia reniformis*, *Agelas oroides*, *Petrosia ficiformis*) and two LMA (*Dysidea avara* and *Crambe crambe*) species that cohabitate the coralligenous community by using a direct *in situ* technique (VacuSIP). Simultaneous sampling of the water inhaled and exhaled by undisturbed animals sharing the same rocky wall in the NW Mediterranean allowed us to measure plankton uptake and the fluxes of dissolved organic (DON and DOC) and inorganics (NH_4^+, NO_x^-) mediated by the sponges. Sponges consumed plankton, DOC, and ammonium in relation to their abundance in ambient water. The plankton retention efficiency was high for all species. When DOC concentration was high (>80 µmol L^{-1}), it accounted for ~90% of carbon intake from the examined sources for the three HMA sponges and *D. avara*. Nitrogen fluxes markedly differed between the two groups: plankton was the main source of nitrogen for LMAs that excreted DON and ammonium. The nitrogenous waste products of LMAs were found to be the major source of nitrogen (up to 97%) for HMAs that efficiently removed DON and ammonium and excreted nitrate. The estimated areal fluxes indicated that the N excreted by LMAs might potentially account for N needs of coexistence HMAs. This illustrates a phenomenon in which a metabolic end-product of the LMA species become a resource for the HMA species. The different capacity of both sponge strategies to use dissolved resources suggests a partial trophic niche separation related to HMA-LMA dichotomy as a mechanism facilitating their dense coexistence in the community. Our findings suggest that a mixed assemblage of sponges (and their associated microbes) is able to utilize the suspended particulate and dissolved material more efficiently than a single species population and may contribute to the understanding of the phenomena of the stability and diversity of dense sponge assemblages in oligotrophic habitats.

Financial support by Ministerio de Educación, Cultura y Deporte (MECD) of Spain is gratefully acknowledged.

Sponge science culture and demography

Christine H.L. Schönberg

School of Earth and Environment and Oceans Institute, The University of Western Australia, Crawley, WA 6009, Australia. christine.schonberg@uwa.edu.au

The science environment is changing over time, creating different challenges to conduct research that may have effects on the scientists themselves. The sponge science community is comparatively small, has a tradition of being interactive and supportive, and is presently used as a case example to assess developments over time by accessing materials relating to international conferences. An email survey in 2015 also provided demographic data based on 377 replies.

The selection of published topics in proceedings of international sponge conferences changed. Contributions on fossil and freshwater sponges and temperate environments decreased, as well as review papers and data syntheses, frequency of aquarium studies, and number of species investigated per publication. Publications on recent sponges, hexactinellids, calcareans, marine, Indo-Pacific and warm-water sponges increased along with number of authors per publication and the proportion of field studies. Historically strong interests in ultrastructure were gradually replaced by molecular approaches, but studies at the community level remained stable. The five sub-disciplines morphology/taxonomy, phylogeny/evolution, physiology, ecology and faunistics retained about equal proportions over time. Contributions related to taxonomy, phylogeny and biodiversity always represented a large part of sponge science published in proceedings, while those on management and conservation were rare.

The community of sponge scientists has grown and became more diverse over time, now representing over 70 nations. Since the first sponge conference the gender distribution evened out to nearly 50 : 50% and presently favours women early and men at late career stages. While stated research interests are generally dominated by physiology and ecology, taxonomy and evolution prevail after retirement. Sponge science has become more dynamic, but maybe also more competitive and less inclusive. Early career scientists have a high turnover rate, and a proportion of about 50% of once-only attendances at later sponge conferences suggests that people may frequently move into other disciplines or out of science. We now face the dual challenge of safeguarding against the loss of some sub-disciplines and young scientists, and fostering the collaborative, helpful culture characteristic of our community.

Reference

C. H. L. Schönberg. Culture, demography and biogeography of sponge science: from past conferences to strategic research? Mar Ecol DO:10.111/maec.12416 (in press)

Sponge Genomics Forum

Similar to recent sponge conferences, we offer our scientific community an informal forum to discuss the latest genomic initiatives and opportunities as they relate to poriferan biology.

Genomics, transcriptomics and specifically comparative approaches, fueled by technological advances in massive parallel sequencing, continue to attract attention, and provide a platform for stimulating scientific enquiry and continued advances.

As a diverse and early-branching metazoan phylum, Porifera remains central to efforts of the Global Invertebrate Genome Alliance (GIGA; http://GIGA-cos.org), a collaborative network aiming to promote standards that will facilitate comparative approaches to invertebrate genomics and collaborations across the international scientific community. The significance of sponges in this context is exemplified by the recent debate on which taxon is the sister group to all other animals, sponges ("Porifera-sister" hypothesis) or Ctenophora ("Ctenophora-sister" hypothesis). Prioritization and increasing urgency of genome projects may also stem from increasing threats to habitats (e.g., coral reefs) and their resident biological diversity.

The sponge community is welcome to contribute to GIGA by adding data to public databases, supporting and highlighting new efforts to increase data sharing capacities, coordination or avoidance of duplicate projects, assist in the sampling and taxonomic inventories, expanding international outreach to developing countries and investing in extensive computational biology and bioinformatics training of young scientists and their ability to interpret sequence data.

In this framework, the recently funded EU Horizon 2020 Marie Skłodowska-Curie Innovative Training Network (ITN) "Comparative Genomics of Non-Model Invertebrates" (IGNITE; www.itn-ignite.eu), in which several projects will work on sponge-related topics, will provide a new platform to advance comparative genome analyses and develop new approaches.

Hexactinellida Identification Workshop

Henry M. Reiswig

We are privileged to have Dr. Henry Reiswig of the University of Victoria and Royal British Columbia Museum give a workshop on the identification of hexactinellid sponges. Henry Reiswig is a world expert on the taxonomy and systematics of Hexactinellida.

The workshop will focus first on discussion of methods used to identify hexactinellids with a demonstration of examination on unknown specimens. Realization that there is a major likelihood that any specimen is an undescribed species should be appreciated and temper reliance on identification keys. The second focus will be on what to do with the new information and how to carry out a description. The final component will be on the secrets of making beautiful SEM images of hexactinellid microscleres.

This workshop is supported by the SponGES project which has received funding from the European Union's Horizon 2020 research and innovation programme (grant agreement No 679849).

Posters Evolution & Systematics

Two new species of Hemimycale (Hymedesmiidae: Poecilosclerida: Demospongiae) from Southeastern Brazil

Larissa Huguenin[1], Sula Salani Mota[2], Eduardo Hajdu[2], Eduardo Leal Esteves[1]

[1] *Departamento de Zoologia, Instituto de Biologia Roberto Alcantara Gomes, Universidade do Estado do Rio de Janeiro, Rua São Francisco Xavier, 524, PHLC, Sala 520, Rio de Janeiro, RJ, Brazil, 20550-013.*
edleaalesteves@yahoo.com.br
[2] *Departamento de Invertebrados, Museu Nacional, Universidade Federal do Rio*

Hemimycale Burton, 1934 is a genus of shallow water marine sponges composed by four species distributed worldwide, of which, one is known from Brazil, i.e. H. insularis Moraes, 2011 (van Soest et al., 2017). The genus is characterized by the presence of strongyles and styles as megascleres and by the lack of acanthostyles and microscleres. In addition, it has characteristic areolated pore sieves (van Soest, 2002). In the present study we describe two new species of Hemimycale from the Southeastern Brazil Ecoregion, in the Warm Temperate Southwestern Atlantic Province. Specimens were collected by SCUBA diving in June and September 2013, at Guriri and Jorge Grego islands (Ilha Grande Bay, southern Rio de Janeiro state). Specimens were deposited in the Porifera collection of Rio de Janeiro state University (UERJPOR). Additional material of Hemimycale sp. nov. 1 from Cabo Frio (northern Rio de Janeiro state), and Arvoredo island (Santa Catarina, Southern Brazil), deposited in the Porifera collection of Museu Nacional, Universidade Federal do Rio de Janeiro (MNRJ), were also examined. Hemimycale sp. nov. 1 is thinly encrusting, salmon pink colored and have rounded to irregular pore sieves (2 – 12 mm wide) and circular oscula (1.2 – 3.7 mm wide). Ectosomal skeleton absent. Choanosomal skeleton formed by strongyles and oxeote tornotes vaguely strewn towards the ectosome, and arranged in subectosomal tufts next to surface. Megascleres: (sub)(tylo)strongyles, straight or slightly curved and smooth (171 – 335/ 2.5 – 5.0 µm); oxeas straight and smooth, with points mucronate or telescopic (236 – 344/ 3.9 – 6.5 µm). Hemimycale sp. nov. 2 is thinly encrusting, reddish orange, with circular to oval pore sieves, slightly raised and enlarged at the apex (0.3 – 4.5 mm wide), and vulcaniform oscula (0.8 – 2.3 mm wide). Ectosomal skeleton absent. Choanosomal skeleton plumose, formed by multispicular ascending tracts of (aniso-)strongyles diverging in tufts next to surface. Megascleres: (Aniso)strongyles, straight and smooth, occasionally with swollen points (138 – 289/ 2.0 – 4.2 µm). Hemimycale sp. nov. 1 is the only species in the genus with oxeote tornotes in addition to strongyles. Hemimycale sp. nov. 2 differs from all other species in the genus by the size and shape of their pore sieves and anisostrongyles. Hemimycale sp. sensu Muricy et al. (1991), from Arraial do Cabo,

References

1. G. Muricy, et al., VII Symposium on Coastal and Ocean Management (1991) 1183–1196.
2. R.W.M. van Soest, Systema Porifera (2002) pp 575–601.
3. R.W.M. van Soest et al., World Porifera Database (2017)Financial support by CAPES and CNPq is gratefully acknowledged.

Financial support by CAPES, CNPq, FAPERJ and FAPESP is gratefully acknowledged.

A new species of Hymeniacidon from Brazil and redescription of Halichondria (Halich.) melanadocia de Laubenfels, 1936

Humberto Fortunato[1], Fabiana Fernandes[2], Maira Lopes[3], Rodolpho M. Albano[3], Thiago de Paula[1], Gisele Lôbo-Hajdu[1] and Eduardo L. Esteves[2]

[1]*Departamento de Genética, Universidade do Estado do Rio de Janeiro, Rio de Janeiro, RJ, Brazil.*
[2]*Departamento de Zoologia, Universidade do Estado do Rio de Janeiro, Rio de Janeiro, RJ, Brazil edlealesteves@yahoo.com.br*
[3]*Departamento de Bioquímica, Universidade do Estado do Rio de Janeiro, Rio de Janeiro, RJ, Brazil.*

Halichondriidae is a family of Suberitida composed by 15 genera distributed worldwide. This is a challenging group for sponge taxonomists, with many species and lack of reliable characters (Diaz et al., 1993; Erpenbeck & van Soest, 2002). In the present study, we describe a new species tentatively assigned to the genus Hymeniacidon and provide a redescription and first record of Halichondria (Halich.) melanadocia de Laubenfels, 1936 from Southeast Brazil, using morphological and molecular data in an integrative approach. Specimens of cf. Hymeniacidon sp. nov. were collected by SCUBA diving at Salvador, Bahia, Northeast Brazil, and Ilha Grande Bay, Southern Rio de Janeiro state, Southeast Brazil, from 2013 to 2015. Specimens of Halich. melanadocia were collected by free diving in 2010, at Itaipú Beach, Niterói, Rio de Janeiro state, Southeast Brazil. Specimens were deposited in the Porifera collections of Rio de Janeiro state University (UERJPOR) and Museu Nacional, Universidade Federal do Rio de Janeiro (MNRJ). Molecular analyses of 18S rRNA sequences 1800 bp long of selected species of Suberitida were performed for the genetic identification of the new species as well as specimens of Hym. heliophila (Wilson, 1911) and Halich. melanadocia collected at Rio de Janeiro. Hymeniacidon sp. nov. is thickly encrusting to massive, with conspicuously bifurcated blinded fistula, a pale beige color in life, and a disorganized skeleton composed by styles and oxeas. Oxeas are relatively thick, short (85 – 262/ 3.2 – 12.0 µm) and rather rare compared to styles (110 – 284/ 2.3 – 9.1 µm), but can be found in all specimens examined. Halich. melanadocia is massive, moss green in life externally and greenish yellow internally shifting to dark brown to black externally and pale beige internally, after fixation in ethanol. Ectosomal skeleton anisotropic, with rounded meshes, and disorganized in the inner parts of the choanosome. Spicules, oxeas of varying sizes (87 – 436/ 2.4 – 12.0 µm). ML analysis of 18S rRNA of Suberitida recovered the same clades found by Redmond et al. (2013, fig. 14). Specimens of cf. Hymeniacidon sp. nov. clustered with Hym. kitchingii Burton, 1935 with 100% bootstrap support in a clade composed by some Halichondria spp., and was distantly related from the clade composed by the type species of the genus, i.e. Hym. perlevis, as well as Amorphinopsis, and other species of Hymeniacidon (Hym. heliophila included) and Halichondria (Halich. melanadocia included). It is suggested here that the clade formed by Hym. kitchingii and the new species may represent a distinct genus of Halichondriidae, which for priory reasons should be named as Rhaphidostyla Burton, 1935 (type: Hym. kitchingii; currently a junior synonym of Hymeniacidon), or a new genus might be created for the inclusion of the new species.

References

[1] M.C. Diaz, S.A. Pomponi, R.W.M. van Soest, Sci. Mar. (1993) 57: 283-306.

[2] D. Erpenbeck, R.W.M. van Soest, Systema Porifera (2002) p. 787-815.

[3] N.E. Redmond et al., Integ. Comp. Biol. (2013) 53: 388-415.

Financial support by CNPq, FAPERJ and CAPES is gratefully acknowledged.

A Messinian paleo-sponge community from northwestern Italy.

Marco Bertolino[1], Gabriele Costa[1], Carlo Avignolo[1], Maurizio Pansini[1], Giorgio Bavestrello[1], Francesco Dela Pierre[3], Francesca Lozar[3], Marcello Natalicchio[4], Donata Violanti[3]

[1] DiSTAV, Università degli Studi di Genova, Corso Europa 26, 16132 Genova, Italy marco.bertolino75@gmail.com

[3] Dipartimento di Scienze della Terra, via Valperga Caluso 35, 10135 Torino, Italy

[4]Institute of Geology, Hamburg University, Bundesstrasse 55, 20146 Hamburg, Germany

In the Messinian (Late Miocene) the Mediterranean basin was affected by a salinity crisis (Messinian Salinity Crisis, MSC, 5.96 – 5.33 Ma) with a devastating impact on marine organisms. Siliceous sponges were very seldom reported from Miocene sediments of Italy (Matteucci & Russo, 2012) and Messinian spicules were known only in Tertiary Piedmont Basin (TPB) (Bonci et al, 1997). Recent findings in the Monferrato region (TPB) found very diversified assemblages, rich in siliceous paleospicules. The study of these fossil remains is a powerful tool to reconstruct the sponge communities of the past, as well as the paleoenvironmental evolution of the Mediterranean area.

This research is based on the Banengo and Moncalvo sections, cropping out on the northern margin of the Piedmont Basin, that preserve the boundary between the Sant'Agata Fossil Marls and primary evaporites of the Primary Lower Gypsum unit, deposited immediately before and during the MSC, respectively.

Five samples, which contained siliceous spicules, were collected in total: 3 from Banengo and 2 from Moncalvo sections. The analysis of peculiar, diagnostic spicules contained in the sediment allowed to identify at least at genus level the sponge taxa living during the Messinian. The samples yielded calcareous nannofossils, foraminifers, diatoms, radiolarians, abundant spicules of siliceous sponges and briozoan fragments. Spicules are strongly fragmented, partly due to sediment compaction, and show signs of chemical corrosion. Most of them are broken and with the surface deeply etched by deep circular marks sometimes developing into tunnels that may reach the often-enlarged axial canal. According to the spicule assemblages the presence of the genera *Geodia, Erylus, Stelletta, Dercitus* and *Alectona* was assessed.

Fossil sterrasters have been measured and compared with those of recent *Geodia* spp. The largest Messinian sterrasters measure 170 µm in diameter. Even larger sterrasters, from earlier epochs, were recorded from sediments dated to the Early Miocene (Aquitanian- Burdigalian) of the Piedmont basin (207 µm) and from the Middle Eocene of the Lessini Hills (257 µm). *Geodia avicula* Brimaud & Vachard, 1986, from the Spanish Miocene has sterrasters up to 250 µm across. All these sterrasters are larger than those occurring in the recent *Geodia* species living in the Mediterranean Sea, apart from *G. pachydermata* (Sollas, 1886), recorded off Marseille, where sterrasters are up to 230 µm across but are oval in shape. In the southwestern Atlantic, *G. australis* Silva and Mothes, 2000 possesses sterrasters up to 350 µm in diameter. A very peculiar orthotriaene with an unusual swelling of the rhabdome that ends with a round extremity was ascribed to *Stelletta*. We were unable to find this type of spicule in the recent and fossil sponge literature.

A new species of *Haliclona* (Haplosclerida: Chalinidae) from sandstone reefs in Ceará (NE Brazil)

André Bispo[1] and Eduardo Hajdu[1]

[1] Laboratório de Taxonomia de Poríferos (TAXPO), Museu Nacional, Universidade Federal do Rio deJaneiro, Quinta da Boa Vista, Rio de Janeiro, Brazil

Haliclona Grant, 1841 is the richest genus of Porifera, comprising more than 400 valid species[1]. This genus is distributed worldwide and especially abundant in shallow waters (intertidal and shallow subtidal), which is also the case along the Brazilian coast. This high diversity is also accompanied by the paucity of skeletal features, leading to a difficult taxonomy. Recent efforts were carried by our team to reach a better assessment of the diversity of poriferans along the Brazilian coast. Therefore, recent expeditions to Northeastern Brazil and its oceanic islands were conducted in 2014 (EXPO-CERN) and 2016 (TAXPO Biodiscovery). This work aims to describe a new species of *Haliclona* (*Reniera*) found in a sandstone reef of Ceará State. Eight specimens were collected through snorkelling in tide pools of a sandstone reef (0.2–1 m depth) at Praia do Boi Choco. They are encrusting, bear a punctate surface with threads running through (Fig 1A–C), soft and fragile consistency, oscula circular and flush with the surface, or slightly elevated (diameter 1.1–1.8 mm). When handled, specimens release mucus. Colour varies from beige (Fig 1A) to lilac (Fig 1B) (even in the same individual, Fig 1C). Skeleton composed of an isodictyal reticulation with nodal spongin, mostly of very regular unispicular triangular meshes. Spicules: oxeas, 110–159 x 2–9 µm, toxas, 7–101 x 0.5–2.5 µm. Other Tropical Western Atlantic *Haliclona* spp approaching the new species in colour alive are *H. implexiformis*, *H. lilacea*, *H. mucifibrosa*, *H. portroyalensis,* and *H. tubifera*. All of them, except for *H. portoyalensis*, lack toxas. On the other hand, *H. portroyalensis* has a very distinct digitate shape, larger oscula (2–3 mm) and longer oxeas (153–210 x 6–9 µm). Other species with toxas in the TWA are *H. melana* and *H. ruetzleri*. The lobate base with oscular chimneys and black colour alive sets *H. melana* apart from the new species. Habit (slender, anastomosing branches), brown colour alive, and sigma microscleres distinguish *H.* ruetzleri. Figure 1. Variability of colour in *Haliclona* (*Reniera*) sp. nov. Scale bars = 1 cm.

References

[1]. R.W.M. Van Soest et al. World Porifera Database (2017) Available from:http://www.marinespecies.org/porifera

Financial support by CAPES and CNPq is gratefully acknowledged.

What about PCP pathway in sponges?

Amélie Vernale [1, 2], Quentin Schenkelaars [2], Emmanuelle Renard[2], André Le Bivic[1] & Carole Borchiellini[2]

[1]Institut de Biologie du Développement de Marseille, Aix-Marseille University, France

[2] Institut Méditerranéen de Biodiversité et d'Ecologie, Aix-Marseille University, France
Carole.borchiellini@imbe.fr

Among pathways needed for epithelium patterning, the Planar Cell Polarity (PCP) signalling components have been identified, in eumetazoans, to play a key role in controlling orientation of epithelial cells within the plane of their sheet. A molecular core has been identified to be involved in patterning such typical organization in bilaterians and cnidarians. Among them, Flamingo (Fmi), Frizzled (Fzd), Dishevelled (Dvl), Van Gogh (Vang), Prickle (Pk) and Diego (Dgo) / Inversin (Invs) are key components of the core PCP pathway whereas others such as Fuzzy (Fuz) and Inturned (Intu) have been described as potential effectors for flagellum orientation. Briefly, the PCP pathway is involved in patterning two different clusters of proteins within bilaterian cells : antagonist interaction between the Fzd-Dvl-Invs complex localized at the distal pole of the cell and the Vang-Pk complex localized proximally in the neighboring cells is required to coordinate cell orientation within the plane. Our transcriptomic and genomic analyses have revealed that, among the 4 sponge classes, only homoscleromorph sponges possess all genes needed for a functional PCP pathway[1]. This astonishing and challenging result now calls for functional studies in the homoscleromorph sponge *Oscarella lobularis* in order to establish the role of these genes in this sponge lineage. By a combination of imaging and immunolocalization techniques using specific antibody against PCP proteins, we explored the reliability of a *bona fide* PCP pathway in this sponge lineage.

References

1. Q. Schenkelaars, L. Fierro-Constain, E. Renard, C. Borchiellini, BMC Evol.Biol. (2016) 16:69.

Financial support by "investissement d'avenir" French Government program, A*MIDEX project (n° ANR-11-IDEX-0001-02) is gratefully acknowledged.

Diversity, distribution and phylogenetic relationships of the North Atlantic lithistid sponges

Francisca C. Carvalho [1], **David Rees** [1], **Shirley A. Pomponi** [2], **Hans Tore Rapp**[1] **& Joana R. Xavier**[1]

[1] Department of Biology and K.G. Jebsen Centre for Deep-Sea Research, University of Bergen, PO Box 7803, N-5020 Bergen, Norway. Francisca.Carvalho@uib.no

[2] Harbor Branch Oceanographic Institute, Florida Atlantic University, Fort Pierce, Florida, USA.

Lithistid sponges, also known as rock sponges, are an artificial group of species characterized by the shared possession of a hypersilicified skeleton composed of articulated spicules (desmas). Initially placed in the order Lithistida, accumulating morphological and molecular evidence has revealed the polyphyletic nature of this group and the different families were allocated to the orders Tetractinellida, Bubarida and Sphaerocladina. At present over 200 species, representing 42 genera and 13 families, are recognized. These are found in tropical or warm temperate regions, at bathyal depths, with some species occurring in shallower water in cave systems. Lithistid sponges of the North Atlantic have received considerable attention, and over 40 species were described to date for this region. However, much information remains scattered in the literature hindering our understanding of biogeographic and evolutionary patterns.

Here we provide a review of the diversity and both geographic and bathymetric distribution of desma-bearing sponges of the North Atlantic, based on a comprehensive literature survey and examination of specimens held in several collections. Using two independent markers (mtDNA CO1 and rDNA 28S gene fragments) we also investigate the phylogenetic relationships between taxa co-distributed on both sides of the Atlantic (e.g. within the genera *Corallistes*, *Neophrissospongia*, *Discodermia*). We further place this new data into a wider phylogenetic context in view of the most recent classification system proposed for the Class Demospongiae.

Financial support by the European Union's Horizon 2020 research and innovation programme to the SponGESproject (grant agreement 679849) and by the US National Oceanic and Atmospheric Administration to the Cooperative Institute for Ocean Exploration, Research, and Technology (grant number NA14OAR4320260) are gratefully acknowledged.

Integrative Taxonomy for the Genus *Ernstia* (Porifera, Calcarea, Calcinea) in the Lesser Antilles, Caribbean Sea

Raisa Rizzieri[1], FernandaAzevedo[1], Báslavi Cóndor-Luján[1], Thierry Perez[2], Michelle Klautau[1]

[1]Universidade Federal do Rio de Janeiro, IB, Av. Carlos Chagas Filho,373, CCS, sala A0-100, Rio de Janeiro, RJ, Brazil, 21941-902. nandaporifera@gmail.com, mklautau@gmail.com.

[2]Institut Méditerranéen de Biodiversité et d'Ecologie marine et continentale, CNRS, Aix Marseille Univ, RD, Avignon Univ. Station Marine d'Endoume, rue de la Batterie des Lions, 13007 Marseille.

The Lesser Antilles are a group of volcanic islands located in the Caribbean Sea and are surrounded by oligotrophic waters, which harbour a great variety of organisms including sponges of the class Calcarea. *Ernstia* is a Calcinean genus diagnosed by the presence of a typical clathroid body and skeleton composed of triactines and tetractines. Tetractines are the most abundant spicules or happen at least in the same proportion as triactines (Klautau *et al*., 2013). This genus has 15 known species originally described from Australia, Brazil, Indonesia, Papua New Guinea and Norway (Van Soest *et al*., 2017). Only one species of *Ernstia* from the Lesser Antilles has been reported but not formally described (Pérez *et al*., submitted). The aim of this study was to assess the diversity of the genus *Ernstia* in the Lesser Antilles using an integrative taxonomic approach (morphology, molecular and ecology). Photos *in situ*, *in toto* slides, spicules micrometry, morphological remarks, scanning electron microscopy and molecular (ITS) data analyses were used to recognize species. Individuals were collected in the PACOTILLES (LIA-MARRIO) campaigns. *Ernstia* species were found in Antigua & Barbuda, Anguilla, Guadeloupe, Saint Vincent, Saint Martin, Martinique and Bequia. Species were mainly collected inside caves in shallow waters (1 to 23.5 meters of depth) with temperatures between 27 and 28 ºC. Some species were found associated with cnidarians and polychaetes. From a total of 24 individuals, 11 species were identified. *Ernstia citrea* (n=3) and *Ernstia rocasensis* (n=1) were originally reported for the Brazilian Oceanic Islands (Azevedo *et al*., submitted). The other nine species are new to science and provisionally endemic to the Lesser Antilles: *Ernstia* sp. nov. 1 (n=7), *Ernstia* sp. nov. 2 (n=4) *Ernstia* sp. nov. 3 (n=2), *Ernstia* sp. nov. 4 (n=3), *Ernstia* sp. nov. 5 (n=1), *Ernstia* sp. nov. 6 (n=1), *Ernstia* sp. nov. 7 (n=1), *Ernstia* sp. nov. 8 (n=1), *Ernstia* sp. nov. 9 (n=1). *Ernstia* sp. nov. 1 was the most abundant species and was also the most widely distributed, being found in three islands, while *E.* sp. nov. 4 and *E. citrea* were found in two islands. The other species were found only in one island each. With the nine new species found in this study, the number of *Ernstia* species rises from 15 to 24 and the Caribbean represents 46% of the total diversity of the genus.

References

1. M. Klautau, F. Azevedo, B. Cóndor-Luján, H. Tore Rapp, A. Collins, C.A. de Moraes Russo. 2013. Integ. and Comp. Biol. 53 (2013) 447-461.
2. Van Soest, R.W.M.; Boury-Esnault, N.; Hooper, J.N.A.; Rützler, K.; de Voogd, N.J.; Alvarez de Glasby, B.; Hajdu, E.; Pisera, A.B.; Manconi, R.; Schoenberg, C.; Klautau, M.; Picton, B.; Kelly, M.; Vacelet, J.; Dohrmann, M.; Díaz , M.-C.; Cárdenas, P.; Carballo, J.L. Accessed at http://www.marinespecies.org/porifera on (2017).
3. T. Pérez, M. C. Diaz, C. Ruiz, B. Cóndor-Luján, M.Klautau, E. Hajdu, G. Lobo-Hajdu, S. Zea, S. A. Pomponi; R. W Thacker; S. Carteron; G. Tollu; A. Pouget-Cuvelier; P. Thélamon; J. Maréchal; O. P. Thomas; A. V. Ereskovsky; J. Vacelet & N. Boury-Esnault. Plos One, *in press*.
4. F. Azevedo, A. Padua, F. Moraes, A. Rossi, G. Muricy, M. Klautau, *in press*.

Financial support by CAPES, CNPq, CNRS and LIA MARRIO.

Revising the taxonomy of a two-sponge associations from Korean waters

Paco Cárdenas[1], Jae-Sang Hong[2], Jean Vacelet[3]

[1] Department of Medicinal Chemistry, Division of Pharmacognosy, BioMedical Center, Husargatan 3, Uppsala University, 751 23 Uppsala, Sweden. paco.cardenas@fkog.uu.se

[2] Department of Ocean Science, College of Natural Sciences, Inha University, Incheon 402-751, Republic of Korea

[3] IMBE UMR 7263, Aix Marseille Université, CNRS, IRD, Avignon Université, 13397 Marseille, France

Two-sponge associations are fairly common but more often involve species from different orders. One exception, and one of the most studied two-sponge association in the field of sponge natural products involves two species belonging to the Tetractinellida order, suborder Astrophorina, but to two different families: *Jaspis* *wondoensis* Sim & Kim, 1995[1] (Ancorinidae family) and the encrusting *Poecillastra wondoensis* Sim & Kim, 1995[1] (Vulcanellidae family). This association was described from the shallow waters of Geomun islands (locality of Wondo), Jeju Strait, South Korea. In this study we examined new material from the Jeju Strait, this time from Yeoseo Island. Spicule morphology and spicule arrangement, as well as the molecular barcode COI, suggest that these species have been placed in the wrong genus and should be reallocated as *Rhabdastrella wondoensis* comb. nov. (Geodiidae) and *Vulcanella wondoensis* comb. nov. (Vulcanellidae). Phylogenetic relationships of these two species are presented.

References

1. Sim CJ, Kim Y-A (1995) A systematic study on the marine sponges in Korea: 12. Tetractinomorpha (Porifera: Demospongiae). The Korean Journal of Systematic Zoology 11 (2):147-158

Financial support from an Inez Johanssons scholarship (Uppsala University) and EU Horizon 2020 programme SponGES under grant agreement No. 679849.

Phylogenetic relationships of the Thrombidae and suggestion of a new Tetractinellida sub-order

Paco Cárdenas[1, 2], Michelle Kelly[3]

[1]Department of Medicinal Chemistry, Division of Pharmacognosy, BioMedical Center, Husargatan 3, Uppsala University, 751 23 Uppsala, Sweden
paco.cardenas@fkog.uu.se

[2]Program in Systematic Biology, Department of Organismal Biology, Evolutionary Biology Centre, Uppsala University, Norbyvägen 18D, 752 36 Uppsala, Sweden

[3]Coasts and Oceans National Centre, National Institute of Water & Atmospheric Research Ltd, Private
Bag 99940, Newmarket, Auckland, New Zealand

The Thrombidae Sollas, 1888 is an enigmatic demosponge family with two unique microscleres forms: a tiny acanthose triaene-like 'trichotriaene', and a minute birotulate 'amphiaster' absent in some species. Prior to Lévi's (1973)[1] placement of Thrombidae in the order Astrophorida Sollas, 1887 (= suborder Astrophorina), the family was thought to be most closely associated with class Homoscleromorpha Dendy, 1905. Although its phylogenetic relationships remained obscure, even in the Astrophorina, this position was followed in the *Systema Porifera*[2]. Today the family contains only six species distributed in two genera: *Thrombus* Sollas, 1886 and *Yucatania* Gómez, 2006. The discovery and sequencing of several new Thrombidae genera and species has provided us with the opportunity to conduct a molecular phylogenetic study, using three molecular markers (COI, 28S and 18S). Our analyses clearly indicate that: (1) the Thrombidae are the sister-group to the recently described family Stupendidae Kelly & Cárdenas, 2016[3] and most surprisingly (2) that the Thrombidae/Stupendidae clade is sister to the lithistid families Scleritodermidae Sollas, 1888, /Siphonidiidae Lendenfeld, 1903 /Azoricidae Sollas, 1888. We propose that this large new clade represents a new Tetractinellida suborder and we discuss which synapomorphies might support this clade.

References

1. Lévi C (1973) Systématique de la classe des Demospongiaria (Démosponges). In: Grassé PP (ed) Traité de Zoologie. Spongiaires, vol 3. Masson & Co., Paris, pp 577-632
2. Uriz MJ (2002) Family Thrombidae Sollas, 1888. In: Hooper JNA, van Soest RWM (eds) Systema Porifera. A Guide to the classification of Sponges, vol 1. Kluwer Academic / Plenum Publishers, New York, pp 163-164
3. Kelly M, Cárdenas P (2016) An unprecedented new genus and family of Tetractinellida (Porifera, Demospongiae) from New Zealand's Colville Ridge, with a new type of mitochondrial group I intron. Zool J Linn Soc 177 (2):335-352

Financial support by NIWA under 'Coasts and Oceans Research Programme 2 Marine Biological Resources: Discovery and definition of the marine biota of New Zealand' (2014/2015 SCI), an Inez Johanssons scholarship (Uppsala University) and the EU Horizon 2020 programme SponGES under grant agreement No. 679849.

First record of *Bolosoma* (Hexactinellida, Euplectellidae) for the Atlantic Ocean and new species

Cristiana Castello-Branco[1], Allen Collins[2,3] and Eduardo Hajdu[1]

[1] Laboratorio de Taxonomia de Poriferos - TAXPO, Departamento de Invertebrados, Museu Nacional / UFRJ, Quinta da Boa Vista, s/n, 20940-040, Rio de Janeiro, RJ, Brasil.
cristianacbranco@gmail.com

[2] Zoologist & Director, NOAA's National Systematics Lab

[3] Smithsonian Institute, National Museum of Natural History, Dept of Invertebrate Zoology, MRC-163, 10th & Constitution Aves. NW, Washington DC 20560, U.S.A.

Bolosoma is a basiphytose euplectellid glass sponge (Hexactinellida) with peduncle, microscleres bearing only discoidal outer ends, and megascleres mainly diactines, hexactines, and rarely pentactines. Eight species of *Bolosoma*, all from the Pacific Ocean, have been described. We report a new species from the Atlantic Ocean, the first such record, specifically the South Atlantic, Rio Grande Rise (RGR). Further, a comparative study of samples from the Smithsonian National Museum of Natural History (NMNH) collection yielded two possibly new species from the Pacific. *Bolosoma* sp. nov. 1 (RGR, 936 m depth) is characterized by a peduncle with cemented diactines (40–80 µm diam.), occasional free diactines with rough extremities (15–20 µm diam.). Choanosomal diactines with rough extremities and rudiments of middle actines (1710–2370 x 5–8 µm), dermal and atrial hexactines (and rare pentactines) smooth with rough extremities, sometimes with short spines along the actine (most frequently in atrial hexactines, 270–830 x 5–8 µm); microscleres discohexasters (70–80 µm diam.), derivates (stauractines, 42–50 µm diam.), and hemidiscohexasters (155–175 µm, primary rosette with 27–43 µm diam.). *Bolosoma* sp. nov. 1 posseses an exclusive microsclere set that differentiates it from all its congeners. The other two putative species are from the North Pacific: *Bolosoma* sp. nov. 2 (Necker Seamount, Hawaii, 1477 m), fragmented (without signs of peduncle) is characterized by choanosomal diactines with rough and lanceolate extremities, sometimes with one of the ends claviform (3650–5000 x 10–22 µm), dermal and atrial hexactines smooth or with a few short spines and rough extremities (300–810 x 25–56 µm, distal actine 100–140 x 30–63 µm); rare pentactines with same shape as hexactines (300–950 x 25–35 µm, distal actine 140–270 x 25–35 µm). Microscleres discohexasters (210–240 µm diam.). These characteristics indicate that it is similar to *B. biocalum*, but differing by having bigger discohexasters (cf. 61–108 µm diam.). Finally, *Bolosoma* sp. nov. 3 (Pigafetta Guyot, to the E of the Marianas Trench, 2028 m) is characterized by champignon-like shape with lateral openings and a peduncle with cemented diactines (1310–2825 x 20–60 µm), few short hexactines and pentactines (195–250 x 2–5 µm) with distal actine shorter and acanthose. Choanosomal diactines with rough extremities sometimes with rudiments of middle actines (1075–2575 x 15–18 µm), dermal and atrial hexactines smooth with rough extremities and distal actine shorter (300–789 x 10–18 µm, distal actine 80–110 x 12–25 µm), atrial hexactines with a few short spines along the actines; rare pentactines (450–680 x 15–18 µm). Microscleres macrodiscohexasters (480–570 µm diam.) and microdiscohexasters (55–60 µm diam.), which is unique among all its known congeners. In addition to the wide geographic distance (at least for *Bolosoma* sp. nov.1), each species presents a unique set of spicules, indicating their distinctiveness from the remaining *Bolosoma* species.

Financial support by CAPES and CNPq is gratefully acknowledged.

On-going speciation of the amphiamerican calcareous sponge *Clathrina aurea*

Báslavi Cóndor Lujá [1], Pedro Leocorny [1], Fernanda Azevedo [1], André Padua [1], Eduardo Hajdu [2], Philippe Willenz [3, 4], Yuri Hooker [5] & Michelle Klautau [1]

[1]Universidade Federal do Rio de Janeiro, Instituto de Biologia, Departamento de Zoologia. Avenida Carlos Chagas Filho, 373. CEP 21941-902. Rio de Janeiro, Brazil. baslavic@gmail.com

[2]Universidade Federal do Rio de Janeiro, Museu Nacional, Departamento de Invertebrados, Quinta da Boa Vista, S/N, CEP 20940-040, Rio de Janeiro, RJ, Brazil.

[3]Taxonomy & Phylogeny, Royal Belgian Institute of Natural Sciences, Rue Vautier, 29, B-1000 Bruxelles, Belgium

[4]Laboratoire de Biologie marine, Université Libre de Bruxelles, Avenue F.D. Roosevelt, 50, B-1050, Bruxelles, Belgium

[5]Universidad Peruana Cayetano Heredia, Laboratorio de Biología Marina, Lima, Avenida Honorio Delgado, 430, Urbanización Ingeniería, San Martín de Porres, Lima, Peru.

Clathrina aurea was considered a Brazilian endemic sponge (1). However, recent studies revealed its presence in the SE Pacific (Peru, 2) and in the Caribbean Sea. In the present work, we assessed the genetic variability and population structure of *C. aurea* along its wide distribution range using rDNA sequences (partial 18S-ITS-partial 28S) and microsatellite *loci*. Fifteen localities were sampled, eight in the Caribbean Sea (n=77), five in the Brazilian coast (NE, SE and S regions; n=68) and two in the southern coast of Peru (n=45). The genetic divergence (p distance) varied from 0 to 1.2%. The variation among Atlantic individuals (Caribbean and Brazil) was 0–0.7%, in Peru 0%, and between Atlantic and Peruvian individuals, 0.7–1.2%. Phylogenetic analyses (ML BI) separated Atlantic and Peruvian individuals in two different clusters with high support values (bootstrap >98% and posterior probabilities >0.9). The phylogeographic network retrieved Atlantic individuals in a cohesive haplogroup 28 mutational-steps distant from the Peruvian haplogroup (Figure 1). STRUCTURE analysis suggested the presence of six structured populations of *C. aurea*: two Caribbean, one Caribbean + NE Brazil, two Brazilian (SE and S), and one Peruvian (Figure 2). The highest allelic contribution to Peru corresponded to the Caribbean + NE Brazil population, which may reflect past gene flow between Atlantic and Pacific populations. Our results suggest an ongoing speciation process in the Peruvian individuals of *C. aurea,* probably as a result of the closure of the Isthmus of Panama (2.8 MY BP, 3).

References

1. G. Muricy, D.A. Lopes, E. Hajdu, M.S. Carvalho, F.C. Moraes, M. Klautau, C. Menegola, U. Pinheiro. Museu Nacional, Rio de Janeiro. (2011) 300.
2. F. Azevedo, B. Cóndor-Luján, P. Willenz, E. Hajdu, Y. Hooker, M. Klautau. Zool. J. Linn. Soc 173 (2015) 787-817.
3. A. O'Dea, HA. Lessios, AG. Coates, RI Eytan, SA. Restrepo-Moreno, AL. Cione, LS. Collins, A. De Queiroz, DW. Farris, RD Norris, RF Stallard, M.O. Woodburne, O. Aguilera, M-P Aubry, W.A., Berggren, A.F. Budd, M.A. Cozzuol, S.E. Coppard, H. Duque-Caro, S. Finnegan, G.M. Gasparini, E.L. Grossman, K.G. Johnson, L.DL. Keigwin, N. Knowlton, E.G. Leigh, J.S. Leonard-Pingel, P.B. Marko, N.D. Pyen- son, P.G. Rachellodolmen, E.L. Soibelzon, J.A. Soibelzon, G.J. Todd, G.J. Vermeij, J.B.C. Jackson. *Sci. Adv.* 2 (2016) e1600883.

Financial support by CAPES, CNPq, CONCYTEC, FAPERJ, GTI to RBINS.

Sponge bottoms off the Amazon River mouth revisited

Fernando Moraes[1], Camille Leal[2, 3], Sula Salani[2], Maíra Ventura[1] & Eduardo Hajdu[2]

[1]Instituto de Pesquisas Jardim Botânico do Rio de Janeiro, Rio de Janeiro, Pacheco Leão, 915/123.22460-030, Rio de Janeiro, RJ, Brazil. fmoraes@mn.ufrj.br

[2]Universidade Federal do Rio de Janeiro, Museu Nacional, Quinta da Boa Vista, s/n, 20940-040, Rio deJaneiro, RJ, Brazil.

[3] Graduate Program in Genetics, Universidade Federal do Rio de Janeiro

The Amazon River strongly influences oceanographic processes at the Atlantic Ocean, changing the environmental conditions along the year and geological periods to build up a powerful biogeographical filter to reef organisms. This outstanding river-ocean interface creates a complex scenario for benthos. The discovery of the emblematic "sponge bottoms" off the mouth of the Amazon River (Collette & Rützler, 1977) revealed that the postulated biogeographical "Amazon Barrier" could support an unexpected reef sponge community as a "sponge corridor" between the Caribbean and Brazil. Dredges and bottom trawls were used to sample the area (23–120 m deep), onboard R/V Atlantis (July 2012) and NHo Cruzeiro do Sul (September 2014), between the French Guiana border to the State of Maranhão in Brazil. A total of 267 sponge samples were deposited at the Museu Nacional/UFRJ, representing 61 taxa in 30 families (Demospongiae - 29 + Calcarea - 01). *Theonella atlantica* and *Didiscus verdensis* were two new records for Brazil, previously known from the Caribbean and the Guiana Shelf or the East Atlantic, respectively. At least five species are new to science (*Arenosclera* spp. 1–2, *Coelocarteria* sp., *Dictyonella* sp., *Geodia* sp.). The central sector of the continental margin harbored a species–rich sponge community comprised by massive/erect specimens associated to rhodolith beds around 55 m depth. The sampling design and the biological material collected have contributed to a better knowledge of the benthic biodiversity patterns along the Brazilian equatorial margin. These specimens are also potential sources of new bioactive compounds, due to the unique environmental conditions imposed by the Amazon plume regime. More than 1.000 images of field procedures and fresh material have been useful to taxonomy and to public outreach, creating international conservation awareness on the extensive Amazon reef system.

Financial support by ANP/Brasoil, CAPES, CNPq, FAPERJ.

Diversity of Porifera in the Aviles Canyons System: COCACE project

Pablo Heres[1, 2], Javier Cristobo[3], Nuria Anadón[4] & Pilar Ríos[3]

1. Instituto Español de Oceanografía. Centro Oceanográfico de Gijón, Av. Príncipe de Asturias 70 bis, 33212 Gijón, Asturias, Spain.

2. Universidad de La Coruña. Rúa da Maestranza, 9, 15001 La Coruña, Spain pablohg93@hotmail.com.

3. Instituto Español de Oceanografía. Centro Oceanográfico de Gijón, Av. Príncipe de Asturias 70 bis, 33212 Gijón, Asturias, Spain.

4. Departamento de Biología de Organismos y Sistemas, Facultad de Biología, Universidad de Oviedo, Spain.

The COCACE expedition (from the acronym of "Campaña Oceanográfica del mar CAntábrico CEntral") of the University of Oviedo was accomplished between February 1987 and February 1988 in the Avilés Canyon and during the same survey were carried out in 43 sampling stations with two types of Benthic gears (anchor dredge and epibenthic Hessler and Sanders model) at depths between 31 and 1400 m. Some of the results of this project related to Cnidarians and other invertebrates have been published in the years following the campaign (Alvarez et al, 1993; Louzao et al, 2010). However, the samples of the Phylum Porifera remained until now without studying (with the exception of description of *Podospongia loveni* Cristobo et al 2002) given the absence of specialists in this group in the Oviedo University.

As a result of this work, a total of 106 samples of sponges have been reviewed, of which 236 microscopic preparations have been made. In this contribution, twenty-four taxa have been identified at the species level and 20 at the generic level. Most of specimens belong to class Demospongiae (98%) with the presence of 1 Calcarea and 1 Hexactinellida. Orders best represented in Demospongiae are Tetractinellida (66%), Axinellida (15%), Poecilosclerida (14%) and Merliida (2%).

Two of the specimens *Characella* sp. and *Hamacantha (Vomerula)* sp., could be new species and would require a later study.

References

Álvarez-Claudio, C. (1993) Hidrozoos bentónicos y catálogo de Antozoos de la Plataforma y Talud Continentales de la Costa Central de Asturias. Universidad de Oviedo. Departamento de Biología de Organismos y Sistemas.

Cristobo, J., Rios, P., Sánchez, F. & Anadón, N. 2009. Redescription of the rare species Podospongia loveni (Porifera) from the Cantabrian Sea. Continental Shelf Research 29, 1157-1164.

Louzao, M., Anadón, N., Arrontes, J., Álvarez –Claudio, C., Funete, D.M., Ocharan, F., Anadón, A., Acuña, J.L., 2010. Historical macrobenthic community assemblages in the Avilés Canyon, NIberian Shelf: Baseline biodiversity information for a marine protected área. Elsevier, Journal of Marine Systems 80, 47-56.

Calcareous sponges of the Western Indian Ocean and the Red Sea

Rob W.M. van Soest & Nicole J. de Voogd

Marine Biodiversity, Naturalis Biodiversity Center, leiden, the Netherlands Nicole.devoogd@naturalis.nl

Past taxonomic studies of Western Indian Ocean and Red Sea Calcarea have been few and sporadic (e.g. Schuffner, 1877, Jenkin, 1908, Row, 1909, Dendy, 1913, 1916, Voigt, in press). Nevertheless approximately 70 species are known from these studies for the considered region, but their descriptions often lack sufficient details for reliable identification. We studied the Western Indian Ocean Calcarea collection kept in the Naturalis Biodiversity Center. Available specimens numbered about 140, collected in the Red Sea, the Seychelles, Maldives, Mayotte and Rodrigues, in addition to incidental samples from Oman, the Lakshadweep Islands, Madagascar, Eastern and South Africa. Using a combination of techniques (in situ and 'on deck' photography, detailed field notes, light microscopic studies and measurements, SEM, and DNA sequencing) we identified 42 species, almost equally divided over two main classes Calcinea (24 spp.) and Calcaronea (18 spp.). In addition, the identified species as well as Indonesian species published in 2015 (see van Soest & de Voogd, 2015) were subjected to extraction and sequencing of the partial 28S gene of nuclear rDNA.

References

Dendy, A. 1913. The Percy Sladen trust expedition to the Indian Ocean in1905 (V). I. Report on the Calcareous Sponges collected by HMS 'Sealark' in the Indian Ocean. Transactions of the Linnean Society of London (2) 16 (1): 1-29.

Jenkin, C.F. 1908a. The Marine Fauna of Zanzibar and British East Africa, from Collections made by Cyril Crossland, M.A., in the Years 1901 & 1902. The Calcareous Sponges. Proceedings of the Zoological Society of London 1908: 434-456.

Row, R. W. H. (1909). Reports on the Marine Biology of the Sudanese Red Sea. XIII. Report on the Sponges, collected by Mr. Cyril Crossland in 1904-5. Part I. Calcarea. *Journal of the Linnean Society. Zoology.* 31 (206): 182-214.

Schuffner, O. 1877. Beschreibung einiger neuer Kalkschwämme. Jenaische Zeitschrift für Naturwissenschaft 11: 403-433 pls XXIV-XXVI

Van Soest, R. W. M.; De Voogd, N. J. (2015). Calcareous sponges of Indonesia. *Zootaxa.* 3951(1): 1-105.

The deep water sponge fauna of Guadeloupe

Nicole J. de Voogd[1], Gydo Geijer[1] & Cécile Debitus[2]

[1] Naturalis Biodiversity Center, 2300RA Leiden, The Netherlands

.*[2] IRD, UMR 6539 Lemar, IUEM Technopôle Bres Iroise, rue Dumont d'Urville 29280 Plouzané, France*

The shallow-water reef sponge fauna of the Caribbean is relatively well known from multiple studies by Van Soest and others, yet surprisingly little is known about the biota of the deep reef and the mesophotic and dysphotic zones. To adequately protect the ecosystem and construct sustainable management plans it is essential to document the biodiversity and to gain an understanding of which processes keep it in place. Recently, an inventory of the deep benthos of the EEZ of Guadeloupe in the bathymetric range of 60-1000 was carried out by the MNHN Paris and the Research Institute for Development (IRD) in the frame of the project Tropical Deep Sea Benthos. This mission allowed the sampling of sponges at different depths by means of trawling and dredging, thus enabling maximum diversity to be inventoried. Over 200 specimens were collected belonging to approximately 60 different sponges species. Here we report on some newly discovered and ill-known species.

The Sponge Collection of the Yale Peabody Museum of Natural History

Daniel Drew, Eric Lazo-Wasem, Janie Wulff.

The Yale Peabody Museum of Natural History

Sponge collection is world-wide in scope, and as the result of a recent NSF funded grant, the data are now fully entered into the Museum's database (KE Emu) and is searchable via the Museum's collections portal. Founded in 1866, the Museum's sponge collection began to grow under Yale's first Professor of Zoology, Addison E. Verrill and his involvement with the U.S. Fisheries Commission. The collection grew tremendously under the stewardship of Willard Hartman, who joined the Museum in 1953 as professor and curator in Invertebrate Zoology until his retirement in 1992. Strengths include collections from the Pacific coast of North America (California), the North Atlantic Ocean (New England and Canadian Maritime Provinces), the Caribbean Sea (Jamaica & Puerto Rico), the South Pacific (Palau, Ifaluk and Micronesia) and Indian Ocean. Hartman spent a year in the latter, and the resulting collection of the Yale Seychelles Expedition (1957-1958) remains a little studied, but highly important resource for future study. More recently collections have been added from Antarctic surveys conducted in 2009 and 2012. Included in the over 15000 lots of sponges are 450 primary and secondary type lots. There are types and schizotypes from noted authors such as Verrill, Hartman, Alpheus Hyatt, Duchassaing & Michelotti and Max de Laubenfels and even as yet unprepared fragments of Lamarck. Many schizoptypes were acquired by Hartman and his students for comparative study material. Also included in the collection are nearly 20000 microslide preparations of sections and spicules. These slides are in the process of being fully digitized via a NSF funded grant and images will be available through the Museum's collection portal; all types will be available as hi-resolution images.

Taxonomic Revision of the Family Heteropiidae (Porifera, Calcarea) in Norwegian Waters

Hilde Strand Dybevik, Adriana Alvizu & Hans Tore Rapp

Department of Biology and KG Jebsen Centre Deep-Sea Research, University of Bergen, Thormøhlensgate 53A, N-5020 Bergen, Norway. Correspondence: hilde.dybevik@student.uib.no

In the last decade, several studies in the Norwegian Sea have shown that calcareous sponges represent a diverse and abundant group, with a wide distribution from the lower littoral to the abyssal zone. However, the number of calcareous species is thought to be underestimated, because they are small, inconspicuous, and therefore easily ignored. Also, the complicated taxonomy and the limited information available for some of the families, such as Heteropiidae, support the need for thorough and comprehensive revisions. Heteropiidae is one of the more diverse families in the subclass Calcaronea, and five species are so far reported from Norwegian waters (*Sycettusa glacialis* (Haeckel, 1870), *Sycettusa kuekenthali* (Breitfuss, 1896), *Sycettusa nitida* (Arnesen, 1900), *Sycettusa murmanensis* (Breitfuss, 1898) and *Sycettusa lanceolata* (Breitfuss, 1898). Through an integrated approach using morphological characters combined with molecular data, this work aims to revise the Heteropiidae sponge fauna in Norwegian waters, to map the distribution of species and to provide a key for their identification.

Financial support was provided by the Norwegian Biodiversity Information Centre (grant to HTR, project number 70184219), the Norwegian Academy of Science and Letters (grant to HTR), the Research Council of Norway (through contract number 179560), and by the European Union's Horizon 2020 research and innovation program (grant agreement No 679849).

Three new *Halisarca*-like sponges (Porifera, Verongimorpha) from tropical seas

Alexander Ereskovsky[1, 2], Pierre Chevaldonné[1], Maude Dubois[1], Marie Grenier[1], Daria Tokina[1] & Thierry Pérez[1]

[1] Institut Méditerranéen de Biodiversité et d'Ecologie marine et continentale (IMBE), Aix Marseille Université, CNRS, IRD, Marseille, France

[2]Dept. Embryology, Saint-Petersburg State University, Saint-Petersburg, Russia

Halisarca belongs to a mono-generic family whose phylogenetic position among Demospongiae has been subject to numerous debates. Nowadays *Halisarca* belongs to a sister clade of the Verongiida among the Verongimorpha, but only a poor number of species have been properly studied and can thus be included in a phylogenetic tree.

We here provide the first descriptions of three new *Halisarca*-like sponges from the tropical zone of the Atlantic region (Caribbean Sea) and of the Pacific (Marquesas, French Polynesia). The first sponge has been collected in St. Lucia and it inhabits vertical sides of big boulders at 4 m depth in open water. The second sponge is from Marquesas, it has been found in two dark caves at 13-19 m depth. The third one was found at 25 m depth on the top of a seamount, East of the Marquesas Archipelago. All species are incrusting sponges living on hard surfaces and are sciaphilic or cave-dwelling. The colour of the first sponge is green-grey and its surface is smooth. The second is white-beige in colour with a lobate surface. The third is pink, with a smooth surface and prominent oscular tubes. The first two species present tubular choanocyte chambers, which is a characteristic trait of *Halisarca*, and they are also characterized by the presence in the mesohyl of peculiar cells displaying inclusions (spherulous, granular, microgranular and vacuolar cells) and symbiotic bacteria, which are different in both species and differ from the *Halisarca* previously studied. However, the third sponge presents large spherical choanocyte chambers and cells with inclusions that have never been found before in any other skeletal-less Demospongiae. Based on a preliminary molecular assessment, the white Marquesan *Halisarca*-like sponge clearly belongs to a sister taxon of *Halisarca*, likely a new genus very genetically distinct from the known *Halisarca*. On the contrary, the current assessment of the pink Marquesan sponge suggests it genetically belongs to *Halisarca*. These new sponges might call for a significant revision of the definition of the Halisarcidae family.

This work was conducted after the "Pakaihi i te Moana" and "Pacotilles" expeditions, the former with support from the French Agency for Marine Protected Areas (AAMP) and the latter in the framework of the LIA MARRIO.

Molecular Biodiversity of Iranian Persian Gulf Sponges

Aref Gholami[1], **Majid Askari Hesni**[1], **Azad Teimori**[1], **Gert Wörheide**[2, 3, 4], **Dirk Erpenbeck**[2, 3]

[1] *Department of Biology, Faculty of Sciences, Shahid Bahonar University of Kerman (SBUK), 76169-14111 Kerman, Iran. arefgholami91@gmail.com*

[2] *Department of Earth- & Environmental Sciences, Palaeontology and Geobiology, Ludwig-Maximilians-Universität München, Richard-Wagner Str. 10, 80333 Munich, Germany*

[3] *GeoBio-CenterLMU, Ludwig-Maximilians-Universität München, Richard-Wagner Str. 10, 80333 Munich, Germany*

[4] *SNSB - Bavarian State Collections of Palaeontology and Geology, Richard-Wagner Str. 10. 80333 Munich, Germany.*

Despite their importance, our knowledge of the biodiversity and phylogeography of Persian Gulf sponges is largely unexplored. However, this knowledge is necessary to better understand the patterns and processes that generated and maintained sponge diversity in this waterbody and to create a foundation for future exploration of the marine natural resources in this area.

Expeditions led by the Shahid Bahonar University of Kerman facilitated the most comprehensive collection for Iranian sponges to date. The collection of almost 100 samples has been DNA barcoded and genetically analyzed to identify operational taxonomic units (OTUs). The sponge identification will subsequently be corroborated by morpho-taxonomy to generate a biodiversity inventory, which will be used to analyze occurrence patterns. Here, first and the currently most comprehensive results are presented about demosponge and calcareous sponge species diversity and their geographic distribution patterns along the Iranian Persian Gulf coastline.

Molecular Taxonomy of African Freshwater Sponges

Dirk Erpenbeck[1, 2], **Sebastian Mai**[1], **Markus Steiner**[1], **Astrid Schuster**[1], **Gert Wörheide**[1, 2, 3]

[1] *Department of Earth- & Environmental Sciences, Palaeontology and Geobiology, Ludwig-Maximilians- Universität München, Richard-Wagner Str. 10, 80333 Munich, Germany. erpenbeck@lmu.de*

[2] *GeoBio-CenterLMU, Ludwig-Maximilians-Universität München, Richard-Wagner Str. 10, 80333 Munich, Germany*

[3] *SNSB - Bavarian State Collections of Palaeontology and Geology, Richard-Wagner Str. 10. 80333 Munich, Germany.*

African sponges, particularly freshwater sponges, are largely understudied, compared to demosponges in most other geographical regions. Recent morphological studies started summarizing our current knowledge and conclude that the species richness of African freshwater sponges is underestimated and that geographic distribution ranges remain obscure. Freshwater sponges (Spongillina) likely share a common ancestor, however their evolution, particularly the radiation into endemic and allegedly cosmopolitan groups is largely unknown. Freshwater sponges of at least 58 species of 17 genera and at least four families are described from Central and Eastern Africa, but the diversity may be largely underestimated, due to limited distinguishable morphological features. The discovery of additional, particular cryptic, species is very likely with the use of molecular techniques such as DNA barcoding. The Royal Museum of Central Africa (RMCA, Tervuren, Belgium) hosts one of the largest collections of (Central) African freshwater sponges and their type material. Holotypes in theory constitute ideal targets for molecular taxonomy, however the success is frequently hampered by DNA degradation and deamination, which are a consequence of suboptimal preservation techniques. Therefore, we genotyped African demosponge holotype material of the RMCA with specific short primers suitable for degenerated tissue and compare the results with the current, morphology-based classification.

New Species And A New Record Of The Genus *Leucilla* (Calcarea, Calcaronea) To The Tropical Brazilian Coast.

Bruna Bahiana & Fernanda F. Cavalcanti

Instituto de Biologia, Universidade Federal da Bahia. Barão de Jeremoabo s/n, Campus de Ondina, Salvador – Bahia, Brazil. 40170-115. fernanda.cavalcanti@ufba.br

The genus *Leucilla* is composed of species of the family Amphoriscidae with inarticulated skeleton and sylleibid or leuconoid aquiferous system, without a disorganized layer of spicules between the subatrial and atrial skeletons. Currently, it has 13 accepted species, and its last described one was *L. endoumensis* by Borojevic and Boury-Esnault in 1986. In the present work, we describe species of *Leucilla* from Salvador, Bahia state, Northeastern Brazilian coast. The specimens were sampled at one meter depth, and fixed and preserved in 96% ethanol. Taxonomic identification followed a standard protocol. Our results reveal the occurrence of three new species and the first record of *Leucilla sacculata* for the studied area. *Leucilla* sp. nov. 1 resembles two known species – *L. endoumensis* and *L. sacculata* – but differs from them due to the organization of the skeleton and to the type of aquiferous system, respectively. *Leucilla* sp. nov. 2 has a skeletal composition similar (but not identical) to that of *L. nuttingi*, but the presence of a continuous layer of microdiactines in the cortical region, easily visible in *L. nuttingi* and absent in the new species, allows the differentiation between them. The third new species, *Leucilla* sp. nov. 3, resembles *L. minuta*, *L. hirsuta* and *L. oblata*. However, it can be recognized due to its choanosomal skeleton formed by one category of triactines and two categories of tetractines, while the other species have only choanosomal tetractines. Finally, *Leucilla sacculata* was originally described to Fernando de Noronha Archipelago (also at the tropical Brazilian domain) during the 19th century and here it is recorded for the first time out of its type locality. Although type material is unknown, the identification was possible based on the original description. Recently, some discussion was raised on the genera *Leucilla* and *Paraleucilla* as the main difference between them is the presence, in the second genus, of a disorganized layer of spicules. This layer is absent in young specimens and in some adults of *Paraleucilla*, leading one to identify them as *Leucilla*. Thus, to avoid misidentification, all the species described here were compared to those comprising both genera, before we conclude that most of them are in fact new to science.

Financial supports by PIBIC/ UFBA, FAPESB, CNPq, PRODOC-PROPCI/ UFBA are gratefully acknowledged.

Taxonomy Of Calcareous Sponges (Porifera, Calcarea) Sampled On Artificial Substrates In A Recreational Marina From The Tropical Brazilian Coast.

Cleslei Chagas & Fernanda F. Cavalcanti

Instituto de Biologia, Universidade Federal da Bahia. Barão de Jeremoabo s/n, Campus de Ondina Salvador – Bahia, Brazil. 40170-115. fernanda.cavalcanti@ufba.br

Artificial substrates submerged in the sea can be quickly colonized by several invertebrates. Thus, they can be used as a method of sampling benthic organisms in areas where scuba diving or snorkeling are not allowed. In the present work, fragments of nautical cables were used to sample calcareous sponges from a recreational marina in Salvador, Bahia State, Northeastern Brazil. Only few taxonomic works focusing on Calcarea had already been developed in this region, and observations from scientific collections and fieldworks reveal that calcareous sponges are easily found there. The cables remained submerged at one meter depth during two months, and after this period they were replaced by new cables from August 2015 to October 2016. In the laboratory, calcareous sponges were removed from them, and taxonomic identification followed standard protocols. Four species were found, being three of them new to science: *Sycon* sp. nov. 1, *Sycon* sp. nov. 2, *Leucilla* sp. nov. and *Leucandra serrata*. The latter species had never been recorded to the coast of Bahia. *Sycon* sp. nov. 1 was the most abundant species. It has no oscular fringe and atrial skeleton composed by triactines and few tetractines, making it slightly hispid. The species has also tufts of diactines not so visible at the end of the distal cones, and tubar triactines that are different from those occurring at the subatrial region. The other new species of the genus, *Sycon* sp. nov. 2, can be easily differentiated from the previous one mainly by its large amount of tetractines in the atrium, in addition to the largest size of diactines and presence of an oscular fringe. Both species resemble *S. frustulosum*, but the size and shape of the diactines are the most remarkable differences among them. The third new species found in the present work is *Leucilla* sp. nov. It is different from all the described species of the genus due to its spicules size and skeletal composition, as it has pentactines. This spicule category was previously described only to *Sycon pentactinale*. Finally, the record of *Leucandra serrata* to the Bahia coast fills an important gap in the distribution of this species, which was found in localities on the Brazilian coast that are 2900 km apart, being our studied area in between these localities. Our results emphasize that leaving artificial substrates in the sea for a short period of time is an efficient method for sampling calcareous sponges, which are among the pioneer organisms to colonize them. The number of new species to science and the new record of *Leucandra serrata* also reveal that our knowledge on the diversity of Calcarea is underestimated in the tropical portion of the Brazilian coast, and the number of species known to Bahia increased from 13 to 17. The lack of data on the spongefauna occurring in the marina makes impossible to recognize if one of these species could be exotic, which is common in areas with heavy boat traffic. Nevertheless, we believe that in the future our results could help in the detection of a possible introduction by calcareous sponges.

Financial supports by FAPESB, CNPq, PRODOC-PROPCI/ UFBA are gratefully acknowledged.

Biodiversity of calcineans (Porifera, Calcarea) from Martinique, Lesser Antilles, Caribbean Sea

Tayara Fontana[1], Fernanda Azevedo[1], Báslavi Cóndor-Luján[1], Thierry Pérez[2] & Michelle Klautau[1].

[1] Universidade Federal do Rio de Janeiro, Instituto de Biologia, Departamento de Zoologia.

[2] Institut Méditerranéen de Biodiversité et d'Ecologie marine et continentale (IMBE), CNRS, IRD, Aix Marseille Université, Université Avignon. Station Marine d'Endoume, Rue de la Batterie des Lions, Marseille, France.

Martinique is an island located in the central portion of the Lesser Antilles (14º51'N -14º22'N), in the Caribbean Sea. Although sponges are one of the most important invertebrate benthic groups in the Caribbean Sea, only 21 species were reported from Martinique and none were calcareous sponges. Therefore, the aim of the present work was to study the diversity of calcareous sponges from Martinique, with a particular focus in the subclass Calcinea. The sponges were collected in 2013 and 2015 by scuba diving in eight localities in Martinique, in depths ranging from three to 30 meters, under the Franco-Brazilian project LIA-MARRIO. Sponges were photographed *in situ* and fixed and preserved in ethanol 93%. Morphological and molecular procedures and analyses were performed in order to identify the 46 collected specimens. Optical and Scanning Electron Microscopy were used in order to characterize the spicules. The nuclear rDNA marker ITS was sequenced. The molecular results were in concordance with the previous morphological determinations. A total of 11 species within five genera were identified: *Arthuria hirsuta* (Klautau & Valentine, 2003), *Clathrina aurea* Solé- Cava, Klautau, Boury-Esnault, Borojevic & Thorpe, 1991, *Leucetta floridana* (Haeckel, 1872) and eight new species. Among the new species there are two *Arthuria*, one *Borojevia*, four *Clathrina* and one *Ernstia*. Considering all the 11 species identified, only *L. floridana* had already been reported from the Caribbean Sea. *Arthuria hirsuta*, originally described from South Africa, suggests an amphi-Atlantic affinity, while *Clathrina aurea*, originally described from Brazil, suggests a faunal connection with the Brazilian coast. The discovery of nine new species provisionally endemic to Martinique is possibly just an artefact of our precarious knowledge of the class Calcarea.

References

[1] M. Klautau, C. Valentine, Zoological Journal of the Linnean Society. 39 (2003)1-62.

[2] Van Soest, R.W.M, Boury-Esnault, N., Hooper. J. N. A., Rützler, K., et al. World Porifera Database. Available: http://www.marinespecies.org/porifera/. Acessed in Janeiro/2017.

Financial support by CAPES, CAPES-COFECUB CNPq and CNRS.

Comparative Transcriptome Analysis Reveals Insights Into The Streamlined Genomes Of Haplosclerid Demosponges

Christine Guzman[1, 2] & Cecilia Conaco[1]

[1] Marine Science Institute, College of Science, University of the Philippines, Diliman, Quezon City 1101 Philippines. cjmguzman@gmail.com

[2] Current address: Okinawa Institute of Science and Technology Graduate University, 1919-1 Tancha, Onna-son, Okinawa 904-0495, Japan

Sponges (Porifera) are one of the most ancestral metazoan groups. They are characterized by a simple body plan lacking the true tissues and organ systems found in other animals. Members of this phylum display a remarkable diversity of form and function and yet little is known about the composition and complexity of their genomes. In this study, we sequenced the transcriptomes of two marine haplosclerid sponges belonging to Demospongiae, the largest and most diverse class within phylum Porifera, and compared their gene content with members of other sponge classes. We recovered 44, 693 and 50, 067 transcripts expressed in adult tissues of *Haliclona amboinensis* and *Haliclona tubifera*, respectively. These transcripts translate into 20, 280 peptides in *H. amboinensis* and 18, 000 peptides in *H. tubifera*. Genes associated with important signaling and metabolic pathways, regulatory networks, as well as genes that may be important in the organismal stress response, were identified in the transcriptomes. Futhermore, lineage-specific innovations were identified that may be correlated with observed sponge characters and ecological adaptations. The core gene complement expressed within the tissues of adult haplosclerid demosponges may represent a streamlined and flexible genetic toolkit that underlies the ecological success and resilience of sponges to environmental stress.

Beyond the sponge barcode: testing the taxonomic utility of microbial diversity analysis using 16s rRna gene sequences among tetillid sponges

Kathryn A. Hall[1] & John N.A. Hooper[1]

[1] Biodiversity and Geosciences Program, Queensland Museum, South Brisbane, Queensland, Australia. kathryn.hall@qm.qld.gov.au

The serious limitations of the DNA barcoding marker (COI mtDNA Folmer fragment) for the taxonomy of sponges are widely acknowledged. The marker is notoriously difficult to amplify using standardised degenerate primers (1) because of the interplay of numerous factors, including the persistence of secondary metabolites in DNA extracts, the presence of contaminating DNA from other marine organisms, and also the incorporation of introns, often near primer binding sites, into the gene itself. Some of these factors are not restricted to the COI barcoding gene, and, along with additional impediments, such as gene order rearrangements, confound attempts to amplify other loci. Currently, we are exploring the practicality of other DNA markers for specimens of Tetillidae (Demospongiae, Tetractinellida) from the Indo-West Pacific, but in view of the multiplicity of obstacles to sponge DNA sequence analysis, we are exploring the utility of microbiome analysis for taxonomic investigations of this group.

A test sample of 20 specimens from a diversity of species and sampling locations was sent to a commercial facility for microbial diversity analysis using partial 16S rRNA genes (V3–V4), visualised using next-gen sequencing technology. Preliminary analysis produced high quality microbiome data for 12 of the samples (60% success rate). In excess of 36, 000 OTUs were identified from this mix of samples, with approximately 3, 000 microbial OTUs recovered per specimen. Some microbial diversity was shared among the samples and a Principal Component Analysis (PCA) was performed. PCA of the microbial OTU data indicated that specimens identified morphologically as the same species were recovered as having similar microbiome compositions. Further, specimens from geographically similar waters, but which were morphologically distinct, were not found to have similar microbiomes, suggesting that the microbiome of the ambient water did not influence the uniqueness of the microbiome of individual tetillid species. Encouraged by these preliminary findings, we are continuing our study using an additional 200 specimens from an array of tetillid species from locations throughout the Indo-West Pacific, including the Great Barrier Reef, Torres Strait, Papua New Guinea, French Polynesia and northern Western Australia. Here we present our new data from these samples and further explore the efficiency of this ecological character as a taxonomic marker and as a dataset for phylogenetic inference.

References

1. O. Folmer, M. Black, W. Hoeh, R. Lutz, R. Vrijenhoek, Mol Mar Biol Biotechnol. (1994) 3 (5) 294–299.

Financial support by the Australian Biological Resources Study (ABRS) is gratefully acknowledged.

Taxonomy of Theonellidae in the Indo-West Pacific

Mary Kay Harper[1], Kathryn A. Hall[2], Merrick Ekins[2], Chris M. Ireland[1], John N.A. Hooper[2,3]

[1]University of Utah Asia Campus, 119 Songdo Munhwa-ro, Building U856, Yeonsu-gu, Incheoen, Korea 21985
[2]Queensland Museum, P.O. Box 3300 South Brisbane Queensland 4101
[3]Eskitis Institute for Drug Discovery, Griffith University, Nathan, QLD 4111, Australia

We used a combined approach of morphological, molecular and chemical datasets to explore the taxonomy of Indo-West Pacific (IWP) Theonellidae Lendenfeld, 1903 (Demospongiae, Tetractinellida, Astrophorina). Based on gross morphology and some secondary metabolite data, 30 specimens were selected from collections from multiple locations throughout the Indo-west Pacific: Solomon Islands, Papua New Guinea, Vanuatu and Australia (Great Barrier Reef). Detailed morphological study of this material revealed an assemblage of sponges with inconsistent morphological features: some lack the articulated desmas associated with specimens ascribed to the type species *Theonella swinhoei* Gray, 1868; others possess tetralophose calthrops, like those seen in specimens of *Theonella mirabilis* (de Laubenfels, 1954); and others are like *Theonella xantha* (Sutcliffe, Hooper & Pitcher, 2010) and appear to have lost tetractinal spicules entirely. We have found microsclere morphology to be taxonomically useful for discriminating among our theonellid species and supporting monophyly of the genus. DNA sequence analysis, using COI barcoding and intergenic spacer regions of mtDNA, validates taxonomic use of the microscleres by recovering monophyly of our specimens among other IWP astrophorine species. Here we characterize our new species and discuss the phylogenetic relationships of the morphologically atypical theonellids.

Six New Species of Verongiid Sponges from Southern Region of Baja California Peninsula, Mexico

Zvi Hoffman[1], Patricia Gómez[2], Carlos Sánchez[1] and Jaime Gómez-Gutiérrez[3]

[1]Departamento de Biología Marina, Universidad Autónoma de Baja California Sur, La Paz, Baja California Sur, Mexico. hoffmanzvi@gmail.com
[2]Unidad Académica Ecología y Biodiversidad Acuática, Instituto de Ciencias del Mar y Limnología, Universidad Nacional Autónoma de México, Mexico City, Mexico
[3]Centro Interdisciplinario de Ciencias Marinas, Instituto Politécnico Nacional, La Paz, B.C.S., Mexico

Description of six new species of Verongiida is presented, four from *Aplysina* and two from *Suberea* collected at Baja California Peninsula, Pacific side of Mexico (2013-2016). Verongiid sponges have a widespread distribution in tropical and subtropical waters. Ecological census and sampling at both coasts of the southern region of the peninsula showed verongiid type sponges highly abundant, but most of them are still unknown for science. A morphologic study from 85 verongiid samples was realized, samples were also compared with type material of the Eastern Pacific *Aiolochroia thiona* (de Laubenfeles, 1930), *Aplysina gerardogreeni*, *A. azteca* Gómez & Bakus, 1992, *A. clathrata, A. revillagigedi* Cruz-Barraza *et al*., 2012, and *Suberea etiennei* van Soest, *et al*., 2011. Skeletal trait and fibres from these yielded six new species, four *aplysinas* and two *subereas*. The four new *Aplysina* species possess polymorphic skeleton ranged from anastomosed to anastomosed-dendritic with intermediate morphologies among them. This new skeleton morphology have been evidenced as diagnostic feature for *Aplysina* sponges of the Eastern Pacific[1], including *Aiolochroia thiona* at Laguna Beach (California, USA). The two new *Suberea* species are quite different inwardly, since one has an encrusting massive shape with a tangled dendritic skeleton and the other has a subspherical habit with a dendritic pattern of long fibres that grow from a complex of inner tangled and anastomosed fibers towards the sponge surface. None of these morphological traits of *Suberea* matches with those observed in the paratype of *Suberea etiennei*. Albeit, a genetic investigation from the six species is carried out and it still in progress. Several diagnostic morphological characters used in verongiid species identification are discussed, concluding that verongiid species show a remarkable species diversity correlated with relatively small distribution range, likewise other species reported in the Gulf of California and the subtropical Eastern Pacific region as well.

References

[1]. P. Gómez, Z. Hoffman, C. Sánchez, B. González-Acosta, C.J. Hernández-Guerrero (in press). *Zootaxa*

Financial support by CONACyT, Copris Group, and UABCS is gratefully acknowledged. We thank Dr. Robert Thacker (Department of Ecology and Evolution Smithsonian Natural History Museum) for his support in a research stay in 2016 of Z.H.

Toward Integrative Taxonomy of Endemic Lake Baikal Sponges Lubomirskiidae

Valeria Itskovich, Olga Glyzina, Alena Yakhnenko, Oxana Kaluzhnaya

Limnological Institute of the Siberian Branch of the Russian Academy of Sciences, Irkutsk, Russia;. itskovich@mail.ru

The endemic sponge family Lubomirskiidae (Porifera; Demospongiae; Spongillina) is an example of species radiation in ancient Lake Baikal. It is a true species flock with 13 described species which are dominant component of the benthos community in the lake. We performed for the first time multi-gene analyses of molecular phylogeny of Lubomirskiidae using several molecular markers: Folmer's CO1 fragment, ITS1-5.8S- ITS2 region, D3 28S rDNA region, CO2-ATP6 intergenic mtDNA region, silicatein gene fragment. Molecular analyses revealed that *Lubomirskia* and *Baikalospongia* genera are not monophyletic. At the same time species *L. baicalensis, B. intermedia, B. bacilifera* and *B. recta* also do not form monophyletic clades. Discrepancy between molecular and morphology data revealed the need integrative taxonomic approach for species delimitation within Lubomirskiidae. We used fatty acid composition of total lipids and composition of prokaryotic symbiotic community as additional markers for species delimitation. Analyses of intra and inter species variability of fatty acid composition of total lipids of three sponge species showed that fatty acid compositions were species specific and detected microalgal contribution to the total pool of fatty acids. 16S rRNA gene sequencing of three sponge species displayed the inter species differences in composition of prokaryotic symbiotic community. Our results revealed that fatty acid composition and sponge microbial diversity probably are perspective markers for integrative taxonomy of Lubomirskiidae.

Financial support by Federal Agency Scientific Organizations project VI.50.1.4 (0345-2016-0002) and RFBR grants № 14-04-00838A, 14-44-04165p is gratefully acknowledged.

Two new records of marine sponges (Demospongiae: Haplosclerida) from the coast of Karachi, Pakistan

Hina Jabeen, Seema Shafique, Zaib-un-Nisa Burhan, Amjad Ali and Pirzada Jamal Ahmed Siddiqui

Centre of Excellence in Marine Biology, University of Karachi, Karachi-75270, Pakistan. hinajabeen14@gmail.com

The coastline of Pakistan is situated about 200 nautical miles of Exclusive Economic Zone in North Arabian Sea, stretched about 1050 km with the coast of Balochistan (800 km) and Sindh coastal region (250 km). Marine sponge persists in this area in mutualistic association with coral communities that enhances species growth and distribution which eventually depends upon variable environmental conditions. The sponge taxa belong to class Demospongiae, order Haplosclerida reported from Karachi coast. *Callyspongia* (*Cladochalina*) *fibrosa* (Family Callyspongiidae) collected from Churna Island (66°36'E, 24°53'N) by SCUBA diving in February 2013 and *Haliclona* (*Reniera*) *cinerea* (Family Chalinidae) collected from the rock pool of Buleji rocky ledge (64°50'E, 24°49'N) in January 2016. Both specimens were identified morphologically through skeletal structure (spicules and spongin) in light and scanning electron microscope. The occurrence of these two species *Callyspongia* (*Cladochalina*) *fibrosa* and *Haliclona* (*Reniera*) *cinerea* are documented as new records from the coastal region of Karachi, Pakistan.

A first assessment of the sponge biodiversity off the coast of mainland Ecuador

Karla Jaramillo[1, 2], Christine Morrow[2], Olivier P. Thomas[3], Jenny Rodriguez[1], Grace P. McCormack[2], Eduardo Hajdu[4]

[1] *Escuela Superior Politécnica del Litoral, ESPOL. Centro Nacional de Acuacultura e Investigaciones Marinas, CENAIM. Km 30.5 via Perimetral, Guayaquil, Ecuador.*

[2] *National University of Ireland Galway, School of Zoology, Ryan Institute, University Road, Galway, Ireland.*

[3] *National University of Ireland Galway, School of Chemistry, Ryan Institute, University Road, Galway, Ireland.*

[4] *Museu Nacional/UFRJ, Depto. Invertebrados, Quinta da Boa Vista, s/n, 20940-040, Rio de Janeiro, RJ, Brasil. kbjarami@espol.edu.ec*

The Pacific coast of South America has been recently studied for its sponge biodiversity from the cold waters of Chile until Peru. However, the coast of Ecuador was still considered a gap in the knowledge of the biodiversity as well as distribution and abundance of sponges along this coast.

A recent project was supported recently at the national level to assess for the first time the biological and chemical diversity of marine invertebrates in this maritime region. We report herein the very first results on the description of sponges at El Pelado Marine Protected Area in the province of Santa Elena-Ecuador. In a first instance, eight sponge species were identified from the shallow waters, using morphological characters and some molecular markers including mitochondrial 16S ribosomal DNA (mt 16S rDNA), cytochrome oxidase subunit I (COI). These species were first shown to belong to seven genera *Callyspongia*, *Mycale*, *Chondrosia*, *Tedania*, *Dysidea*, *Clathria*, and *Plocamiancara*. A particular interest was given to a very common sponge *Callyspongia* sp. usually found in interaction with corals. This may represent an interesting case of sponge-coral interaction that deserves attention.

These first insights into the sponge biodiversity off the coasts of mainland Ecuador revealed a high sponge diversity in a very small area that clearly deserves more detailed examination. This work will give access to key data for the distribution of sponges between the Southern and the Northern coast of South America.

Molecular Taxonomy and Phylogeography of *Ircinia* from Western Australia

Joseph Kelly[1, 2],, Robert W. Thacker[1]

[1] *James Cook University, Townsville, Australia*

[2] *Department of Ecology and Evolution, Stony Brook University, Stony Brook, New York, United States of America. joseph.b.kelly@stonybrook.edu*

Sponges represent a highly diverse group of morphologically simple, sessile, filter-feeding organisms that contribute to benthic biomass and nutrient cycling. Despite their critical ecological significance in marine ecosystems, sponges suffer from difficult species identifications and unresolved phylogenetic relationships. One group in particular, the aspiculate keratose sponges, lack defining mineralized skeletal features and can be difficult to identify. As a result, the richness of keratose sponge communities is typically underestimated in biodiversity censuses. In addition, keratose sponges are often misidentified in museum collections, impeding the characterization of their biogeography and life history.

In this study, we examined the taxonomic, phylogenetic and phylogeographic relationships of keratose sponges of the genus *Ircinia* collected from Western Australia. Molecular phylogenies inferred from the mitochondrial cytochrome oxidase subunit 1 gene delineated multiple clades from a set of specimens corresponding to uncharacterized sponge taxa and several previously recognized, but unnamed, species. Our results stress the urgent need for development of clearly defined sponge taxonomy to enhance assessments of sponge biodiversity, conservation, and environmental management.

Financial support by AIMS@JCU is gratefully acknowledged.

Deeper understanding of deep sea Axinellida: mitochondrial sequencing of a novel abyssal sponge

Nathan J. Kenny[1], Ana Riesgo[1], Helena Wiklund[1], Gordon L.J. Paterson[1], Thomas G. Dahlgren[2, 3,] Adrian G. Glover[1], Sergio Taboada[1]

[1] *Life Sciences Department, The Natural History Museum, Cromwell Road, London SW7 5BD, UK n.kenny@nhm.ac.uk*

[2] *Uni Research, PO Box 7810, 5020 Bergen, Norway*

[3] *Department of Marine Sciences, University of Gothenburg, Sweden*

A novel abyssal sponge, Axinellida sp. nov., is currently the subject of descriptive efforts. This species is endemic to the Clarion and Clipperton Zone (CCZ) in the North East Pacific, a region that has recently become economically viable as a source of polymetallic nodules. Axinellida sp. nov. itself encrusts on these nodules, is an abundant component of the ecosystem at these depths, and our understanding of its ecology and interrelationships is still limited at best.

In order to better characterise this sponge and place it in its phylogenetic context, we sequenced, assembled and annotated its mitochondrial genome using Illumina MiSeq reads and the Velvet and IDBA-UD assemblers. We compared its gene arrangement with other closely related species, and performed Maximum Likelihood and Bayesian Inference analyses using both nucleotide and amino acid data sets.

The mitochondrial genome of this species is 20, 819 bp in length, slightly larger than that of most related species (1). A total of 26 tRNA, 14 protein coding and 2 rRNA genes were present, and all genes possessed the same orientation. Gene order is somewhat different to that seen in other species, with a defined tRNA 'cluster'. Phylogenetic analyses place this species firmly in the order Axinellida, and broadly support heteroscleromorph relationships as formerly proposed (2).

Efforts to understand the wider biology and population connectivity of this unique sponge species continue (Taboada et al., at this meeting), but interpreting these results within a phylogenetic context will enable stronger conclusions to be drawn. The mtDNA sequence presented here will continue to be useful for designing markers suitable for phylogenetic and phylogeographic studies of this unique species, and allow greater understanding of the evolution of the Axinellida and Demospongiae as a whole.

References

1. D. Lavrov, X. Wang, M Kelly, Mol Phylogenet Evol. 49 (2008) 111-124.
2. C. Morrow, P. Cárdenas, Front Zool. 12 (2015) 1.

Financial support from the Natural History Museum of London (DIF SDF14032 to AR) and the EU-MIDAS (Managing Impacts Of Deep Sea Resource Exploitation) and ABYSSLINE (Abyssal Biological Baseline) projects gratefully acknowledged.

Integrative Systematics of Tropical Western Atlantic *Mycale* of the "*immitis*-group"

Dora Leite[1], Thiago S. de Paula[2]; Gisele Lôbo-Hajdu[2]; Eduardo Hajdu[1]

[1] *Universidade Federal do Rio de Janeiro, Museu Nacional, Quinta da Boa Vista, s/n, 20940-040, Rio de Janeiro, RJ, Brazil dorademoura@gmail.com*

[2] *Universidade do Estado do Rio de Janeiro, Instituto de Biologia Roberto Alcântara Gomes, Departamento de Genética, Rua São Francisco Xavier 524, PHLC, sala 205, 20550-013, Rio de Janeiro, RJ, Brazil*

Mycale Gray, 1867 comprises about 250 species, and ranks among Porifera largest genera. Its species are currently classified in 11 subgenera. Some of these are quite large and comprise clearly recognizable species groups, as is the case of the "immitis group", assigned to *Mycale (Mycale)*, characterized by an anisochela markedly curved in profile, and with relatively short head (25–35% of whole microsclere length). Three species of this group have been described from the Tropical Western Atlantic: *M. (M.) alagoana* Cedro, Correia & Hajdu, 2011, from Alagoas (Brazil); *M. (M.) arenaria* Hajdu & Desqueyroux-Faúndez, 1994, from Rio de Janeiro (Brazil) and *M. (M.) immitis* (Schmidt, 1870), from Florida (USA). We have used morphology and molecular data (16S and ITS) to characterize specimens of this species group collected in Brazil and the Caribbean, including type and/or topotypical materials of both Brazilian species. Seventeen specimes were analysed for morphometric analysis, and 14 for molecular. Our results recovered three highly supported cladi in the molecular analyses: clade A *(Mycale* sp. 1*)* comprises individuals from Las Cuevas (Bocas del Toro); clade B *(Mycale* sp. 2*)* comprises individuals from Isla Solarte (Bocas del Toro); clade C *(M. arenaria)* comprises specimens from NE (topotypical with *M. alagoana*) and SE Brazil (including one paratype of the species). *Mycale* sp. 1 differs from *M. arenaria* by the width of its mycalostyles I (8) and II (10), and by the length of the anisochela II (21). *Mycale* sp. 2 differs from *M. arenaria* by the length and width of mycalostyles I (422/10) and II (570/11), and in the length of anisochela II (26) and III (18), sigmas II (35) and III (14) and raphides (77). *M. (M.) immitis* could not be analyzed yet. A PCA recovered specimens from each clade in distinct morphospace positions (ANOSIM) of the "*immitis*-group". Despite the holotype of *M. alagoana* (MNRJ 4624) being the sole specimen with sigmas of type-I, PCA put it together with *Mycale* sp. 1, mainly due to its anisochelae II dimensions. In addition, the paratype of *M. alagoana* (UFALPOR 0139), seemingly without sigmas-I, was retrieved closer to *M. arenaria*. It was thought that NE and SE Brazil contained distinct species of the "*immitis* group", but it turns out to be more likely now that *M. arenaria* is widespread all the way up to the Guiana shelf at least.

Taiwan deep-water sponge collection at the National Museum of Natural Science at Taichung (Taiwan)

Swee Cheng Lim

National University of Singapore Tropical Marine Science Institute 18 Kent Ridge Road, S2S Singapore 119227

The deep-water sponge collection of the National Museum of Natural Science at Taichung is examined and reported for the first time. This collection comprises of over 100 specimens dating back to 1991, up to 4400 m depth from Taiwan waters and they were collected by the museum curators on the research vessel, Ocean Research 1. Some of the localities include Green Island, Orchid Island and Dongsha Atoll. There are over 20 hexactinellids and 20 demospongiae species and they are described in work. The result is compared to deep-water sponge species (some 150 species) that have been described and recorded from the Northwest Pacific. These comprise of mainly of hexactinellids (over 100 species) and some 50 species of demospongiae and a single, record of an unidentified calcareous sponge reported by Koltun. Most of these records were from Japan and Russia waters, north of Taiwan. The composition and distribution of the deep- water sponges in Northwest Pacific are discussed in this work.

Evolution of haplosclerid sponges: insights from kinetid structures

Maria Belinda Longakit[1, 2], Christine Morrow[1] & Grace P. McCormack[1]

Department of Zoology, Martin Ryan Institute, National University of Ireland, Galway, Ireland
Corresponding author email address: bel_longakit@ymail.com

Molecular evidence points to the polyphyletic nature of many taxonomic ranks within the marine Haplosclerida. Three major clades have been recovered via molecualr data, referred to as clades A, B and C. The kinetid structures of species currently classified as *Haliclona,* which represent the three clades were investigated to evaluate whether they could discriminate the clades. Members of the three clades differ in at least three aspects of the kinetid structure, i.e. characteristics of 1) electron dense, and 2) electron clear areas of the transition zone; and 3) presence/absence of a basal foot. The Clade A representatives (i.e. *Haliclona oculata*, type species and *H. urceolus*) have electron dense areas that stretch horizontally along the margins of the peripheral microtubules and narrow at their proximal ends, short electron clear areas and no basal feet. The Clade C representatives (*H. indistincta and H. viscosa*) have electron dense areas that are uniform in thickness, long electron clear areas and basal feet. The Clade B representative on the other hand (*H. simulans*) shared similarity with Clade C on the thickness of electron dense area and with clade A on the length of the electron clear area and absence of a basal foot. Our findings show that within the order Haplosclerida, variations in the kinetid are present and these support the phylogenetic relationship of the order recovered from molecular data.

Spicular Analysis for Reconstructions of Sponge Communities in Modern Coral Reefs

Magdalena Łukowiak

Institute of Paleobiology, Polish Academy of Sciences, ul. Twarda 51/55, 00-818 Warszawa, Poland, e-mail: mlukowiak@twarda.pan.pl

Sponges are a key and inseparable component of modern coral reefs thus the knowledge of their taxonomic diversity is therefore crucial for ecological considerations of coral reef ecosystems. However, some sponge species might be easily overlooked due to their size and cryptic and/or excavating nature. This problem might often be solved using the method of spicular analysis. It enables to recognize spicule morphotypes by means of detailed examination of surficial sediments. Here, the spicular analysis has been applied to study the sponge-spicule assemblage in the lagoon reef of Bocas del Toro, Panama. This method allowed to identify some highly diagnostic spicule morphotypes. They belong to four sponge species, i.e. *Samus anonymus* (1), *Triptolemma endolithicum* (2), *Cliona mucronata* (3), and *Alectona wallichii* (4), that have not been noticed in this area so far. The last two species were previously known only from Indian Ocean, and Japanese and South African waters, respectively. The presence of these species enriches our knowledge of the ecological interactions within the coral reef ecosystem of the studied area. Despite some limitations, the method of spicular analysis proves to be useful as a supplementary tool for the reconstruction of modern shallow-water sponge communities.

Financial support by Polish National Science Center Grant (NCN) no 2013/09/D/ST10/04050, Short Term Fellowship from the Smithsonian Tropical Research Institute, and PalSIRP Sepkoski Grant.

Siliceous Sponges from the Upper Eocene of Eastern Central Ukraine

Magdalena Łukowiak[1], Tetiana Stefanska[2] & Andrzej Pisera[1]

[1] *Institute of Paleobiology, Polish Academy of Sciences, ul. Twarda 51/55, 00-818 Warszawa, Poland, mlukowiak@twarda.pan.pl, apis@twarda.pan.pl*

[2] *Oles Honchar Dnipropetrovsk National University, 72, Gagarin Av., Dnipropetrovsk 49010, Ukraine, ivanovatatyana@rambler.ru*

In the late Eocene (~40 Mya), most of the European continent was covered by a shallow Tethys sea. New study of loose sponge spicules shows that rich and diversified sponge communities existed in this region during that time. The abundant and diversified assemblage of dissociated spicules of eastern Central Ukraine (Middle Dnieper region) reveals the presence of both, "soft" and lithistids demosponges. Rare spicules of homoscleromorphs and extremely rare hexactinellid spicules are also observed.

At least nine families (i.e. Bubaridae, Geodiidae, Pachastrellidae, Thoosidae, Spirastrellidae, Samidae, Agelasidae, Clionaidae, and Placospongiidae) of "soft" demosponges were recognized. Among lithistid demosponges, at least 4 families (Phymaraphinidae, Theonellidae, Vetulinidae, and undetermined family with rhizoclones) were present. Spicules belonging to one plakinid homoscleromorph and a single hexactinellid species were also observed.

We estimate that at least 14 different species of demosponges (including 4 lithistid demosponges), one homoscleromorph and one hexactinellid inhabited this region of the Tethys Sea during the late Eocene. Most of these sponges have not been reported yet from the late Eocene of Ukraine. The taxonomic composition of this spicule assemblage [e.g., presence of *Alectona millari* (1), *Placinolopha sarai* (2)*, Diplastrella megastellata* (3), and *Samus anonymus* (4), and abundant lithistids and extreme rarity of hexactinellids], suggests relatively shallow-water (shelf) environments.

The occurrence of the genus *Vetulina* (5, 6) is significant as it was noted for the first time in the fossil record. As in the case of previously studied Miocene sponge assemblage from Vienna Basin (cf. Łukowiak et al. 2014), these findings suggest Tethyan origin and a wider distribution of some extant sponge taxa in the geological past. Thus, their present- day, geographically restricted range seems to be of a relic character.

References

1. M. Łukowiak, A. Pisera, J. Schlögl, Pal. Zeitschrift 88 (2014) 263-277.

Financial support by Polish National Science Center Grant 2016/21/B/ST10/02332 to A. Pisera.

Varied environments drive rapid divergence in sponge (*Suberites diversicolor*) populations

Diede Maas[1], Ke Bi[2, 3], Stefan Prost[4, 5], Maria Meijer[1], Ludi P. Aji[6], Gandi Purba[7], Rosemary Gillespie[8] & Leontine Becking[1, 8, 9]

[1] Marine Animal Ecology group, Wageningen University & Research, Wageningen, De Elst 1, the Netherlands. diede.maas@wur.nl

[2] Museum of Vertebrate Zoology, Valley Life Sciences Building, University of California, Berkeley, CA, USA

[3] Computational Genomics Resource Laboratory California Institute for Quantitative Biosciences, University of California, Berkeley, CA, USA

[4] Department of Biology, Stanford University, Stanford, USA

[5] Department of Integrative Biology, Center for Theoretical Evolutionary Genomics, University of California, Berkeley, CA, USA

[6] Marine Life Conservation Unit, Indonesian Institute of Sciences (LIPI), Bosnik Raya, Biak, Papua

[7] Marine and Fisheries Department, University of Papua (UNIPA), Manokwari, Papua

[8] EvoLab, Department of Environmental Science, Policy, and Management, University of California, Berkeley, CA, USA

[9] Naturalis Biodiversity Center, Darwinweg 2, Leiden, the Netherlands

The nature of dispersal barriers for marine taxa often remains elusive. Here, we studied the relative role of stochastic and deterministic variables influencing population divergence, by comparing multiple replicate populations of sponges from marine lakes. Marine lakes are land-locked bodies of seawater with a variable connection with the surrounding sea via subterranean fissures. Furthermore, each lake has a distinct environmental regime (defined as water temperature, salinity and pH). Marine lakes with their discrete populations provide a unique model to study early stages of evolution in coastal marine taxa. We selected lakes that have comparable ages (~ 8000 years) and sizes (~15000 m^2), but which vary in degree of connection to the open sea and environmental regimes. Using population genomic methods (double-digest restriction site associated DNA, ddRAD) we studied populations of *Suberites diversicolor* from 8 marine lakes and three adjacent sea locations. In this study ddRAD proved to be a useful and cost-effective method for both phylogeographic and population genomic analyses of sponges. We found strong genetic structure and in most cases strong divergence between populations (pairwise F_{ST} ranged from 0.54 - 0.63). Admixture analyses furthermore showed little gene flow between marine lakes, even between lakes only 1-10 kilometres apart. We found that at large spatial scales (> 200 km), stochastic dispersal limitation plays a large role, while preliminary analysis showed that environment plays a significant role in the connectivity and divergence of marine lakes populations at smaller scales (< 30 km). Hence, varied environments can lead to rapid divergence of sponge populations. Understanding how gene flow corresponds with environmental gradients will improve predictions on adaptive capacities of marine species under different climate change scenarios.

The Netherlands Organisation of Scientific Research ALW-VENI #863.14.020

The freshwater sponge fauna of Madagascar: a first assessment

Renata Manconi[1] & Roberto Pronzato[2]

[1] Dipartimento di Scienze della Natura e del Territorio, Università di Sassari, Sassari, Italy

[2] Dipartimento di Scienze della Terra, dell'Ambiente e della Vita, Università di Genova, Genova, Italy r.manconi@uniss.it

Spongillida fauna of Madagascar was known only for a single record on *Spongilla alba* (family Spongillidae) since more than two centuries (1887) from the northern small island of Nosy-Bé. *Metania madagascariensis* (family Metaniidae) was recently described by us from the central highlands.

Two field campaigns were carried out in 2011 and 2016 for a total of *ca*. 80 sampling sites in a wide altitudinal range 0-1600 m asl, along (a) two transects in the Eastern slope and High Plateau, and (b) three transects in the North-Western slope, South-Western slope, and Central-Eastern High Plateau. Sampling season was selected on the basis of rainfalls trend, i.e. at the end of the dry season (September) characterised by the lowest water level in the major hydrographic basins, facing both East (Indian Ocean) and West (Mozambique Channel). A wide range of water bodies, of all climatic areas (*sensu* Köppen), were sampled i.e. springs, streamlets, streams, rivers, crater lakes, and reservoirs, from pristine rainforests to arid lands, and in areas where forests are now relictual due to alteration by human activities (deforestation, agriculture, mining, and farming). Geographic coordinates, altitude, habitat, and micro-habitat data were collected.

Sponges (*ca*. 80 specimens) were discovered in 13 of the sampled sites, in both lentic and lotic water bodies, from 6 out of 9 Malagasy classified climatic areas. Here we report on new records for Madagascar of 5 genera of Spongillidae, i.e. *Corvospongilla*, *Ephydatia, Eunapius, Radiospongilla*, and *Trochospongilla*. The most widespread genera are *Radiospongilla* (5/13 sites), *Trochospongilla* (3/13 sites), and *Eunapius* (3/13 sites). The majority of the samples (over 50) is still problematic. In some cases it is not possible to ascribe them to a presently known genus of Spongillida. Further investigations at the species level are in progress.

From a biogeographic point of view the 7 genera recorded in Madagascar, including *Spongilla* and *Metania* from previous literature are well represented in several continents with many species. *Ephydatia, Eunapius, Spongilla*, *Radiospongilla*, and *Trochospongilla* are widespread worldwide, while *Corvospongilla* and *Metania* show a prevalent Gondwana range. All recorded genera are known from the Afrotropical Region. Once again field campaign, in unexplored lands, yielded the discovery of a diversified Spongillida fauna.

Research financially supported by Regione Autonoma Sardegna (RAS), INTERREG- EU, PRIN-MIUR, and Fondazione Banco Sardegna.

Systematics of marine sponges from the Bay of Plenty, New Zealand

Sam McCormack [1], Chris Battershill[2], Michelle Kelly[3], Phil Ross[2] & Ian Hogg[2]

[1] University of Waikato, Tauranga, New Zealand samuel.pmccormack@gmail.com

[2] University of Waikato, Tauranga, New Zealand

[3] National Institute of Water and Atmospheric Research Ltd (NIWA), Auckland, New Zealand

Reliable taxonomic assignments are critical to marine conservation strategies, as is an understanding of how biodiversity is distributed. However, the morphological plasticity of marine sponges can make identifications difficult, hence records of distribution patterns can be unreliable and there are frequent gaps in biogeographic knowledge. The need to improve both morphological and molecular based taxonomic methods in order to make it easier to accurately record sponge diversity has been recognised. Here we present a case study of the first taxonomic examination of sponges from a north eastern New Zealand Harbour. Research focused on (1) recording sponge biodiversity from the Bay of Plenty region, (2) undertaking a systematic revision of the fauna correlating classical taxonomy with a modern phylogenetic assessment (3) determine whether identifications based on genetic barcoding are congruent with those produced via traditional morphological methods (alpha taxonomy). Fifty five species are described, of these; there is a possibility of a new genus with eighteen species remaining un-described. We conclude that for New Zealand Demospongiae, sequence variation present in the barcoding region of the COI gene is sufficient to allow for the identification of species.

Progress with Poecilosclerida (Demospongiae: Porifera) – more molecular insights into poecilosclerid phylogeny.

Christine Morrow [1, 2,] Bernard Picton[3] & Grace P. McCormack[1]

[1] Zoology Department, Ryan Institute, School of Natural Sciences, NUI Galway, University Road, Galway, Ireland

[2] Queen's University Marine Laboratory, 12-13 The Strand, Portaferry, Northern Ireland

[3] National Museums Northern Ireland, 153 Bangor Road, Holywood, Northern Ireland

Poecilosclerida with around 2210 species is the largest of the demosponge orders and also one of the most diverse in terms of spicule morphology. In a recent revision of Demospongiae (Morrow & Cardenas, 2015)[1], 5 of the 25 poecilosclerid families were assigned to other orders and the suborder classification, which was based mainly on the presence/absence, and morphology of the chela was abandoned. A new internal classification of Poecilosclerida was considered premature, as there was insufficient molecular data to support it.

The current study is an attempt to fill some the gaps in the molecular classification of Poecilosclerida by analysing newly obtained 18S & 28S rRNA sequences in combination with sequences obtained from previous studies. Species of Hymedesmiidae that possess pore sieves form a monophyletic clade with Crellidae. The genus *Phorbas* appears to be polyphyletic with pore sieve bearing species (including the type taxon *P. amaranthus* Duchassaing & Michelotti, 1864) clustering with Crellidae, whilst species without pore sieves e.g. *P. plumosum* & *P. dives* cluster outside of this clade. The resurrection of *Stylostichon* Topsent, 1892 is proposed for this clade. The study includes 18S & 28S rRNA data from *Desmacidon fruticosum* (Montagu, 1814), the type taxon of Desmascididae Schmidt, 1870. This is the first study to include DNA sequence data from *D. fruticosum* and shows it clustering with *Myxilla (M.) rosacea* [(Lieberkühn, 1859) type taxon of *Myxilla*], inside *Myxilla* Schmidt, 1862 (Myxillidae Dendy, 1922).

This study highlights the enormous amount of work that needs to be done in terms of obtaining DNA sequence data and re-evaluating morphological characters in light of the DNA with the aim of building a more robust phylogeny of Poecilosclerida.

References

[1] Morrow, C., Cárdenas, P., 2015. Proposal for a revised classification of the Demospongiae (Porifera). *Frontiers in Zoology.* 12:7.

We gratefully acknowledge post doctoral funding from the Irish Research Council to C. Morrow.

The peculiar spicules in *Tethyspira*: an apomorphy for *Tethyspira* or a synapomorphy with Raspailiidae?

Christine Morrow [1,2], Bernard Picton[3] & Grace P. McCormack [1]

[1] Zoology Department, Ryan Institute, School of Natural Sciences, NUI Galway, University Road, Galway, Ireland
[2] Queen's University Marine Laboratory, 12-13 The Strand, Portaferry, Northern Ireland
[3] National Museums Northern Ireland, 153 Bangor Road, Holywood, Northern Ireland

Tethyspira Topsent, 1890 is a monotypic genus erected for *Tethea spinosa* Bowerbank, 1874. Topsent initially assigned this genus to Suberitidae but subsequently (Topsent, 1900)[1] created a new family Mesapidae to contain *Mesapos* and *Tethyspira*. *Mesapos* was created for the *Hymeraphia stellifera*, however it has subsequently been returned to *Hymeraphia* (Raspailiidae). The peculiar spination of the acanthostyles are characteristic of *Tethyspira* (Vacelet, 1961)[2].

The distribution of *Tethyspira* is thought to be restricted to the north east Atlantic and Mediterranean where it can be found on wave or current exposed rocky habitats down to 60m. *Tethyspira spinosa* was recorded for the first time from the Mediterranean by Sarà (1958)[3] from a cave in the Gulf of Naples, Sarà assigned it to Poecilosclerina (=Poecilosclerida). Vacelet (1961)[2] reported *Tethyspira spinosa* from Corsica and assigned it to Euryponidae (=Raspailiidae).

Hooper (1991)[4], in his revision of Raspailiidae assigned *Tethyspira* to Raspailiidae (*incertae sedis*) as its taxonomic affinities with Raspailiidae were considered uncertain. Hooper stated that although it has similarities in skeletal structure and spiculation with some raspailiid genera e.g. *Raspaciona,* it is also reminiscent of Hymeniacidonidae. Unlike *Raspaciona* it lacks the ectosomal specialisation, characteristic of raspailiids. The only obvious link between *Tethyspira* and Raspailiidae is the presence of acanthose megascleres.

Based on the external appearance of *Tethyspira* and the skeletal arrangement of ascending parallel bundles of long styles, van Soest et al. (2002)[5] assigned it to Dictyonellidae, interpreting the peculiar spined spicules as an apomorphy for *Tethyspira.*

Our molecular analyses based on 18S and 28S rRNA and mitochondrial COII sequences support the hypothesis that *Tethyspira* is a raspailiid and that the peculiar spined spicules are homologous with basal echinating acanthostyles as in *Eurypon* (Raspailiidae). The lack of ectosomal specialisation in *Tethyspira* whilst unusual amongst raspailiid taxa is not unique as this feature is also absent in *Echinodictyum* and *Amphinomia* (Hooper, 2002)[6].

References

[1] Topsent, E. 1900. Etude monographique des spongiaires de France. III.Monaxonida (Hadromerina). *Archives de Zoologie expérimentale et générale.* (3) 8: 1-331, pls I-VIII.

[2] Vacelet, J. 1961. Spongiaires (Démosponges) de la région de Bonifacio (Corse). Recueil des Travaux de la Station marine d'Endoume 22(36):21-45.

[3] Sarà, M. 1958. Studio sui Poriferi di una grotta di marea del Golfo di Napoli. *Archivo Zoologico Italiano.* 43: 203-281, pls I-II.

[4] Hooper, J. N. A. 1991. Revision of the family Raspailiidae (Porifera: Demospongiae), with description of Australian species. *Invertebrate Taxonomy.* 5(6): 1179-1418.

[5] Hooper, J.N.A.; Van Soest, R.W.M. (Ed.). (2002). Systema Porifera: a guide to the classification of Sponges. Kluwer Academic/Plenum Publishers: New York, NY (USA). ISBN 0-306-47260-0. xix, 1-1101, 1103-1706 (2 volumes) pp.

[6] Hooper, J.N.A. 2002 in Hooper, J.N.A.; Van Soest, R.W.M. (Ed.). (2002). Systema Porifera: a guide to the classification of Sponges. Kluwer Academic/Plenum Publishers: New York, NY (USA). ISBN 0-306-47260-0. xix, 1-1101, 1103-1706 (2 volumes) pp.

We gratefully acknowledge post doctoral funding from the Irish Research Council to C. Morrow.

Clarifying the status of *Raspaciona aculeata* versus *Raspailia aculeata*

Christine Morrow [1,2], Bernard Picton[3] & Grace P. McCormack [1]

[1] Zoology Department, Ryan Institute, School of Natural Sciences, NUI Galway, University Road, Galway, Ireland
[2] Queen's University Marine Laboratory, 12-13 The Strand, Portaferry, Northern Ireland
[3] National Museums Northern Ireland, 153 Bangor Road, Holywood, Northern Ireland

Topsent (1936)[1] erected *Raspaciona* for *Raspailia aculeata* (=*Halichondria aculeata* Johnston, 1842[2]). The type locality for *Raspailia aculeata* is from the coast near Scarborough, east coast of England (coll. Mr Bean). Johnston (1842)[2] described it as follows, "It forms a rude, cellular, brown mass, half an inch in thickness, adhering to its site by a thin membranous basis and hirsute with greyish hairs, formed by the spicula projecting beyond the surface. It is their great length and the circumstance of their protruding beyond the surface, which is characterize the species".

When Topsent (1936)[1] established *Raspaciona* he based it on material which was from the Bay of Beaulieu, Cap Roux and also Banyuls sur Mer, Mediterranean Sea, rather than on the type specimen from the east coast of England. In contrast to the brown sponge described by Johnston, Topsent described his specimen as a brilliant bright red crust with an uneven surface and hispid surface.

We have collected and examined several specimens from the coasts of Britain and Ireland and compared them with the type specimen of Johnston (Norman collection 10.1.1.2327; 2328: Scarborough, collected by Mr. Bean). In terms of external morphology, colour, spiculation and skeletal architecture they match *Raspailia aculeata* (Johnston). We have also collected material from Banyuls sur Mer and the Marseille area (Mediterranean Sea) which matches Topsent's description of *Raspaciona aculeata*. Here we present molecular and morphological data which show that Topsent's *Raspaciona aculeata* is a separate species to *Raspailia aculeata* and we propose a new name for the entity *'Raspaciona aculeata*'.

Raspailia aculeata sensu stricto is very similar to *Raspailia virgultosa* (= *Dictyocylindrus virgultosa* Bowerbank, 1866[3]). The type locality for *Raspailia virgultosa* is from deep water off Shetland. From the description and illustrations given in Bowerbank, it appears to be very similar, if not synonymous with *Raspailia aculeata*. We have examined microscope slide preparations of the type species of both *R. aculeata* and *R. virgultosa* (Norman collection 10.1.1.2352; 2353: off Balta, Sheltand 40-50 fms., 1867) and whilst there are some small differences in the shape and size and of the acanthostyles, we have observed a gradation of morphologies and sizes within our material of *R. aculeata*. Whilst noting the similarities and potential synonymy of *R. virgultosa* with *R. aculeata*, we do not at this stage synonymize the two as we have only studied microscope slides and Bowerbank's description of *R. virgultosa*.

References

[1] Topsent, E. 1936. Sponges observed in the vicinity of Monaco (Part II). Bulletin of the Oceanographic Institute, Monaco (686): 1-70.

[2] Johnston, G. 1842. A History of British Sponges and Lithophytes.(W.H. Lizars: Edinburgh): i-xii, 1-264, pls I-XXV.

[3] Bowerbank, JS 1866a. A Monograph of the British Spongiadae. Volume 2. (Ray Society: London): i-xx, 1-388.

We gratefully acknowledge post doctoral funding from the Irish Research Council to C. Morrow.

Stir it Up! - Support for the movement of the ‘Bob Marley’ sponge, *Pipestela candelabra* from Axinellidae to Bubarida

Christine Morrow [1,2], Olivier Thomas[3], John N.A. Hooper[4,5] & Grace P. McCormack[1]

[1] Zoology Department, Ryan Institute, School of Natural Sciences, NUI Galway, University Road, Galway, Ireland
[2] Queen’s University Marine Laboratory, 12-13 The Strand, Portaferry, Northern Ireland
[3] Marine Biodiscovery Laboratory, School of Chemistry, College of Science, NUI Galway, University Road, Galway, Ireland
[4] Queensland Museum, PO Box 3300, South Brisbane, Queensland, 4101, Australia
[5] Griffith Institute for Drug Discovery, Griffith University, Nathan, Queensland, 4111, Australia

Pipestela candelabra Alvarez, Hooper & van Soest, 2008[1], commonly known as the ‘Bob Marley’ sponge is an erect sponge with multiple cylindrical hollow tubes, reminiscent of Rastafarian dreadlocks. Despite being very common throughout the Great Barrier Reef, Coral Sea, Papua New Guinea and adjacent regions, it was only recently described by Alvarez et al. (2008)[1]. Secondary metabolites from *P. candelabra* contain cytotoxic peptides that selectively inhibited the growth of prostate cancer cells (Tran et al. 2014)[2]. Despite the interest in this species from a biodiscovery perspective, doubt remains regarding its taxonomic affinities.

Alvarez et al. (2008)[1] assigned *Pipestela* to Axinellidae (Halichondrida) noting that it had close affinities with *Cymbastela* and *Auletta*. Morrow & Cardenas (2015)[3] proposed a revised classification of Demospongiae whereby Halichondrida was abandoned, Axinellida was resurrected for Axinellidae, Stelligeridae and Raspailiidae, and Bubarida was established for Bubaridae, Desmanthidae & Dictyonellidae (they cautioned that whilst the type taxa for these families form a monophyletic assemblage, the families themselves are not monophyletic).

In the current study we include for the first time, molecular data for *Pipestela* - 28S rRNA (D3-D5 region) from the type species *P. candelabra* and for *Bubaris vermiculata*, the type taxon of Bubarida. In our molecular analysis *P. candelabra* clusters closely with *Cymbastela stipitata* (type taxon of *Cymbastela*) and *Phakellia ventilabrum* (type taxon of *Phakellia*) inside Bubarida and not with Axinellidae. As our analysis also includes sequence data from *Axinella polypoides*, the type taxon of Axinellidae we can confidently support the reallocation of *Pipestela*, *Cymbastela* and *Phakellia* to Bubarida. From a morphological perspective *Pipestela*, *Cymbastela* and *Phakellia* all possess thin megascleres that are curved, flexuous or sinuous. The megascleres can be oxeas, styles or strongyles, microscleres are absent. In *Axinella sensu stricto* the megascleres are more robust, usually not flexuous or sinuous and microscleres when present are microraphides and trichodragmata.

References

[1] Alvarez, B.; Hooper, J.N.A; Van Soest, R.W.M. 2008. *Pipestela*, a new genus of Axinellidae (Porifera: Demospongiae: Halichondrida) and description of three new species. *Memoirs of the Queensland Museum* 52 (2): 105–118.

[2] Tran, T.D., Pham, N.B., Fechner, G.A., Hooper, J.N., Quinn, R.J. 2014. Potent cytotoxic peptides from the Australian marine sponge *Pipestela candelabra*. *Marine Drugs* 2014 Jun 4; 12 (6):3399-3415

[3] Morrow, C., Cárdenas, P., 2015. Proposal for a revised classification of the Demospongiae (Porifera). *Frontiers in Zoology.* 12:7.

We gratefully acknowledge post doctoral funding from the Irish Research Council to C. Morrow.

A new species of *Hymeraphia* Bowerbank, 1864 from the cold water coral reefs off the south west coast of Ireland.

Christine Morrow[1,2] & A. Louise Allcock[1]

[1] Zoology Department, Ryan Institute, School of Natural Sciences, NUI Galway, University Road, Galway, Ireland
[2] Queen’s University Marine Laboratory, 12-13 The Strand, Portaferry, Northern Ireland

Hymeraphia is a thinly encrusting raspailiid species; to date it is only known from the northeast Atlantic and the Mediterranean Sea. It was considered a monotypic genus until Picton & Goodwin (2007)[1] described two new species from Rathlin Island (Northern Ireland). Recent explorations of the cold water coral reefs off the southwest coast of Ireland using the Marine Institute’s R.V. *Celtic Explorer* and R.O.V. *Holland I* have collected a large number of small encrusting sponges that are either poorly known from the published literature or are new to science.

Here we describe a new species of *Hymeraphia* that is morphologically distinct from other *Hymeraphia* species. 28S rRNA sequences from the variable D1-D2 region show substantial differences between our new species and the other *Hymeraphia* spp. The fact that amongst the Porifera there are still species that are new to science in the relatively well-studied northeast Atlantic is an indication that we are severely underestimating actual sponge diversity.

Small encrusting sponges are often difficult to collect and identify and subsequent molecular analyses can be confounded by problems with insufficient amounts of sample and sponges overgrowing other sponges leading to contamination. As a consequence crusts are often neglected and yet they are important for our understanding of taxonomy, systematics and phylogeography.

References

[1] Picton, B.E.; Goodwin, C.E. (2007). Sponge biodiversity of Rathlin Island, Northern Ireland. *Journal of the Marine Biological Association of the UK.* 87 (6): 1441-1458.

We gratefully acknowledge post doctoral funding from the Irish Research Council to C. Morrow. Deep water samples were collected during cruise CE10004 of R.V. *Celtic Explorer*, using the deepwater Remotely Operated Vehicle *Holland I*, and carried out under the *Sea Change* strategy supported by the Marine Research Sub-programme of the National Development Plan 2007–2013.

Taxonomy of *Corticium* (Porifera: Homoscleromorpha) from Western Australia

Karen Sarmento[1], Anaíra Lage[1], Jane Fromont[2], Guilherme Muricy[1]

[1]Departamento de Invertebrados, Museu Nacional, Universidade Federal do Rio de Janeiro, Brasil.
[2]Department of Aquatic Zoology, Western Australian Museum, Perth, Australia

The genus *Corticium* Schmidt, 1862 (Homoscleromorpha: Plakinidae) is defined by the presence of heterolophose calthrops (candelabra) and includes encrusting to cushion-shaped sponges, with a leuconoid aquiferous system and aphodal choanocyte chambers. Currently seven species are accepted globally, only one of which from Australia: *C. simplex* Lendenfeld, 1907. In this study we redescribe *Corticium simplex* Lendenfeld, 1907 and describe six new species of *Corticium* from Western Australia housed at the Western Australian Museum. One of the species, *Corticium* sp. 1, is massive with peculiar, conspicuous ‘oscule fields’ located on top of some lobes, and another is cushion-shaped (*Corticium simplex*), however, the majority of the species were encrusting, *Corticium* spp. 2–6. Distribution of spicules throughout the sponges varied with species, with some having calthrops mainly in the ectosome and around canals in the choanosome (*Corticium simplex, Corticium* sp. 1), others with a dense crust of candelabra in the ectosome and the choanosome with an alveolar reticulation formed mainly by calthrops (*Corticium* sp. 5). The remainder of the species have a dense skeleton throughout the sponge (*Corticium* sp. 2, *Corticium* sp. 3, *Corticium* sp. 4, *Corticium* sp. 6). Some spicule elaborations were unique to a species such as the candelabra in *Corticium* sp. 4 where the apical actine has an unusual ramification pattern. Some species had aquiferous systems with large canals and a basal cavity (*Corticium simplex, Corticium* sp. 5, *Corticium* sp. 6). This study shows a surprisingly high richness of the genus *Corticium* in Western Australian waters.

Taxonomy of the genus *Plakinastrella* (Porifera: Homoscleromorpha: Plakinidae) from Western Australia

Barbara Fernandes[1, 2], Anaíra Lage[2], Jane Fromont[3] & Guilherme Muricy[2]

[1]Bacharelado em Ciências Biológicas, Pontifícia Universidade Católica do Rio de Janeiro, Brasil.
[2]Departamento de Invertebrados, Museu Nacional, Universidade Federal do Rio de Janeiro, Brasil.
[3]Western Australian Museum, Perth, Australia.

The genus *Plakinastrella* Schulze, 1880 is currently represented by 14 species of encrusting or massive plakinids whose spicules are diods, triods and calthrops, usually with a large size variation. In Australia, only one species of *Plakinastrella* has been reported so far, *P. mammillaris* Lendenfeld, 1907 from SW Australia. The goal of the present study is to identify and describe 12 specimens of *Plakinastrella* from Western Australia housed in the Western Australian Museum. The preparation of spicules and skeleton slides followed the established protocols for Porifera taxonomy. The specimens were separated into four distinct species, all probably new. They are cushion-shaped to massive, with smooth surface, firm to compressible consistency, and the spicules are diods, triods and calthrops of varying size. *Plakinastrella* sp. 1 has cream to light brown color after fixation. The choanosomal skeleton is disorganized or irregularly reticulate. The subectosomal cavities are small, rounded or elongate and the tangential skeleton has primary and secondary meshes circular. Diods are 15-116-235 µm, triod actines 10- 41-99 µm, and calthrops actines 52-141-524 µm. *Plakinastrella* sp. 2 differs from *Plakinastrella* sp. 1 mainly by its color after fixation, dark greyish brown to light brown externally and cream to light brown internally. The choanosomal skeleton is disorganized or irregularly reticulate, with the subectosomal cavities rounded or elongate. It has a tangential skeleton with circular and well defined primary and secondary meshes. Diods are 15-102-188 µm, triod actines 10-41-99 µm, and calthrops actines 52-141-524 µm. *Plakinastrella* sp. 3 is dark brown externally and light brown internally after fixation. The choanosomal reticulation is irregular while the ectosomal skeleton is differentiated, thick, with columnar spicule tracts perpendicular to the surface and subectosomal cavities. The tangential skeleton is well defined with circular primary and secondary meshes. Diods are 15-84-210 µm, and both triods and calthrops are distinctively small, with actines only 7-29-42 µm and 17-20-23 µm, respectively. *Plakinastrella* sp. 4 is brown after fixation, and slightly darker externally than internally. The ectosomal and choanosomal skeletons are dense and disorganized, and without differentiation. Large calthrops are present in both the choanosome and the ectosome. Diods are 20-98-259 µm, triod actines 25-46-109 µm, and calthrops actines 25-138-222 µm. This species is distinguished by its disorganized ectosomal skeleton and the medium-sized calthrops. This study increased the number of species of *Plakinastrella* in Western Australia from one to five, indicating that the diversity of the genus is significantly higher than previously recorded.

High richness of sponges at the mouth of the São Francisco river, in Northeast Brazil: another barrier falls in the Tropical Western Atlantic

Joana Sandes[1, 3], Guilherme Muricy[1], Ulisses Pinheiro[2] & Carmen Parisotto[3]

[1]Museu Nacional, Universidade Federal do Rio de Janeiro, Departamento de Invertebrados, Rio de Janeiro, Brazil.

[2] Universidade Federal de Pernambuco, Departamento de Zoologia, Recife, Brazil.

[3] Universidade Federal de Sergipe, Departamento de Biologia, São Cristóvão, Brazil.

The São Francisco River is one of the most important rivers of Brazil. The continental shelf of Sergipe State in NE Brazil is highly influenced by the plume of sediments brought by the São Francisco, creating a distinct environment predominantly composed of muddy and sandy bottoms. The lack of information about the benthic fauna from this part of the Brazilian continental shelf led many authors to treat this area as a dispersal barrier for benthic organisms, especially corals and sponges (Laborel, 1970; Hechtel, 1976). The aim of this study was to describe the sponge community at the continental shelf of Sergipe State, as part of the monitoring project “Caracterização Ambiental da Bacia de Sergipe e Sul de Alagoas (MARSEAL)”, coordinated by PETROBRAS/CENPES. Samplings were made by trawling in two expeditions during the year 2011, in the dry season (January-February) and in the wet season (June-July). Eighteen sites were sampled at the 10, 25 and 50 m isobaths, arranged in six transects perpendicular to the coast. In each site we weighted each species and calculated the species richness, diversity and evenness of the sponge taxocenosis. Approximately 800 specimens summing up 115 kg wet weight were found in 11 out of the 18 collection sites (61%). They belong to 108 species, of which 66 were identified only to genus and 42 to species level. The most abundant species was *Ircinia* sp. 1 (24.8 kg), followed by *Ircinia strobilina* (14.2 kg), *Aiolochroia crassa* (8.8 kg) and *Myrmekioderma intrastrongyla* (7.0 kg). The total Shannon’s diversity and Pielou’s evenness were H’=1.83 bits.g^{-1} and J=0.27. Shannon’s diversity varied from 0.65 to 3.24 bits.g^{-1} and the total sponge wet weight varied from 3.0 g to 68.7 kg. The diversity, abundance and distribution of the sponge community in the continental shelf of Sergipe State are highly dependent on the sedimentology. The sites with coarse sand and gravel bottoms had higher diversity, evenness and abundance than those with muddy and thin sand substrates. Since the flow rate and sediment load of the São Francisco River are being reduced by droughts and river dams (Medeiros et al., 2014), the proportion of sandy and muddy substrates off its mouth is decreasing, probably leading to an increase in sponge abundance and richness. Here we showed that there is a rich sponge community off the mouth of the São Francisco, which, like the mouth of the Amazon River, should no longer be considered as an effective biogeographical barrier for sponges.

References

1. J. Laborel, Les peuplements de madréporaires des cotes tropicales du Brésil. Annals Univ. Abidjan (série E) 2 (3) (1970) 1-260.
2. G. J. Hechtel, Zoogeography of Brazilian Marine Demospongiae. In: F. W. Harrison, R. R. Cowden, (Eds), Aspects of Sponge Biology. New York & London: Academic Press (1976) 237-260.
3. P. Medeiros, M. Santos, G. Weber, F. Souza, W. Silva, Características ambientais do Baixo São Francisco (AL/SE): efeitos de barragens no transporte de materiais na interface continente-oceano. Geochimica Brasiliensis 28 (1) (2014) 65-78.

Financial support by PETROBRAS/CENPES, CNPq, FAPERJ and FACEPE is gratefully acknowledged.

Rhabdastrella fibrosa Hechtel 1983 and *Geodia corticostylifera* Hajdu et al. 1992 are junior synonyms of *Geodia tylastra* Boury-Esnault, 1973 (Demospongiae: Astrophorina)

Guilherme Muricy

Departamento de Invertebrados, Museu Nacional, Universidade Federal do Rio de Janeiro, Rio de Janeiro, Brasil. muricy@mn.ufrj.br.

The sponge fauna of the Western Atlantic is becoming increasingly well known, but there are several species reported only in the original description and never or very rarely found again. This can be due to this species being either extremely rare or poorly described, hampering their recognition by subsequent authors. Here I investigate the cases of two such species described from Brazil: *Geodia tylastra* Boury-Esnault, 1973 and *Rhabdastrella fibrosa* Hechtel, 1983. After the original descriptions *Geodia tylastra* was never found again and *R. fibrosa* has been reported again only in 2017, in the Guianas. Revision of the two holotypes showed that both are very similar and share a massive, cerebriform shape, a radial skeletal architecture with a well-defined cortex, and both spicule size and shape in SEM with the common Western Atlantic species *Geodia corticostylifera* Hajdu et al., 1992. In the holotypes of all three species the megascleres are oxeas, styles and orthotriaenes and microscleres are sterrasters and oxyasters. The presumed differences previously observed between the three species were mainly due to the lack of photographs of whole specimens and especially of SEM observations of the spicules in the original descriptions of *R. fibrosa* and *G. tylastra*, which were thus almost unrecognizable. According to the ICZN rules, the older name *Geodia tylastra* has priority over the most recent names *Rhabdastrella fibrosa* and *Geodia corticostylifera*, which should be abandoned. *Rhabdastrella fibrosa sensu* van Soest (2017) differs from the holotype in body shape, skeletal architecture and spicule shape, and is given here a new replacement name, *Rhabdastrella vansoesti* sp. nov.

References

1. van Soest, R.W.M. Zootaxa 4217 (2010) 1-225.

Financial support by CNPq, CAPES and FAPERJ is gratefully acknowledged.

Diversity in inferred mitochondrial proteomes in Phylum Porifera

Dennis Lavrov[1], Viraj Muthye

[1]Department of Evolution, Ecology and Organismal Biology, Iowa State University, Ames, Iowa dlavrov@iastate.edu

Mitochondria, subcellular organelles well-known for ATP production through oxidative phosphorylation, are involved in various crucial cellular processes in eukaryotic cells. Mitochondrial genomes in Phylum Porifera show great diversity with respect to size, gene- content and genome-organization [1]. The mitochondrial genome encodes for a minute portion of the mitochondrial proteome, while majority of proteins in the mitochondria are encoded by the nuclear genome and imported into the organelle. Thus, study of mitochondrial evolution and physiology is incomplete without characterizing the mitochondrial proteome. Proteomic experiments which characterize mitochondrial proteins are limited to model species, e.g. MitoCarta2.0 [2]. In this study, we infer and analyze mitochondrial proteomes of 11 sponge species. We use a combination of two approaches: 1] Prediction of N-terminal mitochondrial presequences using TargetP [3] and 2] Reciprocal Best Blast Hit (RBBH) with well- characterized mitochondrial proteomes of human, mouse and yeast (outgroup). We find that the inferred mitochondrial sponge proteomes vary greatly in size. The two calcareous sponges *Leucosolenia complicata* (4958) and *Sycon ciliatum* (3951) have the largest inferred mitochondrial proteomes. While the number of proteins predicted to be mitochondrial by RBBH in the sponges show only a 1.4X difference, the number of proteins predicted by TargetP shows nearly a 12X difference. Around 500 mitochondrial proteins are shared among all four groups in Phylum Porifera - Demospongiae, Homoscleromorpha, Hexactinellida and Calcarea. Nearly 40% of the inferred mitochondrial proteins in the two calcareous sponges *Leucosolenia complicata* and *Sycon ciliatum* have no BLAST hit with the NR database or a RBBH with any of the proteomes under study. 828 protein domains are present in mitochondrial proteomes of all 4 groups of sponges, with Calcarea and Homoscleromorpha having the highest number of group-specific domains.

References

1. D. Lavrov, W.Pett, Genome Biol Evol (2016) 8 (9): 2896-2913
2. S.E.Calvo, C.R. Clauser, V.K. Mootha, Nucleic Acids Res (2016) 44 (D1): D1251-D1257
3. O.Emanuelsson, H.Nielsen, S.Brunak, G. vonHeijne1. J Mol Biol. 2000 Jul 21; 300(4):1005-16.

Financial support by Iowa State University is gratefully acknowledged.

Excavating sponges of Central American Pacific and evidence of a complex of species in *Cliona mucronata*

Cristian Pacheco & José-Luis Carballo

Universidad Nacional Autónoma de México, Instituto de Ciencias del Mary Limnología, 102, Progreso, Col. Santa Catarina, Del. Coyoacán, Ciudad de México

Excavating sponges are one of the main bioeroders in coral reefs worldwide. They have been thoroughly studied in regions like Caribbean, Mediterranean, Indian Pacific and Mexican Pacific. However, there is lack of information in Central American Pacific where only very few records in Panamá and Costa Rica are known. This study provides taxonomic descriptions of species recollected between 2011 and 2016 at nine localities in the Pacific coast of El Salvador, Nicaragua, Costa Rica and Panamá. We identified three orders, three families, five genus and fourteen species of excavating sponges, *Cliona amplicavata, Cliona californiana, Cliona euryphylle, Cliona microstrongylata, Cliona* cf. *mucronata, Cliona pocillopora, Cliona tropicalis, Cliona vermifera, Cliothosa tylostrongylata, Pione* cf. *carpenter, Pione mazatlanensis, Thoosa calpulli, Thoosa mismalolli, Siphonodictyon crypticum* which represent new records for Central America. Also the literature for this region, related with excavating sponges has been reviewed and the taxonomic status of the previous cited species have been updated. A detailed analysis of *Cliona mucronata* was done. This species seems to have a widespread distribution in the Indic Ocean, Pacific Ocean and the Caribbean Sea. Morphological studies and molecular studies using markers such as: COI and 28S, suggest a complex of species between *Cliona mucronata* from Caribbean Sea, Pacific and Indic Ocean.

Suberites From The North Atlantic: Taxonomic Tribulations And Spicule Similitude

Raquel Pereira[1], Mikael Thollesson[1]

[1] *Systematic Biology, Dept of Organismal Biology, Uppsala University, Norbyvägen 18D, SE-752 36 Uppsala, Sweden. raquel.pereira@ebc.uu.se*

The genus *Suberites*, Nardo 1833 was erected for sponges with a velvety surface and confused to alveolar skeleton composed by (sub-)tylostyles, and often with centrotylote, spined, strongyles and/or microxeas. Most of the *Suberites* species are found in shallow, temperate waters, particularly in North Atlantic. However, due insufficient details in many original descriptions, and paucity of morphological characters, the real diversity of this genus is still poorly known. These facts created an extensive list of synonyms for many of the *Suberites* species making it difficult to associate a taxon name to a newly collected specimen. Furthermore, recent studies indicate that neither genus nor family are monophyletic, and the current grouping, based on morphology, is artificial.

In this work we aim to clarify the specific diversity of genus *Suberites* present in North Atlantic by re-examining name-bearing types, as well other historical relevant specimens. This will have further bearings in assessing overlooked species, and will together with molecular markers allow us to obtain a clearer view of species boundaries.

In order to do so we sub-sampled sponge collections in three European museums: the Zoological Museum in Copenhagen (Denmark), the Naturalis Biodiversity Centre (Netherlands), and the Natural History Museum in London (UK).

The preliminary results show that there are useful morphological differences between species, e.g., *Suberites virgultosus* (Johnston, 1842) and *Suberites luetkenii* Schmidt, 1870, which contradicts previous synonymization by Laubenfels (1). Furthermore, we have successfully amplified a small fragment of *coxI* marker (a.k.a mini-barcode) (2) from over half century old formalin fixed museum specimen, and we hope in the future be able to compile a comprehensive barcoding database from the museum specimens which will be further used for validate the morphological species boundaries.

References

1. M. W. de Laubenfels, Smithson. misc. collect. (1953). *121*(6), 1–22;
2. Meusnier. G. A. Singer, J.F. Landry, D. A. Hickey, P. D.Hebert, M. Hajibabaei, M. BMC Genomics (2008), *9*(1), 214.

Financial support by Swedish taxonomic initiative dh 159/09 1.4, and Inez Johansson scholarship is gratefully acknowledged.

The International Associated Laboratory MARRIO (France, Brazil, Ireland): Patterns of sponge biodiversity and chemical diversity from Martinique to Rio de Janeiro

Thierry Pérez [1], Michelle Klautau [2], Olivier P. Thomas [3] and the MARRIO team [4]

[1] *Institut Méditerranéen de Biodiversité et d'Ecologie marine et continentale, CNRS, Aix Marseille Univ, IRD, Avignon Univ. Station Marine d'Endoume, chemin de la Batterie des Lions, 13007 Marseille, France*

[2] *Instituto de Biologia, Departamento de Zoologia, Universidade Federal do Rio de Janeiro, Av. Carlos Chagas Filho 373, CCS, Bloco A, A0-100, Rio de Janeiro, RJ, 21941-902, Brazil*

[3] *Marine Biodiscovery, National University of Ireland Galway, School of chemistry, college of science, University road, Galway, Ireland*

[4] *are also included people from University of Paris VI (France), Universidade do Estado do Rio de Janeiro, Universidade Federal do Bahia, Universidade Federal do San Paulo (Brazil).*

MARRIO is a laboratory without walls, created in 2013, and associating French, Brazilian and Irish scientists to work on three main scientific themes.

Theme 1: Integrative taxonomy for a better understanding of the mechanisms related to the origin of sponge biodiversity. This first topic deals with the biogeographic study of sponge biodiversity in the Caribbean Sea and off the Brazilian coast using independent datasets to develop an integrative approach (morphology, cytology, genetics and metabolomics). In this theme we will (i) improve knowledge on the diversity of sponges from the Caribbean and Brazil; (ii) describe new species from understudied habitats; (iii) access the species distribution in a geographical gradient; (iv) identify endemism; and (v) evaluate the biogeographical proximity between the Caribbean and Brazil, comparing two categories of habitats: fragmented (*e.g.* submarine caves) and non-fragmented.

Theme 2: Populations, phenology and metabolomic variability. Patterns of biodiversity cannot be explained without a good knowledge of the reproductive strategies and of the environmental factors that can influence them. Thus, reproduction mode, sex ratio, production of gametes, reproductive effort, recruitment, and sexual phenotypic plasticity are related to population dynamics, structuring and operation. In this theme, we will (i) consider the life cycle of calcareous and Homoscleromorpha sponges; (ii) analyze the connectivity of Caribbean and Brazilian sponge populations to assess the role of the Amazons as barrier to genetic flow; (iii) describe intra-specific metabolomic variability.

Theme 3: Metabolomics, chemical ecology & development. The third theme concerns more precisely the secondary / specialized metabolites produced by target sponges within the two previous topics. A characteristic of the secondary metabolism is its large diversity and plasticity, which can be induced by adaptation processes of organisms to the environment. This part of the metabolome is then always considered as a «product / indicator» of the natural selection. In this theme, we (i) organize a database on the biodiversity and chemical diversity of Brazilian and Caribbean sponges; (ii) describe secondary / specialized metabolites and their associated bioactivities; (iii) analyze the contribution of symbiotic microorganisms in this metabolism; (iv) define the role of the chemical mediation in the functioning of benthic ecosystems.

LIA MARRIO is an initiative of the French National Center of Scientific Research (CNRS), supported by the Institute of Ecology and Environment (INEE) and Institute of Chemistry (INC), and by Aix Marseille University, CAPES, COFECUB, CNPq and FAPERJ.

New cleistocheliferous species of *Clathria* (*Thalysias*) Duchassaing & Michelotti, 1864 (Microcionidae; Poecilosclerida; Demospongiae) of intertidal zone from Brazil

Thaynã Cavalcanti[1], Rodrigo Alves[1], George Garcia dos Santos[2] & Ulisses Pinheiro[1]

[1] *Universidade Federal de Pernambuco, Centro de Biociências, Departamento de Zoologia, Av. Nelson Chaves, s/n Cidade Universitária CEP 50373-970, Recife, PE, Brazil uspinheiro@hotmail.com*

[2] *Universidade Federal do Cariri, Instituto de Formação de Educadores, Rua Olegário Emídio de Araújo, s/n, 63260-000, Brejo Santo, CE, Brazil*

Clathria (*Thalysias*) Duchassaing & Michelotti, 1864 comprises 97 species worldwide distributed. These species are characterized by two categories of auxiliary styles forming a specialized ectosomal skeleton, the smaller usually forming discrete bundles or a continuous palisade perpendicular to the surface, echinating megascleres present (Hooper, 2002). The presence of cleistocheliferous spicules are found only in one species of *Clathria* (*Thalysias*) from Atlantic Ocean, *Clathria* (*Thalysias*) *sulfocleistochela* Zea, Rodríguez & Martínez, 2014. In Brazil, two species are recorded with the presence of cleistochelae: *Clathria* (*Microciona*) *crassitoxa* Santos & Pinheiro, 2014 and *Clathria* (*Microciona*) *trairae* Santos & Pinheiro, 2014. The aim is described a new species of *Clathria* (*Thalysias*) with cleistochelae from Brazilian coast. The specimens were collected in Pontas de Pedra Beach, Pernambuco State, Brazil (20/IV/2015), in an intertidal zone. *Clathria* (*Thalysias*) sp. nov. is a thickly encrusting sponge, with 1 mm thick, hispid surface and colour orange. Ectosomal skeleton forming erect brushes of large styles through the surface. Choanosoma is composed by subtylostyles organized in disorganized brushes. Pour spongin fibres and distribution of other spicules is not recognized. Spicules are: coanosomal principal styles (287–372.6– 538 / 7–11.2–19 µm): large and smooth; coanosomal small styles (110–157.0–210 / 5– 8.3–12 µm): robust and smooth; tylostyles I (220–268.6–341 / 2–2.6–5 µm): long, thin, smooth, with microspined bases; tylostyles II (96–147.9–165 / 2–2.1–3 µm): long, thin and smooth; cleistochelae I (26–34.1–41): with alae touching, none space between the alae; cleistochelae II (15–17.2–20): shorter but similar to the previous; and toxas (31– 36.3–40 / 1–1.1–1.5): thin and slightly curved. *Clathria* (*Thalysias*) sp. nov is different from the only cleistocheliferous Atlantic Ocean species *Clathria* (*Thalysias*) *sulfocleistochela* by its spicules complement of styles, subtylostyles, acanthostyles, cleistochelae and palmate isochelae. With the description of *Clathria* (*Thalysias*) sp. nov, there are now three cleistocheliferous Brazilian species of *Clathria*, and 98 species of *Clathria* (*Thalysias*) worldwide.

References

1. Hooper, J.N.A. Family Microcionidae Carter, 1875 In: Hooper, J.N.A. & van Soest, R.W.M. (Eds.) Vol. 1. Kluwer Academic / Plenum Publishers, New York, (2002) 432-468.

Financial support by FACEPE (Fundação de Âmparo a Ciência e Tecnologia de Pernambuco) and CNPq (National Counsel of Technological and Scientific Development) is gratefully acknowledged.

Two new species of *Oceanapia* Norman, 1869 (Phloeodictyidae; Haplosclerida; Demospongiae) from slope area of oil and gas exploitation in Rio Grande do Norte State, Northeastern Brazil

Carlos Santos Neto[1], Elielton Nascimento[1], Thaynã Cavalcanti[1] & Ulisses Pinheiro[1]

[1] *Universidade Federal de Pernambuco, Centro de Biociências, Departamento de Zoologia, Av. Nelson Chaves, s/n Cidade Universitária CEP 50373-970, Recife, PE, Brazil uspinheiro@hotmail.com*

The genus *Oceanapia* Norman, 1869 includes sponges with compact external ectosomal crust composed of tangential oxeas, often surrounding a hollow body and numerous ubiquitous fistulae, spicules are oxeas and microscleres, if present, sigmata or toxas (Weerdt 1985). *Oceanapia* currently has 89 valid species, seven are known for Brazilian coast. Two new species of the genus are described for Potiguar Basin, important area of oil and gas exploitation in Northeastern Brazil. Specimens were collected from trawl in a slope area at Rio Grande do Norte State on 2009 and 2011, as part of the Project 'Campanha de Monitoramento Ambiental do Projeto de Caracterização Ambiental do Talude Continental na Bacia Potiguar/ Rio Grande do Norte/ BR' (BPot) sponsored by PETROBRÁS (Petróleo do Brasil S/A). *Oceanapia* sp. nov. 1 consist of a spherical body of 30 cm in diameter. Numerous digitated fistules (0.7–6.5 / 0.5–1.8 cm) of irregular shape are found in the upper side. Surface is hispid and irregular, colour brown (Ethanol 80%). Ectosome composed of an organic layer of single oxeas and debris, supported by a subdermal reticulation. Choanosome includes an irregular network of multispicular tracts. Spicules are oxeas (32–203.8–375 / 2–10.1–13 µm), straight to slightly curved, with acerate, hastate and blunt tips, and sigmas (9–18.2–45 µm). *Oceanapia* sp. nov. 2 has semispherical body, with 7 cm length. Fistules (~1 cm length) located on the top of the body. Rounded oscules on the fistules with 0.2–0.8 diameter. Rough and detachable surface. Colour is cream (Ethanol 80%). Ectosoma with a tangencial crust of spicules. Choanosomal skeleton reticulate with a network of irregular multispicular tracts. Spicules are oxeas (258–284.9–312 / 6–7.7–9 µm), straight to slightly curved, with rounded, telescopic and lobate tips. *Oceanapia* sp. nov. 1 and *Oceanapia* sp. nov. 2 differs from other *Oceanapia* species in Atlantic Ocean by their spicules complement, skeleton architecture and external morphologies. The description of these new species is important to the knowledge of poor known slope areas with high environmental disturber. This study increases to nine species the number of *Oceanapia* from Brazil.

References

1. Weerdt, W.H. A systematic revision of the north-eastern Atlantic shallow-water Haplosclerida (Porifera, Demospongiae): 1. Introduction, Oceanapiidae and Petrosiidae. Beaufortia 35(5), (1985) 61-91.

Financial support by FACEPE (Fundação de Âmparo a Ciência e Tecnologia de Pernambuco) and CNPq (National Counsel of Technological and Scientific Development) is gratefully acknowledged.

The Sponge Genus *Laocoetis* Pomel 1872 (Hexactinellida, Hexactinosida): a Case of Extreme Morphological Conservatism

Andrzej Pisera[1] & Konstantin Tabachnick[2]

[1] *Institute of Paleobiology, Polish Academy of Sciences, ul. Twarda 51/55, 00-818, Warszawa, Poland. apis@twarda.pan.pl*

[2] *P.P. Shirshov Institute of Oceanology, Russian Academy of Sciences, 36, Nakhimovski prospect, Moscow, Russia, 11799 7. tabachnick@mail.ru*

The hexactinellid sponge genus *Laocoetis* Pomel 1872 (earlier known as *Craticularia* Zittel, 1877) belongs to rare examples of a taxon that is based on fossil forms, and its extant representatives have been found only later. Due to the fact that sponges belonging to *Laocoetis* are very characteristic (in result of the regular pattern of canal openings on their surface), they are easily recognizable even by a non-specialist, and thus have a very good fossil record. The fossil sponges of this genus are very common in the Late Jurassic and Cretaceous rocks of Europe, but were also noted in the Australia, Argentina and Antarctica. They occur also abundantly in the Eocene deposits of Spain and Italy, Miocene of Algeria, and in the Pliocene of Sardinia. Despite the fact that these sponges are so common, details of their spiculation (especially ectosomal and gastral spicules) were never properly described. Recent forms, on the other hand, that were discovered only in sixties of the previous century, and that belong to the species *Laocoetis perion* Lévi, 1986, are poorly known because first only small fragments were collected and not all spicular components have been observed. New and well preserved specimens of this sponge from the Madagascar area (the only region where it has been found) allow to study all spicules, including microscleres, and their comparison with exceptionally well preserved the Late Jurassic *Laocoetis parallela* (Goldfuss, 1826) from Poland. The Jurassic specimen, apart from choanosomal dictyonal skeleton, have also ectosomal and gastral spicules preserved, althought microscleres are missing, as it is usually in the fossil state. Comparison of skelton structure (dictyonal skeleton as well as dermal and gastral spicules) of extant and fossil forms, leave no doubts that they belong to different morphospecies. However, observed differences are so small that attribution of extant and fossil forms to the same genus *Laocoetis* is entirely substantiated. It is clear that in the case of *Laocoetis* we deal with the genus that spans at least 150 Ma, being thus a good example of extreme morphological conservatism, already postulated for sponges (Wörheide *et al*. 2008).

References

1. Wörheide G, Epp LS, Macis L.2008. Deep genetic divergences among Indo-Pacific populations of the coral reef sponge *Leucetta chagosensis* (Leucettidae): founder effects, vicariance, or both? *BMC Evol Biol.* 2008. doi: 10.1186/1471-2148-8-24.

Financial support by the Polish National Science Center Grant 2016/21/B/ST10/02332, to A. Pisera.

New Minchinellid Sponge (Calcarea, Lithonida, Minchinellidae) from the Oxfordian (Late Jurasssic) of Russia

Andrzej Pisera[1], Magdalena Łukowiak[1] & Alexandr Guzhov[2]

[1] Institute of Paleobiology, Polish Academy of Sciences, ul. Twarda 51/55, 00-818 Warszawa, Poland, apis@twarda.pan.pl, mlukowiak@twarda.pan.pl

[2] Laboratory of Molluscs Borissiak Paleontological Institute, Profsoyuznaya St., 123 Moscow 117997, Russia, avguzhov.paleo@mail.ru

Minchinellids are calcareans with rigid skeleton composed of articulated, occasionally cemented, spicules (Vacelet 2012, Vacelet *et al*. 2002). Despite their resistant skeletons, they are not common in the fossil record. The oldest minchinellid, *Muellerithalamia* Reitner, 1987, is reported from the Upper Jurassic of Germany (Finks and Rigby 2004). It is composed of monactines, triactines, tetractines and additional cement. Our Late Jurassic finding are minchinellids with basal skeleton composed of articulated tetractines without additional cement. No free spicules have been found. They are small, about 1 to over 5 mm in diameter, round, slightly dome-like sponges with flat base. The fossil specimens are intermediate in morphological features between modern *Plectroninia* Hinde, 1900 and *Monoplectroninia* Pouliquen and Vacelet 1970. They resemble *Plectroninia* in the character of spicules, but in opposition to *Plectroninia*, they have only one size category of tetractines. This last feature makes them similar to *Monoplectroninia.* However, *Monoplectroninia* has very small tetractines, morphologically different from the studied fossil forms. These differences, the fact that free spicules are unknown in the fossil forms, and a large time gap between the fossil and extant forms, allow to propose a new genus for them. Modern *Plectroninia* is common in bathyal zone, while in shallow water it occurs (together with *Monoplectroninia*) only in submarine caves (Vacelet et al. submitted). The Oxfordian minchinellids were found in grey clays along with ammonites and coccolithophores and thus could be interpreted as living in relatively deep (below storm wave base) outer shelf environments. The occurrence of 155-million-year-old minchinellids morphologically very similar to extant forms is another example of high morphological conservatism recognized already among sponges. This fact must be taken into account when discussing the phylogeny of Calcarea in general and Minchinellidae in particular.

References

1. R.M. Finks, J.K. Rigby 2004. *Treatise on Invertebrate Paleontology, Part E (Revised)* Rigby, J.K. ed, Volume 3, Porifera. The University of Kansas, Paleontological Institute, Lawrence (Kansas, USA), 585-733.
2. J. Vacelet 2012. *Treatise on Invertebrate Paleontology On line, Part E (Revised)* Selden P.A. ed., Volume 4, Hypercalcified Porifera. The University of Kansas, Paleontological Institute, Lawrence (Kansas, USA), Chapter 4C, 1-15.
3. J. Vacelet, R. Borojevic, N. Boury-Esnault, M. Manuel M., 2002. *Systema Porifera: A Guide to the Classification of Sponges*. Hooper J.N.A. & Soest R.W.M. van (eds), Kluwer Academic/Plenum Publishers, New York, 1185-1192.

Financial support by the Polish National Science Center Grant 2016/21/B/ST10/02332, to A. Pisera.

A new morphological approach to sponge phylogeny: Homoscleromorpha as a case study

Luis Porras[1], Gert Wörheide[1, 2]

[1]Department of Earth- and Environmental Sciences, Paleontology and Geobiology & GeoBio-Center, Ludwig-Maximilians-Universität München. l.porras@lrz.uni-muenchen.de

Improving our understanding about the phylogeny of sponges is not only central to the debate about the evolution of complexity in animals, it is also essential for the preservation of their biodiversity and future biomedical exploitation.

The use of sequence data in sponge systematics has cleared many previous traditional morphology-based misconceptions, but intra-phylum level relationships still pose some problems. There clearly is a need to produce independent datasets aiming to correct any undetected systematic errors. Morphology is among the simplest solutions, plus, it is the only way to include fossil taxa.

In the past, morphological characters were problematic for reconstructing the phylogeny of sponges, frequently providing little resolution, partly due to the simple bodyplan of sponges and an overreliance on spicule morphology and other highly homoplastic characters, such as body structure. What we propose here is to systematize the knowledge about the embryology and anatomy of sponges in order to build an integrative set for a representative taxon sampling across the phylum. Then, by breaking up complex characters into smaller binary characters we aim to make them comparable and informative across the whole phylum.

We chose homoscleromorphs as a case study here because they share a number of features with both siliceans and calcareans, making them pivotal for our understanding of the sequence of character acquisition in the evolutionary history of sponges. We aim to show why critically constructed morphology sets are necessary, why they are particularly useful for sponge systematics and how we are planning to assemble them.

Integrative taxonomy reveals a new genus and new species of an Antarctic calcinean sponge (Porifera, Calcarea, Clathrinida)

Ana Riesgo[1], Fernanda F. Cavalcanti[2], Nathan J. Kenny[1], Pilar Ríos[3], Javier Cristobo[3], Emilio Lanna[2]

[1] Department of Life Sciences, The Natural History Museum of London, Cromwell Road, London SW7 5BD, UK, A.Riesgo@nhm.ac.uk

[2] Universidade Federal da Bahia, Instituto de Biologia. Rua Barão de Jeremoabo s/n, Ondina, Salvador/Bahia, Brazil. 40170-115.

[3] Instituto Español de Oceanografía, Centro Oceanográfico de Gijon, Avenida Príncipe de Asturias, 70 bis, 33212, Gijón, Spain

In the Southern Ocean, the calcareous assemblage represents approximately 15% of the sponge fauna, with 50 species reported from Antarctica [1, 2]. The Antarctic Calcarea include 11% endemic genera and about 44 endemic species [2]. Among the most abundant and speciose families of calcareous sponges in Antarctica is Leucettidae [2]. While leucettids from Antarctic deep waters are relatively well known [2], the shallow water leucettids are far less studied.

Our study reports on the occurrence of a new genus and species of Leucettidae (Calcinea, Calcarea) from the Southern Ocean, collected in the shallow waters (15 m depth) of Deception and Half Moon Islands, South Shetland archipelago. This new taxon is described based on a combination of morphological and molecular data, including the skeleton composition, description of oocytes, embryos, larvae, and sperm found in the choanosome. While female reproductive elements showed great similarities with those of other calcineans, sperm is reported here for the first time in the whole subclass Calcinea. Sperm cells are flagellated and possess a typical spermatic mid-piece, which is usually observed in cnidarians [3]. In our phylogenetic analyses, our new species appeared as sister species of a clade formed by species of the genera *Leucetta*, *Pericharax* and *Leucettusa*. The proposal of the new genus is supported by morphological features and leads to the reallocation of some species from *Leucetta* to the new genus, which is entirely comprised by Antarctic species so far. Our study reinforces the relevance of integrative approaches in the description of new taxa, and contributes to resolving the poorly known reproductive patterns of Antarctic sponge species.

References

1. R.V. Downey et al. PLoS One 7(2012) e41672
2. H.T. Rapp et al. Zootaxa 3692(2013) 149-159
3. G.W. Hinsch GW. Amer. Zool. 14(1974) 457-465.

Funding by DISTANTCOM project (CTM2013-42667/ANT; Ministry of Economy and Competitiveness of Spain).

New records of *Iotroata acanthostylifera* (Stephens, 1916) and *Janulum spinispiculum* (Carter, 1876) (Porifera) in Flemish Cap (NW Atlantic)

Pilar Ríos[1,3], Francisco Javier Murillo[2,3], Mar Sacau[3], Lucía Alvariño[3], Javier Cristobo[1]

[1] Instituto Español de Oceanografía (IEO), Centro Oceanográfico de Gijón, Av. Príncipe de Asturias 70 bis, 33212 Gijón, Asturias, Spain.pilar.rios.lopez@gmail.com

[2]Bedford Institute of Oceanography1 Challenger Dr, Dartmouth, NS B2Y 4A2, Canada

[3]InstitutoEspañol de Oceanografía (IEO), Centro Oceanográfico de Vigo, Subida Radio Faro, 50, 36390 Vigo, Pontevedra, Spain.

NEREIDA is a Spanish-led multidisciplinary international research project involving active participation by Spain, Canada, UK and Russia. The main objective of the project isthe implementation of the Ecosystem Approach to the fisheries management in order to identify and protect Vulnerable Marine Ecosystems (VMEs) in the NAFO Regulatory Area (NRA) In complying with UNGA Resolutions 61/105 and 64/72, affected nation states, through various regional fisheries management organisations, have responsibility to collect information and implement mitigation measures to ensure the sustainability of deep sea fishing activities according to the principles of the ecosystem approach.

The NEREIDA data collection programme comprised six research cruises conducted between May and July of 2009 and June and August of 2010, on board the Spanish R/V *Miguel Oliver*. The new records were collected in the 4thsurvey (NEREIDA 0610) which covered the southern area of the Flemish Cap. *Iotroata acanthostylifera* (Stephens, 1916) was recorded for the first time off the SW coast of Ireland and four specimens were recorded in three stations between 457 and 1331m depth (Stephens, 1921).

Janulum spinispiculum (Carter, 1876) originally collected in the Cape of St. Vicent (South of Portugal) at 137-684 m depth in *HMS Porcupine* expedition (1869).Kelly *et al*. (2015) summarized the records in the North Atlantic where it was known from the Azores, off the west and north coast of Ireland, the Western Mediterranean Sea, the North Atlantic including Denmark Strait and Iceland, and the Arctic Ocean including the Barents Sea, northern Norway and Spitzbergen between 136 and 1469 m depth.

In this contribution, we add one new record of each species in the Flemish Cap (NW Atlantic), eastern of the Beothuk Knollin NW Atlantic, at 916 m depth. These records are located in an area of high sponge and coral concentrations currently closed to bottom fishing activities to protect sponge grounds VME (NAFO, 2017).

References

Kelly, M.; Erpenbeck, D.; Morrow, C.; Van Soest, R. (2015). First record of a living species of the genus *Janulum* (Class Demospongiae) in the Southern Hemisphere. *Zootaxa.*3980 (2): 255-266 NAFO. 2017. Conservation and enforcement measures. NAFO/FC Doc. 17/01, Serial No N6638. 188 p

Stephens, J. 1921 [1920]. Sponges of the Coasts of Ireland. II. The Tetraxonida (concluded). *Scientific Investigations of the Fisheries Branch. Department of Agriculture for Ireland* 1920(2): 1-75, pls I-VI.

A new sponge-dominated ecosystem found in the Aviles canyon (Cantabrian Sea)

Pilar Rios[1], Francisca C Carvalho[2], Joana R Xavier[2] and Javier Cristobo[1]

[1]Instituto Español de Oceanografía. Centro Oceanográfico de Gijón, C/ Príncipe de Asturias 70 bis, 33212 Gijón, Asturias, Spain. pilar.rios.lopez@gmail.com

[2] Department of Biology and K.G. Jebsen Centre for Deep-Sea Research, University of Bergen, PO Box 7803, N-5020 Bergen, Norway

Sponge-dominated communities are increasingly recognized as key functional ecosystems of the deep-sea. In the past decades, various of such ecosystems have been discovered in the North Atlantic, most of which dominated by species of *Geodia*, *Stryphnus*, *Stelletta*, *Thenea* and *Phakellia* and/or Hexactinellida. Here we report a multispecific aggregation dominated by *Neoschrammeniella bowerbankii*, *Pachastrella monilifera* and *Phakellia robusta*, found between 550-750 m depth in the Corbiro canyon, part of the Avilés canyon system located in the central Cantabrian Sea. From the analysis of the catch resulting from a rock dredge operation we could investigate the diversity and composition of this ecosystem. In terms of biomass, *N. bowerbankii* clearly dominated the community with 70 kg of live specimens and 22 kg of dead specimens collected, followed by *P. monilifera* (20 kg) and *P. robusta* (4 kg). Many taxonomic groups, including other sponges, were found associated with this community, suggesting that it may serve as an important habitat in this area. The future collection of underwater imagery through ROV will allow us to fully describe this community and place it in the context of the North Atlantic deep-sea sponge grounds.

Financial support: this study is part of the SponGES project funded by the European Union's Horizon 2020 research and innovation programme (grant agreement 679849). INDEMARES project was partially funded by the European Commission LIFE + "Nature and Biodiversity" call, and included in the INDEMARES Project (07/NAT/E/000732). The Biodiversity Foundation, of the Ministry of the Environment, was the institution responsible for coordinating this project in which various scientific institutions and NGOs were involved.

Taxonomy of Brazilian Petrosiidae deposited at Museu Nacional / UFRJ

Lívia Rocha, Eduardo Hajdu

Universidade Federal do Rio de Janeiro, Museu Nacional, Quinta da Boa Vista, s/n, 20940-040, Rio de Janeiro, RJ, Brazil. eduardo.hajdu@gmail.com

While over 130 Petrosiidae species are recognized as valid around the world, only eight had been reported from Brazil before this study. The family is distributed in tropical and temperate seas, occurring in a wide depth range (4–1,053 m). Brazilian records comprised *Neopetrosia carbonaria*, *N. proxima*, *N. subtriangularis*, *N. sulcata*, *Petrosia weinbergi*, *Xestospongia grayi, X. kapne* and *X. muta*; and were done mostly in the Northeast region. Our objective was to study Petrosiidae materials from Brazil deposited at the scientific collections of Museu Nacional/UFRJ, undertaking comparisons with type material whenever possible. Collection materials were revised to clear out possible erroneous identifications, generate new records for species previously listed for the country, allow better profiling of intraspecific morphologic variability, and describe new species. The methods used for optical microscopy studies were dissociation of spicules and tangential and transversal anatomic hand-sectioning. From the eight species previously recorded in Brazil, five were re-described in the present study: *viz*. *Neopetrosia carbonaria* (with a new record for Alagoas), *N. proxima* (with new records for Bahia, and the Almirante Saldanha seamount); *Petrosia weinbergi*, *Xestospongia grayi* and *X. muta* (with new records for Ceará, Vitória–Trindade seamounts chain, and off the mouth of the Amazon). *Xestospongia* cf. *wiedenmayeri* was recorded for the first time for the brazilian coast, from Alagoas. Two new species were found, *Petrosia* sp. nov. I, (from Alagoas and Bahia, 5–10 m deep), massive habit and cavernous choanosome, white color with or without purple stains, oxeas I: 133–185 x 5–12 µm, oxeas II: 66–106 x 2–12. *Petrosia* sp. nov. II, (from Pernambuco, Bahia, Espírito Santo and Almirante Saldanha seamount, 15.8–270 m deep), massive to branching habit, varied color (pink to burgundy, white, yellow or beige), ectosomal skeleton formed by the ends of choanosomal tracts, presenting subdermal canals, choanosomal skeleton with rectangular meshes. Oxeas I: 102–305 x 4.8–19.4 µm, oxeas II: 39–97 x 4.8–9.7 µm. The latter was one of the most abundant sponges in the Central V cruise of the REVIZEE Program. *Xestospongia grayi* is considered a junior synonym of *X. muta*. The list of Petrosiidae recorded in Brazil contains nine species now.

Biodiversity of Hymedesmiidae (Porifera, Poecilosclerida) of the Brazilian Coast

Sula Salani[1], Philippe Willenz[2, 3] & Eduardo Hajdu[1]

[1]Museu Nacional, Departamento de Invertebrados, Universidade Federal do Rio de Janeiro, Quinta da Boa Vista, s/n, 2090-040, Rio de Janeiro, RJ, Brazil.

[2]Royal Belgian Institute of Natural Sciences, Taxonomy and Phylogeny, Bruxelles, Belgium.

[3]Université Libre de Bruxelles, Laboratoire de Biologie Marine, Bruxelles, Belgium. sulasm@gmail.com

Only five species of Hymedesmiidae were recorded from Brazil until now: four species of *Phorbas* (*P. amaranthus, P. capixaba, P. fusifer* and *P. hechteli*) and one of *Hemimycale* (*H. insularis*). Recent expeditions along the Brazilian Coast allowed us to recognize 15 species, ten of which are new to science, *Phorbas* (1), *Hymedesmia* (*H.*) (6), *H.* (*Stylopus*) (1), *Hemimycale* (2), including the first record of *Acanthancora* for the Brazilian coast (Fig. 01). The hymedesmioid architecture did not allow differentiation of genera within the family, while the skeletal architecture of pore fields proved to be a specific character. Despite the great affinities between Caribbean and Brazilian marine biota, only one species of Hymedesmiidae was found to occur both in Brazil and the Caribbean, *P. amaranthus*. Twelve species belong only to the Tropical Southwestern Atlantic province, one species belongs only to Warm Temperate Southwestern Atlantic, two belong to both provinces and none belongs to the North Brazil Shelf. The large number of new species found in this family illustrates the importance of studying encrusting species of Porifera, mostly occurring in cryptic microhabitats (sciophilous). The results highlight the richness of the rocky shores of southeastern Brazil and the potential for new species discoveries.

Financial support by CAPES, CNPQ and FAPERJ.

The Western Tropical Atlantic ‘ring’ of rock sponges – A molecular phylogenetic approach using four different markers (28S, 18S, ITS and CO1)

Astrid Schuster[1], Andrzej Pisera[2], Michelle Kelly[3], Shirley A. Pomponi[4], Gert Wörheide[1, 5, 6], Dirk Erpenbeck[1, 6]

1. Department of Earth- & Environmental Sciences, Palaeontology and Geobiology, Ludwig- Maximilians-Universität München, Richard-Wagner Str. 10, 80333 Munich, Germany

a.schuster@lrz.uni-muenchen.de

2. Institute of Paleobiology, Polish Academy of Sciences, u. Twarda 51/55, 00-818, Warszawa, Poland.

3. National Centre for Coasts and Oceans, National Institute of Water and Atmospheric Research, Private Bag 99940, Newmarket, Auckland, 1149, New Zealand.

4. Harbor Branch Oceanographic Institute, Florida Atlantic University, 5600 U.S. 1 North, Ft Pierce, FL 34946, USA.

5. SNSB - Bavarian State Collections of Palaeontology and Geology, Richard-Wagner Str. 10. 80333 Munich, Germany.

6. GeoBio-Center^{LMU}, Ludwig-Maximilians-Universität München, Richard-Wagner Str. 10, 80333 Munich, Germany.

Between 1985 and 2011, numerous oceanographic expeditions in the Western Tropical Atlantic were undertaken by Harbor Branch Oceanographic Institution, Fort Pierce, Florida. Desma-bearing demosponges, historically named ‘lithistid demosponges’, were collected from water depths ranging from two to 950 meters. Those sponges form a polyphyletic group, and are immensely important from a paleontological point of view as they present a fossil record with the highest diversity and best preservation among poriferans. In this study we investigate a substantial part of this extensive collection (~350 specimens) using four different molecular markers (28S, 18S, ITS rDNA, and mitochondrial CO1), representing the largest taxon set ever sequenced for lithistid demosponges from this region. Our molecular systematic approach provides novel insights into the taxonomic diversity and historical biogeography of rock-sponges in the Western Tropical Atlantic.

Dating Demosponge Divergences – New Mitogenomes from ezRAD and the Fossilized Birth-Death Clock Model

Astrid Schuster[1], Sergio Vargas[1], Ingrid S. Knapp[2], Shirley A. Pomponi[3], Robert J. Toonen[2], Dirk Erpenbeck[1, 4,] Gert Wörheide[1, 4, 5]

[1]Department of Earth- & Environmental Sciences, Palaeontology and Geobiology, Ludwig-Maximilians- Universität München, Richard-Wagner Str. 10, 80333 Munich, Germany a.schuster@lrz.uni-muenchen.de

[2]Hawaii Institute of Marine Biology, 46-0007 Lilipuna Road, 96744 Kaneohe, Hawaii, USA

[3]Harbor Branch Oceanographic Institute-Florida Atlantic University, 5600 U.S. 1 North, Ft Pierce, FL 34946, USA

[4]GeoBio-Center^{LMU}, Ludwig-Maximilians-Universität München, Richard-Wagner Str. 10, 80333 Munich, Germany

[5]SNSB - Bavarian State Collections of Palaeontology and Geology, Richard-Wagner Str. 10, 80333 Munich, Germany

An integrative molecular paleobiological approach to better understand the evolution and divergence times within early-branching animal phyla such as Porifera has already been performed, for example for crown-group Hexactinellida and Demospongiae within a node- calibrated Bayesian relaxed molecular clock framework. However, no attempts have yet been made to employ a similar integrative molecular paleobiological approach for demosponges by using the fossilized birth-death (FBD) model. The advantage of FBD compared to several other molecular clock models is the ability to include multiple fossils, without providing morphological data, which can represent either recent taxa or clades. Demosponges, in particular those forming a rigid skeleton of interlocking desmas, are known for their extraordinary fossil preservation and continuous fossil record dating back to the Cambrian (~500 Ma). The majority of these desma-bearing sponges belong to the order Tetractinellida, but some are clearly associated with other demosponge lineages. As an example, molecular phylogenetics showed that the Sphaerocladina, known since the Ordovician, are sister to freshwater sponges, thus representing a key taxon for the reconstruction and understanding the last common ancestor of freshwater and marine sponges. In this study we used 24 fossils and analyzed 33 complete mitochondrial genomes of demosponges, six of which were *de novo* assembled from ezRAD libraries to reconstruct the divergence time for demosponges. ezRAD is an easy-to-implement reduced-genome representation library protocol that allows for the rapid gathering of genome-wide sequence data in non-model organisms. We provide a dated phylogeny of Demospongiae using the FBD model in a relaxed molecular clock framework. Our study provides novel estimates of the divergence times of different demosponge clades with a focus on tetractinellids and the split between Sphaerocladina and freshwater sponges, and discusses the potential usage of this molecular clock model for demosponges.

Deep-water tetractinellid sponges from the Galápagos Islands: first molecular and morphological analysis reveals seven new species

Astrid Schuster[1], Paco Cárdenas[2], Andrzej Pisera[3], Shirley Pomponi[4], Michelle Kelly[5], Gert Wörheide[1, 6, 7], Dirk Erpenbeck[1, 7]

1. Department of Earth- & Environmental Sciences, Palaeontology and Geobiology, Ludwig-Maximilians- Universität München, Richard-Wagner Str. 10, 80333 Munich, Germany. a.schuster@lrz.uni-muenchen.de

2. Department of Medicinal Chemistry Division of Pharmacognosy, BioMedical Centre, Husargatan 3, Uppsala University, 75123 Uppsala, Sweden.

3. Institute of Paleobiology, Polish Academy of Sciences, u. Twarda 51/55, 00-818, Warszawa, Poland.

4. Harbor Branch Oceanographic Institute, Florida Atlantic University, 5600 U.S. 1 North, Ft Pierce, FL 34946, USA.

5. National Centre for Coasts and Oceans, National Institute of Water and Atmospheric Research, Private Bag 99940, Newmarket, Auckland, 1149, New Zealand.

6. SNSB - Bavarian State Collections of Palaeontology and Geology, Richard-Wagner Str. 10. 80333 Munich, Germany.

7. GeoBio-Center^{LMU}, Ludwig-Maximilians-Universität München, Richard-Wagner Str. 10, 80333 Munich, Germany.

The Galápagos archipelago is famed for its exceptional marine fauna and was designated a UNESCO World Heritage Site in 1978. Straddling the equator, its isolated position in the Pacific is influenced by the confluence of cold and warm water currents. The marine invertebrate fauna has been extensively studied and catalogued in recent years, including echinoderms, molluscs, corals and other benthic cnidarians. However, little is known about the deep and shallow water sponge fauna. To date, only 70 sponge species are described, of which 37 are known to be endemic to Galápagos Islands. In particular, no desma-bearing Tetractinellida (Demospongiae) have been discovered, except for one shallow-water species, *Corallistes isabela*. This study focuses on the morphological descriptions of deep-water tetractinellids collected by the HBOI’s Johnson-Sea-Link manned submersible, during the expedition conducted in 1995 and the generation of DNA barcodes for material collected. Morphological descriptions together with the analyses of three different markers (28S rDNA, 18S rDNA, and CO1 mtDNA) reveal seven new species from four different families and five genera: *Neophrissospongia* sp. nov. and *Corallistes* sp. nov. (family Corallistidae), *Racodiscula* (1-3 new species, family Theonellidae), *Craniella* sp. nov. (family Tetillidae) and *Scleritoderma* sp. nov. (family Scleritodermidae). In addition, we re-sampled *Corallistes isabela* from Santiago Island, previously only known from the type locality, Isabela Island.

Morphological descriptions of the ‘lithistid demosponge’ fauna (Porifera, Tetractinellida and Sphaerocladina) from the Western Tropical Atlantic

Astrid Schuster[1], Shirley A. Pomponi[2], Andrzej Pisera[3], Michelle Kelly[4], Gert Wörheide[1,5,6], Dirk Erpenbeck[1,5]

1.Department of Earth- & Environmental Sciences, Palaeontology and Geobiology, Ludwig- Maximilians-Universität München, Richard-Wagner Str. 10, 80333 Munich, Germany. a.schuster@lrz.uni-muenchen.de.

2. Harbor Branch Oceanographic Institute, Florida Atlantic University, 5600 U.S. 1 North, Ft Pierce, FL 34946, USA.

3. Institute of Paleobiology, Polish Academy of Sciences, u. Twarda 51/55, 00-818, Warszawa, Poland.

4. National Centre for Coasts and Oceans, National Institute of Water and Atmospheric Research, Private Bag 99940, Newmarket, Auckland, 1149, New Zealand.

5. GeoBio-Center^{LMU}, Ludwig-Maximilians-Universität München, Richard-Wagner Str. 10, 80333 Munich, Germany.

6. SNSB - Bavarian State Collections of Palaeontology and Geology, Richard-Wagner Str. 10. 80333 Munich, Germany.

The morphological identification of desma-bearing demosponges, historically named lithistids or lithisitd demosponges, has been the focus of several studies from the Northern Atlantic, the Indo- Pacific and the South Pacific region, while the tropical Western Atlantic remains comparatively poorly known. In this study we provide morphological descriptions of taxa collected by Harbor Branch Oceanographic Institution, Fort Pierce, Florida, during expeditions to the Bahamas, Curacao, Turks & Caicos, Puerto Rico, Honduras, Jamaica, Guadeloupe and Bonaire, conducted between 1995 and 2011. Preliminary morphological identifications of 40 taxa indicate that Theonellidae and Corallistidae are the dominant families with the largest geographically distributed faunas amongst the different Caribbean Islands. Representatives of families Neopeltidae and Macandrewiidae are rarer and most likely represent new species. Additionally, several samples were classified as Sphaerocladina. All in all, our morphological inventory of the Western Tropical Atlantic lithistid fauna enlarges the current knowledge on the diversity and distribution of lithistid demosponges from this region.

Gossip – tapping the taxonomic grapevine

Mikael Thollesson [1]

[1] *Dept. Organismal Biology, Evolutionary Biology Centre, Uppsala University, Norbyvägen 18D, SE-752 36 UPPSALA, Sweden. mikael.thollesson@ebc.uu.se*

Taxonomical work on sponges has been made much more tractable by the many excellent resources available, such as Systema Porifera and the World Porifera Database. However, such resources present a synthesis of the current knowledge, whereas the process of taxonomic revisions also involves sifting through, and evaluating, primary sources of nomenclature to arrive at those conclusions. In course of our work on Suberitidae, we implemented the database tool *Gossip* to manage information on taxon names in literature during the process. The central item in *Gossip* is *taxonomic statement*, in this context equivalent to a statement about a name in a specific publication, optionally including a relation to another such statement (e.g., considered referring to same taxon). Collecting taxonomic statements and publications in *Gossip* enables us to trace and visualize the use and relations of names and opinions, e.g., as networks or as timelines, as well as the effects of our own conclusions on the relations.

Gossip is implemented in Java using Spring, backed by a (NoSQL) graph database (Neo4J).

Financial support by Swedish Taxonomy Initiative is gratefully acknowledged.

Taxonomy, distribution and abundance of the shallow common sponges from Nha Trang Bay (Vietnam)

Marta Turon[1] **& Maria J.Uriz**[1]

[1] *Centre d'Estudis Avançats de Blanes, CEAB-CSIC, Accés Cala St.Francesc 14, Blanes, Girona, 17300, Spain. mturon@ceab.csic.es*

Sponges are important components of the benthic communities all over the world; therefore, their identification is on the basis of many ecological studies. However, the true sponge diversity remains underestimated due to both the insufficient taxonomic studies in certain areas and the presence of morphologically cryptic species. Our aim was to characterize the sponge diversity of three differentiated habitats: vertical rocky walls, well-preserved coral reefs, and eutrophic coral reefs in the bay of Nha Trang (Central Vietnam). We photographed and collected 208 sponge specimens along 25 m long transect lines, randomly placed in the three habitats at depths between 3m and 9m. Sponges were identified at the lowest taxonomic level possible by both molecular and morphological features. Partitions encoding the 18S and 28S rRNA, as well as the cox1 mitochondrial gene, were amplified and sequenced to identify the species genetically. External and skeleton characters such as spicule types and sizes through light and electron (SEM) microscopy, as well as their arrangement were also recorded to describe the species in the traditional way (Hooper & Van Soest 2002). The specimens collected belonged to 71 species, 42 genera, 23 families, and 11 orders of Demospongiae. The three study habitats differed in sponge diversity and abundance. Most species were ambient-specific and only two species (*Gellioides cf. gracilis* and *Clathria reinwardti*) inhabited the three sampled habitats and were not found in the reefs explored. Differences were also notable between the well preserved and the highly eutrophic habitats, with higher species richness in the former and higher sponge coverage in the later. The dominant species in the clean environments (*Aaptos suberitioides* and *Neofibularia hartmani*) were absent from the eutrophic zones, which were dominated by *Amphimedon sp.* and *Clathria reinwardti,* (accounting for more that 50% of the sponges).

This study quantifies the most abundant sponges in rocky, well-preserved and polluted coral reefs of Nha Trang Bay by combining molecular and morphological identification, which may ease unambiguous identifications in the future.

References

1. Hooper, J.N.A., van Soest, R.W.M. (Eds.), 2002. *Systema Porifera,* A Guide to the Classification of Sponges. Kluwer Academic/Plenum Publishers, New York.

Financial support by he Spanish Ministry of Science and Innovation through the project MarSymbiOmics (CTM2013-43287-P) is gratefully acknowledged.

Evolution of key biomineralization genes in calcareous sponges

Oliver Voigt[1]**, Maja Adamska**[2]**, Marcin Adamski**[2]**, David J Miller**[3]**, Gert Wörheide**[1, 4]**, Benedetta Fradusco**[1]**, Warren Francis**[1] **& Sofia Fortunato**[3]

[1] *Ludwig-Maximilans-Universität Munich, Paleontology and Geobiology, Department of Earth and Environmental Sciences, Richard-Wagner-Str. 10, 80333 Munich, Germany. oliver.voigt@lmu.de*

[2]*Research School of Biology, ANU College of Medicine, Biology and Environment, The Australian National University, Canberra, 46 Sullivans Creek Road, Acton ACT 2601, Australia.*

[3]*ARC Centre of Excellence for Coral Reef Studies, James Cook University, Townsville, Qld 4811, Australia.*

[4]*GeoBio-Center, Ludwig-Maximilians-Universität München, Richard-Wagner-Str. 10, 80333 München, Germany.*

Members of class Calcarea are the only sponges that produce calcite spicules. The calcareous skeleton generally account for a substantial proportion of the biomass of the animal and, by supporting the soft tissue, enables these sponges to achieve larger body sizes. Amongst sponges, the ability to deposit calcite spicules is a synapomorphic trait of the Calcarea, and is thus a key innovation of the group. The genetic bases of this morphological novelty remain unclear, however. Two sub-classes are recognized within the Calcarea and, to date, the focus has been primarily on one of these, the Calcaronea. Genes implicated in calcification of the calcaronean sponge *Sycon ciliatum* include two sclerocyte-specific carbonic anhydrases, two bicarbonate transporters, and several acidic matrix proteins. Here we investigate additional transcriptomic data for members of the Calcinea, the other subclass of calcareous sponges, to identify homologous biomineralization genes. These data provide insights into the evolution of the sponge biomineralization repertoire from the last common ancestor of Calcarea.

Financial support by the German Research Foundation (DFG, Project VO 2238/1-1) is gratefully acknowledged.

Development of A Multilocus-Based Approach for Sponge (Phylum Porifera) Identification: Refinement and Limitations

Qi Yang[1, 2]**, Christopher M.M. Franco**[1, 2]**, Shirley J. Sorokin**[1, 2, 3]**, Wei Zhang**[1, 2]

[1] *Department of Medical Biotechnology, School of Medicine, Faculty of Medicine, Nursing and Health Sciences, Flinders University, Adelaide, South Australia, SA 5042, Australia qi.yang@flinders.edu.au*

[2] *Centre for Marine Bioproducts Development, Flinders University, Adelaide, South Australia, SA 5042, Australia*

[3] *SARDI Aquatic Sciences, 2 Hamra Ave, West Beach, SA 5024, Australia*

DNA barcoding is an effective approach for sponge (Porifera) phylogenetic classification [1-3]. However, so far no reliable molecular protocol is available to aid species identification; using traditional morphological methods is particularly difficult due to frequent homoplasies [4-6]. To address this gap, we developed a multilocus-based Sponge Identification Protocol (SIP) validated by a sample of 37 sponge species belonging to 10 orders from South Australia. The universal barcode COI mtDNA, 28S rRNA gene (D3- D5), and the nuclear ITS1-5.8S-ITS2 region were evaluated for their suitability and capacity for sponge identification. The highest Bit Score was applied to infer the identity. The reliability of SIP was validated by phylogenetic analysis. The 28S rRNA gene and COI mtDNA performed better than the ITS region in classifying sponges at various taxonomic levels. A major limitation is that the databases are not well populated and possess low diversity, making it difficult to conduct the molecular identification protocol. The identification is also impacted by the accuracy of the morphological classification of the sponges whose sequences have been submitted to the database. Re-examination of the morphological identification further demonstrated and improved the reliability of sponge identification by SIP. Integrated with morphological identification, the multilocus-based SIP offers an improved protocol for more reliable and effective sponge identification, by coupling the accuracy of different DNA markers.

References

1. Wörheide, G. & Erpenbeck, D. DNA taxonomy of sponges—progress and perspectives. *J. Mar. Biol. Assoc. U. K.* **87**, 1629-1633 (2007).
2. Erpenbeck, D. *et al.* The phylogeny of halichondrid demosponges: past and present re-visited with DNA-barcoding data. *Org. Divers. Evol.* **12**, 57-70 (2012).
3. Fontaneto, D., Flot, J.-F. & Tang, C. Q. Guidelines for DNA taxonomy, with a focus on the meiofauna. *Mar. Biodiv.* **45**, 433-451 (2015).
4. Hooper, J. N. A. & van Soest, R. W. M. *Systema Porifera. A guide to the classification of sponges*. (Kluwer Academic/Plenum Publishers, 2002).
5. Plotkin, A., Rapp, H. T. & Gerasimova, E. Phylogenetic reconstruction of Polymastiidae (Demospongiae: Hadromerida) based on morphology. *Hydrobiologia* **687**, 21-41 (2012).
6. Morrow, C. C. *et al.* Congruence between nuclear and mitochondrial genes in Demospongiae: a new hypothesis for relationships within the G4 clade (Porifera: Demospongiae). *Mol. Phylogenet. Evol.* **62**, 174-190 (2012).

Financial supports by the National Natural Science Foundation of China (Grant No.41428 and a Chinese Scholarship Council – Ph.D. Scholarship for Qi Yang are gratefully acknowledged.

First records of shallow-water sponges (Demospongiae) from the largest marine no-take zone in South America, the Nazca- Desventuradas Marine Park (SE Pacific)

Julio C. C. Fernandez[1,3], German Zapata-Hernández[2], Eduardo Hajdu[3]

[1] Programa de Pós-Graduação em Oceanografia, Universidade do Estado do Rio de Janeiro, Rio de Janeiro/RJ, Brazil. juliocesarbio@yahoo.com.br

[2] Departamento de Biología Marina, Universidad Católica del Norte, Coquimbo, Chile. zapata.bm@gmail.com

[2] Museu Nacional, Departamento de Invertebrados, Universidade Federal do Rio de Janeiro,Rio de Janeiro, RJ, Brazil. eduardo.hajdu@gmail.com

Although there are reports of sponges from oceanic islands in the SE Pacific (Thiele 1905; Desqueyroux-Faúndez 1990), the single species this far reported from the entire Nazca-Desventuradas Marine Park is *Pseudosuberites hyalinus*, from 160–170 m depth in the Desventuradas Islands Archipelago (van Soest, 2002). Here, three new species of shallow-water sponges (down to 20 m depth) are described from Desventuradas Islands. *Hemimycale* **sp. nov.** (Fig. 1A), which has the smallest spicules in the genus (subtylotes up to 205 × 3 µm only), is now the fifth known species in the genus, and its first record for the entire Pacific Ocean. *Crella* (*Pytheas*) **sp. nov.** (Fig. 1B), which has the smallest spicules in the subgenus (tornotes up to 168 × 3 µm; ectosomal acanthostyles up to 52 × 2.8 µm; larger choanosomal acanthostyles up to 104 × 3.5 µm; smaller choanosomal acanthostyles up to 66 × 3.5 µm; arcuate isochelae up to 14.5 µm). *Spongia* (*Heterofibria*) **sp. nov.** (Fig. 1C–D), which has the thinnest fibers in the subgenus (only up to 55 µm across), is now the seventh known species worldwide, and the first record of *Heterofibria* for the SE Pacific. In addition, *S.* (*H.*) **sp. nov.** is also recorded here from Easter Island (9.7 m depth).

References

Dequeyroux-Faúndez, R. Spongiaires (Demospongiae) de I'lle de Pâques (Isla de Pascua), *Rev. Suis. Zool.* 97 (1990) 373-409.

Thiele, J. Die Kiesel und Hornschwämme der Sammlung Plate. *Zool. Jahrbücher, Supplementun*, 6 (1905) 407-496.

Van Soest, R.W.M. Family Suberitidae Schmidt, 1870. *Systema Porifera. Guide to the Classification of Sponges* (ed. J.N.A. Hooper and R.W.M. Van Soest), Kluwer Academic/Plenum Publishres: New York, Boston, Dordrecht, London, Moscow, V.1, (2022) 227-244.

Financial support by CAPES, CNPq and FAPERJ (Brazil) is gratefully acknowledged.

Posters Sponges and Microbes

Influence of eutrophication pressure on the resilience and sensitivity of sponge-associated microbial community

Jake Ivan Baquiran* & Cecilia Conaco

The Marine Science Institute, University of the Philippines, Diliman, Quezon City, Philippines
**Email address: jpbaquiran@up.edu.ph*

Marine sponges are important members of benthic communities circumglobally as they are involved in bio-erosion and bio-consolidation of reef structures, provide temporary habitat for reef fish recruits, and have the potential to influence benthic or pelagic processes. These sessile, filter-feeding organisms harbor a great diversity of symbiotic microorganisms. The enigmatic and mutualistic relationship between sponges and microbes is supported by metabolic exchange between host and symbionts. Members of the holobiont can share byproducts of carbon dioxide fixation, nitrogen cycling, secondary metabolite synthesis, and dissolved organic matter uptake and conversion. Shifts in environmental factors may modify relationships between sponges and their symbionts, which could possibly influence the abundance and distribution patterns of some host species. In this study, we transplanted fragments of *Callyspongia* sp. from its natural habitat in a seagrass bed to a coral reef area and to a mariculture area in Bolinao, Pangasinan, Philippines. The associated microbial community of the sponge exhibited changes over the six-week observation period. Transplantation to a mariculture area caused the biggest shift in community, based on denaturing gradient gel electrophoresis (DGGE) fingerprinting analysis. These results emphasize the sensitivity of the sponge microbial community to environmental perturbations, specifically coastal pollution caused by intensive fish farming. Further analysis of the changes in the taxonomic diversity and abundance of functional genes represented in the community will provide an indication of the effect of environmental parameters on the sponge symbionts. The findings from this study may point towards potential applications of sponges or the microorganisms within their tissues in clearing organic matter and nutrients from mariculture areas.

References

1. H. Luter, K. Gibb and N. Webster. Frontiers in Microbiology 5 (2014): 216.
2. L. Pita, P. Erwin, X. Turon and S. López-Legentil. PLoS ONE 8(11) (2013): e80307.
3. R. Simister, M. Taylor, P. Tsai and N. Webster. PLoS ONE 7(12) (2012): e52220.
4. T. Thomas, L. Moitinho-Silva and M. Lurgi et al. 2016. Nature Communications 7 (2016):11870.

This study is funded by the Department of Science and Technology of the Philippines through the Accelerated Science and Technology Human Resource Development Program (ASTHRDP) and a grant from the UP MSI Bolinao Marine Laboratory to JIB. Additional support was provided by the University of the Philippines System (ECWRG 2015-1-011) to CC.

Anti-tumoral activities of the sponges of the *Sarcotragus* genus and their associated bacteria

Yosr BenRedjem Romdhane[1], Leila Ktari[1], Marianna Carbone[2], Maria Letizia Ciavatta[2], Margherita Gavagnin[2], Véronique Mathieu[3], Florence Lefranc[4], Radhia Mraouna[1], Abdellatif Boudabous[5], Robert Kiss[3], Ernesto Mollo[2] and Monia Elbour[1]

[1]Institut National des Sciences et Technologies de la Mer (INSTM), Salammbˆo, 2025 Tunis, Tunisia

[2]Consiglio Nazionale delle Ricerche (CNR), Istituto di Chimica Biomolecolare (ICB), 80078 Pozzuoli, Italy

[3]Laboratoire de Cancérologie et de Toxicologie Expérimentale, Faculté de Pharmacie, Université Libre de Bruxelles (ULB), 1050 Brussels, Belgium

[4]Service de Neurochirurgie, Hôpital Erasme, ULB, 1070 Brussels, Belgium

[5]Laboratoire des Microorganismes et Biomolécules actives, Faculté des Sciences de Tunis, 2092 Tunis, Tunisia. Email: yosr.benredjem@gmail.com

Marine sponges of the *Sarcotragus* genus and their symbiotic bacteria are well known for their anti-inflammatory, antioxidant, antimicrobial and anti-tumoral activities. In aim of chemical and biological investigation for both anti-tumoral and anti-microbial activities, several samples of *Sarcotragus* genus and its symbiotic eubacteria were investigated. First, the chemical processing of sponges samples led to purification of three known furanosesterterpene tetronic acids (FTAs) and three known prenylated hydroquinones (PHQs). Their *in vitro* growth inhibitory properties (six purified compounds) have been evaluated for a panel of five human and on murine tumoral cell lines displaying various levels of sensitivity to proapoptotic stimuli. Surprisingly, FTAs and PHQs elicited distinct profiles of growth inhibitory-responses, differing by one to two orders of magnitude in favor of the PHQs for all cell lines. Secondly, a collection of one hundred and four symbiotic bacterial isolates were obtained from thirty specimens of *Sarcotragus* genus. The antimicrobial activities of the collection were assessed using the agar diffusion tests against a panel of 17 pathogenic bacteria species and one fungal species. The results revealed bioactivity of 14.4% of the collection with remarkable inhibition profiles against Gram + and Gram – bacteria species and the yeast *Candida albicans*. Highest level of inhibition was revealed for symbiotic isolates of *Sarcotragus muscarum* with strongest activity against *Pseudomonas fluorescens*. Besides, active isolates were obtained from *Sarcotragus muscarum and Sarcotragus fasciculatus* mainly sampled from Korbous site. The present data represent the first results of Tunisian sponges' activities investigation for symbiotic bacteria and sponge species and represent a promising high level area for bio production and discovery of new drugs.

Keywords: *Sarcotragus*, antibacterial activity, antifungal activity, anti-tumoral activity, FTA, PHQ, sponge associated bacteria, Tunisian coast.

Microbial community dynamics of the mangrove fire sponge, *Tedania ignis*, following time in a sustained mariculture setup

Alexandra Campbell[1] & Julian Marchesi[1, 2]

[1] School of Biosciences, Cardiff University, Sir Martin Evans Building, Museum Avenue, Cardiff, UK CF10 3AX. CampbellA15@cardiff.ac.uk

[2] Centre for Digestive and Gut Health, Imperial College London, London, UK W2 1NY

Sponges contain multitudes of symbiotic microbes with exceptional diversity. Large sequencing projects, such as the Global Sponge Microbiome Project, have shown the diversity of these microbes. Attempts to obtain enough biomass for more detailed experiments remains an issue hindering some areas of research. To this end, several groups have tried to develop a mariculture approach to grow sponges in the laboratory. What is not clear, however, are whether microbial communities in sponges are stable upon entering an *ex situ* mariculture setup and whether we are capturing the active community within the sponge. Wild specimens of *Tedania ignis* were collected and cultivated in a recirculating mariculture setup. Samples were taken at 0 days, 1 week, 2 weeks, 1 month, and 2 months. Environmental *T. ignis* were collected on another trip and flash frozen. Following extraction of gDNA and generation of cDNA from total RNA, sequencing of the V4 hypervariable region of the 16S rRNA gene was performed on a MiSeq.The results showed high abundances of *Endozoicomonas* and *Candidatus Branchiomonas* across all samples. Populations of *Mycobacteria* and *Sulfurovum* were unique to the gDNA samples, with time point changes consisting mainly of unclassified bacteria. Within the cDNA samples, increases in the abundance of unclassified and rarer bacteria such as *Actibacter* and the family Desulfobacteraceae, were observed. Increases in alpha and beta diversity were seen for both the gDNA and cDNA samples as time increased. This research contributes to understanding how the sponge microbiome fluctuates in mariculture, and also to showing differences in diversity by incorporating cDNA into microbiome analyses.

Financial support from the BluePharmTrain project through the MC-ITN (Project ID: 607786) is gratefully acknowledged.

Comparative study of the microbial diversity in four Mediterranean irciniid sponges

Katerina Skaraki[1, 2], Georgios Kotoulas[1], Antonios Magoulas[1], Adriani Pantazidou[2] & Thanos Dailianis[1]

[1] Institute of Marine Biology, Biotechnology & Aquaculture, Hellenic Centre for Marine Research, Heraklion, Greece. thanosd@hcmr.gr

[2] Department of Ecology & Systematics, Faculty of Biology, National & Kapodistrian Univ. of Athens

Our knowledge regarding the diverse and abundant symbiotic microorganisms hosted by sponges is rapidly expanding through the increased use of next generation sequencing technologies [1]. In the present study, we characterize microbial communities associated with four irciniid sponges by investigating species- and tissue-specific patterns. The examined host species, all collected from Crete, Greece, are *Ircinia fasciculata, I. oros*, *I. variabilis*, and *Sarcotragus spinosulus*). Morphological indentification was validated by analyzing the *COI* and *18S* rRNA genes of the sponge specimen under study. The microbial communities of distinct species and tissue sections (mesohyl and ectosome) were assessed by amplicon pyrosequencing of the *16S* rRNA V5-V6 region. Over 138, 000 high quality sequences were obtained, generating more than 900 operational taxonomic units (OTUs at the 97% sequence similarity level). The most dominant bacterial phyla were Proteobacteria (mostly Gamma- Alpha- and Deltaproteobacteria) and Acidobacteria. Archaeal sequences were affiliated to Crenarchaeota and fewer Euryarchaeota. Interestingly, Cyanobacteria were only hosted in *I. fasciculata* and *I. variabilis*, where high abundances were observed. In *I. variabilis* cyanobacteria were found in both ectosomal and mesohyl samples, while in *I. fasciculata* they were present only in the ectosome. Comparison of the microbial communities associated with the studied sponges revealed very different patterns from the surrounding seawater in their vicinity. In general, strong species-specific patterns were observed for all studied sponges, while tissue specificity was only partially evidenced. This study serves as a baseline for the understanding of ecological interactions for sponges that are common and ubiquitous in the Mediterranean coastal environment, as well as sensitive to environmental fluctuations.

References

1. T. Thomas, L. Moitinho-Silva, M. Lurgi *et al.*, Nat. Commun. 7 (2016) 11870.

Financial support was provided by the European Union project MARBIGEN (FP7- REGPOT-2010-1)

Evidence for the mobility of AMR determinants in a marine sponge holobiont

Stephen A. Jackson[1], Lekha Menon Margassery[1], Alan D.W. Dobson[1]

[1]School of Microbiology, University College Cork, Ireland. a.dobson@ucc.ie

Increasing incidences of antimicrobial resistance (AMR) is a growing and urgent problem where microbial infections are becoming harder to treat. This has serious outcomes for patient morbidity and mortality and also has significant negative economic consequences for patients and healthcare systems alike. Indeed, the recent emergence of colistin resistance in China has resulted in an untreatable infection. Projections by the World Health Organisation (WHO) predict that by 2050, a death will occur every 3 seconds from microbial infections if the issue is not ameliorated before then. The lack of new antibiotics reaching the clinic in recent decades serves to exacerbate the problem. While most reported incidences of AMR derive from clinical isolates from infected patients, little is known about the global distribution and diversity of AMR determinants. Marine sponges (*Porifera*) host diverse and dense microbial populations[1] with densities in high microbial abundance (HMA) sponges eclipsing those of soils and animal digestive tracts. Such a species rich environment may harbour genetic repertoires which aid in competitiveness and survival – including antibiotic production and resistance genes. We have investigated the metagenome of a marine sponge, *Cliona celata,* for the presence of AMR gene fragments conferring resistance to 6 common antibiotics of different classes (Kanamycin, Tetracycline, Chloramphenicol, Nalidixic acid, Erythromycin & Penicillin). We have identified AMR gene sequences in the genomes of sponge isolates, on plasmids from those isolates, from the sponge metagenomic DNA and from the sponge plasmidome. Plasmids from sponge isolates were transformed into *E. coli*, conferring the resistance phenotype on that host. Additionally, we have identified integron gene sequences flanking a gene cassette carrying AMR genes suggesting that these genes may be mobile and shared amongst the sponge-associated microbes. We conclude that marine sponges may be important environmental reservoirs of AMR genes which, via mobility, are shared and maintained.

References

1. Taylor MW, Radax R, Steger D and Wagner M. (2007). Sponge-associated microorganisms: evolution, ecology, and biotechnological potential. *Microbiol Mol Biol Rev* **71**:295–347.

Sponge-derived *Pseudovibrio* species exhibit a promising potential toward the discovery of novel bioactive compounds.

Lynn M. Naughton[1], Stefano Romano[2], Fergal O' Gara[3, 4] & Alan D.W. Dobson[*]

[1] School of Microbiology, University College Cork, Western Road, Cork, Ireland. lynn.naughton@ucc.ie

[2] Department of Microbiology and Ecosystem Science, University of Vienna, Austria.romano@microbial-ecology.net

[3, 4] School of Biomedical Sciences, Curtin University, Perth WA 6845, Australia & BIOMERIT Research Centre, School of Microbiology, University College Cork, Western Road, Cork, Ireland. Fergal.Ogara@curtin.edu.au

**School of Microbiology, University College Cork, Western Road, Cork, Ireland. a.dobson@ucc.ie*

Members of the *Pseudovibrio* genus are frequently the most abundant isolates recovered from the culturable bacterial fraction from marine invertebrates, particularly sponges [1-3]. *Pseudovibrio* species previously isolated from the marine sponge, *Axinella dissimilis* off the south coast of Ireland, display a wide spectrum of inhibitory properties against prominent human pathogens, including Methicillin-resistant *Staphylococcus aureus* (MRSA) and *Salmonella enterica* serovar Typhimurium [4]. This bioactivity has been linked to the production of the antibiotic, tropodithietic acid (TDA) [4]. However, several different antimicrobial activity spectra have been identified amongst these and other members of the *Pseudovibrio* genus [5]. Furthermore, molecular approaches have revealed the potential presence of biosynthetic gene clusters (BGCs) involved in the production of secondary metabolites within the genomes of these bacteria [1]. These physiological and genetic clues hint at the possibility of an array of bioactive compounds being produced by these marine bacteria. Using a genome guided approach, we reveal for the first time a wide variety of diverse BGCs present in the genomes of 21 members of the *Pseudovibrio* genus, isolated from a number of marine sources from different geographic locations. We determined that the most abundant classes of BGC present amongst the isolates (i.e. nonribosomal peptide synthetase (NRPS), polyketide synthase (PKS) and hybrid NRPS/PKS gene clusters) showed a low degree of similarity to known BGCs from other bacteria and demonstrated variability within their biosynthetic units, resulting in several different predicted potential peptide structures. We further corroborate our findings by demonstrating non-TDA related bioactivity amongst the *Axinella dissimilis* derived *Pseudovibrio* isolates using deferred antagonism assays. Our results suggest a promising biosynthetic potential exists amongst the *Pseudovibrio*, toward the production of novel compounds.

References

1. A. Esteves, C. Hardoim, J. Xavier, J. Goncalves, R. Costa. FEMS Microb. Eco. 85 (3) (2013) 519-36.
2. N. Webster, R. Hill. Mar. Biol. 138 (2001) 843-851.
3. A. Muscholl-Silberhorn, V. Thiel, J. Imhoff. Microb. Eco. 55 (1) (2008) 94-106.
4. C. Harrington, F. Reen, M. Mooij, F. Stewart, J. Chabot, A. Guerra, F. Glockner, K. Nielsen, L. Gram, A. Dobson, C. Adams, F. O'Gara. Mar. Drugs. 12 (12) (2014) 5960-78.
5. J. O'Halloran, T. Barbosa, J. Morrissey, J. Kennedy, F. O'Gara, A. Dobson. Journal of Appl. Microb. 110 (6), (2011) 1495-508.

Specialization of Microbiomes in Sponge and Coral Hosts

Cara L Fiore, Jessica K Jarett & Michael P Lesser

School of Marine Science, University of New Hampshire, Durham NH, USA. fiorec@appstate.edu

The transcriptional activity of two microbiome communities, one in the sponge host *Xestospongia muta*, and one in the coral host *Montastrea cavernosa*, were compared using metatranscriptome analysis. Putative mRNA reads were annotated using the HUMAnN pipeline allowing for comparative analysis and the functional categories of metabolic pathways (KEGG Orthology, KO) in the two host organisms. Separately, reads were assembled and annotated in order to reconstruct specific metabolic pathways of interest in the two different communities. As expected, the taxonomic composition of the two microbiome communities differ greatly, with lower phylum-level diversity and dominance of *Proteobacteria* in the corals. The sponge microbiome had higher phylum level diversity with groups such as *Nitrospirae* and *Thaumarchaeota* that were not detected in the coral microbiomes. Comparison of read-normalized pathway abundance indicated that photosynthesis, oxidative phosphorylation, phosphonate and phosphinate, and linoleic acid metabolism were elevated in the coral microbiomes. In contrast, chloralkane degradation, xylene degradation, methane oxidation, and most central metabolic pathways (e.g., nucleotide biosynthesis, vitamin biosynthesis) were elevated in the sponge microbiomes. These differences reveal functional characteristics of each microbiome that likely reflect distinct host-microbe interactions. For example, elevated phosphonate metabolism in the coral microbiome may be a result of phosphonate biosynthesis by the coral host, an ability only recently attributed to corals. Reconstruction of metabolic pathways provided a detailed view of the taxonomic and genetic composition underlying the differential pathways. This work sheds new light on the functional diversity of sponge and coral microbiomes and reveals potential metabolic specialization of microbiomes within different invertebrate hosts.

Insights into the microbial diversity of the Mediterranean marine sponge *Haliclona fulva* (Demospongiae: Haplosclerida)

Erika Garcia-Bonilla[1], Pedro de Brito Brandão [2], Thierry Pérez[3], Olivier P. Thomas [3, 4] & Howard Junca[1]

1 RG Microbial Ecology: Metabolism, Genomics & Evolution; Div Ecogenomics & Holobionts | Microbiomas Foundation, Chía, Colombia. ejgb30@gmail.com

2 Laboratorio de Microbiología Ambiental y Aplicada. Departamento de Química, Facultad de Ciencias. Universidad Nacional de Colombia, Bogotá, Colombia.

3 Institut Méditerranéen de Biodiversité et d'Ecologie Marine et Continentale IMBE, UMR 7263 CNRS, Marseille, France.

4 School of Chemistry, Marine Biodiscovery, National University of Ireland, Galway, University Road, Galway, Ireland.

Over the course of the holobiont evolution, marine sponges and assemblages of specific microorganisms had established a symbiotic relationship in which both parts are codependent to perform ecological functions and to colonize different environments. In this study, the microbial community of *Haliclona fulva* and its metabolome were characterized from samples collected in the Mediterranean Sea. Additionally, the influence of the microbiome on seawater surrounding healthy cultured sponge specimens was evaluated in aquaria. Results showed that the microbial community was dominated by EC94 and Cenarchaeales orders, both representing 90%. Core community was composed by 21 members, some belonging to Cyanobacteria, Bacteroidetes and SBR1093. The analysis of seawater samples revealed that there was a strong influence of the sponge microbiome, where abundances of EC94 and Cenarchaeales were extremely higher when compared to extensively reported open seawater core microbiomes. At metabolome level, fulvynes and renierines were identified (1, 2). In general, we found that *H. fulva* exhibited a very characteristic microbiome composition, with highly abundant and defined eubacterial and archaeal types that are otherwise found in very low relative quantities in the marine environment. Thus *H. fulva* could be a natural source and reservoir of those microorganisms. This finding suggests that this symbiotic relationship is highly specific and could have a significant impact contributing to the biological fitness, metabolite production and activity of this sponge species.

References

1. Cimino G, De Stefano S. 1977. Tetrahedron Lett. 15:1325–1328.
2. Nuzzo G, Ciavatta ML, Villani G, Manzo E, Zanfardino A, Varcamonti M, Gavagnin M. 2012. Tetrahedron 68:754–760.

Financing support by Colciencias, Grant EcosNord-Colciencias research cooperation and mobility exchange program (Convocatoria 652-2014). Erika Garcia-Bonilla acknowledges financial support by Colciencias-Colfuturo, Doctoral Grant (Convocatoria 528-2011).

Does a Sponge's Genotype Influence its Microbiome?

Sarah Griffiths[1], Luca Lenzi[2], Anita Lucaci[2], Donald Behringer[3, 4], Mark Butler IV[5] & Richard Preziosi[1]

1 Division of Biology and Conservation Ecology, Manchester Metropolitan University, Chester Street, Manchester, UK. Griffiths.sarahm@gmail.com

2 Centre for Genomic Research, Institute of Integrative Biology, University of Liverpool, Liverpool, UK

3 School of Forest Resources and Conservation, Program in Fisheries and Aquatic Sciences, University of Florida, Gainesville, Florida, USA.

4 Emerging Pathogens Institute, University of Florida, Gainesville, Florida, USA.

5 Department of Biological Sciences, Old Dominion University, Norfolk, Virginia, USA

The microbial communities associated with sponges have attracted a lot of research interest due to their exceptional diversity and complexity. Much remains unknown about the nature of these communities and their interactions with their hosts, but it is clear that they remain host specific despite constant exposure of the host to highly diverse seawater bacterial communities during filter feeding. Although strong microbiome differences exist among sponge species, there are limited studies examining the extent of microbiome variability within species. In other systems, specific genotypes of host or dominant species have been found to influence associated communities, leading to knock-on effects on ecosystem processes and services, sometimes termed 'community genetic effects'. In this study, we investigate the effect of host sponge genotype on the composition of its associated microbial community in *Ircinia campana* (Dictyoceratida, Irciniidae). We use microsatellites to genetically characterise the sponge hosts, and Illumina sequencing of the V4 hypervariable region of 16S rRNA gene to characterise their microbial communities. In doing so, we investigate the variability among microbiomes in the same host species and examine the relationship between host genotype and microbial community composition to address the question: Do more genetically similar hosts harbor more similar microbial communities?

Financial support by the Natural Environment Research Council (NERC) and the NERC Biomolecular Analysis Facility (NBAF) is gratefully acknowledged.

Do sponge microbiomes depend on past water prokaryotic assemblages?

Carla Huete -Stauffer[1] , Joan Cáliz[1] and Maria J. Uriz[1]

[1] *Centre d'Estudis Avançats de Blanes (CEAB)-Consejo Superior de Investigaciones Científicas (CISC)*

The sponge-associated microbial communities are recognized to be mostly species- specific and enriched of certain taxa compared to that of the surrounding environment[1]. Comparison among the sponge microbiome and the water microbial community at the time of sampling show how distinct the communities are. However, water microbial community is dynamic and highly subjected to temporal changes and, in general, to water conditions[2]. Since the microbial community in the sea water changes in its composition and/or relative taxa abundances with time, these changes might influence the composition of the sponge microbiomes in different time lapses. These comparisons preclude conclusions about possible differential enrichment in the sponge tissues of microbes present in the water in previous months to the sampling date. Up to date, studies comparing the sponge-associated microbial community to that present in the water at several time-lags before the sponge was sampled are, to our knowledge, non- existent. Nevertheless, the stability of the sponge microbial community in time has not been largely studied either. We hypothesize that changes in prokaryote diversity occurring in the recent past in the seawater (i.e. months before) may influence the sponge microbiome months after. Our aims were to i) determine whether the microbiome of *Dysidea avara* changes in time and, ii) whether this change is related to changes in the water prokaryotic community with time. With these purposes, we monitored a population of *Dysidea avara* in the Mediterranean for more than a year (14 months) and sampled seasonally a series of random individuals (n=12) as well as monthly samples of the water surrounding the sponges. Water flowing through the channels or microbes attached to the surface are washed previously to DNA extraction, so that remnants of microbes from the water are unlikely to be present at significant amounts when sequencing, which allows assumptions about the specificity of the microbial community found within the sponges. We applied high throughput 16S rRNA amplicon sequencing using universal primers, to further analyze and compare the prokaryotic communities in the water and the sponges at the given times. Some environmental parameters, i.e. temperature, were also considered to explain the possible changes in the prokaryotic communities.

References

[1.] U. Hentschel, J. Piel, S.M. Degnan, M.W. Taylor, Nat. Revs. Microb. 10 (2012) 641-654

[2.] Frías-López J, Shi Y, Tyson GW, Coleman ML, Schuster SC, Chisholm SW, DeLong EF, PNAS 105(10) (2008) 3805–3810

This research was financially supported by BluePharmTrain (FP7 People-ITN, Ref.2013-667786) and MARSYMBIOMICS (Spanish MINECO, CTM2013 43287- P), given to MJU.

In Situ Responses of the Sponge Microbiome to Ocean Acidification

Nora Kandler[1], Muhammad Abdul Wahab[2], Sam Noonan[2], James Bell[1], Nicole Webster[2], and Heidi Luter[1,2]

[1]*School of Biological Sciences, Victoria University of Wellington, Wellington, New Zealand nora.kandler@vuw.ac.nz*

[2]*Australian Institute of Marine Science, Townsville, Qld, Australia*

Microbes are intimately associated with their sponge hosts and can have a major effect on sponge function and fitness, making it important to consider these relationships when studying the impacts of climate change on sponge assemblages. Ocean acidification and global warming are threatening modern reef ecosystems and the Intergovernmental Panel on Climate Change (IPCC 2014) predicts an ocean surface pH decrease of 0.06-0.32 by the end of the century. Morrow et al. (2015) examined the bacterial community composition of three sponge species in Papua New Guinea (PNG) at two sites with different $p\mathrm{CO}_2$ levels (346-624 µatm) and found significant differences for two of the species, with *Cyanobacteria* and *Proteobacteria* OTUs being the primary drivers of variation. To assess the flexibility in microbial symbiosis in response to ocean acidification, we performed a replicated reciprocal transplant experiment with *Coelocarteria singaporensis* and *Stylissa massa* at the same PNG seep sites as used by Morrow and colleagues, comparing how the microbial communities of transplanted sponges changed over time (T=0, T=9 days, T=7 months). The 16S rRNA gene was sequenced using universal primers targeting bacteria and some archaea. Prior to transplantation (T=0), sponge microbiomes were largely consistent with previous reports (Morrow et al. 2015), with the primary exception being an abundant archaeal OTU in *C. singaporensis*, which was not evident in previous studies that utilized different primers. Across all samples, *S. massa* showed a significant difference based on sampling time, with a *Thaumarchaetota* OTU nearly doubling between T=0 and T=7 months. A shift in the microbiome of *C. singaporensis* was observed upon transplantation, with the microbial communities of samples transplanted from the control site to the vent site displaying higher abundances of a *Cyanobacteria* OTU (*Synechococcus*) and a *Chloroflexi* OTU than samples transplanted within the control site. However, the microbial communities of samples transplanted from the vent site to the control site were not significantly different to those samples transplanted within the vent site. Overall, our results suggest that microbial communities associated with sponges are not always static in a changing environment and can change in ways that may ultimately benefit their sponge hosts.

References

[1] K. M. Morrow, D. G. Bourne, C. Humphrey, E. S. Botté, P. Laffy, J. Zaneveld, S. Uthicke, K. E. Fabricius, N. S. Webster. Natural volcanic CO_2 seeps reveal future trajectories for host-microbe associations in corals and sponges. The ISME Journal 9 (2015) 894-908.

[2] IPCC. Climate Change 2014: Synthesis Report. Contribution of Working Groups I, II, and III to the Fifth Assessment Report of the Intergovernmental Panel on Climate Change (2014). Geneva, Switzerland.

Functional transcripts indicate phylogenetically diverse active ammonia-scavenging microflora in sympatric sponges

Guofang Feng[1], Wei Sun[1], Fengli Zhang[1], Sandi Orlić[2] & Zhiyong Li[1]*

1State Key Laboratory of Microbial Metabolism, School of Life Sciences & Biotechnology, Shanghai
Jiao Tong University, Shanghai 200240, China
*2RuđerBošković Institute, Bijeničkacesta 54, 10000 Zagreb, Croatia *zyli@sjtu.edu.cn*

Symbiotic ammonia-scavengers contribute to effective removal of ammonia in sponges. However, the phylogenetic diversity and *in situ* activity of ammonia-scavenging microflora between different sponge species are poorly addressed. Here, transcribed ammonia monooxygenase gene (*amoA*), hydrazine synthase gene (*hzsA*) and glutamine synthetase gene (*glnA*) were analyzed to reveal the active ammonia-scavenging microflora in the sympatric sponges *Theonella swinhoei*, *Plakortis simplex*, *Phakellia fusca*, and seawater. Archaeal *amoA* and bacterial *glnA* transcripts rather than bacterial *amoA*, *hzsA*, and archaeal *glnA* transcripts were detected in the investigated sponges and seawater. The transcribed *amoA* genes were ascribed into two Thaumarchaeota ecotypes, while the transcribed *glnA* genes were interspersed among the lineages of Cyanobacteria, Tectomicrobia, Poribacteria, Alpha-, Beta-, Gamma- and Epsilonproteobacteria. In addition, transcribed abundances of archaeal *amoA* and bacterial *glnA* genes in these sponges have been quantified, showing significant variation among the investigated sponges and seawater. The transcriptome-based qualitative and quantitative analyses clarified the different phylogenetic diversity and transcription expression of functional genes related to microbially-mediated ammonia scavenging in different sympatric sponges, contributing to the understanding of *in situ* active ecological functions of sponge microbial symbionts in marine nitrogen cycling.

Cinachyrella as a model sponge genus for evolution, microbial symbiosis and experimental biology

Jose V. Lopez[1], Nidhi Vijayan[2], Marie L. Cuvelier[1], Cole G. Easson[1], Emily Blake[3], Astrid Schuster[4], Alexandra M. Campbell[6] Yasmin Khan[1], Paco Cárdenas[5]

[1]Halmos College of Natural Sciences and Oceanography, Nova Southeastern University, Ft Lauderdale FL

[2] Kewalo Marine Laboratory, University of Hawaii, 41 Ahui St, Honolulu HI USA

[3]Center for Collaborative Research, Nova Southeastern University, Ft Lauderdale FL USA

[4]Department of Earth- & Environmental Sciences, Palaeontology and Geobiology, Ludwig- Maximilians-Universität München, Richard-Wagner-Str. 10, 80333 Munich, Germany

[5]Department of Medicinal Chemistry, Division of Pharmacognosy, BioMedical Center, Husargatan 3, Uppsala University, 751 23 Uppsala, Sweden

[6] School of Biosciences, Cardiff University, Cardiff, UK

Our laboratory has been studying the sponge genus *Cinachyrella* for the past six years, as it is a common resident of Western Atlantic and Caribbean reefs, including the Florida Reef Tract. At least four, and perhaps up to six, *Cinachyrella* species (*Cinachyrella kuekenthali, C. alloclada 1 & 2, C. apion and C. arenosa)* occur or overlap in the Western Atlantic area. Several traits support the genus use as an experimental system: this sponge can be maintained for weeks and months in aquaculture, can reproduce via viviparous propagation or asexually (albeit at irregular times and unknown cues), and appears resistant to fouling. To date, a draft *Cinachyrella* transcriptome, metagenome and multiple microbiomes from various individuals have been sequenced. We have studied *Cinachyrella* spp. in the field and in laboratory experiments to investigate changes in holobiont physiology and microbial community structure in response to stressors such as crude oil and antibiotics. Electron microscopy of the holobiont ultrastructure has revealed both low and high microbial abundances in various *Cinachyrella* spp. For example, *Cinachyrella kuekenthali* and perhaps other congeners could be considered as high microbial abundance (HMA) sponges via TEM. A broader question regarding *Cinachyrella spp.* and other potential model sponges regards the specificity of their microbial symbiont communities (microbiomes), and their potential effects on holobiont divergence and speciation. For example, a recent study has shown that the presence of mitochondrial group I introns has divided sympatric *Cinachyrella* individuals into at least two *C. alloclada* species; there is also strong correlation of intron presence/absence with divergence in the microbiome composition of these same individuals. This finding suggests that host genetics (i.e. host divergence) can have a strong influence on microbiome structure, via currently unknown factors, even for visually identical, sympatric sponges which appear to have slight genetic differences.

Microbiome changes in diseased *Geodia barretti*

Heidi Luter[1, 2], Raymond Bannister[3], Steve Whalan[4], Tina Kutti[3], Mari Carmen Pineda[2], Nicole Webster[2]

1 School of Biological Sciences, Victoria University of Wellington, Wellington, New Zealand. h.luter@vuw.ac.nz

2 Australian Institute of Marine Science, Townsville, Australia

3 Institute of Marine Research, Bergen, Norway

4 Marine Ecology Research Centre, Southern Cross University, Lismore, Australia

While reports of sponge disease are becoming more frequent, nearly all cases have involved shallow-water, tropical species. Here, we describe the first disease syndrome affecting the deep-water sponge, *Geodia barretti.* Diseased individuals displayed a brown/black discolouration of their tissue, extensive levels of necrosis and tissue disintegration, as well as increased levels of fouling (Fig. 1). Video survey transects revealed up to 20% of the *G. barretti* population in Korsfjorden, Norway displayed disease symptoms. Comparison of the microbial communities between healthy and diseased sponges using 16S rRNA gene sequencing revealed highly distinct community profiles between the different health states. In particular, diseased individuals exhibited higher abundances of taxa commonly associated with diseased and stressed marine invertebrates, including *Bacteroidetes*, *Firmicutes* and *Deltaproteobacteria*. In addition, three Operational Taxonomic Units (OTUs) were found to be exclusively present in diseased individuals and were shared between the disease lesions and the apparently healthy tissue of diseased individuals, suggesting a non-localised infection or dysbiosis. A number of putative pathogens were also elucidated, including a *Bacteroidetes* OTU which shares highest sequence similarity to a bacterial sequence previously associated with *Porites* White Patch Syndrome. Therefore, future experimental work should focus on examining the mechanisms of infection and the functional roles these microorganisms play in disease etiology.

Microbial Community Composition of the Demosponge *Haliclona amboinensis* (Order Haplosclerida) in Bolinao, Philippines

Michael Angelou Nada and Cecilia Conaco

Marine Science Institute, University of the Philippines, Diliman, Quezon City 1101 Philippines

Marine sponges are sessile filter-feeding animals responsible for processes such as reef consolidation and structuring of benthic ecosystems. In addition, sponges link bentho-pelagic processes essential for the retention and transfer of reef-derived nutrients. The sponge microhabitat supports distinct and diverse communities of microbes that contribute to the holobiont metabolic potential. However, only a subset of sponges have been studied in terms of their microbial community composition and this knowledge gap makes it difficult to assess the role of microbial communities in sponges and their potential impacts on biogeochemical cycling and ecosystem processes. In this study, the microbial community composition of *H. amboinensis* was determined. Three replicates of *H. amboinensis* and seawater samples were collected in Malilnep Channel, Bolinao, Pangasinan and sequenced on the Illumina MiSeq300 platform targeting the V3-V4 region of the 16S rRNA gene. Results from the 16S rRNA analysis revealed specific differences in microbial community composition of *H. amboinensis* and the surrounding water. In particular, *H. amboinensis* communities were dominated by Actinobacteria, Planctomycetia, Gamma-proteobacteria, Alpha-proteobacteria and Cyanobacteria. Among these OTUs, Actinobacteria and Planctomycetia were rarely detected in the seawater community suggesting that these taxa are specific to *H. amboinensis*. Although the relative abundance of particular taxa were variable across samples, diversity indices and ordination analysis indicate that *H. amboinensis* houses a relatively stable assemblage of microbes consistently dominated by Actinobacteria, Planctomycetia and Proteobacteria, which is similar to the *A. queenslandica* microbiome. The results of this study highlight the core microbiome of the demosponge, *H. amboinensis*, and provide a basis for future studies aiming to identify the potential response of the sponge holobiont to environmental perturbations and climate change.

References

[1] C. Guzman and C. Conaco. Sci. Rep. 6 (2016) 18774-18784.

[2] J. M. de Goeij, D. van Oevelen, M. J. A Vermeij, R. Osinga, J. J. Middelburg, A. F. P. M. de Goeij and W. Admiraal. Science. 342 (2013) 108-110.

[3] R. A. Fieth, M. A. Gauthier, J. Bayes, K. M. Green and S. M. Degnan. Front. Mar. Sci. 3 (2016) 228.

[4] L. Rix, J. M. de Goeij, C. E. Mueller, U. Struck, J. J. Middelburg., F. C. van Duyl, F. A. Al-Horani, C. Wild, M. S. Naumann and D. van Oevelen. Sci. Rep. 6 (2016) 18715-18726.

[5] T. Thomas, D. Rusch, M. Z. De Maere, P. Y. Yung, M. Lewis, A. Halpern, K. B. Heidelberg, S.

[6] Egan, P. D. Steinberg and S. Kjelleberg. The ISME Journal. 4 (2010) 1557-1567.

This research project is supported by thesis grants from the DOST-ASTHRDP and the UP MSI Bolinao Marine Laboratory to M.A.N. and a grant from the University of the Philippines System (ECWRG 2015-1-011) to C.C.

Phase shifts in microbial symbiont community associated with compromised immunity and death in *Cliona celata* from Skomer Marine Conservation Zone, UK.

Joanne Preston[1] and Mark Burton[2]

1 Institute of Marine Sciences, School Biological Sciences, University of Portsmouth, Ferry Road, Portsmouth, PO4 9LY, UK. Joanne.preston@port.ac.uk.

2 Skomer Marine Conservation Zone, Natural Resource Wales, Fisherman's Cottage, Martin's Haven, Pembrokeshire, SA62 3BJ, UK. Mark.Burton@cyfoethnaturiolcymru.gov.uk.

Healthy, functional sponges drive biogeochemical cycles via bentho-pelagic coupling and provide essential ecological services to the marine environment[1]. Sponges filter large volumes of seawater consuming the microbes there in, and are often implicated in water quality control[2]. During 2013/14, black necrotic tissue, and heavy fouling (notably by barnacles or red algae) were observed in *Cliona celata* at several locations across Skomer Marine Conservation Zone (SMCZ). Sponge tissue necrosis is a stark and worrying indication of reduced resilience and function in one of the most important groups in benthic marine communities. Sponge disease and mass mortality have been associated with extreme sea surface temperature (SST) events in the Mediterranean and tropical waters[3]. This, however, is the first record of sponge disease in the UK. The cause is unknown, but is not presently correlated with abnormal SST. We present 16S rRNA based metagenomic analysis of microbial communities in healthy, fouled and necrotic *Cliona celata* sponges from SMCZ. Dramatic shifts in microbial community composition was observed between the different states of sponge, and furthers our understanding of the role of microbial symbioses in conferring immunological resilience in sponges. This research provides insight into the role of microbial symbionts in reduced functionality and sponge mortality in temperate sponges and could provide the basis of an early biomarker for shifts in benthic ecosystem functioning linked to environmental stressors.

References

1. Maldonado, M., M. Ribes, and F.C. van Duyl, Adv. Mar. Biol. 62 (2012) 113-82.
2. Bell, J.J., Estuar. Coast. Shelf Sci. 79(3) (2008) 341-353.
3. Cebrian, E. *et al*., PLoS One, 6(6) (2011) e20211.

Financial support by Natural Resource Wales is gratefully acknowledged.

Biogeography of prokaryote communities in Indo-Pacific giant barrel sponges.

Thomas Swierts[1], Daniel F. Cleary[2] & Nicole J. de Voogd[1]

[1] Naturalis Biodiversity Center, Leiden, the Netherlands Thomas.Swierts@naturalis.nl

[2] CESAM, Universidade de Aveiro, Aveiro, Portugal

Sponges are one of the oldest living multicellular animals and form symbiotic relationships with complex communities of microorganisms. Many symbionts are sponge host-specific, which is potentially a derivative of co-speciation. However, host- specificity is not necessarily a result from co-speciation, but could also be a result from the fact that certain physical substructures of the sponge offer distinct microenvironments that have supported niche differentiation leading to similar host species specificity patterns. To better understand the driving forces behind the biogeography of sponge associated microbes, research should include closely related sponges with broad distributions and a similar body plan. Giant barrel sponges have a broad distribution on coral reefs around the globe with a complex phylogeny and are thus an ideal model to study the impact of geography and phylogeny on the microbial communities of sponges on an ocean wide scale. In the present study we compared the prokaryotic community of 49 giant barrel sponges from regions across the Indo-Pacific. The results of the present study do not provide strong evidence that host-specificity is related to phylogeny and thus co-evolution in giant barrel sponges. In contrast, our results indicate a strong effect of geography on the sponge prokaryote community. This is to the best of our knowledge the first study that included intricate phylogenetic relationships on an ocean wide scale for comparing the sponge microbiome.

Genetic Variability of SpongeCyanobacteria Symbioses across the Caribbean

Robert W. Thacker [1], Kenan O. Matterson [2], Cole G. Easson [3], Christopher J. Freeman [4]

[1] Department of Ecology & Evolution, Stony Brook University, Stony Brook, New York 11790, USA
robert.thacker@stonybrook.edu

[2] National Museum of Natural History, Smithsonian Institution, Washington, DC 20560, USA

[3] Halmos College of Natural Sciences and Oceanography, Nova Southeastern University, Dania Beach, Florida 33004, USA

[4] Smithsonian Marine Station, Fort Pierce, Florida 34949 USA

Marine sponges frequently host symbiotic, unicellular cyanobacteria classified as *Synechococcus spongiarum*. Previous investigations used Sanger sequencing of the cyanobacterial 16S23S ribosomal RNA internal transcribed spacer (ITS) region to document 13 distinct clades of *S. spongiarum*. These clades are hypothesized to vary in host specificity from generalists to specialists, but the expense and labor involved in Sanger sequencing has limited replication across multiple geographic areas. We developed a highthroughput method to obtain ITS sequences using the Ion Torrent nextgeneration sequencing platform, multiplexing 61 specimens that represented 14 species from 6 locations, as well as positive (cloned sequences inserted into plasmid vectors) and negative controls. Quality filtering and analysis using the mothur pipeline identified 16, 951 *S. spongiarum* sequences, which were subsequently clustered into the 13 known clades. Individual sponge specimens hosted an average of 2.6 *S. spongiarum* clades (ranging from 1 to 5 clades), while individual *S. spongiarum* clades occurred in 1 (Clade G) to 13 (Clade B) host sponge species. The relative abundance of clades hosted by some species varied significantly among locations; for example, *Aplysina cauliformis* hosted 99% Clade A in Martinique but only 33% Clade A in Panama. Similarly, *Ircinia felix* hosted 100% Clade J in Panama, but only 55% Clade J in the Bahamas and Martinique. These data suggest that selective pressures exerted by hosts and/or environmental conditions vary across the Caribbean. Future work will use this method to determine whether experimental manipulations of environmental conditions can change the relative abundance of *S. spongiarum* clades within individual hosts.

Microbial Communities of the Marine Sponge *Xestospongia Muta* at Microhabitat Transitions show Increased Diversity with Depth, a Core Stable Microbiome across Different Seasons and Concurrent Metabolomic Profiles.

Marcela Villegas-Plazas[1], Juan A. Sanchez[2], Dietmar H. Pieper[3] Olivier P. Thomas[4]and Howard Junca[1]

[1] RG Microbial Ecology: Metabolism, Genomics & Evolution, Div Ecogenomics & Holobionts, Microbiomas Foundation, Chia, Colombia, info@microbiomas.org

[2] Laboratorio de Biología Molecular Marina (BIOMMAR), Departmento de Ciencias Biológicas, Universidad de los Andes, Bogotá, Colombia

[3] Microbial Interactions and Processes Research Group, Helmholtz Centre for Infection Research, Braunschweig, Germany

[4]School of Chemistry, Marine Biodiscovery, National University of Ireland Galway, Ireland

Xestospongia muta is one of the most abundant sponge species of the coral reef communities at the Caribbean Sea. Its high ecological significance makes this species a suitable holobiont model for further understanding of the relationships between its symbiotic bacteria and the secondary metabolism it produces. The aim of our study was to identify the composition and changes of the bacterial symbiotic communities and the sponge metabolomic profiles and whether they might be related to environmental conditions such as depth or season, and also if there are correlations between the relative abundance of bacterial symbionts and the concentration of main sponge metabolites. Microbiome composition was determined using Illumina MiSeq platform (V5-V6 region of 16S rRNA gene), and metabolomic analyses were carried out by UHPLC-DAD-ELSD. We identified significant variations in the structure of the communities in relation to the season. We observed a clear increasing trend for bacterial diversity with depth. The metabolic profile evidenced shifting patterns with similarities not ascribed to depth or season and mainly composed by two predominant brominated polyunsaturated fatty acids. No statistically significant dependence was found between any OTU/metabolite pair. A *X. muta* core microbiome across all the specimens collected could be defined; it is composed by

23 different OTUs collectively representing between 10-25% of the total relative abundance.

References

1. Fiore CL, Jarett JK, Lesser MP. Symbiotic prokaryotic communities from different populations of the giant barrel sponge, Xestospongia muta. *Microbiologyopen* 2013;**2**:938–52.
2. Thomas T, Moitinho-Silva L, Lurgi M *et al.* Diversity, structure and convergent evolution of the global sponge microbiome. *Nat Commun* 2016;**7**:11870.

Financial support by the European Commission to EC/FP7 research project consortium MAGICPAH (KBBE-2009-245226), the Colombian Administrative Department for Science, Technology and Innovation - Colciencias for financial support through grants EcosNord-Colciencias (Convocatoria 652-2014) and "*Joven Investigador*" 2012 fellowship to M. Villegas-Plazas and the Universidad de Los Andes for the MSc scholarship to M. Villegas-Plazas is gratefully acknowledged.

Egg deposition by *Rossia palpebrosa* (Cephalopoda: Rossiinae) in deep-sea sponges, in temperate Northwest Atlantic and fringes of polar Canadian Arctic

Vonda E. Wareham Hayes[1], Susanna Fuller[2] & Elizabeth Shea[3]

[1]Department of Fisheries and Oceans Canada, 80 East White Hills Road, St. John's, Newfoundland and Labrador, Canada A1C 5X1 vonda.wareham@dfo-mpo.gc.ca

[2]Ecology Action Centre, 2705 Fern Lane, Halifax, Nova Scotia, Canada B3K 4L3

[3]Delaware Museum of Natural History, 4840 Kennett Pike, Wilmington, DE, USA 19807.

One of the key ecosystem functions of sponges is the provision of habitat. Here we illustrate one association between a deep-water sponge [Porifera: *Mycale* (*Mycale*) *lingua* (Bowerbank, 1866)] and its functional role to a small cephalopod (Cephalopoda: Rossiinae), in temperate Northwest Atlantic and fringes of the polar Canadian Arctic Oceans. In Canada, there is an ongoing effort to identify Ecologically and Biologically Significant Areas for conservation and protection within Canadian jurisdiction, as well as, in adjacent international waters (referred as Vulnerable Marine Ecosystems). As part of this effort, sponges have been collected opportunistically in multispecies research surveys as part of a new initiative, commencing in 2009, to systematically document and speciate sponges. One species identified was *Mycale* (*Mycale*) *lingua*, a common deep-water hexacinellid found from Baffin Island Shelf to the Grand Banks of Newfoundland. Sponge samples were observed with clusters of eggs embedded in the sponge body, nestled within the long spicule tracts. Eggs were identified as the sepiolid cuttlefish *Rossia palpebrosa* Owen, 1834, based on examination of the stage of 28 embryos found developing within the tissue walls of several species of sponges. Eggs showed multiple stages of development, with at least two hatchlings- miniature replicas of adults. Eggs were primarily deposited in *Mycale* (*Mycale*) *lingua*, with additional observations in *M. loveni* (Fristedt, 1887), *Melonanchora elliptica* Carter, 1874, *Iophon piceum* (Vosmaer, 1882), and several unidentified sponges. Densities ranged from 4-18 eggs/sponge; however majority of sponge samples were retrieved in pieces (<15cm) due to fragility of tissue combined with sampling method |(i.e. research trawl activity), making densities conservative estimates. The ecological importance of *R. palpebrosa* as a global prey species is not well understood in this region but are believed to constitute a significantly element in marine food webs. This work highlights the importance of *Mycale* sponges as nurseries for early life stages of *R. palpebrosa* in the Northwest Atlantic, and adds to the general acceptance that sponges play an important role in the provision of habitat, particularly in the deep sea.

Financial support by Fisheries and Oceans Canada is gratefully acknowledged

Structure and Dynamics of Microbiomes Associated with Marine Sponge *Tedania* sp. During Life Cycle

Jing Zhao[1*], Shufei Wu[1], Dexiang Wang[1]

[1]College of ocean and earth science of Xiamen university, Xiamen, 361005, China;
**Corresponding author:sunnyzhaoj@xmu.edu.cn*

The sponge-microorganism association is a classic, complex and primitive phenomenon in nature. The sponge life cycle offers an excellent opportunity to understand the structure, dynamics and stability of microbiomes. *Tedania* sp. is a dominant sponge that is ubiquitous in the Southeastern China Sea. By high-throughput sequencing and Transmission Electron Microscope (TEM), a detailed profile of sponge- associated microbiomes at 7 life stages was described, including adult, embryo-containing spawning adult, embryo, pre-competent larva at 2 hr, 4 hr and 8 hr, post-larva within 1-2 hrs after settlement, and a seawater sample. The microbial consortia associated with the sponges were relatively consistent, and each was different from the seawater microbiome. In a total of 15098 OTUs, 1089 with low abundance which were clustered within 22 bacterial phyla were identified as being exclusively present in sponges. Vibrionales and Mycoplasmatales, which were widespread in the coastal seawater (21.8% and 3.6%), were rare in marine sponges at each developmental stage. The associated microbiomes from each life stage of *Tedania* sp. exhibited a diverse structure and distribution. At the adult stage, Synechococcales (phylum Cyanobacteria) was the dominant bacterial order (up to 37%), but it occurred at an lower frequency in the other samples. Enterobacteriales, Xanthomonadales and Burkholderiales were markedly higher in the larval and settlement stages than in the adult stages. The pre-competent larvae at 8 hr could be a significant event, as indicated by a sharp increase in the OTUs, diversity indices and richness estimates compared with the other samples. Some rare bacterial groups in other sponge stages (<0.01%) and seawater (<0.2%), such as Clostridia (5.6%), Bacteroidia (2%) and e-proteobacteria (1.1%) increased drastically in the HL8. A similar result was confirmed in vertebrates and invertebrates: members of Bacteroidetes and Clostridia are metabolically complementary and affect cell differentiation and development of the epithelium [1-3]. It suggested that the HL8 stage could be a turning point to higher developmental stages with the drastic changes of symbiotic microbiome. In conclusion, this work greatly advances our understanding of the establishment and maintenance of the sponge-microbe association, particularly the potential roles of microbes in the host.

References

1.J Xu, M K Bjursell, J Himrod et al., Science. 299 (2003) 2074-2076.

2. S Fraune and T C Bosch. Proc. Natl. Acad. Sci. U. S. A. 104 (2007) 13146-13151.

3. L Wrzosek, S Miquel, M L Noordine et al., BMC. Biology. 11(2013) 1-13.

Financial support by the Scientific Research Project of Xiamen Southern Ocean Center (Grant 14GYY74NF38) and China Ocean Mineral Resources R&D Association (Grant No. DY-125-22-QY-18) is gratefully acknowledged.

Posters Biomaterials

Sustainable cultivation of sponges in the Eastern Mediterranean Sea: Integrated aquaculture with fish farms

Philip Nemoy[1], Ehud Spanier[1, 2], Dror Angel[1, 2]

[1] Department of Maritime Civilizations, Leon H. Charney School of Marine Sciences, University of Haifa, Israel, Philip.nemoy@gmail.com

[2] Leon Recanati Institute for Maritime Studies, University of Haifa, Israel

Integrated aquaculture of sponges in conjunction with fish farms has been examined by several workers[1, 2]. Existing evidence for the ability of sponges to incorporate effluents from fish cultivation[3] supports the use of sponges as extractive species in Integrated Multi Trophic Aquaculture (IMTA). Co-cultivation of sponges and finfish may result in lower environmental footprint in comparison with monoculture (cultivation of only finfish or only sponges). The present study explores the ecological and technical aspects of sponge cultivation by IMTA at open-sea and land-based fish farms.

Aquaculture on the Mediterranean coast of Israel focuses on finfish production in marine pen nets and inland ponds. Expansion to the offshore zone and diversification of local aquaculture are expected in the near future.

The sponge *Chondrosia reniformis* is abundant on subtidal rocks along the coast, and it has been selected for aquaculture trials due to its high content of collagen, which is valued by the biomedical sector. In our experiments the growth of *C. reniformis* was monitored at an open-sea fish farm and in an integrated fish-sponge tank for a period of 8 months. We also measured the fluxes of dissolved inorganic nitrogen and oxygen through the sponge in order to reveal if sponge-mediated nitrification is enhanced by increased concentrations of ammonium in seawater, which is common in the vicinity of fish farms.

The survival and growth of *C. reniformis* in our experimental IMTA settings were reasonable when compared to other studies, but still insufficient for commercial operations. It is noteworthy that the sea-based culture resulted in lower sponge survival and growth than the land-based one, suggesting that land-based cultivation is a plausible alternative to sea-based farming of some sponge species.

The results and observations of sponge growth and its physiological response to ammonium enrichment provide the groundwork for the use of sponges as extractive species in oligotrophic IMTA systems. Given the generally positive acceptance of new concepts by local aquaculture operators, further evidence is needed regarding the economic profitability in order to promote the adoption of spongiculture by the industry.

References

1. Osinga, R. *et al.* (2010). Sponge aquaculture trials in the East-Mediterranean Sea: new approaches to earlier ideas. *Open Marine Biology Journal*, 4: 74–81.
2. Milanese, M. et al. (2003). The marine sponge *Chondrilla nucula* (Schmidt, 1862) as an elective candidate for bioremediation in integrated aquaculture. *Biomolecular Engineering*, 20(4): 363–368.
3. Ledda, F. D. *et al.* (2014). Mariculture for bacterial and organic waste removal: a field study of sponge filtering activity in experimental farming. *Aquaculture Research*, 45(8): 1389–1401.

Financial support by the FP7 IDREEM project (www.idreem.eu) is gratefully acknowledged.

Isolation and identification of sterols from *Haliclona* sp. from Taiwan

Merran Dunford[1, 2], Sanjeevan Ranjendran[1], Patric Jonsson[1], Ping-Jyun Sung[3], Fang-Rong Chang[4], Achyut Adhikari[5], Sunithi Gunasekera[1], Paco Cárdenas[1]

[1] Department of Medicinal Chemistry, Division of Pharmacognosy, BioMedical Center, Husargatan 3, Uppsala University, 751 23 Uppsala, Sweden. paco.cardenas@fkog.uu.se

[2] Department of Pharmacy and Pharmacology, University of Bath, Bath BA2 7AY, UK

[3] National Museum of Marine Biology and Aquarium, Pingtung 944, Taiwan

[4] Graduate Institute of Natural Products, College of Pharmacy, Kaohsiung Medical University, Kaohsiung 80708, Taiwan

[5] International Centre for Chemical and Biological Sciences, H. E. J. Research Institute of Chemistry, University of Karachi, Pakistan

Sponges are known to harbor a wide spectrum of bioactive compounds of potential pharmaceutical value. In the current study, sterols were isolated from the shallow water *Haliclona* sp. from South Taiwan, and their antimicrobial activity was investigated. A normal phase, open-column chromatography procedure was adopted to isolate sterols from the sponge extract. From the initial NMR experiments, the most abundant compound in the sponge extract was suggested to be β-sitosterol present in a mixture with several other sterols. Subsequently a preparative TLC was utilized to further separate the sterol mixture by using β-sitosterol as a reference. The NMR analysis of the isolated peak having similar R_f value as β-sitosterol from the preparative TLC procedure, gave evidence of a partially purified sterol mixture with the presence of a sterol with an additional double bond to β-sitosterol. The partially purified sterol mixture was determined to have no activity on *Escherichia coli* and *Staphylococcus aureus* at a concentration of less than 0.5 mg/mL.

Financial support from the EU Erasmus programme, the EU Horizon 2020 programme SponGES under grant agreement No. 679849 and an International Collaborative Research Grant (Swedish Research Council).

Deep-sea sponge grounds associated with canyons and seamounts of the Cantabrian Sea

Javier Cristobo[1,2], Pilar Rios[1], Francisco Sánchez[3] & Joana R. Xavier[4]

[1]Instituto Español de Oceanografía (IEO), Centro Oceanográfico de Gijón, Avd. Príncipe de Asturias 70 bis, 33212 Gijón, Asturias, Spain. cristobo@gi.ieo.es

[2]Departamento de Zoología y Antropología Física, Universidad de Alcalá, Alcalá de Henares, Spain

[3]Instituto Español de Oceanografía. Centro Oceanográfico de Santander.

[4] Department of Biology and K.G. Jebsen Centre for Deep-Sea Research, University of Bergen, PO Box 7803, N-5020 Bergen, Norway.

The Cantabrian Sea, located in the South of the Biscay Bay of Biscay is a topographically rich area, comprising several important geomorphological structures such as canyons, seamounts and deep-sea basins that harbour a variety of benthic ecosystems, such as cold-water coral reefs and sponge grounds. Two of such structures – the Aviles Canyon System and Le Danois Bank – have been selected as case study areas in the scope of the EU-funded H2020 project SponGES.

The Avilés Canyon System is a complex canyon and valley system designated since 2014 as a Site of Community Importance as defined in the EC Habitats Directive. The complex is constituted by three main canyons of different morphostructural character: La Gaviera, El Corbiro and Avilés Canyon that have been relatively well characterized in the course of the Life+ INDEMARES project lead by IEO. A peculiar multispecific ground dominated by *Neoschrammeniella bowerbanki*, *Pachastrella monilifera* and *Phakellia robusta* has been found in El Corbiro between 550-750 m depth. In addition, several communities dominated by the glass sponge *Aphrocallistes beatrix* were found between 814 and 1199 m.

Le Danois Bank is a large seamount that rises sharply from the Bay of Biscay abyssal plain at nearly 5000m to 425m at its summit. This seamount was the subject of the ECOMARG project coordinated by IEO during which dense aggregations of *Pheronema carpenteri* and *Phakellia* spp., along with large specimens of *Geodia* sp. (up to 15kg in weight) and of the cup-shaped *Asconema setubalense* (1m in height) were found at 500 m depth. Targeted for many decades by bottom-fisheries (trawl, gillnets and bottom longline) Le Danois was designated a Marine Protected Area in 2011 making it a good case study to investigate recovery trajectories after the establishment of protection measures.

The distribution, community composition and diversity associated to these temperate grounds will be further investigated in the coming years in the course of the SponGES project.

Financial support. This study is part of the SponGES project funded by the European Union's Horizon 2020 research and innovation programme (grant agreement 679849). INDEMARES project (07/NAT/E/000732) was partially funded by the European Commission LIFE + "Nature and Biodiversity" call.

Metabolic characterization of marine sponges, genus Xestospongia using NMR-based metabolic profiling techniques.

Lina M. Bayona[1], Young Hae Choi[1], Hye Kyong Kim[1], Nicole J. de Voogd[2], Peter G.L. Klinkhamer[3]

[1] Natural Products Laboratory, Institute of Biology, Leiden University, Leiden, The Netherlands

[2] Naturalis Biodiversity Center, Leiden, The Netherlands.

[3] Plant Ecology and Phytochemistry, Institute of Biology, Leiden University, Leiden, The Netherlands

Marine organisms are being paid great attention as source of bioactive molecules. Their chemical diversity is very different from terrestrial organisms and this difference serve another set of chemical resource for life science. Of the marine organisms, sponges have been investigated for long time and fount to be one of the most prolific resources of new bioactive compounds, increasing the chemical list by more than 200 new molecules every year. Despite of the chemical diversity, as other marine organisms, the collection as a resource, sponges often have problem with sustainability such as large amount of collection and maintaining chemical quality. Overcoming these problems cultivation of the sponges in controlled aquarium and chemical synthesis of target bioactive compounds have been employed but due to many limitations, the approaches have not been successful yet. Another attempt for sponge production is to investigate them in systems biology way. Particularly, the use of metabolomics to uncover biological or environmental factors influencing metabolome of sponges is one of the most urgent issues in the field.

In this study, as first attempt, we worked for 1H-NMR metabolomics of sponge samples together with multivariate analysis to gain insight into the relation between metabolome and age. As a model, we used 33 samples of the genus *Xestospongia* collected in Taiwan and Martinique and the metabolomics data obtained from 1H NMR analysis were correlated with ages.

We found that samples collected in Martinique there were differences in the metabolic production between juvenile specimens and oldest ones. However, this clear difference was not stablished for the specimens collected in Taiwan. Probably due to the range of ages in Taiwan was smaller than for Martinique. This result may lead to future understanding of changes in production of different families of compounds during different stages of growth on these organisms.

Sponge-derived compounds from Australian chromodorid nudibranchs

Ariyanti S. Dewi [1], Karen L. Cheney [2], Anne E. Winters [2], Holly E. Urquhart [2], Gregory K Pierens [3], Jack K. Clegg [1], Joanne T. Blanchfield[1] & Mary J. Garson[1]

[1]School of Chemistry and Molecular Biosciences, University of Queensland, Australia ariyanti.dewi@uq.net.au

[2]School of Biological Sciences, University of Queensland, Australia

[3]Center of Advanced Imaging, University of Queensland, Australia

As part of our ongoing research of the chemical ecology of Australian nudibranchs, we investigated the secondary metabolites of chromodorid nudibranchs that were sequestered from their sponge diets. Four species of chromodorid nudibranchs were collected along the coast of Queensland and were dissected into mantle and viscera tissues. The chemistry of each specimen was investigated and the distribution of the isolated compounds was analysed. Specimens of *Goniobranchus coi* were found to contain a series of rearranged diterpenes in both the mantle and viscera extracts, including a new compound namely chromolactol possessing an unusual stereochemistry of the [3.3.0]-dioxabicyclo octane ring. From the extract of *Ardeadoris egretta*, more spongian diterpenes were isolated, along with a new 7á-hydroxy-dendrillol-3 that was concentrated in the viscera tissue.[1] The extract of *A. egretta* was toxic and unpalatable against the brine shrimp *Artemia salina* and the shrimp *Palaemon serenus*, respectively.

Different from the other two, nudibranchs of the genus *Miamira* from Southeast Queensland were found to contain hydroxy and methoxy polybrominated diphenyl ethers. A new hydroxy polybrominated diphenyl ether has also been isolated from the mantle extract of *Miamira magnifica.* The extract of *M. magnifica* was highly active in the toxicity assay with an LD_{50} value of 58 μg/mL.[2]

References

1. White, A. M., Dewi, A. S., Cheney, K. L., Winters, A. E., Blanchfield, J. T., Garson, M. J. Nat. Prod. Commun. 11 (2016), 921–924.
2. Dewi, A. S., Cheney, K. L., Urquhart, H. H., Blanchfield, J. T., Garson, M. J. Mar. Drugs. 14 (2016), 198-205.

Financial support by the Australia Awards (ASD, AEW), Australian Pacific Science Foundation (KLC) and the University of Queensland (ASD, KLC, MJG) is gratefully acknowledged.

Visualizing the spatial distribution of barettins and barrettides in the deep-sea sponge *Geodia barretti* using MALDI-TOF mass spectrometry imaging

Gabriella Krogius[1], Mohammadreza Shariatgorji[2], Per Andrén[2], Paco Cárdenas[1]

[1] Department of Medicinal Chemistry, Division of Pharmacognosy, BioMedical Center, Husargatan 3, Uppsala University, 751 23 Uppsala, Sweden. gabriella.krogius@gmail.com

[2] Department of Pharmaceutical Biosciences, Biomolecular Imaging and Proteomics, National Center for Mass Spectrometry Imaging, BioMedical Center, Husargatan 3, Uppsala University, 751 23 Uppsala, Sweden.

Barettins[1] and barrettides[2] are specialized metabolites found in the deep-sea North Atlantic sponge *Geodia barretti* (Demospongiae, Tetractinellida, Geodiidae). The three known barettins are mono- or dibrominated cyclic dipeptides (Trp+Arg), with a very distinct isotopic pattern. They have been shown to have antioxidant, anti-inflammatory, anti-coagulant and antifouling activities. Barrettides are 31 amino-acid long disulfide- containing peptides with antifouling activity. The aim of this study was to visualize the spatial distribution of barettins and barrettides in *G. barretti*, to learn more about the biological role of these compounds and hopefully gain some insight into the producer of these compounds: the sponge and/or its associated microbes. Several 20 μm thick sections through the cortex and the underlying choanosome were analyzed with Matrix- Assisted Laser Desorption Ionization (MALDI) mass spectrometry imaging (MSI), with and without gelatin embedding. We examined the spatial distribution of several compounds including barettins and other unknown brominated compounds. Some have a homogeneous distribution while others seem to be localized in certain areas in the section.

References

1. Hedner E, Sjögren M, Hodzic S, Andersson R, Göransson U, Jonsson PR, Bohlin L (2008) Antifouling Activity of a Dibrominated Cyclopeptide from the Marine Sponge *Geodia barretti*. J Nat Prod 71 (3):330-333
2. Carstens BB, Rosengren KJ, Gunasekera S, Schempp S, Bohlin L, Dahlström M, Clark RJ, Göransson U (2015) Isolation, Characterization, and Synthesis of the Barrettides: Disulfide- Containing Peptides from the Marine Sponge *Geodia barretti*. J Nat Prod 78 (8):1886–1893

Financial support from the EU Horizon 2020 programme SponGES under grant agreement No. 679849 and from the 'SciLife lab Mass Spectrometry Imaging Platform' (Uppsala University).

Bioelectrometallurgical Application of Poriferan Chitin

Iaroslav Petrenko[1], Vasilii V. Bazhenov[2], Marcin Wysokowski[3], Teofil Jesionowski[3] and Hermann Ehrlich[1]

[1] Institute of Experimental Physics, TU Bergakademie Freiberg, Leipziger Str. 23, 09599 Freiberg, Germany. Hermann.Ehrlich@physik.tu-freiberg.de

[2] European XFEL GmbH, Holzkoppel 4, 22869 Schenefeld, Germany

[3] Institute of Chemical Technology and Engineering, Faculty of Chemical Technology, Poznan University of Technology, Berdychowo 4, 60965 Poznan, Poland

Marine demosponges of the Verongida order represent renewable source of unique prestructured three dimentional skeletal networks made of chitin. Such chitinous scaffolds isolated from Aplysina aerophoba and Ianthella basta sponges can be used as novel templates for deposition of metals such as copper and copper oxides. In contrast to traditional Extreme Biomimetics methods which are based on high temperature reactions, here, we propose an alternative way based on electrochemical plating. This method allows creation of 3D composite materials with metallic and metal oxide nanostructures within their surfaces. The nanostructured metallic phases obtained on and within chitinous fibres of poriferan origin represents replicas of the original nanofibrous substrate. Functionalization of sponge chitin with metals opens new fields for their practical application as catalysts.

Financial support by DFG Grant EH 394/3-1 (Germany), Krüger Research School, Biohydrometallurgical Center for Strategic Elements (BHMZ) at TU Bergakademie Freiberg (Germany), as well as PUT research grant03/32/DSPB/0706/2017 (Poland) are gratefully acknowledged.

The Giant Basal Spicule of *Monorhaphis* Sponge Revisited

<u>Andrzej Pisera</u>[1], Magdalena Łukowiak[1], Konstantin Tabachnick[2] & Hermann Ehrlich[3]

[1] *Institute of Paleobiology, Polish Academy of Sciences, ul, Twarda 51/55, 00-818 Warszawa, Poland. apis@twarda.pan.pl, mlukowiak@twarda.pan.pl*

[2] *P.P. Shirshov Institute of Oceanology, Russian Academy of Sciences, 36, Nakhimovski prospect, Moscow, Russia, 117997. tabachnick@mail.ru*

[3] *Institute of Experimental Physics, TU Bergakademie Freiberg, Leipziger Str. 23, 09599 Freiberg, Germany. hermann.ehrlich@physik.tu-freiberg.de*

Basal spicule of hexactinellid sponge *Monorhaphis* is probably the largest single biosilica- based structure on Earth. The single spicule can reach nearly 1 cm in diameter and over 2 meters of length. During the last decade, it became a model of hexactinellid spicules structure and formation.

We have examined several new specimens of this spicule and have discovered that some descriptions and interpretations of the *Monorhaphis* spicule structures reported previously by Müller and his co-workers (Wang et al. 2011 with references) must be questioned. According to their observations, the majority of the spicule body is composed of regular smooth siliceous laminae, but two most external layers differ in morphology and structure. The most external layer called "banded ribbon layer" was first described as made of a solid fibrous collagen but later its siliceous composition has been proven. The sculpture of the second layer, occurring directly below, was described as depressions with elevated rims that housed sclerocytes.

Our studies show that such complex structure characterize only some parts of the spicule and have confirmed that the ribbon layer is siliceous, not organic. We have found that, in opposition to a solid glassy structure of all more internal lamellae, banded ribbon layer is porous and composed of granular silica. On the contrary to earlier reports, we can demonstrate that the penultimate layer is covered with regularly developed and distributed elevations, not with depressions. Those elevations fit tightly into depressions in the lower (overhanging) surface of the banded ribbon layer. The structure of the penultimate layer is exactly the same as all internal lamella i.e. glassy and without visible porosity. It is worth to mention that the apparent depressions cannot house sclerocytes, because in in later stage of development in hexactinellids occurs only sclerosyncytium. Our observations clearly show that the elevations in *Monorhaphis* spicules are developed by progressively stronger folding of the surface of superimposed thinner layers. It is not clear why and how such structures developed, but we speculate that the outer banded ribbon layer of silica may be an adaptation to help sponge to keep on the spicules and not to glide down on a very smooth silica surface. The elevations of the penultimate layer that fit into depressions of the lower surface of banded ribbon layer help to stabilize (fix) this layer.

References

1. X. H. Wang, M. Wiens, H. C. Schröder, K. P. Jochum, U. Schloßmacher, H. Götz, H. Duschner, W. E. G. Müller, J. Experimental Biol. 214 (2011) 2047-2056.

Financial support by the Polish National Science Center Grant 2016/21/B/ST10/02332 to A. Pisera.

Identification, Purification and Characterization of Proteins with Cytotoxic/Antitumor Activity from *Chondrosia reniformis*

<u>Sonia Scarfì</u>[1], Marina Pozzolini[1], Andrea Abbona[1], Matteo Paccagnella[2], Annalisa Salis[2], Gianluca Damonte[2] & Marco Giovine[1]

[1]*Department of Earth, Environment and Life Sciences (DiSTAV), University of Genova, Genova, Italy*

[2]*Centre of Excellence for Biomedical Research, University of Genova, Genova, Italy*

The majority of medicines come from natural resources, and in particular a great number of bioactive molecules (more than 10, 000) have been isolated until now from the marine environment, with hundreds of new compounds still being discovered every year [1]. The richest sources of sea natural products are invertebrates with Porifera being the most prolific phylum. Sponge-derived bioactive compounds show the most varied activities: antifungal, anti-HIV, antiviral, antibacterial, but the predominant action is cytotoxic/antitumor with more than 800 compounds so far identified in this category.

Sporadic observations on the behavior of the marine sponge *Chondrosia reniformis* pointed out a possible production of cytotoxic compounds in stress conditions able to kill neighboring organisms. The aim of this work was to purify and possibly characterize the compound causing said activity by means of a step by step purification followed by *in vitro* cytotoxicity analyses (MTT test) on a series of human tumor cell lines (leukemia, breast cancer, pulmonary carcinoma) as well as on healthy primary cells (fibroblast and blood mononuclear cells). The MTT tests showed a predominant cytotoxicity on tumor cells compared to healthy cells, thus pointing out a possible antitumor activity. Furthermore, preliminary experiments surprisingly showed that most cytotoxic/antitumor activity was confined to the protein fraction of the crude hydrophilic extract. Thus, different methods of protein fractionation were used to isolate the bioactive protein for a final high definition mass spectrometry (HD-MS) characterization. Namely, the purification steps were: a 10 kDa-cut-off dialysis, a 30% ammonium sulphate protein fractionation and a HPLC separation by gel filtration. After the latter step, a particular low-MW HPLC peak retained the antitumor activity, thus this fraction was separated in a 2D gel electrophoresis showing the presence of three protein bands. The bands from the gel were then trypsin-digested and the derived peptides analyzed in HD-MS obtaining the sequence of a series of peptides.

Finally, through an in silico analysis comparing the peptide sequences to the *C. reniformis* transcriptome previously obtained in our lab, we were able to identify three possible protein candidates for the cytotoxic/antitumor activity: a protein with a trefoil factor domain and two unknown proteins showing no homology to known sequences. Actually, homologues of the first protein from higher Metazoa already show in literature an involvement in stress conditions, especially in epithelial injuries. Finally, we plan for the future to obtain the three proteins in recombinant form for further characterization studies.

Research supported by EU (FP7 grant agreement n: 266033 SPonge Enzyme End Cell for Innovative AppLication-SPECIAL).

References

1. Proksch P, Edrada RA, Ebel R. Appl Microbial Biotechnol, 2002, 59: 125-134

Two new sesterterpenes isolated from the Antarctica sponge *Phorbas bergmontae* Hajdu & Teixeira, 2011

<u>Hiren Solanki</u>[1], Carlos Angulo-Preckler[2], Kevin Calabro[1], Navdeep Kaur[1], Conxita Avila[2] & Olivier P. Thomas[1]

[1] *National University of Ireland, Galway, School of Chemistry, Marine Biodiscovery, Ryan Institute, University Road, Galway, Ireland.*

[2] *University of Barcelona, Department of Animal Biology (Invertebrates), Faculty of Biology, Biodiversity Research Institute (IrBIO), Av. Diagonal 643, 08028 Barcelona, Catalonia, Spain. h.solanki1@nuigalway.ie*

Chemical investigation of sponges has been mainly focused on tropical and temperate waters, while cold water sponges have attracted much less attention. Among 18 sponges collected from Antarctic waters, 2 species were selected as their extracts exhibited the highest antimicrobial and anti-predator or anti-biofouling activities. Chemical investigation of the first species identified as *Phorbas bergmontae* Hajdu & Teixeira, 2011 led to the isolation of three new sesterterpenes **1-3** but also of the already described analogues: suberitenone B and oxaspirosuberitenone. The structure elucidation of the new compounds was performed mostly by NMR data analyses and mass spectrometry. Compound **1** and **2** exhibit an oxaspirosuberitenone skeleton while compound **3** belongs to the typical suberitenone class. Compounds **1-3** mostly differ from the already described compounds from another sponge *Suberites* sp. from Antarctica only in positions 0-6 and 0-20 with an inversion between the acetyl and the hydroxyl groups.

Posters Ecology

North-western Australia: a sponge biodiversity hotspot

Jane Fromont[1, 2], **Muhammad Azmi Abdul Wahab**[2, 3], **Oliver Gomez**[1, 2], **Merrick Ekins**[4], **Monique Goverdina Geerruida Grol**[5], **John N.A. Hooper**[4, 6]

[1] *Department of Aquatic Zoology, Western Australian Museum, Locked Bag 49, Welshpool DC, WA 6986, Australia*

[2] *Western Australian Marine Science Institution, Entrance 2 Brockway Road, Floreat, WA 6014, Australia*

[3] *Australian Institute of Marine Science, Indian Ocean Marine Research Centre, The University of Western Australia (MO96) 35 Stirling Hwy, Crawley WA 6009, Australia m.abdulwahab@aims.gov.au*

[4] *Queensland Museum, PO Box 3330, South Brisbane, QLD 4101, Australia*

[5] *CoralWatch, Queensland Brain Institute, The University of Queensland, St. Lucia, QLD 4072, Australia*

[6] *Eskitis Institute for Drug Discovery, Griffith University, Nathan, QLD 4111, Australia*

The biodiversity of sponges of the Pilbara region, north-western Australia, was assessed using datasets amalgamated from the Western Australian Museum and the Atlas of Living Australia databases. Using the Integrated Marine and Coastal Regionalisation for Australia (IMCRA), differences in biodiversity between Pilbara bioregions were also determined. The Pilbara accounts for a total of 1164 Linnean and morphospecies and is considered to be a global biodiversity hotspot for marine sponges. A high level of “apparent endemism” was recorded with 78% of species found in only one of six bioregions, and with less than 10% confirmed as widely distributed. The Ningaloo, Pilbara Nearshore and Pilbara Offshore bioregions contain >250 species and are recognised as having the highest conservation value, followed by the North West Shelf with 232 species. Species compositions differed between bioregions, with those that are less spatially separated sharing more species. Notably, the North West Province bioregion (110 species) exhibited the most distinct species composition, highlighting it as a unique habitat within the Pilbara. While sponge biodiversity is apparently high, incomplete sampling effort in parts of the region was identified, with only two sampling events recorded for the Central West Transition bioregion. Furthermore, only 15% of records in the dataset are presently described (Linnean) species, highlighting the continuing need for taxonomic expertise for the conservation and management of marine biodiversity resources.

This research was funded by the Western Australian Marine Science Institution (WAMSI) as part of a Dredging Science Program, and made possible through investment from Chevron Australia, Woodside Energy Limited and BHP Billiton as environmental offsets, and by co-investment from WAMSI Joint Venture partners. This research was also enabled by data and information provided by Chevron Australia. The commercial entities had no role in data analysis, decision to publish, or preparation of the presentation. The views expressed herein are those of the authors and not necessarily those of WAMSI.

Silica concentration influence on sponge spicule dimensions

Belinda Alvarez[1], **Wim Clymans**[1], **Gary Prentice**[3], **Katharine Hendry**[3] **& Daniel Conley**[1]

[1] *Lund University, Department of Geology, Lund, Sweden. belinda.alvarez@geol.lu.se*

[2] *Digital Optics, Auckland, New Zealand*

[3] *Department of Earth Sciences, University of Bristol, UK*

Silicon isotope composition of sponge spicules has been positively correlated to the ambient silica (dissolved Si) concentration and proposed as a good estimator of silica conditions in past oceans [1, 2]. In this work we explored relationships between the dimensions of sponge spicules and the availability of silica in the sponge habitat to identify potential morphometric variables that could complement the relationships derived from isotopic studies.

Seventeen individuals belonging to 15 sponge species, with similar megascleres in their skeletons (styloids, styles and subtylostyles) and collected at six stations with different concentrations of ambient silica (12, 56, 75, 84, 107 and 119 µM) were selected to explore these relationships. The, area, length and width (at 100 equidistant points along each spicule), were measured in 30 non-broken megasclere spicules of each individual. Measurements were made on digital images of the spicules with an algorithm developed in V++ Precision

Digital Imaging System v 5.0 (Digital Optics, Ltd).

The dimension of spicules based on the morphometric variables considered, showed a great variability among the selected species and no apparent correlation with the concentration of silica. The inter-specific variation in the size of spicules is less at stations with DSi>75 µM. In those stations, species show a higher frequency of spicules in smaller size categories. The maximum dimensions are also recorded in these stations but not in a linear way in relation to the DSi concentration.

The results indicate that the variability of spicule dimensions is more likely to be species-related than controlled by the availability of silica or other environmental correlated parameters of their habitats. Extrapolations of silica conditions in past environments derived from spicule dimensions found in fossil records or sediment cores should be therefore carefully considered. Sizes and frequencies of size classes on the other hand might continue to be useful morphometric characters to differentiate sponge species, despite some claims that they are not constant within species.

Financial support by Knut and Alice Wallenberg Foundation to DJC is gratefully acknowledged.

References

1. Hendry KR, Georg RB, Rickaby REM, Robinson LF, Halliday AN (2010) Deep ocean nutrients during the Last Glacial Maximum deduced from sponge silicon isotopic compositions. Earth and Planetary Science Letters 292: 290-300.
2. Hendry KR, Robinson LF (2012) The relationship between silicon isotope fractionation in sponges and silicic acid concentration: Modern and core-top studies of biogenic opal. Geochimica et Cosmochimica Acta 81: 1-12.

Initial report on nine newly discovered glass sponge reefs in British Columbia, Canada

Stephanie K. Archer[1], Glenn Denison[2] and Anya Dunham[1]

[1]Fisheries and Oceans Canada, Pacific Biological Station, 3190 Hammond Bay Road, Nanaimo, BC V9T 6N7, Canada

[2]Marine Life Sanctuaries Society of British Columbia, PO Box 54193, Lonsdale West, North Vancouver, BC V7M 3L5. Stephanie.Archer@dfo-mpo.gc.ca

Glass sponge reefs are built by dictyonine hexactinellid sponges. These sponges are characterized by fused spicules that result in the persistence of skeletal structural integrity after the sponges' death. This property allows for reef formation as larval sponges settle on the structure provided by previous generations of sponges. Glass sponge reefs have only been documented in shelf habitats in the North East Pacific from Portland Canal to the Strait of Georgia. Recently nine small reefs in Howe Sound, British Columbia, Canada, were discovered by a citizen science group using a drop camera. Here we present the results of a survey of these nine reefs using Fisheries and Oceans Canada's ROV. A total of 19 transects (1-3 per reef) were conducted between September 29 and October 2, 2016. A forward facing high-definition video camera collected continuous video used to assess megafauna community structure. A downward facing still camera automatically took a photo every 15 seconds. The still photos were used to assess percent cover of live and standing dead sponge. These reefs, similar to others in the Strait of Georgia, are constructed by *Aphrocallistes vastus* and *Heterochone calyx*. They are the shallowest known glass sponge reefs, with some reef pinnacles as shallow as 20 m. The reefs have high live sponge cover ranging from 4 to 25%. Standing dead sponge cover was also high ranging from 5 to 42%. We documented a diverse megafaunal community associated with the reefs including several species of sponges, fish, crabs, and other crustaceans. Overall these newly discovered reefs appear healthy and represent a substantial increase in the number of known glass sponge reefs, an ecosystem that, until recently, was thought to be extinct.

Diversity of sponge species in the coralligenous community along the eastern Adriatic

Tatjana Bakran-Petricioli[1], Silvija Kipson[1] & Donat Petricioli[2]

[1]Department of Biology, Faculty of Science, University of Zagreb, Rooseveltov trg 6, HR-10000 Zagreb, Croatia. tatjana.bakran-petricioli@biol.pmf.hr

[2]D.I.I.V. Ltd., for marine, freshwater and subterranean ecology, Obala Petra Lorinija 52, HR-23281 Sali, Croatia

Porifera is one of the most representative and diverse groups of animals present in the Mediterranean coralligenous community. Up till now more than 300 species of sponges have been recorded in this habitat threatened with a number of human activities. Recent study of highly valuable but highly understudied coralligenous assemblages along the eastern Adriatic Sea revealed high species richness and significant inter-site and inter-depth variability of macrobenthic biodiversity. The aim of this work was to assess diversity of sponge taxa present in the coralligenous of the Eastern Adriatic Sea. We analysed our database with over 2000 specimens of sponge species that we sampled and determined over the last 15 years from more than two hundred locations along the Croatian coast. Among 125 determined species, 68 were recorded in coralligenous, but not exclusively, many of them were also present in the community of semi-dark caves. We also performed underwater photo-sampling of coralligenous community dominated with the red gorgonian (*Paramuricea clavata*) on six locations, three in the central and three in the north Adriatic. Analysis of photos revealed 46 distinct categories (taxa) of sponges. Among them 21 were possible to determine to a species level and 11 to a genus level. In our contribution we discuss these results in light of previous studies carried out elsewhere in the Mediterranean.

Carbon cycling by the deep-sea glass sponge *Vazella pourtalesi*

Martijn C. Bart[1], Gabrielle J. Tompkins-MacDonald[2], Jasper M. de Goeij[1]

[1] Department of Freshwater and Marine Ecology, Institute for Biodiversity and Ecosystem Dynamics, University of Amsterdam, Post Office Box 94248, 1090 GE Amsterdam, Netherlands m.c.bart@uva.nl

[2] Bedford Institute of Oceanography, 1 Challenger drive, Dartmouth, NS B2Y 4A2, Canada

Deep-sea sponge grounds are abundant and complex reef structures on the ocean floor. They support rich associated faunal communities and act as feeding grounds and nurseries for various commercial fish species[1]. Despite their importance, deep-sea sponge grounds have received little to no attention as to how they function, which hampers proper understanding of these vulnerable ecosystems. The emerging view is that sponges play a key role in deep-sea food webs and biogeochemical cycles[2, 3]. We quantified the uptake, transfer, and release rates of dissolved and particulate organic carbon by the deep-sea glass sponge *Vazella pourtalesi*, using *ex situ* flow chamber experiments. Preliminary results show that *V. pourtalesi* efficiently takes up a wide variety of particulate organic carbon sources, and that bacterial uptake rates are on average eight times lower than for encrusting tropical sponges. Additionally, *V. pourtalesi* seems not able to utilize viral particles. These results provide the first indication on the ecological role of deep-sea *V. pourtalesi* glass sponges in carbon cycling and deep-sea ecosystems.

References

1. C. Cathalot, D. van Oevelen, T.J. Cox et al. Frontiers Mar. Sci., 2 (2015) 1-12.
2. L. Rix, J.M. de Goeij, C.E. Mueller et al. Sci Rep. 6 (2016) 18715.
3. A.S. Kahn, G. Yahel, J.W.F. Chu et al. Limnol. Oceanogr. 60 (2015) 78-88.

Financial support by the EU Horizon2020, project, grant Agreement 679849, is gratefully acknowledged.

Cohort Analysis and Kinship of the Hexactinellid Sponge *Vazella pourtalesi* on an Artificial Substrate

Lindsay Beazley[1], Ellen Kenchington[1], Sarah Thompson[1], Joana R Xavier[2], Fred Whoriskey[3]

[1] Fisheries and Oceans Canada, Bedford Institute of Oceanography, Dartmouth, Nova Scotia, Canada. Lindsay.Beazley@dfo-mpo.gc.ca

[2] Department of Biology and K.G. Jebsen Centre for Deep-Sea Research, University of Bergen, PO Box 7803, N-5020 Bergen, Norway

[3]Ocean Tracking Network, Dalhousie University, Halifax, Nova Scotia, Canada

The hexactinellid *Vazella pourtalesi*, commonly known as the "Russian Hat" sponge, forms a globally unique monospecific sponge ground on the Scotian Shelf off Nova Scotia, Canada. Under Fisheries and Oceans Canada's (DFO) 2009 Policy for Managing the Impact of Fishing on Sensitive Benthic Areas, two areas equating to 197 km^2 were closed to all bottom fishing activities in 2013 to protect this unique population of sponges. It was recently discovered that a tracking array consisting of over 200 acoustic moorings situated off Nova Scotia from Halifax to the shelf break owned by Dalhousie University's Ocean Tracking Network (OTN) is heavily biofouled by *Vazella pourtalesi* (Figure 1). This provides a unique opportunity to collect high quantities of sponges of a known age during future servicing of these moorings. In collaboration with the EU- funded Horizon2020 SponGES project and the OTN, DFO is conducting size-frequency and cohort determination analyses of *Vazella pourtalesi* collected from the moorings. A detailed kinship study that will investigate the genetic relatedness of sponges on the moorings and the dispersal distance between kin will also take place. Additionally, information on the spatial population structure, growth rate and basic reproductive biology will be deduced from these samples. The results of these studies will serve to increase our understanding of the ability of this species to recover in the face of anthropogenic impact and assess whether DFO's two closure areas are adequate for its conservation.

Financial support: this study is part of the SponGES project funded by the European Union's Horizon 2020 research and innovation programme (grant agreement 679849).

A survey of the shallow water sponge fauna of the Cyprus island (Eastern-Mediterranean)

Marco Bertolino[1], Alexia Setti[1], Gabriele Costa[1], Valentina Giussani[2], Maurizio Pansini[1] & Roberto Pronzato[1]

[1] *DiSTAV, Università degli Studi di Genova, Corso Europa 26, 16132 Genova, Italy marco.bertolino75@gmail.com*

[2] *ARPAL - Dip. Biotossicologia ambientale, via Fontevivo 21L, 19125 La Spezia, Italy*

The Mediterranean Sea, with over 650 sponge species recorded in total and a percentage of endemics around 50%, is one of the marine areas richest of porifera. Notwithstanding this the sponge fauna of the Levantine Basin (30°-35° East of Greenwich) is still poorly known. As to Cyprus in particular, just one paper deals of freshwater sponges and other 3 report on 3 protected species of marine sponges. More detailed is the information about commercial sponge fishery and its decline after the dramatic 1986 disease.

This first scuba diving survey of the shallow water Cyprus sponge fauna allowed to identify 32 sponge taxa in total (23 at species level and 8 at genus level) from 5 sampling sites at 2-15 m depth. Keratosa, with 15 species, are the most common order. According to the presence/absence in the different sites, the most common species are: *Chondrosia reniformis* (5/5), *Crambe crambe* (4/5), *Haliclona* (*Rhizoniera*) *sarai, Phorbas fictitius* and *Sarcotragus spinosulus* (3/5).

From a biogeographic point of view the Cyprus sponge fauna shows a clear Atlanto- Mediterranean affinity (17 spp) without prevalence of species with either Mauritanic or Lusitanic affinity. Seven species (32%) out of the 23 identified in total result Mediterranean endemics, a percentage significantly lower than that of the whole Mediterranean Sea. Ten sponge species are recorded in the Levantine Basin for the first time. The majority of species are common and previously reported by several authors from Mediterranean Sea; only 1 species (*Petrosia* (*Petrosia*) *clavata*) can be considered rare, being recorded no more than 6 times in the past. *P.* (*Petrosia*) *clavata* is here reported for the third time, but probably it was confused with *P.* (*Petrosia*) *ficiformis*.

Focusing on the Keratosa, to which belong the majority of recorded taxa, the complete absence of Dendroceratida could be ascribed to their actual rarity in the Mediterranean Sea (e.g. Darwinellidae), but also to their inconspicuous aspect. Among Dictyoceratida the family Irciniidae is represented by 7 taxa of *Ircinia* and 4 of *Sarcotragus*; the family Spongiidae by 2 taxa of the genus *Spongia*. Cyprus is one of the traditional sites of fishery and trade of bath sponges. The severe diseases at the end of the last century virtually stopped this activity, making very rare, or locally extinct, the 5 species of *Spongia* (*S. lamella*, *S. mollissima*, *S. officinalis* and *S. zimocca*) and 1 of *Hippospongia* (*Hippospongia communis*) supporting this fishery. The record of *Spongia zimocca* could be an important sign of new recruitment of this traditionally exploited and much sought-after bath sponge.

For the sponge sampling Demetris and Periklis Kletou are gratefully acknowledged.

Fine-scale population structure of tetillid sponges in a tropical reef lagoon

Cecilia Conaco, Michael Angelou Nada, Jake Ivan Baquiran & Patrick C. Cabaitan

Marine Science Institute, University of the Philippines, Diliman, Quezon City 1101 Philippines pcabaitan@msi.upd.edu.ph

With the increasing incidence of disturbance caused by anthropogenic activities and thermal stress events related to climate change, many reefs have transformed from being dominated by corals to being dominated by other biota, such as macroalgae and sponges. These shifts influence the dynamics of benthic reef populations. Sponges represent some of the most adaptable benthic organisms and may be found in diverse marine ecosystems. Yet, few have assessed sponge populations and their interaction with other reef biota. Here, we surveyed the benthic populations of tetillid ball sponges, tentatively identified as *Cinachyrella* sp., on four bommies in a tropical reef lagoon in Bolinao, northwestern Philippines. Ball sponges are common on these bommies, with an average abundance of 3.6 individuals per sq. m. and an average size of 3.4 cm. The abundance, size frequency distribution, and morphology of the ball sponges varied across bommies. Based on spicule morphology and microbial profiling, the sponge balls could be classified into two groups that vary in abundance between the eastern and westernmost bommies. Fine-scale differences in the population structure of the sponges despite close proximity of the bommies within the reef may reflect differences in species distribution as influenced by the gradient of physicochemical parameters in the environment. Interestingly, all the ball sponges exhibit frequent interactions with other biota, particularly the spaghetti sponge, *Callyspongia samarensis*, as well as corals. Ball sponges also contribute to reef structure, forming the base of the territories of farmer damselfish on the upper surface of the bommies. The tetillid sponges showed no obvious negative effects on other biota. However, further studies exploring its potential influence on recruitment of corals and other benthic organisms need to be conducted.

References

1. van Soest RWM and Rutzler K (2002) Family Tetillidae Sollas, 1886. In Systema Porifera: A Guide to the Classification of Sponges. Hooper JNA and Van Soest RWM (eds). Kluwer Academic/Plenum Publishers, New York.
2. Cuvelier, M. L., Blake, E., Mulheron, R., McCarthy, P. J., Blackwelder, P., Thurber, R. L. V., & Lopez, J. V. (2014). Two distinct microbial communities revealed in the sponge Cinachyrella. *Frontiers in Microbiology*, *5*, 1–12.

Financial support by the Marine Science Institute of the University of the Philippines is gratefully acknowledged.

Antarctic Sponges and Climate Change: Responses from Individual to Community Levels

César A. Cárdenas[1], Marcelo Gonzalez-Aravena[1], Eduardo Hajdu[2], Nicole Trefault[3], Shane W. Geange[4] & James J. Bell[5]

[1]*Departamento Científico, Instituto Antártico Chileno, Punta Arenas, Chile. ccardenas@inach.cl*

[2]*Museu Nacional, Departamento de Invertebrados, Universidade Federal do Rio de Janeiro, Rio de Janeiro, RJ, Brazil.*

[3]*Center for Genomics and Bioinformatics, Faculty of Sciences, Universidad Mayor, Santiago, Chile.*

[4]*Department of Conservation, Wellington, New Zealand.*

[5]*School of Biological Sciences, Victoria University of Wellington, Wellington, New Zealand.*

The Antarctic Peninsula has undergone drastic changes in air and water temperature over the last fifty years and continues to experience some of the most rapid climatic warming on the planet. The projected changes in temperature constitute major threats to ecosystem functioning, services and integrity, as they can affect key functional species and associated ecosystem processes. Sponges play important roles in community dynamics, as microhabitat providers and also positively influencing diversity and composition of Antarctic benthic communities. Recent evidence suggests their diversity and abundance in algae-dominated rocky reefs in the western Antarctic Peninsula (WAP) has been underestimated. This highlights that the existing knowledge on sponge assemblages and the functional roles they play in vast zones of the WAP is still incomplete. The long-term goal of this work is to evaluate the utility of sponge species as indicators environmental perturbation with Antarctic benthic communities.

The objectives of this proposal, which are a step towards attaining the long-term goal, are to generate baseline data on the distribution of Antarctic sponge species and their microbial communities against which future temperature-induced changes can be assessed, and to undertake initial evaluations of the effect of temperature increases on the ecophysiological performance of Antarctic sponges. Sponge assemblages have been monitored for 2 years at different sites around Doumer Island (64°52'24''S; 63°36'00''W), Palmer Archipelago, Antarctic Peninsula. Preliminary results confirm previous evidence suggesting the presence of diverse sponge assemblages in zones that are typically dominated by canopy-forming algae (e.g. *Himantothallus grandifolius*). In addition, high throughput sequencing shows the existence of diverse bacterial communities associated with different Antarctic sponges. It is critical to increase our understanding of the dynamics of Antarctic sponges from a molecular to community level, which will help our understanding of current patterns, which is essential for informing our ability to detect future changes in these communities resulting from increasing temperatures.

Financial support by FONDECYT 11150129 is gratefully acknowledged.

New Ice-Free Areas in Antarctic shallow-waters: an Opportunity for Sponge Colonization?

Cristian Lagger[1], César A. Cárdenas[2]

[1]*Instituto de Diversidad y Ecología Animal (IDEA), CONICET-UNC and Facultad de Ciencias Exactas, Físicas y Naturales, Universidad Nacional de Córdoba, Argentina.*

[2] *Departamento Científico, Instituto Antártico Chileno, Punta Arenas, Chile. ccardenas@inach.cl*

The Antarctic Peninsula has warmed significantly over recent decades, being considered among the fastest warming regions on Earth. This warming has profound influences on the cryosphere including ice shelf collapses and a decrease in extent and seasonality of sea-ice. Furthermore, the majority of glaciers have retreated during the last 60 years. Particularly, the Fourcade Glacier surrounding Potter Cove (South Shetland Island, Antarctica) shows an accelerated retreat affecting the hydrographical characteristics of the cove; hence, driving significant changes in the established benthic communities. In addition, the glacier retreat has also uncovered a new rocky island representing an excellent opportunity to study colonization and succession processes in Antarctic ecosystems. We sampled the *new* island by photo-transects taken up to 30 m depth by SCUBA diving, six years after that it was freed of ice (March 2010). Here, we report a particular benthic assemblage characterized by high species richness, diversity and structural complexity with a well-developed three-dimensional structure, dominated by filter feeders at all depths.

Sponges were the second most important group in terms of abundance in the new island with a mean of 3.03 ± 0.32 percent cover. Total abundance of sponges decreased markedly across the bathymetric gradient, with the lowest cover (0.9 ± 0.31%) recorded at 30 m depth. The sponge *Haliclona* sp. 2 was the most abundant taxa, representing between 25 and 70% of total sponge coverage. We registered large individuals reaching more than 50 cm in length (sponges of up to 0.02 m^3). Considering if individuals have settled and grown for only six years, it will represent a high growth rate, higher than previously reported for demosponges in Polar Regions, hence confirming recent findings reported from East Antarctica and challenging the widely held assumption of low velocity processes in Antarctic benthos. However, it also opens the question of whether these sponges could have been present under the glacier in ice refuges and now have been exposed to open sea conditions. Sedimentation will increase under the current scenario of glacier retreat, affecting filter- feeders and other sessile benthic organisms such as sponges, which may be vulnerable. For this reason, sponges may constitute suitable indicators of climate induced perturbations along the Antarctic Peninsula. On the other hand, the opening of new areas available for sponge colonization that could take place at previously unexpected velocity, shows the need for a better understanding on the interactions between physical and biological variables and how they affect sponge assemblages

Financial support by FONDECYT 11150129 is gratefully acknowledged.

Deep-Sea sponges from the Cape Verde archipelago collected during RV Meteor cruise M80/3

Frine Cardone[1&*], Matthias López Correa[2&], Jacek Raddatz[3], Thor Hansteen[4]

[1]*Department of Biology, University of Bari, Bari, Italy.*

[2]*GeoZentrum Nordbayern (GZN), Universität Erlangen, Loewenichstr. 28, D-91054 Erlangen, Germany.*

[3]*Goethe University, Institute of Geosciences, Altenhöfer Allee 1, D-60438 Frankfurt am Main, Germany.*

[4] *GEOMAR, Wischhofstr. 1-3, D-24148 Kiel, Germany.*

[&] *These authors contributed equally to this work*

**Conference presenter: frine.cardone@uniba.it*

During RV-Meteor cruise M80/3 the submarine volcanoes of the Cape Verde archipelago have been examined with the ROV QUEST6000 to document and sample the volcanic rocks and the associated biological communities of cold-water corals and sponges. Our current work is focused on creating a basic inventory of the common sponge species and a description of the rare sponge species. The sponge samples have been collected between 767 and 3753 m, corresponding to a temperature decline of 7.2 to 2.9°C and a salinity decline from 34.99 to 34.86 g/kg. The explored environments most commonly comprised volcanic rock escarpments with fresh mafic rocks, which served as substrate for encrusting sponges. The second most abundant substrates were Pleistocene to recent skeletons of cold-water corals which littered the flanks of the submarine volcanoes. Sandy to muddy siliciclastic substrates were encountered only scarcely. Overall the sponge macrofauna was dominated by Hexactinellidae mainly belonging to the subclass Hexasterophora. *Aphrocallistes beatrix* was a common element within the fossil *Lophelia* grounds between 767 and ~900 m depth. Several species of Cladorhizidae and other small hexactinellid sponges had been found in the framework of *Hertwigia falcifera* at 1403 m depth. On the flanks of Cabo Verde Seamount at 950 m (N15°18'/W021°53') the candelabrum-shaped hexactinellid sponge *Sarostegia oculata* had been found associated with a large number of polychaetes placed inside axial cavities of the branches. Furthermore, all the atrial cavities of the sponges were closed by a parchment, which contained planktonic foraminifera. Interestingly, these spots served as preferred settlement sites of zoanthids.

We further examine the endolithic sponge inventory, based on their spicules and tissues encased in calcitic (*e.g. Keratoisis*) and aragonitic cold-water corals (*e.g. Lophelia*), which served as substrates. Their trace morphology is explored with the vacuum epoxy- cast embedding technique and SEM, revealing a rich ichnocoenoses, dominated by fungal traces and bioeroding sponges.

Diversity and abundancy of intertidal zone sponges on rocky shores of NSW, Australia: patterns of species distributions, abundance and diversity.

Caroline Corodnis[1], Andy Davis[2]

[1]*School of Biological Sciences, University of Wollongong, Wollongong, NSW 2522, Australia. ccbds989@uowmail.edu.au*

[2] *Director of the Institute for Conservation Biology and Environmental Management, School of Biological Sciences, University of Wollongong, Wollongong, NSW 2522, Australia.*

A primary measure to manage biodiversity loss in marine ecosystems is to define priority areas for conservation based on biodiversity hotspots and the distribution of key organisms. Sponges (Porifera) are a highly diverse group that, despite playing a wide range of important functional roles, still poorly represented in monitoring and conservation programmes. They are also an important component of sessile benthic communities, acting as competitors, symbionts, hosts of symbionts, consumers, and prey. I investigated sponge diversity and distribution on the rocky intertidal shores of south eastern Australia. I used quantitative surveys (2 hour timed searches) on 14 intertidal rock reefs along the Illawarra Coast, NSW, Australia. The relative importance of sedimentation, wave exposure and habitat complexity was also examined at the between-reef scale. In parallel, patterns in sponge biodiversity were compared with those for the phylum Mollusca, providing a more comprehensive assessment of the bioregional invertebrate fauna. My sponge survey resulted in 12 new occurrences of sponge species for the Illawarra Region, many of these undescribed. Although more data are required to determine which variables are drivers of patterns of distribution and abundance. These data will contribute formulating advice regarding to the establishment of comprehensive and representative intertidal protected areas in the Hawkesbury Shelf Marine Bioregion of NSW, Australia.

References

1. K. Benkendorff, A. Davis, Biodiversity and Conservation. 11 (2002) 1959-1973.
2. N. Myers, R. A. Mittermeier, C. G. Mittermeier, G. A. B. Fonseca, J. Kent, Nature. 403 (2000).
3. J. Bell, Estuarine, Coastal and Shelf Science. 79 (2008) 341-353.
4. J. Wulff, Can. J. Zool. 84 (2006) 146-166.

Financial support by CAPPES Foundation is gratefully acknowledged.

Space-time evaluation of the composition and abundance of boring sponges on Abrolhos Bank shallow reefs, Bahia, Brazil

Fernanda Cervi[1], Fernando Moraes[1], Claudia Karez[1], Rodrigo Moura[2], Gilberto Amado-Filho[1]

[1]Instituto de Pesquisas Jardim Botânico do Rio de Janeiro, Rio de Janeiro, Pacheco Leão, 915/123. 22460-030, Rio de Janeiro, RJ, Brazil.

2 Instituto de Biologia, Universidade Federal do Rio de Janeiro.

Boring sponges are key players in the ecology of coralline reefs. By removing minute carbonate particles (microchips), sponges contribute to the weakening of the reef framework while increase the production of fine sediments. They are positively affected by rising temperature, acidification and eutrophication, being good bioindicators of local and global stressors. The Abrolhos Bank is the largest reef complex in the South Atlantic, harboring a unique biodiversity and providing several important ecosystem services. The aim of the present work was to determine the composition and abundance of boring sponges along a spatial and temporal gradient on the Abrolhos Bank. Fixed photo-quadrats (1.800 images) and randomly line transects (400 m^2) were employed on shallow (4-9 m depth) reefs from coastal (Pedra de Leste - PL) and mid-shelf areas (Parcel dos Abrolhos - PAB). In the former methodology, sampling occurred in 2008- 2009 and from 2013 to 2016, while in the latter it was in 2013 and 2016, always in the summer. Five species of boring sponges were recorded: *Cliona carteri, C. delitrix, C. schmidti, C. varians* & *Siphonodictyon coralliphagum*. The most abundant species was *C. carteri*, reaching 20.4 ind.m^{-2} at PAB in 2014 and frequent in > 80% of the samples, followed by *C. delitrix* (maximum of 1.7 ind.m^{-2} at PAB in 2013 and frequent from 7- 20 % of the samples). Mean cover of boring sponges was low (1.5 % at PAB and 0.006 % at PL) while density was high (12.7 ind.m^{-2} PAB and 1.8 ind.m^{-2} PL), compared to other reefs in the Caribbean and Australia. Crustose coralline algae was the main substrate type bored (70%) by sponges. An increase in boring sponges abundance was observed on Abrolhos shallow reefs from 2013, probably due to the environmental stress caused by higher seawater temperature, representing thermal anomalies during two consecutive summers (2013/2014).

Financial support by ANP/Brasoil, CNPq, CAPES, FAPERJ.

Mediterranean *Cystoseira* forests *vs*. barren: the case of sponges

Gabriele Costa[1], Marco Bertolino[1], Stefania Pinna[2], Chiara Bonaviri[3], Andrea Padiglia[2-1], Roberto Pronzato[1] and Renata Manconi[2]

[1]Dipartimento per lo Studio del Territorio e delle sue Risorse (DISTAV), Università degli Studi di Genova, Genova, Italy
[2]Dipartimento di Scienze della Natura e del Territorio (DipNeT), Università degli Studi di Sassari, Sassari, Italy
[3]Dipartimento di Scienze della Terra e del Mare (DiSTeM), Università di Palermo, Palermo, Italy. gabrielecosta@me.com

Mediterranean *Cystoseira* forests represent a suitable substrate for the recruitment of many benthic species. In marine ecosystems at temperate latitudes, the reduction of predation or harvesting of sea urchins, *Paracentrotus lividus* (Lamarck, 1816) and *Arbacia lixula* (Linnaeus, 1758), can increase their abundance and provoke a shift from EMA (Erected Macroalgae Assemblages) to ECA (Encrusting Coralline algae Assemblages) that characterizes the so-called "*barren* state" (Bonaviri *et al.*, 2009). The transition from EMA to ECA state is expected to result in dramatic changes in community structure and ecosystem functioning and detrimental effects on coastal fauna that uses macroalgae for shelter, recovery, food, and settlement. Moreover, positive feedback processes may prevent a return of the community to pristine conditions (Suding *et al.*, 2004). In this paper, the Porifera taxonomic richness has been studied in EMA and ECA in six Mediterranean sites. In total we have recorded 31 sponge taxa. Results revealed that the EMA state hosts 25 sponge taxa while a notably lower taxonomic richness characterize the barren state 15 sponge taxa. As for the habitus we noticed that those with massive, encrusting and insinuating sponges are in greater numbers in the EMA state while the boring ones are dominant in the ECA state.

References

1. C. Bonaviri, T. V. Fernandez , F. Badalamenti, P. Gianguzza, M. Di Lorenzo, & S. Riggio, Fish versus starfish predation in controlling sea urchin populations in Mediterranean rocky shores. (2009) *Mar. Ecol. Prog. Ser.*, *382*, 129-138.
2. K. N. Suding, K. L. Gross, & G. R. Houseman. Alternative states and positive feedbacks in restoration ecology. (2004). *Trends Ecol. Evol.*, *19*(1), 46-53.

First characterization of the deep-sea sponge communities on seamounts of the Galapagos Marine Reserve

Marie F. Creemers[1], Salomé Buglass[1], Henry Reiswig[2], Sarah Griffiths[3], Evelyn Taylor-Cox[3], Robert Winch[3], Amanda Bates[4], Patricia Martí Puig[1]

[1] Charles Darwin Foundation, Santa Cruz, Galápagos Islands, Ecuador. marie.creemers@alumni.ulg.ac.be
[2] University of Victoria, Victoria, Canada
[3] School of Science and the Environment, Manchester Metropolitan University, Manchester, United Kingdom
[4] Ocean & Earth Sciences Department, University of Southampton, Southampton, United Kingdom

Seamounts on the Galápagos platforms provide numerous ecosystem services of great economical interest for the tourism and fishery sectors. Recognized by the United Nations as priority habitats under international law, interest in seamounts has recently risen with regards to ensuring sustainable practices to manage human activities and to conserve biodiversity. On the Galápagos platform, seamounts are estimated to be as numerous as 300; nonetheless, little is known about their faunal assemblages.

Deep-sea sponges are one of the habitat-forming benthic taxa that can be observed around seamounts. In addition to their great economic interest for the pharmaceutical industry, deep-sea sponges enhance habitat complexity and biodiversity. Due to their ecological importance, sponge conservation is crucial to preserving seamount ecosystems. Baseline information on deep-sea sponges is therefore necessary to increase our current knowledge of the benthic fauna of seamounts and to improve the management of sponge-associated systems within the Galápagos Marine Reserve (GMR).

With the upcoming plan for a new zonation scheme for the GMR, characterizing seamount habitats and biodiversity has arisen as an important priority. Consequently, the Charles Darwin Foundation (CDF) initiated the *Seamounts of the Galápagos Marine Reserve* project in partnership with the Galápagos National Park directorate (GNP).

In order to explore seamounts of the GMR and establish a baseline inventory of their fauna, a cruise was conducted aboard the E/V *Nautilus* and biological samples were collected on three seamounts by the Remotely Operated Vehicle (ROV) *Hercules*. A total of thirteen species of sponges were morphologically identified, nine demosponges and four hexactinellids, whose eleven specimens are potentially new to sciences. Among the potential new species (84% of the specimens collected), one of each class is believed to belong to new genera, according to both morphological and genetics results.

These preliminary results encourage our team to further investigate the mysterious sponge biodiversity of the Galápagos seamounts and contribute to the maintenance and development of a sustainable management plan for the Galápagos Marine Reserve.

Financial support by the MER Consortium Joint Program Board is gratefully acknowledged.

Understanding Functional Morphology of the Sponge Aquiferous System by Using Computed Tomography (CT) Scan Technique

Azraj S. Dahihande, Narsinh L. Thakur

azrajdahihande@gmail.com
CSIR- National Institute of Oceanography, Dona Paula- 403 004, Goa, India

The aquiferous system, one of the major structural components of sponge morphology has multiple repeated units called aquiferous modules[1]. Detailed 3D-reconstructions of sponge aquiferous system have been elucidated with corrosion cast[2], and synchrotron radiation based X-ray microtomography[3]. However, a working model of the sponge aquiferous system is yet to be demonstrated. In the present investigation, Computed Tomographic (CT scan) technique was applied to understand the functioning of the aquiferous system in live specimens of sponge *Ircinia fusca* (massive growth form) and *Cinachyrella* cf. c*avernosa* (spherical growth form). A radio opaque dye was used to obtain real time information of the water path inside the aquiferous system. Axial slices of the sponge CT scan revealed the progression of dye inside the canals. Interestingly, dye released near the sponge base consistently followed the same path and exited from the nearest oscula. Similar pattern was observed in the field experiments while estimating the sponge-pumping rate by using flourocien dye. The pumping rate of *I. fusca* was 95-165 % higher than *C.* cf. *cavernosa*, which can be attributed to more number of oscula, larger choanocyte chambers (histological observations) and wider canals (CT scan) in this sponge. Though the pattern of aquiferous system was similar in both sponges, CT scan images showed highly convoluted canal system in *C.* cf. *cavernosa,* which explains the lower pumping rate. This investigation demonstrates the functional morphology of the sponge aquiferous system and highlights the potential application of biomedical technique like CT scan in understanding the functional anatomy of marine invertebrates.

References

1. Ereskovsky, A. V. (2003). Problems of coloniality, modularity, and individuality in sponges and special features of their morphogeneses during growth and asexual reproduction. Russian Journal of Marine Biology, 29(1), S46-S56.
2. Bavestrello, G., & Burlando, B. (1988). The architecture of the canal systems of Petrosia ficiformis and Chondrosia reniformis studied by corrosion casts (Porifera, Demospongiae). Zoomorphology, 108(3), 161-166.
3. Nickel, M., Donath, T., Schweikert, M., & Beckmann, F. (2006). Functional morphology of Tethya species (Porifera): 1. Quantitative 3D-analysis of Tethya wilhelma by synchrotron radiation based X-ray microtomography. Zoomorphology, 125(4), 209-223.

Acknowledgement: We are grateful to The Director of National Institute of Oceanography (CSIR). We thank Suyash Naik, Shriraj Jakhalekar and Aabha Deshpande for help with the fieldwork. We greatly appreciate the efforts and helpful suggestions from Vinayak Mestry, Ganpat Sawant, Shukur Shaikh and Dr. Charudutt Sambhaji for scanning the sponge samples. This work was supported by CSIR funded project 'Ocean Finder' (PSC0105).

What processes shape sponge biodiversity patterns?

Christiaan A. de Leeuw[1], Rosemary Gillespie[2], Agustin Capriati[1], Leontine E. Becking[1, 2, 3]

[1] *Marine Animal Ecology, Wageningen University & Research, The Netherlands, christiaan.deleeuw@wur.nl*

[2] *Department of Environmental Science, Policy, and Management, University of California, Berkeley, CA, USA*

[3] *Naturalis Biodiversity Center, Leiden, the Netherlands*

The abundance and composition of species in communities is determined by multiple stochastic and deterministic processes. However, the complexity of most marine ecosystems makes it difficult to independently investigate factors contributing to the assembly of communities.

Here, we aim to test the relative contribution of neutral dispersal limitation versus selective environments in the formation of sponge biodiversity patterns. We compare 17 marine lakes in Papua, Indonesia, which are of comparable ages and sizes, but vary in environmental regimes and in degree of connection to the open sea.

Marine lakes can be found in geographical clusters and represent a unique combination of multiple heterogeneous environments with varying degrees of connection to the open sea, drawing from the same species pool (the surrounding sea and mangroves). These lakes thus represent multiple replicates of community assembly under varying environments. Environmental conditions are stable within lakes and range from similar to the surrounding sea to very harsh: temperatures from 30-42 °C, pH 7.1-8.3, salinity 11-31 ppt.

Using a combination of genetic and morphological data to identify species and their evolutionary history, and replicates of photo transects, we assessed species abundance, distributions and community phylogenetics per lake. Preliminary results show that the formation of sponge biodiversity patterns is largely shaped by deterministic processes related to environment. Particularly when the environment is harsh (i.e. extreme high temperature or low salinity), diversity is significantly lower. However, stochastic processes such as priority effects likely also play a role, especially on species composition.

Financial support by The Netherlands Organisation of Scientific Research (ALW-VENI #863.14.020) and the Lerner-Gray Fund for Marine Research (American Natural History Museum) is gratefully acknowledged.

Seagrass attributes and seascape patterns as drivers of sessile invertebrate distribution in a coastal biogenic environment

Marie-Claire Demers

Understanding the patterns of distribution of sessile epifaunal invertebrate communities in seagrass meadows is an important precursor to determining the ecological processes shaping ecosystem function in this disappearing habitat. To uncover patterns in the spatial distribution of sponges and ascidians within *Posidonia australis* meadows, I investigated small-scale biogenic characteristics, large-scale seascape patterns, and the abundance of a common seagrass-associated fish species. Linear regressions and generalised linear models were used to determine the relationships between 21 predictor variables and several response variables. Response variables included; 1) sponge diversity, abundance and volume, 2) ascidian diversity and abundance, and 3) the abundance of two common sponge species (*Haliclona* spp. and *Tedania* (*Tedania*) sp.). Distributional patterns of sessile epifaunal invertebrates in seagrass meadows were influenced by both small-scale seagrass characteristics and large-scale seascape patterns. They were not affected by the abundance of a common fish species. The scale over which patterns were apparent differed greatly between sponges and ascidians, suggesting that these different phyla respond to differing drivers of pattern. The biogenic characteristics of seagrass such as the density and length of shoots were found to be important determinants of sponge distribution. Hydrodynamic baffling and nutrient availability are thought to play a role in this interaction. The distribution of a common sponge species complex, *Haliclona* spp. was found to be influenced by depth. This species is a suspected phototroph and its distribution is believed to be dependent on irradiance associated with depth. Seascape patterns influenced the distribution of ascidians inhabiting seagrass meadows. Meadows neighbouring abundant reefal habitats consistently harboured low ascidian species richness. This study provided an initial investigation of the factors driving this threatened community and should be perceived as an important stepping stone in designing future experiments. I conclude by highlighting the importance of manipulative experiments to further explore the underlying processes driving the patterns identified in this study.

Re-examining the under-explored NW Pacific abyssal sponge assemblages of the Kuril-Kamchatka and Okhotsk Sea

Rachel Downey[1], Melanie Fuchs[3] & Dorte Janussen[2]

[1] *School of Environment & Society, Australia National University, Canberra 2601, Australia*
Conference presenter: rachel.downey@anu.edu.au

[2] *Senckenberg Natural History Museum & Research Institute, Frankfurt am Main, 60325, Germany*

[3] *Goethe Universität, Frankfurt am Main, 60555, Germany*

Chronic under-sampling is evident in all marine taxa that inhabit remote and open ocean regions, and particularly deep-sea habitats at bathyal to hadal depths. The abyssal realm (3000 – 6000 m depth) is one key region in which considerable research effort is essential in order to fully understand global biodiversity, assess current and future climatological and ecological trends, and implement effective conservation management. The NW Pacific is considerably under-sampled for sponges at all depths, with less than 1% of global sponge records found in this sector[1].

The abyssal sponge fauna of the NW Pacific region has been re-examined during the recent collaborative German and Russian KuramBio (Kurile-Kamchatka Biodiversity Study) and SokhoBio (Sea of Okhotsk Biodiversity Study) expeditions. Combining our new sponge data with rare previous expedition data from this region has enhanced our understanding of the abyssal sponge fauna. Our new research highlights the patchiness, rarity, high biomass of glass sponges and the exceptional and unique richness of the carnivorous sponge family in this region[2]. We discuss faunal connectivity and processes that are potentially driving the distribution patterns and richness that we see in the NW Pacific. The importance of utilising several forms of sampling equipment in the collection of abyssal sponges is illustrated within this study.

References

1. OBIS, 2014. Data from the Ocean Biogeographic Information System. Intergovernmental Oceanographic Commission of UNESCO. Web. http://www.iobis.org (consulted on 2014/04/16).
2. Downey RV, & Janussen, D. 2015. New insights into the abyssal sponge fauna of the Kurile–Kamchatka plain and trench region (Northwest Pacific). Deep Sea Research Part II: Topical Studies in Oceanography, 111, 34-43.

Financial support by the Australian Graduate Research Training Programme is gratefully acknowledged.

New insights into the temporal and spatial impacts of the Larsen AB ice shelf collapse on sponge assemblages

Downey Rachel[1, 2], Laura Fillinger[3], Dorte Janussen[2], Tomas Lundälv[4] & Claudio Richter[3]

[1] School of Environment & Society, Australia National University, Canberra 2601, Australia
Conference presenter: rachel.downey@anu.edu.au

[2] Senckenberg Natural History Museum & Research Institute, Frankfurt am Main, 60325, Germany

[3] The Swedish Institute for the Marine Environment, University of Gothenburg, Sweden

[4] Alfred Wegener Institute, 27568 Bremerhaven, Germany

Regional warming in the western sector of the Antarctic has been observed since the 1950s. In 1995, this warming led to the collapse of the Larsen A ice-shelf, followed by the Larsen B ice shelf in 2002. Research expeditions in 2007, 2011, and 2013 were conducted by a multi-disciplinary team to track and monitor the ecological and oceanographic changes in this region[1].

Our project assesses how sponge assemblages have responded to ice-shelf collapse in the Larsen AB region. Sponges play a key role in Southern Ocean benthic communities, important both for biomass and as a habitat for many other organisms in the Antarctic. We utilise taxonomy, ROV imagery, and environmental data to understand sponge response to ice-shelf collapse. Pioneer and depth traits are applied to determine changes in the ecological succession of sponge assemblages and connectivity with the shelf and deep-sea.

Our project highlights the importance of hexactinellids as pioneers and colonisers in this region. Utilising the powerful combination of ROV imagery and taxonomic identification, we have observed an unprecedented doubling and tripling respectively of hexactinellid sponge biomass and abundance at Larsen A [2]. Our results explore how sponges are one of the ecological ‘winners’ of the Larsen ice-shelf collapse.

References

1. Gutt, J., Barratt, I., Domack, E., et al. 2010. Biodiversity change after climate- induced ice-shelf collapse in the Antarctic. Deep-Sea Research II. doi:10.1016/j.dsr2.2010.05.024
2. Fillinger, L., Janussen, D., Lundalv, T., Richter, C. 2013. Rapid glass sponge expansion after climate-induced Antarctic ice shelf collapse. Current Biology, Vol. 23. pp. 1330-1334

Financial support by Ant-ERA (SCAR Antarctic Scientific Research Programme) and Australian Graduate Research Training Programme are gratefully acknowledged.

Sponges in semi-submerged caves of the North of Bulgaria (Black Sea)

Alexander V. Ereskovsky[1, 2], Oleg A. Kovtun[3], Konstantin K. Pronin[3], Dirk Erpenbeck[4]

[1]Mediterranean Institute of Marine and Terrestrial Biodiversity and Ecology (IMBE), Aix Marseille University, CNRS, IRD, Station marine d’Endoume, rue de la Batterie des Lions, 13007 Marseille France

[2]Biological Faculty, Saint-Petersburg State University, Universitetskaya nab. 7/9, St. Petersburg, Russia

[3]Odessa National I. I. Mechnikov University, st. Dvoryanska, 2, Odessa, 65026 Ukraine

[4]Department of Earth and Environmental Sciences, Palaeontology & Geobiology and GeoBioCenter, Ludwig- Maximilians- Universität München, Munich, Germany,

Marine caves have revealed the unique biocoenotic and ecological characteristics of these habitats. Sessile benthic species associated with cave habitats typically show a marked zonation from the cave entrance to the inward end of the cave. Sponges can dominate in cave habitats. In the present work sponge biodiversity and their spatial variability in three semi- submerged caves was surveyed in a region poorly explored for its cavernicolous biodiversity, i.e. the North of Bulgaria (Black Sea). Three semi-submerged caves with lengths of 50 to 83 m and volumes of 936 m^3 to 2291 m^3 have been investigated. All of them are karst in origin. In the investigated caves, we inventoried 10 sponge species based on preliminary morphological analysis. All recorded species belong to the class Demospongiae and have previously been recorded also in adjacent open sea waters. These species are tolerant to different hydrological conditions, mostly temperature and salinity. Some of them have wide geographical distribution. Sponge distribution in all investigated caves in general is similar, but there are differences of species composition and distribution depending on cave relief and hydrodynamics. The species composition of sponges from the semi-submerged caves of Bulgaria is quite different from the sponge composition in Crimea caves.

Financial support by grants from Russian Foundation for Basic Research n° 15-04-07554 is gratefully acknowledged.

Integrative investigation of an unprecedented epizootic event affecting endemic sponges of Lake Baikal

Alexander Ereskovsky[1], Annabelle Voorhoeve[1], Stéphane Greff[1], Lubov I. Chernogor[2], Sandrine Chenesseau[1], Igor Khanaev[2], Sergey I. Belikov[2], Olivier P. Thomas[3], Thierry Pérez[1]

[1] Institut Méditerranéen de Biodiversité et d’Ecologie marine et continentale (IMBE), Aix Marseille Université, CNRS, IRD, Marseille, France

[2] Limnological Institute of the Siberian Branch of the Russian Academy of Sciences, Ulan-Batorskaya 3, Irkutsk 664033 Russia

[3] National University of Ireland Galway, Marine Biodiscovery, School of Chemistry, Galway, Ireland.

The Baikal is an emblematic lake listed by UNESCO among the World Heritage Sites, harboring an exceptional biodiversity with an unusual rate of endemism, which is currently experiencing an unprecedented ecological crisis. One possible explanation is a rapid change of the water quality due to tourism development along the Baikal shores combined to a lack of wastewater treatment plan.

Sponges are keystone components of the aquatic ecosystem functioning. They are well known for their biological responses facing changes in water quality. Among eighteen sponge species mostly endemic to Lake Baikal, one of them, *Lubomirskia baikalensis* (Pallas, 1773) is a large erect growth form shaping underwater landscapes.

We present herein a preliminary study which takes place in the framework of a French-Russian collaboration. It aims at the understanding of the mechanisms behind the disease outbreaks, and its putative relationship with other ecological events such as bloom of green algae *Spirogyra* colonizing the Lake bottom and/or development of cyanobacterial veils often observed on sponge surface. Among symptoms of disease, the most striking one is true “sponge bleachings”, similar to those observed in tropical coral reefs, and which is likely related to the release of their symbiotic dinobionts. Various approaches were used to identify some putative pathogens, and to assess the physiological disorder they induce. We present results on a) cytological investigation of necrotic tissues in order to localize putative pathogens or to highlight effects on tissue and cell organization; b) metabolomics in order to assess the consequences of bleaching on the sponge metabolism and especially on its ability to produce chemical defenses.

Financial support by grants from PRC CNRS - RFBR n° 216483 & 16-54-150007 is gratefully acknowledged.

Sponge species associated with *Posidonia oceanica* meadows along the coast of the Aegean Sea (Turkey)

Alper Evcen, Melih Ertan Çinar

Ege University, Faculty of Fisheries, Department of Hydrobiology, 35100, Bornava, İzmir. alperevcen@gmail.com

Posidonia oceanica is a sea grass endemic to the Mediterranean Sea. Its complex rhizome network and large leaves provide a variety of microhabitats for benthic species. The studies on the sponge diversity associated with *P. oceanica* are scarce and limited with some areas in the Mediterranean Sea. The present study aims to elucidate the sponge community structures in *P. oceanica* meadows in the eastern Mediterranean. A plenty of replicated benthic samples were collected at 28 stations at depths ranging from 0 to 35 m in summer 2016 by scuba–diving and snorkeling. In the preliminary analysis of samples, we found a total 25 species belonging

3 classis and 12 orders. The frequently species in the area were *Aplysina aerophoba, Spirastrella cunctatrix, Crambe crambe, Chondrilla nucula, Ircinia variabilis* and *Sarcotragus foetidus*. The majority of species were found to be settled on the rhizome layer of the sea grass, but *Sycon raphanus* occurred both on leaves and rhizomes. The diversity of sponges changed with regards to depths and locations.

Keywords: Sponge, Porifera, *Posidonia oceanica*, Aegean Sea, eastern Mediterranean Sea

Glass Sponge Distribution in Relation to Abiotic Factors and Predators – A Large-Scale Regional Study in the Weddell Sea, Antarctica

Luisa Federwisch[1, 2], Santiago Pineda Metz[1, 2], Nils Owsianowski[1], Dieter Gerdes[1], Dieter Piepenburg[1] & Claudio Richter[1, 2]

[1] Alfred-Wegener-Institut, Helmholtz-Zentrum für Polar- und Meeresforschung, Bremerhaven, Germany luisa.federwisch@awi.de

[2] University of Bremen, Bremen, Germany

Glass sponges (Porifera, Hexactinellida) are important structuring components of the benthos in Antarctic shelf regions. They can grow up to 2 m in height and form extensive sponge beds in some areas, dominating the benthic biomass and providing habitat for a variety of other animals. However, much of their ecology is still unknown to date, including the factors determining their distribution and abundance.

In the current study, we investigate glass sponge distribution and abundance in the south-eastern Weddell Sea in relation to environmental factors (water mass characteristics, currents, ice cover), as well as food availability and abundance of predators. During two recent expeditions with RV Polarstern in 2013/14 and 2015/16, we collected photos and videos of the ocean floor by using different gear equipped with HD cameras: an Ocean Floor Observation System (OFOS), a Remotely Operated Vehicle (ROV), and a multi grab (MG). For each of 28 stations, 30 images are selected and analysed for abundance and species composition of glass sponges and their predators, as well as substrate characteristics.

In addition to that, we measured temperature, salinity, concentrations of dissolved and particulate silicon, and bacterial cell numbers. Furthermore, model and/or satellite data on current strength, mean annual ice cover and chlorophyll a concentration as a proxy for productivity will be included in the study. Glass sponge abundance will be analysed in relation to the environmental data and predator abundance in order to identify the factors determining the abundance and distribution of glass sponges in the south-eastern Weddell Sea. Our findings will provide an important baseline to assess how glass sponge communities might change in a changing Antarctic environment.

Biological habitat preference of the exotic ophiuroid *Ophiothela mirabilis* on marine sponges from Brazil

Humberto Fortunato[1, 2], Gisele Lobo Hajdu[2]

[1] Programa de Pós-Graduação em Oceanografia, Universidade do Estado do Rio de Janeiro, Rio de Janeiro, Brazil. hfmfortunato@gmail.com

[2] Laboratório de Genética Marinha, IBRAG, Universidade do Estado do Rio de Janeiro, Rio de Janeiro, Brazil.

Space is the most limiting factor in marine shallow waters. Brittlestars are commonly found associated to marine sponges with low species-specific interactions. Although, the non-indigenous *Ophiothela mirabilis* has been observed since 2000 in almost the entire coast of Brazil, interacting with more than 30 sessile or sedentary benthic species (Hendler et al. 2012; Mantelatto et al. 2016), any quantitative study was applied. Our aim was to quantify the density of exotic Echinodermata on the sponges' basebionts and to relate these interactions with growth type and surface form of these marine sponges. All possible interactions were photographed from 2013 to 2016, at 25 different sites, from Ceará to Rio de Janeiro states. However, we only found ophiuroids at Bahia and Rio de Janeiro states. All ophiuroids found on the sponges were counted. We found a strong positive correlation between sponges' abundance and ophiuroid's density (r=0.79). We observed 37 sponge species, represented by 261 individuals with eight different morphotypes and 14 types of surface. Of 5122 non-indigenous ophiuroids encountered, 32% were over *Mycale angulosa* and 26.3% over *Callyspongia* sp. 2. *Desmapsamma anchorata* (10.3%) and *Monanchora arbuscula* (8.9%) were also observed commonly associated to *O. mirabilis*, but less frequently. More than 43% of the brittlestar preferred digitate sponge shapes, and 39.6%, conulose surface type. Although we did not see any preference in relationship to the basibiont color, *O. mirabilis* is a generalist guest/epibiont with a slight preference to live on organisms with erect shape and conulose surface. This way, it can hug on sponge's substrate, but does not hide from possible predators. To study the interactions between exotic and native species is essential to understand how the non-indigenous species act on the new environments, and further experimental assays are being prepared to analyze if this association is related to physical and/or chemical mechanisms.

References

1. G. Hendler, A.E. Migotto, C.R.R. Ventura, L. Wilk, Coral Reefs 31 (2012) 1005.
2. M. C. Mantelatto, L.F. Vidon, R.B. Silveira, C. Menegola, R.M. Rocha, J.C. Creed, Mar. Biodiv. Rec. 9:8 (2016) doi10.1186/s41200-016-0013-x.

Financial support by CAPES AUXPE CIMAR 1986/2014 is gratefully acknowledged.

Mediterranean Deep-Sea Sponges From The MedSeaCan And CorSeaCan Cruises

Maïa Fourt[1], Nicole Boury-Esnault[1], Jean Vacelet[1], Thierry Pérez[1], Adrien Goujard[2], Pierre Chevaldonné[1] & the MedSeaCan-CorSeaCan technical & scientific teams

[1] Institut Méditerranéen de Biodiversité et d'Ecologie marine et continentale, CNRS, IRD, Aix Marseille Université, Avignon Université, Station Marine d'Endoume, rue Batterie des Lions 13007 Marseille, France

[2] GIS Posidonie, Campus de Luminy, Océanomed, Case 901, 13288 Marseille Cedex 09, France

The MedSeaCan and CorSeaCan cruises took place along the French continental shelf margin, from the Spanish border to Monaco (MedSeaCan) and along the western coast of Corsica (CorSeaCan). These two series of cruises were the very first attempt to systematically explore the French Mediterranean deep-sea canyons. In this area, the canyon heads, as well as the offshore rocky banks of the continental shelf were explored between 100 and 600 m. The surveys of 43 sites (34 canyons and 9 rocky banks) were all conducted with a manned submersible and an ROV. The surveys aimed at providing a reference state of the ecosystem through direct observation and the collection of photographic, video and biological samples, all integrated in a georeferenced database. Images and data treatment revealed the important presence of Porifera and its specific diversity. For this phylum, although some taxonomical difficulties where encountered, we have significantly extended our knowledge on the bathymetrical and geographical distribution of species common along the explored area (*e.g. Poecillastra compressa, Thenea muricata, Rhizaxinella* spp.). New localisations of some rarely encountered species (e.g. *Lycopodina hypogea*, *Haliclona (Halichoclona) magna, Leiodermatium pfeifferae, Stylocordyla pellita*) have been recorded, and for some of them the living context has been observed for the first time in the Mediterranean Sea (*Cladorhiza* cf. *abyssicola*). Finally these explorations have allowed the description of three new Hexactinellida in the genera *Sympagella*, *Farrea* and *Tretodictyum* as well as new biomolecules (aromatic alkaloid from *Latrunculia citharistae* and steroidal saponins from *P. compressa*), some of them being bioactive. The prominence of sponges in some parts of the deep rocky habitats of the Mediterranean has led us to revise the existing French typology of deep-sea habitats by adding a 'facies of large sponges'.

References

1. G. Genta-Jouve, N. Francezon, A. Puissant, P. Auberger, J. Vacelet, T. Perez, A. Fontana, A.A. Mourabit, O.P. Thomas, Structure elucidation of the new citharoxazole from the Mediterranean deep- sea sponge Latrunculia (Biannulata) citharistae. Magnetic Resonance in Chemistry 49 (2011) 533–536.
2. N. Boury-Esnault, J. Vacelet, H.M. Reiswig, M. Fourt, R. Aguilar, P. Chevaldonné, Mediterranean hexactinellid sponges, with the description of a new Sympagella species (Porifera, Hexactinellida). Journal of the Marine Biological Association of the UK 95 (2015) 1353–1364.
3. M. Fourt, A. Goujard, T. Pérez, J. Vacelet, P. Chevaldonné, the scientific team of the MedSeaCan and CorSeaCan cruises, French Mediterranean submarine canyons and deep rocky banks: a regional view for adapted conservation measures, in: Proceedings of the 1st Mediterranean Symposium on the Conservation of Dark Habitats (Portoroz, Slovenia, 31 October 2014). RAC/SPA Publ., Tunis (2014) 33–38.
4. N. Boury-Esnault, J. Vacelet, M. Dubois, A Goujart, M. Fourt, T. Pérez, P. Chevaldonné New hexactinellid sponges from deep Mediterranean canyons. Zootaxa (2017).

Financial support by French Marine Protected Areas Agency (AAMP), the Mistral / Biodivmex program, the Labex "Objectif Terre - Bassin Méditerranéen (OT-Med)".

The availability of map resources for the distribution, degradation status and threats to sponge assemblages in the European Seas – initial baselines in the MERCES project

Vasilis Gerovasileiou[1], Thanos Dailianis[1], Nadia Papadopoulou[1], Katerina Sevastou[1], Christopher J. Smith[1], Teresa Amaro[2], Trine Bekkby[3], Meri Bilan[4], Christoffer Boström[5], Emma Cebrian[6], Carlo Cerrano[2], Roberto Danovaro[2], Dario Fiorentino[7], Simonetta Fraschetti[8], Karine Gagnon[5], Cristina Gambi[2], Anthony Grehan[9], Bernat Hereu[10], Silvija Kipson[11], Jonne Kotta[12], Cristina Linares[10], Martina Milanese[13], Telmo Morato[4], Henn Ojaveer[12], Helen Orav-Kotta[12], Antonio Sarà[13], Rachael Scrimgeour[14], İnci Tüney Kızılkaya[15], Elizabeth Grace Tunka- Eronat[15]

[1] Hellenic Centre for Marine Research, Greece, vgerovas@hcmr.gr; [2] Università Politecnica delle Marche, Italy; [3] Norwegian Institute for Water Research, Norway; [4] Instituto do Mar Centro da Universidade dos Açores, Portugal; [5] Åbo Akademi University, Finland; [6] Institut d'Ecologia Aquàtica, Universitat de Girona, Spain; [7] Alfred Wegener Institute, Germany; [8] Consorzio Nazionale Interuniversitario per le Scienze del Mare, Italy; [9] National University of Ireland Galway, Ireland; [10] University of Barcelona, Spain, [11] Faculty of Science - University of Zagreb, Croatia; [12] University of Tartu, Estonia; [13] Studio Associato GAIA, Italy; [14] UNEP World Conservation Monitoring Centre, United Kingdom; [15] Mediterranean Conservation Society, Turkey

Within the MERCES project (http://www.merces-project.eu/), one of the first objectives is to catalogue existing and available maps for marine habitats, along with their degradation status and restoration potential in the European Seas. In order to reach this objective, an extensive review has been performed and a catalogue compiled with mapping sources for (a) marine habitats, (b) degraded marine habitats, and (c) pressures and mechanisms that could potentially drive key-habitat changes in them. In its current form, the MERCES WP1 catalogue includes a total of approximately 900 entries with meta-data regarding various marine habitats, assemblages and marine areas. These entries include published records, web resources, and grey literature (i.e. project reports, technical documents, and unpublished data). Information about sponge assemblages covers only 6% of the catalogue's entries highlighting a potential gap in relevant broad- scale mapping initiatives. In half of the available sources (52%), sponge assemblages were found together with those of anthozoans (e.g. cold water corals, coral gardens, gorgonian forests), suggesting that these two biological features often co-exist and/or are treated together in broad-scale mapping initiatives. Available mapping sources for sponge assemblages mainly concern the deep-sea (53%) and sublittoral hard substrate habitats (31%) of the North-East Atlantic Ocean (55%) and the Mediterranean Sea (38%). More specifically, the main habitats/assemblages identified were deep-sea sponge aggregations and mixed coral/sponge fields, sublittoral rocky and coralligenous beds. Several information sources underline a significant – though not quantified – decline in deep sponge fields, along with recorded mortality events for the shallow ones. The most frequently highlighted threats for these assemblages are: bottom trawling, climate change, dumping, land-based activities, harvesting, minerals exploration, scientific research, and marine litter. Interestingly, most of the catalogue entries (71%) were derived from grey literature, indicating a valuable – yet often overlooked – source of information.

This research has received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No 689518 (MERCES: Marine Ecosystem Restoration in Changing European Seas).

World Register of marine Cave Species (WoRCS): a tool for evaluating sponge diversity in marine caves and anchialine systems of the world

Vasilis Gerovasileiou[1], Alejandro Martínez[2], Leontine E. Becking[3, 4], Guilherme Muricy[5], Fernando Álvarez[6], Geoff Boxshall[7], William F. Humphreys[8], Damià Jaume[9], Peter J. van Hengstum[10], Hiroshi Yamasaki[11], Nicole Boury-Esnault[12], Thierry Perez[12], Eleni Voultsiadou[13], Stefanie Dekeyzer[14], Wim Decock[14], Bart Vanhoorne[14], Leen Vandepitte[14], Nicolas Bailly[1, 15], Thomas M. Iliffe[10]

[1] Hellenic Centre for Marine Research, Greece, vgerovas@hcmr.gr;[2] CNR-ISE, Italy; [3] Marine Animal Ecology, Animal Science Group, Wageningen University, Netherlands; [4] Naturalis Biodiversity Center, Netherlands; [5] Departamento de Invertebrados, Museu Nacional, Universidade Federal do Rio de Janeiro, Brazil; [6] Universidad Nacional Autónoma de México, Mexico; [7] Department of Life Sciences, Natural History Museum, UK; [8] Department of Terrestrial Zoology, Western Australian Museum, Australia; [9] IMEDEA (CSIC-UIB), Mediterranean Institute for Advanced Studies, Spain; [10] Texas A&M University at Galveston, USA; [11] Leibniz Institute for Evolution and Biodiversity; Museum für Naturkunde, Germany; [12] IMBE-UMR7263 CNRS, Universite´ d'Aix-Marseille, Station Marine d'Endoume, France; [13] School of Biology, Aristotle University of Thessaloniki, Greece; [14] Flanders Marine Institute/Vlaams Instituut voor de Zee (VLIZ), Belgium; [15] FishBase Information and Research Group, Philippines

As reservoirs of sponge diversity, marine caves have attracted the interest of sponge researchers from around the world at an early stage. The need to compile all the existing largely scattered information on the sponge diversity of this unique ecosystem has been recently recognized and some regional overviews came out. The World Register of marine Cave Species – WoRCS (www.marinespecies.org/worcs), a Thematic Species Database of the World Register of Marine Species – WoRMS, offers a valuable resource for an integrated approach to this issue. The aim of WoRCS is to create a comprehensive taxonomic and ecological database of species known from marine caves and anchialine environments worldwide. Within this thematic database, the cave-related information is managed by the WoRCS thematic editors in collaboration with the taxonomic editors of WoRMS, who manage the taxonomic content. The database is an online open source and includes information on the biology, ecology, and distribution of all species. Data on sponge distribution in marine caves are linked to the Gazetteer of the Marine and Anchialine Systems of the World, which is part of the Marine Regions information system and includes geographical and geological information for all study areas. Currently, the database includes 1629 species belonging to 19 phyla as well as 573 relevant literature sources. With 423 accepted species, Porifera is the richest in species phylum of sessile metazoans in the database, covering 26% of the existing records. Demosponges predominate with 365 species, followed by 33 calcareans, 24 homoscleromorphs and 1 hexactinellid. In their attempt to catalogue the world sponge diversity in marine caves, the WoRCS thematic editors and collaborators have initiated an exhaustive overview of all sources, including unpublished data from their expeditions. Herein the followed methodology, available sources and tools along with preliminary results of this initiative are presented. The main goal of this initiative is to describe distribution patterns in this fragmented ecosystem, to highlight unique elements of sponge diversity and provide a baseline for future conservation actions.

Sponge biodiversity of the shallow sublittoral Antarctic Peninsula

Claire Goodwin [1,], Katharine Hendry[2], Jade Berman[3]

[1] Atlantic Reference Centre, Huntsman Marine Science Centre, St Andrews, NB, Canada claire.goodwin@huntsmanmarine.ca

[2] Department of Earth Sciences, University of Bristol, UK

[3]Ulster Wildlife Trust, Belfast, Northern Ireland, UK

Currently the diversity and abundance of sponges on shallow Antarctic reefs is likely to have been significantly underestimated (Cardenas et al. 2016). The difficulty of identifying sponges *in situ* has led to them being recorded simply as 'Porifera' in many studies, despite often being the dominant phylum on Antarctic hard substrates. We collected sponge specimens from 22 sites (0-24m depth) spanning from King George Island, South Shetland Islands (62°12.185'S) to Jenny Island, Marguerite Bay (67°43.325'S). Sampling was undertaken by SCUBA which enabled study of the large boulders and bedrock walls, these tend to be particularly sponge rich and unlikely be well sampled by remote methods. The survey was carried out from a 26.5m vessel which enabled access to sites inaccessible to larger vessels; these included little studied areas such as the Biscoe Islands. In total 309 specimens were collected encompassing 24 species of which four were new to science. Records of the appearance of sponge were obtained, including some which have not previously been seen *in situ*, and these are being developed into a resource for researchers working in this area.

References

1. C.A. Cárdenas, E.M. Newcombe, E. Hajdu, M. Gonzales-Aravena, S.W. Geange, and J.J. Bell, Polar Biology 35 (2016): 1, 30532.

Financial support by the Leverhulme Trust (RPG–2012–615), Antarctic Science Bursary, the Trans-Antarctic Association, the Shackleton Scholarship Fund and the Royal Society is gratefully acknowledged.

Engaging recreational SCUBA divers in recording sponge biodiversity

Claire Goodwin[1], Bernard Picton[2], Charlotte Bolton[3]

[1] Atlantic Reference Centre, Huntsman Marine Science Centre, St Andrews, NB, Canada claire.goodwin@huntsmanmarine.ca

[2] National Museums Northern Ireland, Belfast, Northern Ireland
3 Marine Conservation Society, Ross-on-Wye, UK

Seasearch is a project for volunteer sports divers who have an interest in what they are seeing underwater, want to learn more, and want to help protect the marine environment around the coast of Britain and Ireland. The main aim is to map near-shore habitats and species. Engaging volunteers in recording some of the more difficult and less charismatic taxonomic groups, such as porifera, can be challenging. There can be issues with ensuring correct identifications, compounded by a lack of identification resources aimed at divers. However, the records obtained are extremely valuable in determining distribution and status of species. Here we discuss some of the benefits and challenges involved in engaging volunteers in sponge recording and the tools and resources that have proved useful.

In situ arrests of glass sponge (Hexactinellida) feeding currents in response to suspended sediments

Nathan Grant & Sally P. Leys[1]

[1] Department of Biological Sciences, University of Alberta, 116 Street & 85 Avenue, Edmonton, Canada ngrant@ualberta.ca

Off the Pacific coast of Canada, glass sponges (Class Hexactinellida) form deep-water reefs, akin to shallow-water coral reefs. They feed, respire and recycle nutrients at the reefs via continuous pumping. In 2008, Tompkins-MacDonald and Leys showed that in flow through tanks, hexactinellids temporarily halt their feeding currents when stimulated by sediment. This behaviour, termed the “arrest-recovery response”, is thought to be a protective response against stimuli like suspended sediments that may clog or damage a sponge’s aquiferous system. In a laboratory experiment, the introduction of suspended sediment caused action potentials to traverse the glass sponge syncytial tissue and induce an “arrest” of excurrent flow[1]. This arrest behaviour, while protective, limits the time available to a sponge for feeding and respiration which may have a negative effect on a sponge’s health. Sediment suspended by bottom-trawling near the reefs could be a behavioural instigator that permanently harms the sponge reefs. In 2015 an experiment was carried out at Fraser Reef, a kilometer-long sponge reef in the Strait of Georgia, British Columbia, Canada, to assess whether sediment triggers feeding current arrests in the field. Flowmeters were placed over sponge oscula to measure excurrent flow. Ambient flow and turbidity were recorded with an acoustic Doppler current profiler and optical backscatter sensors respectively. Sediment was suspended upstream of the sponges using the remote operated vehicle ROPOS. We found that reef-building glass sponges do arrest their feeding currents in the field. Eight of the recorded feeding current arrests were highly correlated with increased suspended sediment concentrations. Fisheries and Oceans Canada has recently established the Hecate Strait and Queen Charlotte Sound sponge reefs as Canada’s largest Marine Protected Area[2]. However, a 200 m adaptive management zone adjacent to the reefs would allow potential trawl fisheries adjacent to the sponges. During a 2017 research cruise to the Hecate Strait sponge reef, we aim to quantify the cost feeding current arrests have on sponge health and determine the threshold concentration of suspended sediments that induce arrests of glass sponge feeding currents. By comparing the threshold of response with concentrations of sediments suspended by bottom-trawling we can determine the distance from the reefs that trawling no longer influences sponge health. Our results show that suspended sediment does affect glass sponges, and suggests that a substantial buffer zone excluding bottom-contact fishing is needed for adequate and enduring protection of the sponge reefs.

References

1. Tompkins-Macdonald, G. J. & Leys, S. P, Marine Biology. 154 (2008) 973–984
2. Fisheries and Oceans Canada. *Pacific Region Coral and Sponge Conservation Strategy*. (2010).

Financial support by NSERC Strategic Network (CHONe) and NSERC Discovery/RTI grants to Sally P. Leys is gratefully acknowledged.

Prince Albert’s underwater caves: Sponge fauna of unusual artificial reefs at Monaco

Marie Grenier[1], César Ruiz[1], Nicolas Bonnet[2], Christophe Lejeusne[3], Jean Vacelet[1], Raphael Simonet[2], Pierre Chevaldonné[1], Thierry Pérez[1]

[1] Institut Méditerranéen de Biodiversité et d’Ecologie marine et continentale, CNRS, IRD, Aix Marseille Université, Avignon Université, Station Marine d’Endoume, rue Batterie des Lions 13007 Marseille, France

[2] Direction de l’Environnement, 3 avenue de Fontvieille 98000 Principauté de Monaco.

[3] UPMC Université Paris 6, Sorbonne Université, UMR 7144, Station Biologique de Roscoff, 29688 Roscoff, France

Fifteen years ago, Monaco extended its main harbor seaward by constructing additional jetties. One of these was a “floating” concrete structure, 145 m long and 30 m wide, set on a cuboid hollow base about 40 m high. This basal structure was flooded with seawater through holes left open in the concrete at 22-23 m, that are wide enough (1 m) to allow scientific divers to enter. They are therefore artificial mimics of underwater caves of various configurations and confinement patterns. The first type is a series of 8 cuboid vertical caves (called “caissons”), going from 14 m to 38 m depth, with a main entrance at 22 m and 2 smaller communications with the open sea at 14 m. The second type (called “cathedrale”) consists in one very large cavity, going from 23 m to 39 m depth, with 4 openings in its ceiling. Since the entrances are narrow, these rooms present vast areas that are totally dark, with very low water circulation, high degree of confinement, and thus severe oligotrophy. The entrances being shallower than their deepest parts, these structures tend to trap denser cold waters year-round. This environmental context is similar to that of some natural underwater caves and deep sea habitats.

In 2005, we began a survey of these original mesocosms to follow the recruitment and the development of benthic communities expected to include some representatives of natural underwater caves. Temperature regime was followed hourly in different structures and at various depths (6 data loggers), together with an annual survey of the colonization dynamics at three distances from the entrance inside the two types of “caves” (total of 6 locations and 60 photo-quadrats/yr). Each exploration was used to complete a species inventory, with a special attention to sponges. The long term monitoring showed a quick colonization: the highest species diversity was surprisingly recorded in 2007. However, it was followed by a stabilisation and fluctuations at a lower level. In 2015, ten years after the survey began, highest species diversity is half what it was in 2007. The most remote and confined areas are as expected displaying very low diversity values. The highest colonization was observed at 20 m, near the entrances of “caissons” and the lowest at 35 m, in both sites of the “cathedrale”. After 15 years, although the mobile fauna is clearly dominated by cave species (mysids, decapod crustaceans, teleost fish), the sponge fauna of these artificial caves is composed of a mixture of opportunistic species, rather common in harbor conditions (*e.g. Crambe crambe*, *Chondrosia reniformis*), and of cave-dwelling species (*e.g. Diplastrella bistellata*, *Haliclona fulva*, *Merlia deficiens*, *Oscarella microlobata*, *Oscarella viridis*, *Plakina trilopha*). These concrete artificial caves appear too unstable for a sessile community to settle and mature on the long term. Indeed we observed that the smooth concrete surfaces did not allow for large growth forms to hold in time, and regular accumulations of dying organisms on the floor likely induced some anoxic events in the deepest parts of these systems.

Genetic Population Structure of *Ircinia campana* and *Spheciospongia vesparium* in the Greater Caribbean

Sarah Griffiths[1], Donald Behringer[2, 3], Mark Butler IV[4], Thierry Pérez[5], Evelyn Taylor-Cox[1] and Richard Preziosi[1]

[1] Division of Biology and Conservation Ecology, Manchester Metropolitan University, Chester Street, Manchester, UK. Griffiths.sarahm@gmail.com

[2]School of Forest Resources and Conservation, Program in Fisheries and Aquatic Sciences, University of Florida, Gainesville, Florida, USA.

[3]Emerging Pathogens Institute, University of Florida, Gainesville, Florida, USA.

[4]Department of Biological Sciences, Old Dominion University, Norfolk, Virginia, USA.

[5] Institut Méditerranéen de Biodiversité et d'Ecologie Marine et Continentale, UMR CNRS 7263, IRD 237, Aix Marseille Université, Marseille, France.

In the Caribbean seascape sponges are abundant, biodiverse and have many varied and important functional roles. Understanding how genetic diversity is distributed spatially is important for defining population units, inferring connectivity, gene flow and dispersal capabilities, and predicting resilience. In this study, we investigate the genetic population structure of two common Caribbean demosponges: *Ircinia campana* (vase sponge; Dictyoceratida, Irciniidae) and *Spheciospongia vesparium* (loggerhead sponge; Clionaida, Clionaidae). These large sponges are dominant members of hard bottom ecosystems in the Florida Keys (Florida, USA), where sponge communities have suffered mass mortalities caused by cyanobacterial blooms. This has had suspected knock-on effects through the ecosystem, including on associated faunal abundances, and on the susceptibility of the ecosystem to further blooms. Both species are also common and often conspicuous members of coral reef and lagoon ecosystems throughout the Caribbean. In this study, we use newly developed microsatellite markers to study genetic population structure in these two species at various spatial scales. Samples were collected from several locations across the geographic range of distribution of the species (including fine-scale sampling in the Florida Keys), and levels of genetic diversity and its distribution were examined within and among locations. This research contributes to the understanding of Caribbean sponge population dynamics, and will help to inform ecosystem restoration efforts for vulnerable sponge communities in the Florida Keys by enabling predictions of resilience and recovery patterns among mortality-affected locations.

Financial support by the Natural Environment Research Council (NERC) is gratefully acknowledged.

Integrating (Meta)genomics data into sponge symbiont cultivation

Johanna Gutleben, Catarina Carolina Sales e Santos Loureiro, Hauke Smidt, Detmer Sipkema

Laboratory of Microbiology, Stippeneng 4, 6708 WE Wageningen, Netherlands. johanna.gutleben@wur.nl

Introduction: Marine sponges (*Porifera*) harbour distinct and diverse microbial communities. These symbionts potentially produce sponge-derived, pharmaceutically interesting metabolites and hence cultivation of these microbes has gained focus in the scientific community. However, most microbial symbionts have evaded cultivation to date, thus a promising approach is to mine meta-omics data for *in silico* physiological traits that can be integrated in high-throughput cultivation strategies.

Goals: This study aimed to integrate genomic information into the design of novel cultivation media and develop a high-throughput experimental strategy targeting the cultivation and isolation of the sponge- associated candidate phylum *Poribacteria*. Additionally, this work set out to increase the cultivable fraction of the microbial community associated with the sponge *Aplysina aerophoba*.

Methodology: A collection of low-nutrient media was designed based on the predicted carbohydrate degradation metabolism of *Poribacteria*[1, 2]. To further optimize the medium design, we aimed to mimic conditions from the sponge mesohyl niche by adding the sponge-derived antibiotic Aeroplysinin-1. In total, 240 cultivation conditions were created, and isolates were identified by 16S rRNA gene amplicon sequencing.

Results: 1758 colonies were picked, and 1463 PCR products were analysed, resulting in a total of 128 cultivated OTUs. Amplicon sequencing revealed that no *Poribacteria* isolates were obtained. Nearly 70% of isolates were *Alphaproteobacteria*, of which *Pseudovibrio* and *Ruegeria* OTUs were the only two OTUs isolated from all media. Phylogenetic diversity varied significantly in different media and was influenced by medium dilution and the antibiotic Aeroplysinin-1, however, no novel OTUs were isolated in this study. Only 1.8% of the OTUs were observed in both the cultured fractions and the sponge community, which was dominated by *Chloroflexi*, *Actinobacteria* and *Cyanobacteria*.

Conclusion: The largest part of the sponge-associated microbial community remains uncultivated despite tailor made media designs and a high throughput cultivation approach. Nonetheless, the media formulations developed here have potential as enrichment media for specific microbial groups.

1. Siegl, A. *et al.* Single-cell genomics reveals the lifestyle of Poribacteria, a candidate phylum symbiotically associated with marine sponges. *ISME J.* **5,** 61–70 (2011).
2. Kamke, J. *et al.* Single-cell genomics reveals complex carbohydrate degradation patterns in poribacterial symbionts of marine sponges. *ISME J.* **7,** 2287–300 (2013).

The distribution of Ostur in relation to physical variables within the Faroe-Shetland Channel

Joshua Davison[1], Nils Piechaud[1], Phil Hosegood[1], Kerry L. Howell[1]

[1] Marine Institute, Plymouth University, Drake Circus, Plymouth, UK. joshua.davison@students.plymouth.ac.uk

The range of ecological functions and ecosystem services provided by deep-sea sponge aggregations has resulted in these habitats being considered Vulnerable Marine Ecosystems under United Nations General Assembly Resolution 61/105. Understanding the distribution of these habitats is critical to future spatial management efforts, and the key to predicting their distribution lies in understanding the role of environmental drivers. Accumulations of large suspension feeders are hypothesised to aggregate near the shelf break in regions of internal wave formation. The causal link is thought to be an increase in the supply of food related to the incidence of internal waves which results in resuspension of particulate organic matter on which the sponges feed. There is, however, almost no empirical evidence to support this hypothesis for deep-sea sponge aggregations, although there is strong circumstantial evidence. We tested the relationship between sponge density and oceanographic variability (as a measure of internal wave presence) for a known sponge aggregation in the Faroe-Shetland Channel.

18 video transects, ranging from 422-979m depth were conducted in the study region. 220 images were analysed and all taxa identified to morphotypes and quantified. Temperature and salinity data from 18 CTDs were obtained from the British Oceanographic data centre spanning 18 years (1984-2002), and variability in both calculated over the depth range. Linear regression was used to test the relationship between sponge density and temperature variability. The model showed a statistically significant relationship between sponge density and temperature variation, with the highest sponge densities occurring at depths of greatest temperature variability. Greatest particulate flux and current velocity occurred deeper than the depth of known sponge aggregations suggesting these areas are sub optimal for sponge aggregation presence. Our data broadly support current theory on drivers of deep sea sponge aggregation distribution.

Financial support by the UK Department for Trade and Industry and Plymouth University is gratefully acknowledged.

Oases of diversity: East-Mediterranean mesophotic sponge grounds

Tal Idan [1], Sigal Shefer[1, 2], Tamar Feldstein [1, 2], Ruth Yahel [3], Dorothée Huchon[1, 2], Micha Ilan[1, *]

[1] Department of Zoology, George S. Wise Faculty of Life Sciences, Tel Aviv University, Ramat Aviv, Tel Aviv 6997801, Israel

[2] The Steinhardt Museum of Natural History, Israel National Center for Biodiversity Studies, Tel Aviv University, Ramat Aviv 6997801, Israel

[3] Science Division, Israel Nature and Parks Authority, Givat Shaul, Jerusalem 95463, Israel

Although sponges are a diverse and abundant phylum, data regarding East-Mediterranean sponge communities are scarce, outdated, and limited to shallow water (1, 2, 3). This research aims to expand the knowledge of the sponge fauna along the Mediterranean shore of Israel by studying a diversity of habitats. Among the examined habitats, are the newly-discovered mesophotic sponge grounds that lie on a submerged sandstone ridge at 100-130 m depth, and studied here using a remotely- operated vehicle (ROV). On that ridge, are two of the studied locations, Herzliya and Atlit, in the form of a series of pinnacles raising ca. 30m above the sea floor. The third location, Haifa, is an extension of the terrestrial Carmel mountain ridge, elevated up to 40m from the surrounding sea floor. In the mesophotic ecosystems, sponges are the phylum with the highest live coverage and serve as environmental engineers creating complex three dimensional structures that attract invertebrates and fish.

During quantitative surveys conducted at the three locations, the ROV was used to take photo–quadrats as well as samples. The sponge grounds were found to maintain rich and diverse communities, with 47, 52 and 65 species in Atlit, Haifa and Herzliya respectively. The maximal species overlap between any two sites was 63%, and only 26% of the species were found in all three sites (Figure 1). Several of the mesophotic species are documented for the first time from the Levant basin, while others might be novel species. The mesophotic species include some that disappeared from the east Mediterranean shallower habitats decades ago, and were re-discovered as flourishing in the mesophotic habitats. We suggest that the mesophotic sponge grounds may serve as refugia for species stressed by the rising temperatures in shallow waters, and by other anthropogenic disturbances affecting mostly the shallower coastal habitats.

References

1. Gottlieb E (1959) Study of the benthos in Haifa Bay: ecology and zoogeography of invertebrates. PhD Diss Hebrew University Jerusalem
2. Levi C (1957) Spongiaires des cotes d'Israel. Bulletin of the Research Council of Israel 6B:201-212
3. Tsurnamal M (1968) Studies on the Porifera of the Mediterranean Littoral of Israel. PhD Diss Hebrew University Jerusalem

Financial support by the Ministry of Science and Technology, the Ministry of National Infrastructures, Energy and Water Resources, and Israel Nature and Parks Authority, is gratefully acknowledged.

Studies on sexual reproduction and secondary metabolite profile of the sponge *Ircinia fusca* (Carter) (Demospongiae: Dictyoceratida)

Shriraj S. Jakhalekar & Narsinh L. Thakur

CSIR National Institute of Oceanography, Dona Paula 403 004, Goa, India.

Sexual reproduction in sponges with emphasis on formation of gametes, embryonic development, larval morphogenesis and post-larval-settlement growth has been studied using light and electron microscopy in some species of family Irciniidae Gray (order Dictyoceratida Minchin). Though there are about 450+ marine sponge species recorded from the Indian coast, no information is available on sexual reproduction of these organisms. Sexual reproduction in *Ircinia fusca* (Carter), collected from the central west coast of India, was monitored over a period of two years. Eggs, spermatocysts and developing embryos in the brooding chambers were studied by standard histological methods (microtechnique) and light microscopy. It was observed that *I. fusca* is a hermaphrodite ovoviviparous sponge and reproduces during the post-monsoon season (November–February). Reproductive effort of the sponge was found to be highest in the months of December and January. Sponges produce diverse secondary metabolites. Trade-off between the secondary metabolite production and primary biological processes, like growth and reproduction, has been demonstrated in sponges, which support the 'optimal defense theory'. To understand the possible relation between reproduction and secondary metabolite production in *I. fusca*, metabolic profiles of the sponge were analysed using LC-MS and HPLC during its reproductive and non- reproductive phases. Noticeable difference in metabolic profiles of *I. fusca* was observed during reproductive and non-reproductive periods. Present study describes and illustrates the sexual reproduction in *I. fusca* and suggests its possible influence on the secondary metabolite production, which further needs to be investigated in detail.

Time to Revisit the Western Indian Ocean Ecoregions and Hotspots: A Numerical Zoogeographical Analysis Using Sponges as a Case Study

Liesl Janson[1*], Steve Kirkman[1] and Toufiek Samaai[1,2]

[1]*Department of Environmental Affairs, Branch Oceans and Coasts, Oceans and Coasts Research, Marine Biodiversity and Ecosystems Research, Cape Town, South Africa.*

[2]*MARE, University of Cape Town, Cape Town, South Africa.. ljanson@environment.gov.za*

In the phase of changing climate and disturbance and loss of marine habitats, conservation of at least a representative sample of the ecosystem diversity in global biodiversity hotspots has become a priority. This is where biogeography can provide information for conservation, through demarcation of ecoregions, based exclusively on the actual species distributions. The tropical Indo-West & East Pacific is the largest coastal realm on earth with the WIO been partitioned into 9 ecoregions by Spalding et al. (2007). An analysis of the large-scale patterns of sponge species richness has, however, never been performed in the WIO. Hence, the present analysis attempts (1) to determine the zoogeography of the shallow-water sponges, (2) whether they correlate with the WIO ecoregions as proposed by Spalding *et al*. (2007), (3) how sponge biodiversity is distributed in the WIO. Records of WIO marine sponges were compiled from (1) all known published and unpublished records and observations as well as from (2) collections. A species presence/absence matrix with a resolution of 1° latitude/longitude was constructed. Species matrices in equal operational geographical units were subjected initially to a chronological analysis, where the species richness hotspots, centers of endemism and areas of endemism were mapped. Subsequently the data matrices were numerically analysed with (a) a phenetic approach: cluster analysis approach and (b) a parsimony approach: parsimony analysis of endemism (PAE), where the chronological areas of endemism are numerically confirmed. Results of chronological mapping provide insights for conservation prioritization in the southern and northern extremes of the WIO. Chronological as well as the numerical identification of areas of endemism clearly define the Natal- , Mozambique Channel- and Mascarene Plateau ecoregions as biogeographical barriers within the WIO. Species turnover is also at its lowest within and between the Mascarene Plateau, Somali Bassin and Mozambique Channel ecoregions. On the other hand, species turnover is at its largest at the southern extreme. i.e. at the boundary between Natal and Delagoa ecoregions. The biogeographic ecoregionalisation reconfirms the current ecoregions as identified by Spalding et al. (2007). As a serendipitous discovery, we found that Rapoport's rule does not hold in the WIO.

Financial support by the Department of Environmental Affairs: Oceans & Coasts Branch is gratefully acknowledged.

Sponge communities of the Antarctic Peninsula: influence of environmental variables on species composition and richness

Dorte Janussen[1], Daniel Kersken[1]

[1] *Department Marine Zoology, Senckenberg Research Institute and Nature Museum, Senckenberganlage 25, 61325 Frankfurt a. M., Germany*

Sponge communities on the Antarctic continental shelf currently represent one of the most extensive sponge grounds in the world, and all sponge classes are known to occur in the Southern Ocean. Main objectives of this study conducted at the tip of the Antarctic Peninsula were (1) to identify all sampled sponges and (2) to investigate whether the species composition and species richness of Southern Ocean sponge communities in the area of the Antarctic Peninsula are significantly influenced by environmental variables. The studied material originated from 25 AGT catches and was sampled during the expedition ANT-XXIX/3 of RV Polarstern. Samples were collected in three large-scale areas in the vicinity of the Antarctic Peninsula: Bransfield Strait, Drake Passage and Weddell Sea. The following six environmental variables were measured from bottom water samples (except for sea-ice cover): depth (m), light transmission (%), oxygen (lmol/kg), salinity, sea-ice cover (%) and temperature (^{o}C).

Two hundred and sixty-three sponge samples were analyzed, and 81 species of 33 genera from all Porifera classes were identified. Total numbers of sponge species per sample station ranged from 1 to 29. A detrended correspondence analysis and a backward-stepwise model selection were performed to check whether species composition and richness were significantly influenced by environmental variables. The analyses revealed that none of the measured environmental variables significantly influenced species composition but that species richness was significantly influenced by (1) temperature and (2) the combination of temperature and depth. Results of this study are of crucial importance for development, performance and assessment of future protection strategies in case of ongoing climatic changes at the Antarctic Peninsula.

References

1. D. Kersken, B. Feldmeyer, D. Janussen, Polar Biol. 39 (2016) 851–862 (DOI 10.1007/s00300-015-1875-9).

Financial support by the DFG (project JA-1163/17-1) is gratefully acknowledged.

Ecology of *Halichondria corrugata*, a Common Endemic species in the Northern Gulf of Mexico

Kathleen Kaiser

Department of Biology, Florida State University, Tallahassee, FL, 32306, USA kkaiser@bio.fsu.edu

The Florida Gulf of Mexico coast extends over both tropical and subtropical zones resulting in an intermingling of fauna typical to both zones. Cold winter water temperatures historically limited the distribution of many tropical species and allowed sub-tropical species to thrive. In the past 60 years average winter sea surface temperatures have increased 2-3°C in the Northern Gulf of Mexico, potentially allowing range expansion of tropical species and extinction of endemics. While poleward range expansion is possible for species along the Atlantic coast, species in the Gulf of Mexico face land barriers that prevent northward movement. *Halichondria corrugata* Diaz, van Soest & Pomponi, 1993 is endemic to the northern Gulf of Mexico and may be threatened by extinction due to its limited distribution. The natural history of this species is unknown, and we have started identifying factors that influence its growth and distribution.

H. corrugata population dynamics and growth rate are influenced by factors specific to their habitat. In fouling communities, growth may be influenced by light availability as this sponge harbors photosynthetic symbionts. On the other hand, in seagrass beds, population dynamics are influenced by predatory control. The sea star, *Echinaster spinulosus* feeds on *H. corrugata* in seagrass beds, but the sponge is able to escape predation by associating with decorator crabs. Time-series census surveys of *H. corrugata*, *E. spinulosus*, and the decorator crab suggest that sponge abundance is influenced by decorator crab abundance, particularly when *E. spinulosus* is abundant. Habitat also appears to influence genetic relatedness of *H. corrugata* populations. Somatic tissue grafts, which provide an approximation of clone membership, reveal that *H. corrugata* individuals from seagrass communities readily fuse while individuals from fouling communities do not. This suggests that *H. corrugata* in fouling communities recruit as larvae while *H. corrugata* in seagrass beds are propagated via asexual fragmentation.

Financial support by the PADI Foundation, and FSUCML Graduate Student Research Scholarship is gratefully acknowledged.

Achilles' Heels and Trojan Horse of the Ecologically Aggressive Sponge *Halichondria panicea* (Pallas, 1766)

Vyacheslav V. Khalaman[1], Alexander Yu. Komendantov[1], Yulia I. Mukhina[2] Tatyana G. Shaposhnikova[2]

[1]The White Sea Biological Station, Zoological Institute RAS, St. Petersburg, Russia. VKhalaman@gmail.com
[2]St.-Petersburg State University, St. Petersburg, Russia

Some marine epibenthic species can be regarded as 'ecologically aggressive' organisms. These organisms possess a high growth rate and they are able to grow well over both clear surface and substrata which were previously occupied by other sessile animals and plants. Most of ecologically aggressive species are sponges (Russ 1982). One of them is *Halichondria panicea* (Pallas 1766) wide spreading in North Atlantic and North Pacific. In spite of high growth rate (Barthel 1986; Thomassen & Riisgård 1995) and toxicity (Dyrynda 1983) this sponge nowhere occupies all available hard substrata. It would hold for the White Sea too, where in contrast to Alaska's shore (Knowlton & Highsmith 2000) any predator, which would be able to regulate abundance of *H. panicea*, does not inhabit. So, we tried to ascertain other biotic factors that contain the expansion of *H. panicea* in the White Sea. The fouling communities that develop on artificial substrata were chosen as a model of epibenthic assemblage involving *H. panicea*. The dominant competitor of long-term fouling communities in the White Sea is either blue mussel *Mytilus edulis* or solitary ascidia *Styela rustica*, but *H. panicea* is optional component of these assemblages (Khalaman 2001). Individuals of *H. panicea* are distributed in a mosaic manner and do not extend over large areas as a continuous growth. However, *H. panicea* essentially modifies a fouling community where the sponge is (Khalaman & Komendantov 2011). By means of laboratory and field experiments the following facts were revealed.

1. The survival and growth rates of *H. panicea* are extremely low in mussels' fouling community. The vicinity of adult specimens of *S. rustica* also negatively impacts on growth rate of the sponge (Khalaman & Komendantov 2016).

2. Excretory-secretory products (ESPs) of most mass fouling animals such as bivalve *M. edulis* and *Hiatella arctica*, ascidia *S. rustica* and *Molgula citrina* have a negative influence on settlement and metamorphosis of the sponge larvae, but ESPs of brown algae *Saccharina latissima* promote these processes (Khalaman et al. 2011).

3. Whereas low concentrations of ESPs of *H. panicea* significantly stimulate metamorphosis of conspecific larvae, moderate and high concentrations of these products kill those larvae (Khalaman et al. 2014).

4. The restoration of *H. panicea* after the post spawning degradation lasts not less than two years.

Thus, wide expansion of *H. panicea* in fouling communities of the White Sea can be restrained both by a competitive ability of other epibenthic organisms and by some biological traits of this sponge. The brown algae *S. latissima* is likely to facilitate an invasion of *H. panicea* in fouling communities.

References

G.R. Russ. Oecologia. 53 (1982) 12-19.

D. Barthel. Mar. Ecol. Prog. Ser. 32 (1986) 291-298.

S. Thomassen, H.U. Riisgård, Mar.Ecol. Prog. Ser. 128 (1995) 239-246. P.E.J. Dyrynda. Dev. Comp. Immun. 7 (1983) 621-624.

A.S. Knowlton, R.C. Highsmith. Mar. Ecol. Prog. Ser. 197 (2000) 285-291.

V.V. Khalaman. Rus. J. Mar. Biol. 27 (2001) 227-237.

V.V. Khalaman, A.Yu. Komendantov. Rus. J. Ecology 42 (2011) 493-501. V.V. Khalaman, A.Yu. Komendantov. Biol. Bull. (Rus.). 43(1) (2016) 69-74.

V.V. Khalaman, Yu. I. Mukhina, A.Yu. Komendantov. Rus. J. Mar. Biol. 37 (2011) 494-500.

V.V. Khalaman, N.M. Korchagina, A.Yu. Komendantov. Rus. J. Mar. Biol. 40 (2014) 36-42.

Shallow-Water Sponge Restoration in Florida Bay

Shelly Krueger[1]

[1]University of Florida Institute of Food and Agricultural Sciences, Florida Sea Grant, Gainesville, Florida, United States. shellykrueger@ufl.edu

Sponges are the dominant features of the nearshore hard-bottom habitats of the Florida Keys, where more than 60 sponge species provide ecosystem services by filtering the water of picoplankton and providing structural complexity and essential fish habitat for a diverse array of fish and invertebrates. Unfortunately, a series of harmful cyanobacteria blooms in the early 1990s, 2007 and 2013 caused massive sponge die-offs, resulting in the decimation of sponge communities in Florida Bay. 22 of the 24 most common shallow-water sponge species experienced >90% mortality rate. Recovery is protracted because sponge larval duration is short (6-8 hours) and currents within Florida Bay do not transport larvae far from the parent sponges. To accelerate sponge recolonization in Florida Bay, a research-outreach partnership was created between the University of Florida/Florida Sea Grant, Old Dominion University, the Florida Fish and Wildlife Conservation Commission and multiple non-governmental agencies to scale-up sponge restoration using novel techniques developed by Dr. Mark Butler at Old Dominion University. 8 transplant species (loggerhead *Spheciospongia vesparium*, golfball *Cinachyrella australiensis*, vase *Ircinia campana*, stinker *Ircinia felix*, brown branching, sheepswool *Hippospongia lachne*, glove *Spongia graminea*, and yellow *Spongia barbara*) were propagated at 4 nurseries and 9 research sites to establish best management practices with the program goal to restore >15, 000 sponges in Florida Bay. Raising stakeholder awareness about the ecosystem services sponges provide is critical, as they are the dominant filter feeders in Florida Bay and essential habitat for two economic drivers in the Florida Keys: spiny lobster *Panulirus argus* and bonefish *Albula vulpes*. Florida Sea Grant facilitated the education and outreach component to foster community involvement via a multimedia campaign using local radio, newspapers, fact sheets, and events to train volunteers to assist with sponge restoration. Community involvement is an important component to engender stakeholder support, and increasingly, research grants in the United States are requiring an outreach component. Organizations like Florida Sea Grant can assist scientists to share their research with non-scientists, and to facilitate the organization of volunteer events to propagate and transplant sponges for ecosystem restoration.

Today's environmental conditions influence in the tomorrow's reproduction of five tropical demosponges

Emilio Lanna, Bruno Cajado, Jéssica da Hora, Ubaldo Porto, Carine Santos,
Vivian Vasconcellos

Universidade Federal da Bahia, Instituto de Biologia, Salvador, Brazil. emiliolanna@gmail.com

The Orton's rule predicts that reproduction of tropical marine invertebrates should be continuous due to the low variation of the environmental conditions in this region. Although this rule was already questioned for several invertebrate lineages, with some exceptions, this rule seems to still be useful for sponges. Nonetheless, a strong bias in the number of studies in temperate areas weakens the rule, being the Tropical Western Atlantic Ocean one of the largest gaps in our knowledge. We investigated the reproductive cycle and the fecundity of five species of Demospongiae in Salvador, Brazil, aiming to determine the effect of some environmental parameters (EPs) on the timing, population engagement in reproduction and the fecundity of the species. The populations of *Aplysina solangeae, Cladocroce caelum, Desmapsamma anchorata, Dysidea janiae* and *Tedania ignis* reproduced continuously from June 2013 to July 2015, with low percentage of individuals engaged in reproduction and low fecundity. For each species, we found a set of models containing different EPs to explain the investigated reproductive traits. In general, the effect of the EPs on the percentage of reproductive individuals and in fecundity was delayed in one to three months. Temperature was one of the factors that best explained the reproduction of the species, with a delay of one month being the factor most consistently found among the models. Our findings suggest that the Orton's rule is partially sustained, as the species reproduced continuously, but challenges the lack of the influence of the temperature and other EPs in the reproduction of sponges. As these animals are important components of the benthos, global warming may affect the local communities and ecosystems by changing the reproductive dynamics of sponges.

Financial support by CNPq, CAPES, FAPESB, PROPCI-PRODOC-UFBA are gratefully acknowledged.

Reproductive cycle and fecundity of *Heteropia* sp. (Calcarea, Porifera): a putative non-indigenous sponge in the Atlantic Tropical Ocean

Vanessa Batista, Emilio Lanna

Universidade Federal da Bahia, Instituto de Biologia, Salvador, Brazil. nessabatista_nti@hotmail.com emiliolanna@gmail.com

Heterotopia sp. belongs to the subclass Calcaronea and the family Heteropiidae. It has been considered a potentially introduced specie in Brazilian waters, as individuals of the species are conspicuous in harbors and ports along the Brazilian coast. To investigate the reproductive cycle of this putative alien species is important to better understand its invasion as well as the ecological aspects affecting this dynamics. Therefore, this work aims to investigate the reproductive biology of *Heteropia* sp. on the coast of Salvador, Bahia, Brazil. We also investigated the effects of some environmental factors on the reproductive dynamics of *Heteropia* sp. For this work, 10 specimens were collected monthly during 13 months, from april 2015 to april 2016, using formalin 4% for fixation. After the fixation period (24 h), we weighted the specimens and proceeded with the samples for a standard histology protocol. In order to evaluate the effect of the environmental factors on the reproductive cycle, we obtained data from specific websites for each environmental parameter studied (chlorophyll, precipitation, low tides, photoperiod), except for the temperature, which was obtained by a dattaloger positioned near the collection site. We ran simple and multiple linear regression analyzes to evaluate the relationship of the environment with reproduction of *Heteropia.*

We observed that *Heteropia* sp. was reproductive throughout the study. The reproductive elementes were found spread in the mesohyl of the sponge. Embryos were incubated in the mesohyl until the larvae were released, characterizing the species as viviparous, as expected for the class Calcarea.We found, in November 2015, the highest density means of oocytes and larvae, with 30.72 ± 14.83 oocytes.mm^{-2}and 17.13 ± 14.82 larvae.mm^{-2}, respectively. Embryos were more abundant in October and November 2015, with densities of 13.46 ± 3.94 embryos.mm^{-2} and 13.14 ± 10.61 embryos.mm^{-2}, respectively. The wet weight of the sponges does not seem to influence in the reproduction output of the species. However, among the environmental parameters, the model containing a combination of the one and two months delay of the clorophyll, the low tide of the month, and the one and three months delay of the temperature was the one that better explained the reproductive dynamics of *Heteropia* sp. These results were expected because some studies that relate environmental parameters as a possible response to the reproductive effort of marine invertebrates show that temperature may influence the reproductive effort. In this way, we can affirm that the combination of environmental parameters can influence the reproductive effort of *Heteropia* sp. This study shows that the large fecundity of *Heteropia* sp. reinforces the possibility of the species be an invasive organism. If its invasive status is proved to be false, at least our results indicates that it is has a reproductive pottential to colonize new areas.

Financial support by CNPq, FAPESB, PROPCI-PRODOC-UFBA are gratefully acknowledged.

Sexual reproduction of *Dysidea janiae*, a tropical Dictyoceratida in association with a calcareous alga

Bruno Cajado & Emilio Lanna

Universidade Federal da Bahia, Instituto de Biologia, Salvador, Brazil. emiliolanna@gmail.com

The dyctioceratid *Dysidea janiae* lives with the endozoic calcified red alga *Jania adhaerens* that supports its skeleton. It is one of the most abundant sponges at Todos os Santos Bay, Northeastern of Brazil, but basic aspects of its reproductive biology remains unknown. Therefore, we conducted a 2-year long study (June 2013 to September 2015) to describe the gametogenesis and embryogenesis of this species and to analyse the influence of algae thalli on reproduction. We collected ten samples per month and analysed them through histological methods. *Dysidea janiae* is viviparous and gonochoristic with a continuous but small reproductive effort, ratifying the pattern detected in others shallow-water tropical sponges. Spermatogenesis and oogenesis were asynchronous among individuals, with different cohorts co-occurring in both males and females. Spermatogonia maturation was also asynchronous at the spermatic cyst level, with three different stages occurring at the same time in the same cyst. Spermatic cysts [56.6 (±11.92) µm (mean±SE) in diameter] were typically ovoid, surrounded by a thin follicle of flattened cells and were larger than oocytes [43.8 (±14.45) µm]. A layer of nurse cells appeared at the beginning of oocytes maturation and remained until the embryonic stage. Initially the nurse cells formed a monolayer, but we observed an increase in the number of layers until the early-embryonic stage. At late-embryonic stage there was a decrease in the number of nurse cells layers and an increase on the size of the embryo [162.1 (±20.55) µm]. Cleavages were chaotic, generating cells with different sizes with no clear pattern of distribution. The cells of the embryo acquired the yolk granules from the nurse cells apparently by their transient pseudopodia. Embryonic development leaded to a parenchymella larva [181.7 (±17.09) µm], as well as in others Dictyoceratida. The mature parenchymella was solid and bullet-shaped with amoebocytes-like cells with evident nucleus internally; there were basophils and compact amoebocytes-like cells below the mono-stratified cylindrical-shaped epithelium. The asynchrony within the spermatic cyst is unusual in Demosponges, but their size and the female reproductive elements are similar to others Dictyoceratida. This alga-sponge symbiosis is apparently obligatory and it seems that there were a high specificity in the settlement of the larva, because the reproductive elements were not always near to the algae thalli, despite it occupied a large area at the sponge tissue. As no algae propagule are found within the larvae, the acquisition of the algae by the sponge is probably caused by a trial and error relationship of the larvae, surviving only those that find *J. adhaerens* after being spawned.

Financial support by PROPCI-PRODOC/UFBA, CNPq and FAPESB are gratefully acknowledged.

External and internal anatomy of *Cladocroce caelum* (Haplosclerida, Demospongiae)

Jéssica da Hora and Emilio Lanna

Universidade Federal da Bahia, Instituto de Biologia, Salvador, Brazil. [jessiedahora@gmail.com; emiliolanna@gmail.com]

Morphological characters are essential for the understanding of phylogenetic trees, being of pivotal importance those studies focusing on the anatomy of organisms. Most Demospongiae have choanocytes in contact with the mesohyl, while in the majority of the sponges of Haplosclerida, the choanocytes are separated from the mesohyl by pinacocytes. The haplosclerid *Cladocroce caelum* is found along all the Brazilian coast, but little is known about their biology. It is an abundant sponge at Salvador city coast and it has several associated organisms, being important for the maintenance of local biodiversity. In addition, to understand the anatomy of *C. caelum* can help to uncover gaps in the phylogeny of Haplosclerida and even Demospongiae. Thus, the objective of this work was to describe the organization and body structure of *Cladocroce caelum* aiming to understand whether the organization of the aquiferous system is similar to other studied Haplosclerida. Fragments of specimens were collected through skin dive at different localities in Salvador, NE, Brazil. The fragments were subjected to standard histological techniques and transmission and scanning electron microscopies. It was noted that *C. caelum* has, in general, repent or repent-branched habits. The species had an exopinacoderm composed of a monolayer of pinacocytes, which also delineates the inhalant and exhalant canals. The mesohyl is poorly developed and is formed by collagen fibrils, spongin fibers of the multi-spicular tracts, and few cell types, such as archeocytes and collencytes. The choanocyte chambers occupy a large portion of the sponge tissue, forming a dense choanosome. The choanocyte chambers of *C. caelum* present an apopyle delimited by flattened apopylar cells, differently from others haplosclerids that usually have cone cells delimiting the apopyles. Analyzing the main cells and structures of *C. caelum* it can be observed that they agree with what has been observed in demosponges. However, the choanocyte chambers of *C. caelum* are not in agreement with the classifications proposed for others demosponges, existing the possibility that it has a different (new) pattern of organization of choanocyte chambers, besides presenting some peculiarities probably relevant for the phylogeny of Haplosclerida. The description of the external and internal morphology of *Cladocroce caelum* can contribute to a better knowledge of the evolution of Porifera.

Financial support by CNPq, FAPESB, PROPCI-PRODOC/UFBA are gratefully acknowledged.

Distribution, diversity, and function of glass sponge (Porifera, Hexactinellida) reefs in Hecate Strait, British Columbia, Canada

Lauren Law[1], Sally Leys

[1]Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada. lkl@ualberta.ca

Glass sponge reefs are unique to Hecate Strait, British Columbia, Canada and are among the most ecologically productive ecosystems on the planet. They function in deep-sea nutrient recycling and form complex habitat structures that increase biodiversity. The Government of Canada recently established the reefs as a marine protected area (MPA) to curtail threats from trawling and oil/gas exploration. The proposed MPA boundaries were determined from reef polygons mapped using multibeam echosounders, which to date remains the only prediction of reef locations. Furthermore, progress in effectively managing and monitoring this MPA is currently hindered by a lack of baseline data on reef distribution, diversity, and function. We used a remotely operated vehicle (ROV) in 2015 to conduct photographic surveys of the reefs and analyzed the images to map reef distribution and determine the community structure of resident fauna. Within the regions predicted to be reef by multibeam mapping, only 30% of the area can be considered functional reef while another 10% of reef lies outside these regions. The local species abundance of fish and crustaceans is 67% higher on highly rugose reef features compared to flat non-reef structures. Animals are associated with the reef at a species-specific level in which squat lobsters and rockfish are commonly found on live and dead glass sponge while shrimp and flatfishes correspond to buried glass sponge. The reefs are also an important host to numerous non-hexactinellid sponges, including a new species of the encrusting sponge *Desmacella*. Species of *Desmacella* may be more widespread than previously imagined, but it is still unknown whether these species live parasitically or symbiotically on the reefs. This study garners baseline data for the Government of Canada to improve their capacity at monitoring changes in the health and function of sponge reef ecosystems.

Financial support by NSERC-CGSM and CHONE II is gratefully acknowledged.

Using Compound Specific Isotopic Analysis of Amino Acids to Discern Trophic Mode in Sponges From Shallow to Mesophotic Depths

Keir J. Macartney[1], Michael P. Lesser[1*]

[1] University of New Hampshire, School of Marine Science and Ocean Engineering, Durham NH, USA,
**Contact author: mpl@unh.edu*

On coral reefs around the world, but particularly in the Caribbean, sponges are ubiquitous, functionally important, and increase in size and diversity from shallow to mesophotic depths (3-150 m). Sponges play an important role in benthic-pelagic coupling via filtration of large quantities of picoplankton and picoeukaryotes, and many sponges harbour symbiotic cyanobacteria and contribute fixed carbon via photoautotrophy. Therefore, understanding the trophic ecology of sponges is an important component of their roles n coral reefs. One approach to assessing the trophic mode (i.e., dependence of photoautotrophy versus heterotrophy) and trophic position is to use carbon and nitrogen isotopic compositions. Our previous work has used this approach over shallow to mesophotic depths and while significant differences in $\delta^{13}C$ and $\delta^{15}N$ values over the depth gradient were detected our ability to discriminate between the use of different trophic resources is limited the isotopic compositions represent a mixed signal of the sponge host and its microbiome that is difficult to unravel. Improvements in isotopic approaches include the use of compound specific isotopic analysis (CSIA) of amino acids. This approach promises to improve our ability to assess the trophic ecology of sponges along a shallow to mesophotic depth gradient. In CSIA both $\delta^{15}N$ (trophic versus source amino acids) and $\delta^{13}C$ (essential versus non- essential amino acids) values can be used effectively to unravel trophic sources and metabolic processes with better resolution than bulk tissue isotope analysis (1).

Preliminary $\delta^{13}C$ values of amino acids from samples of the sponge *Xestospongia muta* shows that most essential amino acids become more positive with increasing depth (10, 30, 61 and 91 m) and that leucine, isoleucine and phenylalanine showed statistically significant (ANOVA: $P<0.05$) depth differences. Similarly, $\delta^{13}C$ values of the non-essential amino acid aspartic acid showed a similar, and significant, pattern of decreasing $\delta^{13}C$ values with increasing depth. Looking qualitatively at the isotopic values of sponges and potential end members consumed by sponges that include bacterioplankton and microalgae (eukaryotic and prokaryotic picoplankton) as previously described (2), the preliminary data suggest an increased reliance on heterotrophic bacteria with increasing depth. Looking more systematically at several sponge species as well as both detrital and water column end members is predicted to be significantly more quantitative in discerning carbon and nitrogen flow through the shallow to mesophotic depth range when including the latest analytical approaches for amino acid CSIA

References

1. Boecklen WJ, Yarnes CT, Cook BA, James AC (2011) On the use of stable isotopes in trophic ecology. Ann Rev Ecol Syst 42: 411-440
2. Larsen T, Ventura M, Andersen N, O'Brien DM, Piatkowski U, McCarthy MD (2013) Tracing carbon sources through aquatic and terrestrial food webs using amino acid stable isotope fingerprinting. PLoS ONE 8: e73441

Financial support by NSF is gratefully acknowledged.

Photographic bioeroding sponges in turbid environments

Joe Marlow[1], Jamaluddin Jompa[2], James Bell[1]

[1] Victoria University of Wellington, School of Biological Sciences, Wellington, 6140, New Zealand.
Joe.marlow@vuw.ac.nz

[2] Research and Development Centre on Marine, Coastal and Small Islands, Hasanuddin University, Makassar, Indonesia

Bioeroding sponges are thought to be a comparatively resilient group to the factors that stress and kill corals, and are increasing in abundance on many degraded reefs globally. Many of these bioeroding sponge species harbour endosymbiotic *Symbiodinium* dinoflagellates, an association that aids bioerosion rates and sponge growth. As reef degradation at local scales, particularly in South East Asia, is often associated with watershedbased pollution (and associated turbidity) we also examined the capacity of one such zooxanthellate sponge to photoacclimate to reductions in light availability. We investigated photoacclimation of *Cliona* cf. *orientalis* on reefs in Indonesia using light reducing shades (70 & 95% reduction) and *in situ* PAM fluorometry over a period of 25 days and after 14 days of recovery. *C.* cf. *orientalis* demonstrated an ability to photoacclimate to levels of extreme light reduction and recover within a relatively short period of time. A lack of corresponding tissue loss or evidence of necrosis during this period suggests that these sponges may not be obligative phototrophs and that symbiont derived nutrition is primarily facilitating bioerosion.

Financial support by Victoria University of Wellington and Operation Wallacea is gratefully acknowledged.

Adaptive mechanisms and physiological effects of suspended and settled sediment on barrel sponges

Emily McGrath

Victoria University of Wellington. emily.mcgrath@vuw.ac.nz

Coral reefs across the Indo-Pacific are among the most diverse in the world but remain vulnerable to the multitude of stressors affecting global reef health. Coastal development and resultant sedimentation are of particular concern in this region. Sponges are important components of coral reef communities and would be expected to be negatively affected by sedimentation, yet in the Wakatobi Marine National Park, Indonesia, degraded reefs characterised by high levels of sedimentation and low coral cover support large populations of the ecologically important giant barrel sponge *Xestospongia testudinaria* (Lamarck 1815). Barrel sponges largely influence abiotic and biotic water characteristics, yet tolerance and responses to sedimentation are unknown. This study examined the physiological effects of short-term exposure of *X. testudinaria* to suspended sediment. When exposed to environmentally relevant suspended sedimentation concentrations of 75 and 150 mg l^{-1} *X. testudinaria* respiration rates increased compared to controls; this suggests that suspended sediment exposure has significant effects on sponge physiology. Sponge mucus production as a mechanism to remove settled sediment was reported for the first time and sediment clearance was filmed *in situ* over the course of 24 hours. Sponges produced mucus in response to settled sediment addition, with a mean clearance rate of 10.82 ± 2.04% h^{-1} (sediment size fractions 63-250 µm). Mucus production is an effective but slow mechanism allowing sponges to survive in high sedimentation environments. Our results show that there are likely to be energetic consequences for sponges living sedimented environments, which may influence the energy available for other demographic processes.

Cliona aff. *viridis* as a possible bioindicator on a tropical coral reef experiencing multiple sources of stress

Sambhaji G. Mote *[1], Kalyan De[1], Afreen Hussain[1], Christine H.L. Schönberg[3], Toufiek Samaai[2] & Baban S. Ingole[1]

[1] CSIR–National Institute of Oceanography, Dona Paula, Goa, India.
** sambhajimote41@gmail.com*
[2] Department of Environmental Affairs, Oceans & Coasts Research, Cape Town, South Africa.
[3] University of Western Australia, Crawley, Australia.

Due to environmental changes over the last few decades, bioerosion rates of calcium carbonate materials appear to be increasing globally, a process that can be driven by sponges. In the Indian region studies on sponge-coral interactions and on the ecology of bioerosion are very scarce. However, some faunistic studies had reported *Cliona viridis* complex species, which have been described as bioindicators for coral reef health. We conducted shallow reef surveys (3-8 m) in the Malvan Marine Sanctuary (MMS) and at Grande Island on the west coast of India Nov. 2015-Dec. 2016 using 50 m line intercept transects. We monitored live coral coverage, growth rates and coverage of coral boring sponges together with environmental factors (suspended particulate matter, nutrient concentrations, pH, salinity and temperature). Sponges were identified by morphological and molecular means using ITS1 and 28S RNA.

At the sample sites at the west coast of India the aqueous pH in the sampling areas ranged from 8.0 to 8.1 in premonsoon and 7.9 to 8.1 during postmonsoon season, whereas average temperatures ranged from 23.3°C to 31.5°C. We observed levels of mean SPM between 24.01 mg/L and 22.90 mg/L during the study period. Settlement of filamentous algae on bleached coral colonies was higher compared to non-bleached colonies and coral substrate infested with the bioeroding sponge. We confirmed the occurrence of species from the *Cliona viridis* and the *Cliona celata* complex. *In situ* observations monitored lateral expansion of *Cliona* spp. spreading over the surface of coral rubble and live corals. The sponge infestations were mainly observed on coral species such as *Porites compressa, Favites melicerum, Pseudosiderastrea tayami* and *Turbinaria mesenterina*. We determined (1) an infestation frequency by these sponges for 25% of the sclerectinians in the MMS and 15 % at Grande Island and, (2) that sponge bioerosion by the *Cliona* spp. caused detachment and dislodgement of live coral, thus affecting their survival. Prelimanary results indicated that lateral growth of *Cliona* sp. 1 (aff. *viridis*), reached about 5 cm yr^{-1}, overgrowing and infesting live coral. By relating environmental data to sponge occurrences, we concluded that variability in pH, temperature and sedimentation in the study areas resulted in different levels of abundance and coverage of bioeroding sponges and turf algae. The sponges and algae increased with lowered pH, and higher rates of sedimentation on reefs that had experienced elevated levels of temperature. The increased dominance of *Cliona* spp. and algae appeared to be an important indicator for reduced coral reef health and was interpreted as a warning sign for coral reef deteriotion on the west coast of India.

Financial support: We acknowledge financial support from Rajiv Gandhi Science and Technology Commission (Project code GAP2871) and United Nation Development programme (Project code GAP 2858).

New approaches to quantifying bioerosion by endolithic sponge populations: applications to the coral reefs of Grand Cayman

Gary Murphy [1], Chris Perry[1], Paul Chin[2] and Croy McCoy[2]

[1] Geography Department, University of Exeter, Exeter, UK. garymurphy1@gmail.com
[2] Department of Environment, Cayman Islands Government, Cayman Islands

Bioerosion is a critical process on coral reefs, influencing reef structural integrity and complexity and generating significant amounts of sediment. While the excavating sponges are known to be amongst the most important fauna within macroborer communities, their contribution to total bioerosion on coral reefs is not well understood; census surveys are rarely employed by monitoring agencies, and there is little data on the erosion rates of different species. Here, we estimate bioerosion rates for two Caribbean sponge species with different growth forms (*Siphonodictyon brevitubulatum* — α-form and *Cliona tenuis* — β-form) and describe new approaches to estimating bioerosion by sponge communities. By categorising the growth form of different species, suitable growth form related bioerosion rates were applied to census survey data, along with a previously published rate for *Cliona delitrix* (γ-form), to estimate bioerosion by sponge communities on Grand Cayman reefs. Results indicate distinct habitat preferences for the two most abundant sponge species, *Cliona tenuis* and *Cliona caribbaea*. Mean sponge bioerosion across eight sites was 0.1 kg $CaCO_3$ m^{-2} yr^{-1}. Visible cover by α-growth-form excavating sponges caused a disproportionately high level of bioerosion in comparison with cover by β-growth-form species. Therefore, it is important to consider growth forms and excavation strategies when assessing bioerosion by sponge communities. Our present level of understanding of bioerosion by sponge species is limited, and more research is clearly required. However, the approaches described here can generate instant, meaningful results on sponge abundance and bioerosion and would complement many current benthic monitoring regimes. Furthermore, they create a framework for the provision of data, which is relevant to both coral reef management and to developing our understanding of how bioeroding sponge populations influence reef structure and carbonate budgets.

Financial support by the University of Exeter and the Cayman Islands Department of Environment is gratefully acknowledged.

Using siliceous spicules in the *Posidonia oceanica* “matte” to discover past dynamics of the sponge community.

Alice Oprandi[1], Gabriele Costa[1], Maurizio Pansini[1], Giorgio Bavestrello[1] & Marco Bertolino[1]

[1] DiSTAV, Università degli Studi di Genova, Corso Europa 26, 16132 Genova, Italy. oprandi.ali@alice.it

The skeleton of most of sponge species consist of siliceous spicules. After the sponge death, siliceous spicules persist for a long time in the sediments contrasting dissolution and represent a valuable tool to assess the diversity of past sponge communities (Bertolino et al., 2012). The reduced re-suspension occurring within the meadows of the sea-grass *Posidonia oceanica*, makes these habitats a stable deposit for sponge spicules, trapped in a coherent sedimentary sequence inside the network of rhizomes progressively buried, called ‘matte’ and interpretable on a temporal scale.

By means of a vertical corer manually operated during sections of diving work, we collected samples of sediment (in triplicate) along the matte profile, at 0.5 m and 2 m depth, respectively, in the *P. oceanica* meadow of Punta Pedale (Eastern Ligurian Sea). Sponge spicule amounts were evaluated by microscopical analyses. Significant differences were found between the number of entire spicules occurring in the shallower matte of *P. oceanica* (7756 ± 6457 spicules g^{-1}) compared with that from the deeper sediment (2911 ± 1628 spicules g^{-1}). The percentage of spicules showing marks of dissolution never exceeded 15% of the total spicule number in all the studied samples. The only recognizable genus of demosponge found in the deeper layer is *Geodia,* identified on the base of its sterrasters. This genus is also present in the shallower layer together with spicules coming from species of *Chondrilla*, *Suberites*, *Cliona*, *Dercitus*, *Agelas* and *Crella*. It is remarkable that *Geodia* is nowadays no more present in the *Posidonia* meadow area.

The record of a layer of sediment rich in sponge spicules at a depth of 50-60 cm inside the mattes of *P. oceanica,* confirms previous data coming from other meadows of the Ligurian Eastern Riviera (Bertolino et al., 2012). The temporal variations of sponge abundance in the studied place, resulting from the spicule trend, is probably due to historical anthropogenic disturbances. In fact the low spicule content of the deep layer reflects the impact of the construction of the littoral road along the western board of the meadow occurred at the beginning of the twentieth century. The sponge rich layer could represent a period of recovering that was stopped by the rapid urban development that occurred in this part of the Ligurian Riviera in the sixties of 1900 with a deep impact on the littoral benthic assemblage of the area.

References

1. M. Bertolino, B. Calcinai, S. Capellacci, C. Cerrano, A. Lafratta, M. Pansini, A. Penna, G. Bavestrello. *Posidonia oceanica* meadows as sponge spicule traps. Ital. J. Zool. 79(2) (2012) 231-238.

Research on Annual Growth and Large-scale Transplantation of Red Sponge, *Mycale phyllophila* (Porifera: Demospongiae)

Huilong Ou[1], Dexiang Wang[1], Jing Zhao[1], Jun Chen[1] & Shaoxiong Ding[1]

[1] State-Province Joint Engineering Laboratory of Marine Bioproducts and Technology, college of Ocean and Earth Sciences, Xiamen University, Xiamen, China, 361102

In order to solve the supply shortage of pharmaceutical sponges as well as to promote mining of active products and selection screening, our research focuses on the annual growth rate and large-scale transplantation of the sponge *Mycale phyllophila* which is a common species in coastal water of Fujian, China. For the experiment of annual growth rate, an approach of aquaculture *in situ* using nylon ropes and randomly picked up 30 individuals of sponges for cultivation was applied. The growth rate of every single individual was recorded monthly, and the temperature and light of the seawater were record automatically during the experiment. The growth rate of *M. phyllophila* correlated significantly with seawater temperature ($p<0.05$). In summer, the growth rate of sponge length was up to (541.47±103.68) % and the perimeter growth rate is up to 229.63%. The growth strategies of *M. phyllophila* were that they prefer to occupy more growing space by covering the substrate before expanding their thickness. For the large- scale transplantation of the red sponge, the nylon ropes were used as the substrates for sponge to attach. Altogether about 23, 170 pieces of sponge in the field were explanted, from June 27th, 2013 to September 10th, 2014 the day they were harvested. The initial biomass of the sponge used for the large-scale explant is 98.28 kg and finally 1.8 tons of sponge biomass was harvested, and the average mass growth rate of the large-scale explant was 1831.5%. The final survival rate of the sponge was about 65%. According to the results, we suggest that explant experiment on the sponge should be done around April to May when the water temperature is warm enough for sponge to heal more easily. The large-scale explant of the *M. phyllophila* successfully acquired considerable sponge biomass, which is an ideal way to solve the supply problem of natural products.

Keratosa sponges stranded on the Sardinia coasts: a long term study

Andrea Padiglia[1, 2], Renata Manconi[2], Tiziana Cubeddu[3], Roberto Pronzato[1]

[1]Dipartimento di Scienze della Terra, dell’Ambiente e della Vita, Università di Genova, Genova, Italy

[2]Dipartimento di Scienze della Natura e del Territorio, Università di Sassari, Sassari, Italy

[3]Dipartimento di Medicina Veterinaria, Università di Sassari, Sassari, Italy andreapadiglia@alice.it

Taxonomic richness and geographic distribution of sponges were evaluated on the basis of stranded sponges collection along the Sardinia Island shores for testing the efficiency of a revisited ancient sampling method. Long term monitoring (*ca*. 20 years) resulted in the collection of more than 2000 specimens of Keratosa in 54 sites scattered along *ca*. 1900 Km of the Tyrrhenian Sea and Sardinian Sea coasts.

We recorded 20 species of the order Dictyoceratida belonging to 7 genera *i.e. Ircinia*, *Sarcotragus*, *Scalarispongia*, *Cacospongia*, *Fasciospongia*, *Spongia*, and *Hippospongia* of Irciniidae, Spongiidae, and Thorectidae. Some rare species were recorded. The most common species is *H. communis* (28 out 54 sites). All the six Mediterranean species of *Spongia* are widespread. As for the Mediterranean species of Irciniidae we recorded 5 out 7 species of *Ircinia* and 4 out 4 species of *Sarcotragus*. The three species of Thorectidae are less abundant (<10 records). Among other Demospongiae only stranded specimens of *Axinella damicornis* were also found.

From a biogeographic point of view, the comparison among the four selected sectors of Sardinia (N, E, S, and W) shows strict similarity (>85 %) between West and North coasts, while South and East coasts differ widely in composition of sponge assemblages. Comparing the stranded sponge fauna (Irciniidae, Spongiidae, and Thorectidae) of Eastern and Western Sardinian coasts *vs*. literature data (mainly SCUBA records) referred to the Balearic/Catalan seas (Spanish coasts) and the Tyrrhenian Sea (Italian coasts), the result is the similarity of the Balearic/Catalan/Tyrrhenian dataset, while the Sardinian dataset diverges notably.

A similar comparison of stranded sponges *vs*. the *in situ* sponge assemblages (snorkeling and SCUBA records) of a target site (MPA Capo Caccia-Isola Piana) in NW-Sardinia shows low similarity (67%).

The presence and wide distribution of all Mediterranean species of bath sponges in Sardinia represent positive evidence of the conservation status of these threatened species after the widespread epidemic diseases of the last decades of the past century. Finally this simple, low cost sampling method seems to be absolutely powerful and sustainable for monitoring large coastal areas worldwide to assess the presence of species with conspicuous spongin skeleton *e.g.* many Keratosa taxa.

Research financially supported by Isola dell’Asinara Marine Protected Area, BAMMBO Project‘Sustainable Production of Biologically Active Molecules of Marine Based Origin’ (FP7 KBBE-2010-4-265896), INTERREG-EU, PRIN-MIUR, Regione Autonoma Sardegna (RAS-LR7/2007-CRP-60215-2012), Master&Back (RAS), and Fondazione Banco Sardegna.

Demospongiae taxonomy and diversity at two sites within the Western Indian Ocean region

Robyn P. Payne[1], **Toufiek Samaai**[2, 3], **Mark J. Gibbons**[1], **Sven Kerwath**[4] **& Denham Parker**[4]

[1] *University of the Western Cape, Department of Biodiversity and Conservation Biology, Private Bag X17, Bellville 7535, Cape Town, South Africa robynppayne@gmail.com*

[2] *Department of Environmental Affairs, Oceans and Coasts Research, PO Box 52126, Victoria and Alfred Waterfront, Cape Town, South Africa*

[3] *Marine Research Institute (MA-RE), University of Cape Town, Private Bag X3, Rondebosch 7701, Cape Town, South Africa*

[4] *Department of Agriculture, Forestry and Fisheries: Fisheries Branch, Private Bag X2, Rogge Bay 8012, Cape Town, South Africa*

Since 2014, two South African-led projects have been underway to document the Demospongiae diversity at two sites within the Western Indian Ocean. The first entailed an expedition to Walters Shoal, a poorly studied shallow seamount located on the South Madagascar Ridge. Sponges were collected via SCUBA and a roughed benthic dredge, from the peak and down two opposing slopes of the seamount, to a depth of 500 m. Completed in 2015, the findings of this study will be presented.

The second site is the Amathole region of the Eastern Cape (South Africa), which encompasses the Amathole Marine Protected Area. Historically, the sponge fauna of this region has been documented in a handful of taxonomic papers that describe new species or records but lack detailed descriptions and require taxonomic revision. Thus, as a component of the Imida Frontiers Project (ACEP IV), the aim is to investigate the shallow-water Demospongiae diversity within the region. The connectivity between this area and adjacent regions will also be assessed, as well as the spatial variability of sponge assemblages according to a bathymetric gradient. Sampling was undertaken in 2016, during two cruises aboard the RV *Ellen Khuzwayo*, where over one thousand sponges were collected via a roughed benthic dredge across depths of 20 to 200 m. In addition, 43 ROV dives were completed in January/February 2017, providing insight into *in situ* sponge assemblages. This study is expected to discover range extensions and species new to science, with the data further used to identify ecologically sensitive areas, as well as aid the management of these habitats and the commercially important fishes they support.

Financial support was provided by the African Coelacanth Ecosystem Programme (ACEP (DST-NRF); Grant Number 97969). Resources were provided by the Department of Agriculture, Forestry and Fisheries (DAFF), Department of Environmental Affairs (DEA), South African Institute for Aquatic Biodiversity (SAIAB) and the South African Environmental Observation Network (SAEON).

Experimental manipulation in interspecific interactions among 3 species of sponges associated with roots of *Rhizophora mangle.*

Jeannette Pérez[1], **Cruz-Motta, J.J.**[2], **Díaz, M.C.**[3]

[1] *Universidad Simón Bolívar, Venezuela. perezjeannette@gmail.com*

[2] *Department of Marine Sciences, University of Puerto Rico, Puerto Rico.*

[3] *Oceanographic Center, Nova Southeastern University, Dania Beach, FL 33004, USA.*

In the Caribbean, the roots of *Rhizophora mangle* serve as substrate for a great diversity and abundance of sponge species. Since these species distribution has been found to be very variable in small scales (between roots), we explore the potential role of spatial interactions between sponge species as one of the processes that could explain this variability. This study had the objective to experimentally place common mangrove associated sponge species (*Biemna. caribea*, *Mycale microsigmatosa* and *Tedania ignis*) to interact in their natural environment and to follow the dynamics of these interactions in time. Our experimental design included all possible combinations between pairs of species, varying the availability of the substrate between them and the density of sponges. Photographic records were taken at different times for 94 days. Each studied species presented different strategies in gaining or protecting their space. *B. caribea* maintained and gained new space until it interacted directly with the other two species, and overgrew them, without apparent damage to their tissues; *M. microsigmatosa* evaded the contact with the other species, growing in the opposite direction or displacing its tissue onto the free substrate; while *T. ignis* only maintained its space. These results suggest that species posses different intrinsic strategies to gain or protect space. These strategies are associated to diverse mechanisms of growth rate, growth forms (plasticity in displacing their tissue), and/ or production of allelochemicals. Thanks to the intensive monitoring carried out in different and short times, it was possible to verify fast growth plasticity of the species *M. microsigmatosa*. Because the dynamism, and short time span of the interactions between species of mangrove sponges it is important to make observations over time, and not single time-point observations, since one could arrive to wrong conclusions.

Spatial-temporal variation of natural sponge interactions associated with *Rhizophora mangle* roots in Morrocoy National Park, Venezuela.

Jeannette Pérez[1], **Cruz-Motta, J.J.**[2], **Díaz, M.C.**[3]

[1] *Universidad Simón Bolívar, Venezuela. perezjeannette@gmail.com*

[2] *Department of Marine Sciences, University of Puerto Rico, Puerto Rico.*

[3] *Oceanographic Center, Nova Southeastern University, Dania Beach, FL 33004, USA.*

The roots of *Rhizophora mangle* in the Caribbean sea serves as substrate for a great diversity of marine sponges, Both abiotic and biotic factors make the system structure very dynamic in time. The scope of this study was to evaluate the intra and interspecific interactions natural of sponges at different spatial and temporal scales, associated with *R. mangle* roots in the Morrocoy National Park, Venezuela. Three localities were selected according to their oceanic influence (protected, medium and exposed), where the frequency of occurrence of different species of sponges and the direct interactions between them were estimated. In total 538 roots were evaluated (76% presented sponges) and a total of 32 species were identified. The total frequency of pairs of interactions increased according to the local oceanic influence, ie, the protected locality had the lowest frequency (N = 6) and the biggest exposed location (N = 102). *Mycale microsigmatosa* was the most frequent species in interacting with neighboring sponges both in the protected and exposed localities, while *Tedania ignis* was in the intermediate locality. Interaction matrices and hierarchical networks of overgrowth varied spatially and temporally, either in the species involved or in their hierarchical position. The dynamics of interactions between some sponges in these systems seem to be very dynamic in short time, so that their studies should consider the history and evolution between them.

Hatchability of gemmules in Spongillidae and Metaniidae (Porifera: Spongillida) at different inland waters

Ludimila Calheira[1], **Emilio Lanna**[2] **& Ulisses Pinheiro**[1]

[1] *Universidade Federal de Pernambuco, Departamento de Zoologia, Recife, Brazil. uspinheiro@hotmail.com*

[2] *Universidade Federal da Bahia, Instituto de Biologia, Salvador, Brazil.*

Inland waters experience extreme environmental conditions, nevertheless the fauna has several adaptive strategies for these unfavorable conditions (Manconi & Pronzato 2007). Freshwater sponges produce resisting bodies that contain totipotent cells and specialized spicules peculiar to armed gemmules called gemmuloscleres. Completely formed gemmules exhibit low metabolic rates and may become dormant (Manconi & Pronzato 2002). Most freshwater sponges undergo a period of dormancy at some time during the year, typically during periods of environmental stress, until hatching occurs (Reiswig et al. 2009). Until now, few species had their hatchability tested against different environmental conditions. Here we test the hatching capacity of the gemmules of two species: *Tubella variabilis* (Bonetto & Ezcurra de Drago, 1973) (Spongillidae) and *Drulia ctenosclera* Volkmer & Mothes, 1981 (Metaniidae) from freshwater sponges in different inland waters from Northeastern Brazil. Three treatments were tested for hatching (T): T1 (water of *Tubella variabilis* collection site); T2 (water of *Drulia ctenosclera* collection site); T3 (mineral water). For each treatment, three replicates with 30 gemmules were used. The gemmules were observed daily during 30 days. Data analysis was performed using ANOVA and a posteriori Tukey test. Results showed that there was a significant difference ($p < 0.001$) between treatments and between species, but there was no significant difference between the species in the treatments. Thus, we can infer that there is a difference on hatchability of gemmules in different types of water, even those with similar morphological complexity. Results clearly show that each species has a different capacity of hatching.

References

1. R. Manconi, R. Pronzato. Suborder Spongillina subord. nov.: Freshwater sponges. In: Hooper JNA, van Soest RWM (eds) Systema Porifera: A guide to the classification of sponges, Kluwer Academic/Plenum Publishers, New York, (2002) pp 921-1021
2. R. Manconi, R. Pronzato. Gemmules as a key structure for the adaptive radiation of freshwater sponges: a morphofunctional and biogeographic study. In: Custódio MR, Hajdu E, Lobo-Hadju G, Muricy G (eds) Porifera Research:Biodiversity, Innovation and Sustainability, Museu Nacional, Rio de Janeiro, (2007) pp 61-77.
3. H.M. Reiswig, T.M. Frost, A. Ricciardi. Porifera. In: Thorp JH, Covich AP (eds), Ecology and Classification of North American Freshwater Invertebrates, Elsevier, Academic Press, New York, (2009) pp 91-123.

Financial support by FACEPE (Fundação de Amparo a Ciência e Tecnologia de Pernambuco) and CNPq (National Counsel of Technological and Scientific Development) is gratefully acknowledged.

Sponges of the Langseth Ridge: Mapping sponge distributions under ice with a towed camera / sonar platform

Autun Purser[1], Simon Dreutter[1], Beate Slaby[2], Hans Tore Rapp[3], Ute Hentschel[2] & Antje Boetius[1, 4, 5]

[1] *Deep Sea Ecology and Technology, Alfred Wegener Institute, Bremerhaven, Germany Autun.purser@awi.de*

[2] *Marine Microbiology, GEOMAR Helmholz Centre for Ocean Research, Geomar, Kiel, Germany*

[3] *Department of Biology and KG Jebsen Centre for Deep-Sea Research, University of Bergen, Bergen, Norway*

[4] *Max Planck Institute for Marine Microbiology, Bremen, Germany*

[5] *MARUM, University of Bremen, Bremen, Germany*

During the recent 2016 PS101 *Polarstern* cruise to the Langseth Ridge in the high Arctic (87ºN 60ºE) a modified camera sled incorporating forward looking and side scan sonar systems was used to collect image, video and acoustic data across a selection of sponge dominated ecosystems. The region surveyed is covered by ice throughout the year and therefore challenging to survey by remotely operated or autonomous vehicles.

The tethered system was successfully towed at a flight height of 1.5 – 3.5 m through ice by *Polarstern*, collecting data from the peaks and flanks of three seamounts marking the intersection of the Langseth Ridge with the ultra-slow spreading Gakkel Ridge rift valley. Throughout numerous survey dives georeferenced optical and acoustic data were collected showing the peaks of the seamounts (shallowest peak ~580m depth) to be almost fully covered by 20 – 30 cm diameter astrophorid sponges, to depths of approaching 1200 m. Individual sponges could be readily identified in the side scan sonar data at distances of up to ~40 m to the port and starboard sides of the vehicle.

Here we present high resolution images and 3D mosaics of the sponge communities surveyed, acoustic maps of their distribution and initial interpretations of these results.

Funding: Cruise PS101was funded AWI via Grant No. AWI_PS100_01. BS, HTR and UH received support for this study through the SponGES project funded by the European Union’s Horizon 2020 research and innovation programme (grant agreement 679849).

An Analysis of the Relationship between Sponge Cover and Coral Recruitment

Tia Rabsatt[1], Andia Chaves-Fonnegra[1], Marilyn Brandt[1] Lauren Olinger[1], Deborah Gochfeld[2], Julie Olson[3]

[1]*University of the Virgin Islands, St. Thomas, US Virgin Islands, USA*
[2]*University of Mississippi, University, MS, USA*
[3]*University of Alabama, Tuscaloosa, AL, USA*

Corals play an important role in coral reef ecosystems, including providing habitat and food to other organisms on the reef. Coral cover has declined drastically over the last several decades due to several factors, including coastal development and climate change. In contrast, sponge cover has been increasing on some reefs. In this project, we hypothesized that increases in sponge cover is inhibiting coral recruitment. To test his hypothesis, we deployed recruitment tiles at six shallow water reef sites surrounding the island of St. Thomas, US Virgin Islands. After six months, the surrounding area of recruit tiles was photographed and the tiles were collected for analysis. A second set of tiles was then deployed and collected after an additional six months. Numbers of coral recruits were recorded through examination of the plates, and the percent coverage of coral, sponge and macro-algae was quantified in the surrounding area of the plates using image analysis software. Coral recruit density was found to be positively related to the surrounding percent coral cover but no relationship was found with sponge cover.

Financial support provided by the HBCU-UP program at the University of the Virgin Islands, a NOAA CRCP grant to M. Brandt, D. Gochfeld, and J. Olson, and Virgin Islands EPSCoR.

Is the Gibraltar Strait the real southern boundary for Northeast Atlantic sponges?

Ana Ramos[1], Fran Ramil[2] & Marcos González-Porto[2]

[1] *Instituto Español de Oceanografía, Centro Oceanográfico de Vigo, Subida a Radio Faro 50-52, Vigo (Pontevedra) Spain. ana.ramos@vi.ieo.es*

[2] *Faculty of Marine Sciences, University of Vigo, Campus Lagoas.-Marcosende, Vigo (Pontevedra), Spain*

The location and protection of especially vulnerable habitats, as cold-water coral reefs or long-lived sponge grounds, has recently turned a priority aim of deep-sea biological research and deep-sea fisheries management (FAO, 2009).

Although the Northwest African deep-sea benthos is still poorly know, the trawling surveys carried out in the framework of Spanish and Norwegian surveys provided a large- scale overview on the distribution of megabenthos biodiversity in this area (Ramos et al., 2015). Within the 1225 trawl stations accomplished from Guinea to the Strait of Gibraltar between 20 and 2000 m depth, the sponges reached an occurrence of 40% (546 stations), but only the 1.1% of the abundance and 8.0% of the megabenthic biomass (wet weight). Between the Strait of Gibraltar (36ºN) to Cape Blanc latitude (21ºN), mainly in northern Moroccan and Western Saharan slope, hexactinellids and demosponges constituted high diverse and abundant taxa, reaching to 45% of benthic biomass (Ramos et al., 2015). An impressive amount of sponges are currently conserved as part of the EcoAfrik’ faunistic collections (Vigo, Spain) for its later study.

Among the main and more frequent species, we have identified the big demosponges *Geodia megastrella*, *Geodia barretti*, *Isops pachydermata* and *Leiodermatium lynceus*, and the glass sponges *Pheronema carpenteri*, *Aphrocallistes beatrix*, *Regadrella phoenix* and *Hyalonema* spp. Nevertheless, South to Cape Blanc, along the Mauritanian slope, sponges are practically absent. Despite the intensive deep-water sampling program carried out during the four *Maurit* surveys (325 trawl stations between 80 and 2000 m depth), comparable sponge grounds were not found (Ramil and Ramos, in press). In this area, the big Geodiidae seems constrained to hard bottoms habitats: canyon edges and Wolofs’ seamount (Ramos et al., in press) and the sponge fauna of the slope soft bottoms was only represented by small-sized species. Environmental factors linked to the existence of different hydrological conditions (upwelling, primary productivity, oxygen concentrations, etc.) and geomorphological features (unstable muddy bottoms, turbiditic currents, sediment slides) southwards Cape Blanc, could explain the pattern of sponges distribution along this Northeast Atlantic area.

References

FAO (2009) International Guidelines for the Management of Deep-sea Fisheries in the High Seas. Rome, 73pp.

Ramil & Ramos. In: Ramos et al. (eds.) Deep-sea ecosystems off Mauritania: Research of marine biodiversity and habitats in the NW African margin. Springer (in press).

Ramos et al. (2015) In: Valdés & Déniz González (eds) Oceanographic and biological features in the Canary Current Large Marine Ecosystem. IOC Tech. Ser. 115: 231-244.

Ramos, A., Sanz, J.L, Ramil, F. (eds.) Deep-sea ecosystems off Mauritania: Research of marine biodiversity and habitats in NW African margin. Springer, Heidelberg (in press).

Sponge grounds of seamounts along the Arctic Mid-Ocean Ridge – Diversity, distribution patterns and oceanographic setting

Hans Tore Rapp[1], Marte Torkildsen[1], Adriana Alvizu[1], Francisca C. Carvalho[1], Tone Ulvatn[1], Bernt R. Olsen[1], Martyn Roberts[2], Andy Davies[2], Furu Mienis[3], Joana Xavier[1]

[1]*Department of Biology and KG Jebsen Centre for Deep-Sea Research, University of Bergen, PO Box 7803, N-5020, Bergen, Norway. hans.rapp@uib.no*

[2]*School of Ocean Sciences, Bangor University, Menai Bridge, LL59 5AB, Wales*

[3]*NIOZ Royal Netherlands Institute for Sea Research, P.O. box 59, 1790 AB Den Burg - Texel, The Netherlands*

Several multidisciplinary surveys made by UoB to the Arctic Mid-Ocean Ridge (AMOR) have revealed deep-sea ecosystems of conservation importance such as hydrothermal vents, cold seeps and seamounts in this area. Several seamounts along the Mohns- and Knipovich Ridges have been explored, with special emphasis on the Schultz massif, a large seamount rising from 3500 to approximately 550 m depth. Fine-scale bathymetric mapping was done by use of AUV and ROV-mounted multibeam sonars, water mass characteristics have been investigated by extensive use of CTD and analysis of water samples. Biological sampling by means of ROV, sleds, trawls and cores, supported by high-definition video imagery capture, revealed seemingly rich and undisturbed benthic communities mostly dominated by sponges, anthozoans and ascidians. Here we report our findings regarding the composition and distribution of sponge-dominated communities along a depth gradient (summit, slope and base) of this seamount. The summit and shallower areas (550-700 m) are inhabited mainly by dense aggregations of glass sponges (*Schaudinnia rosea*, *Trichasterina borealis*, *Scyphidium septentrionale* and *Asconema foliata*) along with tetractinellids (*Geodia parva*, *G. hentscheli*, *G. phlegraei and Stelletta raphidiophora*). The slope is characterized by *G. hentscheli* and the hexactinellid *Amphidiscella monai* while the deeper areas (>2000 m depth) are dominated by the demosponges *Radiella sarsi*, *Tentorium semisuberites* and *Thenea abyssorum* alongside with the glass sponges *A. monai*, *Caulophacus arcticus* and *Asconema megaatrialia,* revealing a shift in the community composition with depth. Deeper areas with barren grounds are characterized by highly abundant calcareous sponges. The dominating sponge fauna found on the Schultz massif represent a core group of ground-forming species shared between a number of seamounts along this ridge system.

Financial support by the European Union's Horizon 2020 research and innovation programme to the SponGES project (grant agreement 679849) is gratefully acknowledged.

Solitons shape Antarctic hexactinellid sponge communities

Claudio Richter[1], Laura Fillinger[2], Dorte Janussen[3], Tomas Lundälv[4], Luisa Federwisch[2], Nils Owsianowski[2], Moritz Holtappels[2]

[1]*Alfred-Wegener-Institut Helmholtz Zentrum für Polar- und Meeresforschung & Universität Bremen*

[2]*Alfred-Wegener-Institut Helmholtz Zentrum für Polar- und Meeresforschung*

[3]*Forschungsinstitut & Naturmuseum Senckenberg*

[4]*Sven Lovén Centre for Marine Sciences, University of Gothenburg*

Non-linear solitary internal waves (or solitons) are generated where strong tidal flows interact with topography in stratified waters. Here we report on gargantuan solitons (>200 m amplitude) in the Antarctic peninsula region likely resulting from the interaction of tidal flows with the ice shelf. Mixing of surface production and resuspension of bedload material may enhance microbial processes in the benthic boundary layer and favour growth conditions for hexactinellid sponges. Soliton-enhanced sponge growth and dispersal of propagules may have helped to boost the growth of hexactinellid sponges following the collapse of the Larsen A ice shelf. Sponges knocked over in the direction of current jets (>1 m/s) testify to the importance of rare events in shaping Antarctic megafaunal communities.

Large-scale distribution of bird's nest sponge *Pheronema carpenteri* (Thomson, 1869) along Northwest African slope

Pilar Ríos[1,3], Marcos González-Porto[2], Fran Ramil[2] and Ana Ramos[1]

[1] *Instituto Español de Oceanografía, Centro Oceanográfico de Vigo, Subida a Radio Faro 50-52, Vigo, (Pontevedra) Spain. pilar.rios.lopez@gmail.com*

[2] *Facultad de Ciencias del Mar. Universidad de Vigo. Campus Lagoas-Marcosende. Vigo 36310. Pontevedra. Spain*

[3] *Departamento de Zoología y Antropología Física, Universidad de Alcalá, Alcalá de Henares, Madrid, Spain*

Pheronema carpenteri (Thomson, 1869) is a deep-sea hexactinellid that can be found forming dense aggregations, which are considered particularly vulnerable to extractive anthropogenic activities (Xavier et al., 2015). The species has been previously recorded in North Atlantic European margin and Mediterranean Sea between 90 and 4789 m depth (Tabachnick, 2014), and in Moroccan slope from 355 to 2077 m depth (Boury-Esnault et al., 1996; Barthel et al., 1996).

We present the distribution, occurrence, abundance and biomass patterns of *P. carpenteri* along Northwest Africa margin, based on the collections and quantitative data obtained during the 11 Spanish and Norwegian trawling surveys (2004-2012) carried out from the Gibraltar Strait (36ºN) to Sierra Leone border (8ºN) between 20 m to 2000 m depth (Ramos et al., 2015).

Nest sponges were collected in 112 of the 1225 trawl stations, which represent an occurrence of the 8.4% in Northwest Africa. However, if we consider only the locations where sponges were gathered (546 stations), its occurrence reached the 20.5%, representing, moreover, almost one third of the numerical abundances (29.3%) and the half of the sponges wet weight (50.2%).

The main distribution feature is that *P. carpenteri* was only found in Moroccan and Western Saharan slope, being completely absent south of Cape Blanc. From Cape Spartel (north Morocco, 35º32'N) to south of Cape Barbas (21º39´), *P. carpenteri* spread in an almost continuous band between 512 and 1861 m depth, but showing a significant decreasing trend in its mean occurrence along these 14 degrees of latitude. The main picks of density and biomass were located in Sahara waters, between Cape Boujador and Dackla (26ºN-25ºN) where we found local densities that reached to 1,700 individuals and 150 kg by 0.1 km^2. However, considering the global sponge's assemblages, the density and biomass of *P. carpenteri* exhibited opposite patterns, being the first relatively highest Northern Morocco (84%), and the second ones in Sahara waters (81%).

The possible relationships of these distribution patterns with the hydrological factors that shape this Eastern Boundary Upwelling System are discussed and the main *Pheronema* aggregations are identified for laying a baseline for the protecting of this vulnerable habitat.

References

Barthel, D., Tendal, O.S., Thiel, H. (1996) Marine Ecology 17 (4): 603-616.

Boury-Esnault, N., Pansini, M., Uriz, M.J. (1994) Mém Mus nat d'Hist natl, 160: 1-174. Ramos et al. (2015) In: Valdés & Déniz González (eds) Oceanographic and biological features in the Canary Current Large Marine Ecosystem. IOC Tech. Ser. 115: 231-244.

Tabachnick, K.A. (2014) Invertebrate Zoology, 11(1): 231–239.

Xavier, J.B., Tojeira, I., van Soest, R.W.M. (2015) J Mar Biol Ass UK, 95(7): 1389–1394.

Light dependent allelopathic activity of the tropic sponge *Pseudoceratina* sp.

Sven Rohde[1], Peter Schupp[1]

[1] *University of Oldenburg, ICBM, Oldenburg, Germany.*

Coral reefs face dramatic shifts in their community composition and abundance of species. An increasing number of reports states that sponges are becoming more abundant and in some areas the dominating benthic organisms on coral reefs. In some locations like the Caribbean there is increasing evidence that coral reefs are shifting from coral dominated to sponge dominated reefs. So far, it is disputable whether sponges just profit from newly available space due to coral decline, or whether the actual environmental conditions favour sponges and allow them to outcompete corals actively.

One potential mechanism why sponges are successful competitors is the production of bioactive compounds.

It has been well established that sponges use secondary metabolites to defend themselves against predatory fish and invertebrate predators. Studies on sponge allelopathic compounds are however mostly lacking. We investigated the chemical ecology of a particular dominating sponge (*Pseudoceratina* sp.) in the Gulf of Thailand. This sponge was covering large areas of the benthic substrate and overgrew various other invertebrate species including corals. Bioactivity screenings of *Pseudoceratina* extracts demonstrated weak antimicrobial activity, but highly active antifeeding properties. *Pseudoceratina* is harbouring photosynthetic microbial symbionts and it is unknown whether the sponge or the symbionts are producing the active metabolites. In order to investigate allelopathic activities of *Pseudoceratina* and the source of the active compounds, we conducted field experiments with competing coral species under different light regimes. We assessed whether the holobiont *Pseudoceratina* is reducing the fitness of corals by allelopathic means and whether it is the sponge or the symbionts producing the allelopathic agents. The results give further insight whether sponges are actively outcompeting competitors by production of bioactive compounds or if they are opportunistically occupying free space from dead coral substrate.

Decadal dynamics of Indonesian sponge assemblage: roles of endogenous and exogenous drivers

Alberto Rovellini[1], Matthew Dunn[2], Elizabeth A. Fulton[3], Shane A. Richards[3], David J. Smith[4], Jamaluddin Jompa[5], Nicole S. Webster[6] and James J. Bell[1]

Conference presenter: James.Bell@vuw.ac.nz
[1] *School of Biological Sciences, Victoria University of Wellington, Wellington, New Zealand*
[2] *National Institute of Water and Atmospheric Research (NIWA), Wellington, New Zealand*
[3] *CSIRO Oceans and Atmosphere, Hobart, Tasmania, Australia*
[4] *Coral Reef Research Unit, School of Biological Sciences, University of Essex, Colchester, United Kingdom*
[5] *Universitas Hasanuddin, Department of Marine Science, Makassar, Indonesia*
[6] *Australian Institute of Marine Science, Townsville, Queensland, Australia*

Despite the many functional roles that sponges perform on tropical coral reefs[1,2], information about population dynamics and temporal changes in species composition of sponge assemblages is limited. In this study, we considered temporal variation in an Indonesian coral reef sponge assemblage over 12 years. Sponge density followed a very consistent pattern of initial growth, following decline and final recovery over the studied period. A combination of unconstrained and constrained ordination methods[3] showed that species composition varied over time too, and that a few abundant sponge taxa were responsible for the observed dynamics. This suggests that either one or a combination of multiple drivers may affect several species in the assemblage[4]. We tested a set of three hypotheses to identify these potential drivers: correlation of sponge density with water temperature (I) and fish abundance (II), and presence of density-dependent regulation (III). Sponge density showed no correlation with the mean satellite-derived sea surface temperature (climatologies from December to March) preceding each sampling (I). Abundance of spongivores was weakly correlated with sponge density at the studied reef (R^2 0.65, p-value 0.056). However, abundance of herbivores and invertivores showed a strong positive correlation with sponge density, suggesting that these fish guilds might respond to the same covariates driving sponges (II). A deterministic demographic model of sponge dynamics, incorporating the assumption of density dependence, was fitted to population growth data, but it could not capture apparent local fluctuations. This means that density-dependence alone could not be identified as a driver of the observed dynamics (III). We conclude that sponge density can fluctuate by as much as one order of magnitude in a few years, driven by the dynamics of a few dominant species. This pattern may result from a synergy of exogenous and endogenous drivers, as none of the tested covariates was able to explain the dynamics of the assemblage alone. The remarkable variations in density and composition of this sponge assemblage over time highlight the value of long-term datasets when studying natural systems.

References

1. J. L. Wulff, Can. J. Zool. 84 (2006) 146–166
2. J. J. Bell, Estuar. Coast. and Shelf. Sci. 79-3 (2008) 341-353
3. M. J. Anderson & T. J. Willis, Ecology 84-2 (2003) 511-525
4. C. L. J. Frid, P. R. Garwood, L. A. Robinson, J. Marine Syst. 77-3 (2009) 227-236

Value-added in Thai Pottery by Biological Materials from Freshwater Sponges

Nisit Ruengsawang[1], Petch Suthiporn[1], Wilailak Chuchuay[2], Narumon Sangpradub[3] & Renata Manconi[4]

1Division of Biology, Rajamangala University of Technology Krungthep, Bangkok, Thailand nisit.r@rmutk.ac.th
2Division of Industrial Product Development, Rajamangala University of Technology Krungthep, Bangkok, Thailand
3Department of Biology, Khon Kaen University, Khon Kaen, Thailand
4Dipartimento di Scienze della Natura e del Territorio, Università di Sassari, Sassari, Italy

Biodiversity surveys of freshwater sponges in Northeast Thailand highlighted that sponges e.g. *Corvospongilla* spp. commonly colonize cages of fish culture (tilapia) in rivers and reservoirs. The high amount of sponge biomass clog the nets and limit water circulation in and out the cages causing various harms for fishermen. We attempted to manage this problem by various approaches in the framework of an applied research project. We focus on a) the development of sustainable management of freshwater sponges in the tropics, b) the improvement of pottery quality by introducing a valuable biomaterial (SiO_2 spicules) in the traditional manufacturing process to increase the value-added in Thai pottery, and c) the support on eco-friendly wild aquaculture by reducing its impact by bioremediation (sponges filtering activity) to gain positive effects on food security, habitat modification, and conservation of wild fisheries as traditional practice in Southeast Asia. Sponges were collected after fish harvesting, when cages were cleaned by air-drying for cage maintenance. Appropriated ratio of mixture clay including clay, sand and siliceous spicules were tested for shrinkage and strength of pottery. New designed products were created for value-added from traditional products. Prototype products were tested, and consumer willingness to pay for sponge pottery was also examined. An educational program to involve local populations in sustainable exploitation of natural resources was also planned.

References

1. R. Manconi, N. Ruengsawang, V. Vannachak, C. Hanjavanit, N. Sangpradub, R. Pronzato, J. Limno. 3320 (2013) 313-326.
2. N. Ruengsawang, N. Sangpradub, C. Hanjavanit, R. Manconi, Zootaxa. 3320 (2012) 47-55.
3. S. K. Mcintosh, K. C. MacDonald. J. Field Archaeol. 16 (1989) 489–494.

This work was financial support by Rajamangala University of Technology Krungthep.

Combining Metabarcoding and Metabolomics to better understand the ecological success of Homoscleromorpha sponges in underwater caves

César Ruiz[1], Thierry Pérez[1], Olivier P. Thomas[2]

[1] *Institut Méditerranéen de biodiversité et d'Ecologie Marine et Continental (IMBE), UMR CNRS 7263, IRD 237, Aix-Marseille Université, Avignon Université, Station Marine d'Endoume, Marseille, France. cesar.ruiz@imbe.fr*

[2] *National University of Ireland Galway, Marine Biodiscovery, School of Chemistry, University Road, Galway, Ireland.*

Underwater caves are original habitats of ecological interest. Indeed they can be considered extreme due to marked physical gradients such as light, hydrodynamics and food availability which make them good mesocosms of deep sea ecosystems. Underwater cave ecosystems were mostly studied in the few places of the Mediterranean Sea, often focusing on specific taxonomic groups. Overall, those studies revealed similar faunistic traits and ecological functioning. Homoscleromorpha sponges are well represented in underwater caves, and some species can be cave-exclusive. However, very little is known about the factors explaining their ecological success in such a constraining environment. We hypothesized that the microbiome and/or metabolome of these sponges may confer adaptation capability. On a large collection of samples from Mediterranean and Caribbean submarine caves, we undertook metabarcoding and metabolomic fingerprinting analyses to identify putative patterns in microbial and chemical diversity that may be related to sponges' ecological habit. Some of these patterns seem to be explained by the taxonomy of the sponge and/or the geographical area, so these two approaches can be used in integrative taxonomy. More interesting, we have found that ecological traits like habitat occupation inside caves (semi-obscure, obscure) or species distribution can be explained by the presence of particular microbial groups or the production of exclusive metabolites. Our results seem to confirm our former hypothesis, however the functional role of those microorganisms and metabolites must be analyzed to understand their contribution to the adaptation of Homoscleromorpha sponges to marine caves.

This work takes place in the framework of the LIA MARRIO, and was funded by the CNRS, the Total Founda-

tion and Colciencias-Colfuturo.

South Orkney Islands: a poorly sponge-studied region of the White Continent. Results of Argentinean Antarctic Cruises 2012 and 2014

Laura Schejter[1], Javier Cristobo[2] & Pilar Ríos[2]

1. Consejo Nacional de Investigaciones Científicas y Técnicas (CONICET) & Instituto Nacional de Investigación y Desarrollo Pesquero (INIDEP-ARGENTINA).
Paseo Victoria Ocampo Nº1, 7600, Mar del Plata, Argentina. schejter@inidep.edu.ar
2. Instituto Español de Oceanografía. Centro Oceanográfico de Gijón, Av. Príncipe de Asturias 70 bis, 33212 Gijón, Asturias, Spain.

The South Orkney Islands are among the poorest studied areas regarding sponge fauna in Antarctica. In 1986 the Spanish Expedition Antártida 8611 sampled 6 stations in the region, but the sponge data remains unpublished. Sará *et al*. (1992) reviewed the demosponge fauna of Antarctica and the South Orkney region had recorded only 8 species. Lately, van Soest *et al.* (2012) mentioned 9 species for the same region. A recent search through OBIS database for this marine Ecoregion recorded about 300 unpublished records, most of them not identified to species level (R. Downey, pers. comm.). These numbers highlight a gap in the knowledge of the South Orkney fauna. During two Argentinean Antarctic Research Cruises (2012 and 2014) onboard R/V "Puerto Deseado" 17 sites in the mentioned region were sampled. Sponge samples were separated from trawl catches and constituted in 4 sites the main component of the catch in terms of relative biomass. Sponge richness per site varied between 1 and 20 (based on morphotypes, and including hexactinellids).

A list of the recorded Demospongiae (mainly Poecilosclerida) comprised a total of 32 taxa of which 1 is a new species (*Coelosphaera (Coelosphaera*) sp. nov.) and at least 21 are new records for Orkney islands. Orders Spirophorida, Astrophorida, some species of Haplosclerida and Class Hexactinellida were also recorded and are still in study. The best represented species in the sampled stations were: *Iophon unicorne*, *I. gaussi*, *Lissodendoryx (Ectyodoryx) ramilobosa*, *Tedania (Tedaniopsis) tantula.* Other new records for the area were: *Raspailia (Hymeraphiopsis) irregularis, Myxilla (Burtonanchora) lissostyla, M. (Myxilla) mollis, Mycale tylotornota, M. fibrosa, Clathria (Axosuberites)* cf. *nidificata, Artemisina apollinis, Crella (Pytheas) crassa, Isodictya* cf. *kerguelenensis, I. verrucosa, I. lankesteri, Microxina charcoti, M. benedeni, Inflatella belli, Calyx* cf. *arcuarius, Myxodoryx hanitschi, Axinella antarctica, Haliclona (Gellius)* sp., and *Haliclona* sp. Except for *Mycale (Oxymycale) acerata* (also recorded), *Iophon unicorne* and *Calyx arcuarius* the other species have never been formally recorded in South Orkney Islands.

References

Sarà M, Balduzzi A, Barbieri M, Bavestrello G & Burlando B (1992). Biogeographic traits and checklist of Antarctic demosponges. *Polar Biology* 12: 559-585.

Van Soest RWM, Boury-Esnault N, Vacelet J, Dohrmann M, Erpenbeck D, De Voogd NJ, Santodomingo N, Vanhoorne B, Kelly M & Hooper JNA (2012) Global Diversity of Sponges (Porifera). PLoS ONE 7(4): e35105. doi:10.1371/journal.pone.0035105

Financial Support: Instituto Nacional de Investigación y Desarrollo Pesquero y Dirección Nacional del Antártico (Argentina). PICT 2013-0629 to LS.

Contribution to the description of *Fibulia myxillioides* (Burton, 1932) and new records of the species at Burdwood Bank, after 90 years of its unique collection date

Laura Schejter[1], Javier Cristobo[2], Pilar Ríos[2]

[1] Instituto Nacional de Investigación y Desarrollo Pesquero (INIDEP), Mar del Plata, Argentina. schejter@inidep.edu.ar
[2] Instituto Español de Oceanografía (IEO), Centro Oceanográfico de Gijón, Av. Príncipe de Asturias 70 bis, 33212 Gijón, Asturias, Spain.

Fibulia myxillioides (Burton, 1932) was described as *Plumocolumella myxilliodes* based on the specimens collected in the Malvinas (Falkland) Islands region onboard RRS "William Scoresby" in 1927 and 1928. The species was recorded in 9 sites in the mentioned area, and its distribution comprises Malvinas Is. and Burdwood Bank (SW Atlantic Ocean). However, besides these records, no information regarding this species was published since then, with the exception of the genus transfer, first to *Xytopsaga* by De Laubenfels (1936), based on the type specimen and other specimens collected during the same expedition, and lately to *Fibulia* by van Soest (2007). Burton´s original description consisted in a synthetic paragraph and a draw of two complete specimens, with only few measures (and no ilustrations) of the spicules. In this contribution, we add

5 recent records of the species in Burdwood Bank about 90 years after its original (and unique) collection and record date, from samples collected during research cruises developed during 2013 and 2016, both onboard the RV "Puerto Deseado". We update the bathymetric range of the species from 81-267m (in Burton, 1932) to 608 m. We also describe and provide images of the yellow-brownish coloration in the living specimens and we present, for the first time, SEM images of all the spicules, with the recorded range of measures for Burdwood Bank. Based on the evidence and a bibliographic review, this is an endemic species from Malvinas/ Burdwood Bank region, and the oceanographic conditions (Malvinas Current) are probably related with the distribution pattern.

References

Burton, M. (1932). Discovery Reports.6: 237-392, pls 48-57.

Laubenfels, M.W. De. (1936). Carnegie Institute of Washington Publication 467 (Tortugas Laboratory Paper 30) 1-225, pls 1-22.

van Soest, R. (2007). *Fibulia myxillioides* (Burton, 1932). In: Van Soest *et al*. (2016).World Porifera Database (accessed in February 2017).

Financial support: CONICET, INIDEP (Argentina) and PICT 2013-0629 to LS.

Biogeographic and bathymetric distribution of coral-eroding sponges

Christine H.L. Schönberg[1], James K.-H. Fang[2], José-Luis Carballo[3], Max Wisshak[4] and Lydia Beuck[4]

[1] School of Earth and Environment and Oceans Institute, The University of Western Australia, Crawley, WA 6009, Australia. christine.schonberg@uwa.edu.au
[2] Benthic Resources and Processes Research Group, Institute of Marine Research, 5005 Bergen, Norway
[3]Instituto de Ciencias del Mar y Limnología, Universidad Nacional Autónoma de México, Mazatlán 82040, México
[4]Senckenberg am Meer, Marine Research Department, 26382 Wilhelmshaven, Germany

Environmental change is progressing at an alarming rate and leads to widespread coral demise. Bioeroding sponges have been called bioindicators of environmental change on coral reefs, they are thought to be comparatively resistant to environmental stress, and they can potentially drive reef carbonate budgets further towards net erosion. Some species of bioeroding sponges received much attention, but others have not been mentioned in the literature since their original description. This situation obstructs our progress in research. We therefore synthesized available published data across all 260 accepted and 13 presently undescribed species, generating annotated faunistic checklists per bioregion and presenting global distribution patterns (Schönberg et al. in press). We strongly suggest that 'cosmopolitan' species are usually species complexes that need to be resolved with molecular means. The best-studied area in shallow waters is the Caribbean, harbouring one fourth of all known species, but global patterns are more strongly influenced by Indo-Pacific species. We have inadequate knowledge on the species from shallow depths in the NE Indic, of the central Pacific and Japan. Along a bathymetric gradient the composition of taxa changes, favouring clionaids in depths less than 100 m, while *Spiroxya*, *Alectona, Delectona* and small species of *Siphonodictyon* become dominant at greater depth. Overall, bioeroding sponges in deep water are much less well studied (18% of the evaluated species, see below) than in shallow and warm waters (77%). At many locations bioeroding sponges have not been studied since the 1800s, and it would be desirable to conduct new surveys that involve morphological as well as molecular species identification.

References

C. H. L. Schönberg, J. K.-H. Fang, J.-L. Carballo. Bioeroding sponges and the future of coral reefs. In: J. J. Bell, J.-L. Carballo (eds) Climate change, ocean acidification and sponges. Springer, Berlin, Heidelberg (in press).

Coelocarteria singaporensis – an unexpected bioeroding sponge?

Christine H.L. Schönberg[1]

[1] School of Earth and Environment and Oceans Institute, The University of Western Australia, Crawley, WA 6009, Australia. christine.schonberg@uwa.edu.au

Historically, only the papillate and encrusting Clionaidae, the Thoosidae, and *Siphonodictyon* spp. were regarded as sponges that erode calcium carbonate. Over time it was recognized that massive Clionaidae, the Spirastrellidae, *Zyzzya* and *Cornulella* spp. are also bioeroders. Bioerosion capabilities of some other groups and species have been discussed, i.e. whether they actively erode or only insinuate themselves into pre- existing cavities where they 'nestle' (*Cornulum*, A*morphinopsis*, *Dercitus*, *Holoxea*, *Triptolemma* and *Samus* spp.). A paper by de Laubenfels (1954) and a recent publication by Rützler et al. (2014) described further unusual and unexpected sponge species as bioeroders (*Haliclona*, *Timea*, *Aplysinella* and *Suberea* spp.), which suggests that the ability to bioerode may be much more widely distributed across sponge taxa than previously thought. During fieldwork on the central Great Barrier Reef, another such sponge was found that was not expected to bioerode: *Coelocarteria singaporensis* (Carter, 1883). *C. singaporensis* is a massive-fistular sponge that lives either buried in sediments or fills gaps and cracks in coral rock. A piece broken off a specimen attached to coral rock showed that marginal tissue had penetrated into the rock, and that the sponge body was surrounded with bioerosion chambers. This is the first isodictyid reported as being a bioeroder. Future sampling of replicate specimens will allow more detailed investigations and confirmation of its bioeroder status. At this stage, I hypothesise that bioerosion capabilities in sponges commonly co-occur with a tendency to inhabit sediments (psammobiosis) and the habit to agglutinate or incorporate calcareous debris (see Schönberg 2016). It is therefore not unlikely that sponge taxa that commonly contain species with endopsammic or particle-collecting tendencies will reveal further bioeroders.

References

1. M. W. de Laubenfels. The sponges of the West-Central Pacific. Oregon State Monogr, Studies Zool 7 (1954) 1-320.
2. K. Rützler, C. Piantoni, R. W. M. van Soest, M. C. Diversity of sponges (Porifera) from cryptic habitats on the Belize barrier reef near Carrie Bow Cay. Zootaxa 3805 (2014) 1-29.
3. C. H. L. Schönberg. Happy relationships between marine sponges and sediments – a review and some observations from Australia. J Mar Biol Ass UK 96 (2016) 493-514.

Sponges don't like pumice, they like hard rock!

<u>Peter J. Schupp</u>[1], Sven Rohde[1], Sadie Mills[2], Jackson Cahn[3], Kathrin Busch[4], Tanja Stratmann[5], Dennis Versluis[1], Lars-Eric Petersen[1], Michelle Kelly[6], Tessa Clemens[1], Gert Wörheide[7]

[1] Institut for Chemistry and Biology oft he marine Environment (ICBM), Carl-von-Ossietzky University
Oldenburg, Schleusenstr. 1, 26382 Wilhelmshaven, Germany
<u>Peter.schupp@uni-oldenburg.de</u>

[2]NIWA, 301 Evans Bay Parade, Greta Point, Wellington, New Zealand

[3]Institute of Microbiology, ETH Zurich, Vladimir-Prelog-Weg 1-5/10, 8093 Zurich, Switzerland

[4]GEOMAR, Marine Microbiology, Düsternbrooker Weg 20, D-24105 Kiel, Germany

[5]NIOZ – Royal Netherlands Institute for Sea Research, Korringaweg 7, 4401 NT Yerseke, Netherlands

[6]NIWA, 41 Market Place, Viaduct Harbour, Auckland, New Zealand

[7]Department of Earth & Environmental Sciences, Ludwig-Maximilians-Universität München, Richard-Wagner-Str. 10, 80333 München, Germany

During the deep-water expedition aboard the German research vessel SONNE (cruise SO254) in February 2017 a total of 211 sponges were collected on a North-South transect from 29° South to 49° South along the East coast of New Zealand. Those sponges, as well as other invertebrates, were collected with the remotely operated vehicle (ROV) ROV KIEL 6000 from as shallow as 100 m down to 4200 m water depth. A total of 360 specimens were collected by the ROV. Taxonomic identification using traditional microscopy as well as through DNA barcoding are ongoing.

A first analysis revealed that at the northern stations from 29° South to 39° South were dominated by Hexactinellida (total of 102 specimens/ 7.3 per site) with Demospongiae being less abundant (total of 45 specimens/ 3.2 per site). The southern stations from 41° South to 45° South on the other hand were dominated by Demospongiae (54 specimens/ 13.5 per site), with only a low abundance of Hexactinellida (2 specimens/ 0.5 per site).

Sponge diversity comprised the orders Hadromerida, Halichondrida, Haplosclerida, Lithistida, Poecilosclerida, Tetractinellida, Verongida and several yet to be identified demosponge species. Hexactinellida diversity included the orders Amphidiscosida, Hexactinosida, Lyssacinosida and several yet to be identified species.

One difference that was noted between the different ROV stations was that sponges in general were more common on hard substrate, i.e., volcanic bedrock, while they were rare to absent on slopes dominated by muddy sediment with occasional pumice rocks. Several of the northern sites were also geologically active (e.g. Raoul Island, Maccauley Island), and had much higher abundances of Octocorals compared to sponges. Since most Octocorals also require hard substrate for attachment, it appears that sponges prefer different hard substrate compared to the Octocorals, which seemed rather abundant on the pumice substrate. As these are just preliminary observations directly form the recent SONNE Expedition SO254, further analysis as to possible factors contributing to the observed sponge distribution are ongoing, such as investigations on differences in water chemistry and nutrients among the different sites.

Financial support by BMBF 03G0254A, SO254 PORIBUGNEWZ is gratefully acknowledged.

How to Protect a Mesophotic Sponge Ground – A Case Study

<u>Sigal Shefer</u>[1, 2,] Tal Idan[1], Tamar Feldstein[1, 2], Ruth Yahel[3], Dorothée Huchon[1, 2], Micha Ilan[1]

[1] Department of Zoology, George S. Wise Faculty of Life Sciences, Tel Aviv University, Ramat Aviv, Tel Aviv 6997801, Israel

[2] The Steinhardt Museum of Natural History, Israel National Center for Biodiversity Studies, Tel Aviv University, Ramat Aviv 6997801, Israel

[3] Science Division, Israel Nature and Parks Authority, Givat Shaul, Jerusalem 95463, Israel

In recent years explorations for natural gas and oil have been carried out along the Israeli coast of the Mediterranean, as a future center for the petroleum industry. Last November, the Israel Ministry of Energy launched a competitive process for new offshore exploration licenses, after more than four years during which sea exploration permits were not given. The new process offers 24 blocks within Israel's exclusive economic zone, containing an estimated 6.6 billion oil barrels and about 2, 137 billion m^3 of natural gas. Some of these blocks are located in proximity to newly-discovered mesophotic sponge grounds. In these mesophotic ecosystems, sponges create complex structures that attract both invertebrates and fish, thereby serving as environmental engineers and creating marine oases in an otherwise a relatively homogeneous environment. The proposed physical activities (e.g. drilling, pipeline installation, structure or vessel anchoring to sea bottom, piling-up of drilling cuttings), have the potential to cause irreversible physical damage to benthic rock habitats. Moreover, the drilling lubricants and thin sediment deriving from such excavations and suspended in the water column, could cover and clog the sponges' filtering apparatus.

The Ministry of Energy launched a Strategic Environmental Assessment (SEA) in order that gas and oil exploration and production could be carried out while also maintaining the normal and sustainable functioning of the ecological marine environment, with minimum interference, disturbances, and damage. The habitat mapping team defined four vulnerability levels: 1. Low 2. Moderate; 3. High; 4. Very high (unique species). Our aim was to assess the level of vulnerability applicable to the local mesophotic sponge ground. The data we provided were collected during six expeditions to the Herzliya deep site (~100m, using ROV), at which 98 sponge specimens were sampled from four pinnacles. We found that the sponge grounds maintain a rich and diverse community with an estimated 63 species, and a high sponge percentage cover (~35%). Some of the mesophotic species are documented for the first time from the Levant basin, while others might be novel species. Moreover, a comparison revealed only a slight overlap between the shallow and the mesophotic sponge communities along the Israeli coast, with merely nine species that thrive across this entire depth range. Those species that are confined to the mesophotic depth along the Israeli coast, grow at shallower depths in other parts of the Mediterranean. The findings that the sponge grounds contain species unique to the Levant Basin, the significant difference found between pinnacles, and that the mesophotic community may also serves as a refuge and possible breeding ground for other species, helped us to convince the decision-makers to give the mesophotic sponge ground at the Herzliya site the highest vulnerability level. We suggest that this approach could serve as a case study for science-based conservation.

Trade-off between growth, reproduction and spatial competition of the intertidal marine sponge *Cinachyrella* cf. *cavernosa*

Anshika Singh and Narsinh L. Thakur

CSIR-National Institute of Oceanography, Dona Paula 403 004, Goa, India anshika.singh17@gmail.com

In space-limited environment like intertidal rock pools, sessile marine organisms maintain their space by using allelochemicals, the production of which may influence their primary life processes such as growth and reproduction. In the present investigation, growth, regeneration and asexual reproduction (budding) of the marine sponge *Cinachyrella* cf. *cavernosa* were monitored in presence and absence of the spatial competition from its aggressive neighbour zoanthids, *Zoanthus sansibaricus*. The field experiments were carried out by tagging sponges growing with and without competitor in intertidal rock pools at Anjuna - Goa, central west coast of India, for two consecutive years. The sponges growing with the zoanthids showed significant ($p<0.05$) reduction in their growth (36-69%), regeneration (30-76%) and asexual reproduction (45-60%). Analysis of sponge's crude extract for secondary metabolites led to the isolation of a cytotoxic compound 'ß-sitosterol', the production of which was recorded highest (34-87%) in sponges, growing with zoanthids. At its natural concentration, this compound showed significant toxicity (LD_{50}=92.9ppm) to symbiotic zooxanthellae of zoanthids, which indicates its possible role in allelopathic interaction of the sponge with its spatial competitor. The present investigation shows interplay between primary (growth, regeneration, reproduction) and secondary (spatial competition) life processes of the marine sponge and supports earlier reported observations of trade-off hypothesis.

Financial support by PSC0105 (Ocean Finder) is gratefully acknowledged.

Biogeographic Connectivity of Sponge Communities in the Tropical Atlantic

Marc Slattery [1, 2], Michael P. Lesser[3], Deborah J. Gochfeld[2], M. Cristina Diaz[4], Elizabeth Kintzing[3]

[1]Department of BioMolecular Sciences, University of Mississippi, Oxford MS, USA
slattery@olemiss.edu

[2]National Center for Natural Products Research, University of Mississippi, Oxford MS, USA

[3]School of Marine Science and Ocean Engineering, University of New Hampshire, Durham NH, USA

*[4]***, Nova Southeastern University, *** FL, USA*

Sponges are one of the most diverse marine taxa and an increasingly dominant constituent of tropical Atlantic coral reefs. The ecological importance of these sponges is unequivocal. They provide important food and habitat for a variety of coral reef species, play a significant role in benthic-pelagic coupling via filtration of bacterioplankton, and they can either stabilize or degrade the reef matrix. In addition, symbiotic microbes represent both phototrophic conduits of energy for coral reef communities and a major source of nitrogen cycling. Although our knowledge of sponge ecology has increased dramatically over the last few decades, there are still many questions to be answered. Key among these questions is the degree of spatial variability in sponge diversity between reefs, and the role this plays in the structure and function of coral reefs. As shallow coral reefs worldwide are increasingly degraded by natural and anthropogenic stressors, mesophotic coral ecosystems (~30-150 m) represent potential refugia that might act as seed-banks for coral reef resilience. Our data indicate that sponge diversity varies with depth and site. Our goal is to assess differences in sponge communities between shallow and mesophotic reefs among reefs in the tropical Atlantic (Bahamas and Cayman Islands, to date), to identify local and regional drivers of biodiversity and the degree of connectivity within the Caribbean basin.

Calcarea on the shelf edge of the Great Australian Bight, Australia

Shirley Sorokin[1], Michelle Klautau[2], Lisa Goudie[3], Andrea Crowther[4], Jane Fromont[5], Anita Mary George[6], Sam McCormack[7], Muhammad Azmi Abdul Wahab[8]

[1] SARDI Aquatic Sciences, West Beach, Adelaide, South Australia shirley.sorokin@sa.gov.au

[2] Universidade Federal do Rio de Janeiro, Brasil

[3] Lisa Goudie consultancy, Sandringham, Victoria

[4]South Australian Museum, North Tce, Adelaide, South Australia, Australia

[5]Western Australian Museum, Welshpool, Western Australia, Australia

[6]Queensland Museum, South Brisbane, Queensland, Australia

[7]University of Waikato, Tauranga, New Zealand

[8]Australian Institute of Marine Science, Perth, Western Australia

A broad-ranging benthic survey in the Great Australian Bight (GAB) identified a diverse calcareous sponge fauna in shallower waters (≤ 200 m depth) and an apparent absence of the group in deeper waters (400 m to 3000 m). Sponges were sampled, along with other benthos, at depth-stratified stations in December 2015, as part of the first characterisation of deep benthic communities in the GAB. Of the sponge species collected, 16% were Calcarea, and apart from *Leucetta* sp. all the specimens were small (< 5 cm in length). In total, they made up 1.8% of the overall sponge biomass. Twenty-nine species of Calcarea were identified, 12 of the subclass Calcaronea and 17 of the subclass Calcinea. The most diverse genus was *Ascoleucetta* and the most widespread species was *Leucettusa lancifera*. Seven species are new to science: *Ascoleucetta* (four species), *Ute* n. sp. (one species), *Ernstia* n. sp. (one species) and *Leucettusa* n. sp. (one species). Calcarea have been thought to be depth-limited by the oceans' Calcium Compensation Depth, but previous work has shown that this occurs deeper than 1000 m in the GAB[1] and so the apparent depth limitation of Calcarea may not be due spicule solubility but to other factors. The benthic collection was part of the first characterisation of deep benthic communities in the Great Australian Bight ecosystem to provide a baseline for monitoring future anthropogenic impacts. This work was funded by the Great Australian Bight Research Program, a collaboration between BP, CSIRO, the South Australian Research and Development Institute (SARDI), the University of Adelaide, and Flinders University. The Program aims to provide a whole-of-system understanding of the environmental, economic and social values of the region; providing an information source for all to use.

References

1. N.P. James, Y. Bone and T. Kurtis Kyser, J. Sed. Res 75(3) (2005) 457-467

Dominance and diversity of deep-water sponges on the shelf edge and slope of the Great Australian Bight, South Australia

Shirley Sorokin[1], Lisa Goudie[2]

[1] SARDI Aquatic Sciences, West Beach, Adelaide, South Australia shirley.sorokin@sa.gov.au

[2] Lisa Goudie consultancy, Sandringham, Victoria

Sponges constituted over a quarter of the species count (191 spp., 28%) and biomass (27%) in invertebrate benthic collections along depth-stratified stations (200 - 3000 m depth) in the Great Australian Bight, southern Australia. Two species dominated the sponge biomass. The haplosclerid fan sponge *Callyspongia (Callyspongia)* sp. made up 27% of the total sponge biomass and dominated the shelf edge (200 m) and the tetractinellid *Thenea* sp. made up 42% of the total sponge biomass, dominated the slope and was the most widespread species, being found at all depths between 400 and 3000 m with the highest concentration at 1000 m. Both sponges were found at all longitudinal transects. Overall, there was little overlap of species between depths, with 93% of species only occurring at one depth. The benthic collection was part of the first characterisation of deep benthic communities in the Great Australian Bight ecosystem to provide a baseline for monitoring future anthropogenic impacts. This work was funded by the Great Australian Bight Research Program, a collaboration between BP, CSIRO, the South Australian Research and Development Institute (SARDI), the University of Adelaide, and Flinders University. The Program aims to provide a whole-of-system understanding of the environmental, economic and social values of the region; providing an information source for all to use.

Oxygen consumption and nutrient fluxes of deep-sea sponges

Tanja Stratmann[1] and Dick van Oevelen[1]

[1] *NIOZ Royal Netherlands Institute for Sea Research, Department of Estuarine and Delta Systems, and Utrecht University, P.O. Box 140, 4400 AC Yerseke, the Netherlands. tanja.stratmann@nioz.nl*

Sponges can form extensive reef systems, e.g. off the west coast of Canada (1) and Norway (2), but our knowledge on their role in carbon and nutrient cycling is extremely limited (3, 4). A few initial reports indicate that this may be substantial, as community respiration rates within sponge grounds were measured to be ten times higher than community respiration rates of near-by sediment (2, 3).

During the recent RV Sonne cruise SO254, 17 individual deep-sea sponges of the classes Demospongiae and Hexactinellida were collected with the ROV Kiel 6000 in the exclusive economic zone (EEZ) of New Zealand (SW Pacific) between 595 and 1467 m depth. These sponges were incubated individually in the dark at in-situ temperature for 5 hours in closed incubation chambers onboard RV Sonne. At the begin and at the end of the incubations water samples were taken for the determination of nutrient concentration (phosphate, silicate, ammonia, nitrate, nitrite), whereas oxygen concentration in the incubation chambers was measured continuously.

We will present oxygen utilization and nutrient exchange fluxes for these sponges and attempt a first extrapolation to aerial rates using video footage from the ROV.

References

1. M.M. Hogg, O.S. Tendal, K.W. Cornway, S.A. Pomponi, R.W.M. van Soest, J. Gutt, M. Krauter, J.M. Roberts, UNEP-WCMC Biodiversity Series. 32 (2010) 33-37.
2. T. Kutti, R.J. Bannister, J.H. Fosså, Cont. Shelf Res. 69 (2013) 21-30.
3. C. Cathalot, D. van Oevelen, T.J.S. Cox, T. Kutti, M. Lavaleye, G. Duineveld, F.J.R. Meysman, Front. Mar. Sci. 2 (2015) 37.
4. A.S. Kahn, G. Yahel, J.W.F. Chu, V. Tunnicliffe, S.P. Leys, Limnol. Oceanogr. 60 (2015)78-88.

Patterns of *Cliona delitrix* prevalence in a near-shore artificial reef system

Holly Trew[1], Henri Vallès[1]

[1]*Department of Biological and Chemical Sciences, University of the West Indies, Cave Hill, Barbados hvtrew@gmail.com*

Growth of the coral framework on reefs is constantly counteracted by erosion from both physical and biological sources. Excavating sponges are the primary bioeroders on Caribbean reefs, causing weakening and breakdown of the reef structure. The bio- eroding role of excavating sponges has attracted considerable attention because of the poor current state of many coral reefs across the region. This study examined the prevalence of *Cliona delitrix*, one of the Caribbean's most common excavating sponges, within a system of six shallow shipwrecks in Carlisle Bay, Barbados. Located within 50m of each other, the shipwrecks are subject to the same broad environmental conditions, but vary in their age (from 15 to 98 years old) as well as in the successional stage of their coral communities, with regard to coral species and colony size-frequency, that play host to *C. delitrix*.

The shipwrecks are a prime tourist destination, with approximately 500, 000 snorkelers/divers visiting them each year, thus subjecting them to regular nutrient inputs from fish feeding, sunscreen, and human urine. Because *C. delitrix* abundance has been previously linked to anthropogenic nutrient enrichment and tourist visitation rates vary considerably and consistently among wrecks, this system provides an interesting opportunity to assess the impact of human presence on *C. delitrix* prevalence over relatively small spatial scales.

On each wreck, each individual *C. delitrix* outcrop (n=919) was mapped and measured. Conditions associated with each outcrop were also recorded, including substrate type/species (beneath and immediately adjacent to the sponge), depth, and zooanthid occurrence. *C. delitrix* prevalence was measured across 2, 899 colonies belonging to seven massive coral species and varying in size (between 5 cm to >50 cm in diameter) Nutrient inputs to the different wrecks were assessed via stable isotope analysis from samples of *Dictyota* algae, *C. delitrix*, and *Diadema antillarium* urchins.

Pending results from stable isotopes, preliminary analyses indicate that approximately 7.5% of all live coral colonies within the system are colonized by *C. delitrix*, accounting for 3% of total live coral surface area. The most common coral host was *Siderastrea sidereal,* followed by *Diploria strigosa.* There was a strong colony size-dependent effect on *C. delitrix* prevalence: ranging from 4.2% to 28.6% for the smallest and largest corals, respectively. An understanding of relative abundances of *C. delitrix* within different reef communities can illuminate the role of this particular sponge, and bioeroders in general, in community succession. The relationship between tourism, nutrient enrichment, and bioerosion is of particular interest as it is an issue that affects many reefs worldwide and is crucial for management of near-shore reef ecosystems.

Financial support by The University of the West Indies is gratefully acknowledged.

Mutualistic relationship between host sponge *Spongia* (*Spongia*) sp. and its endosymbiotic bivalve *Vulsella vulsella*

Remi Tsubaki[1]

[1] *Research and Development Center of Marine Bioscience, Japan Agency for Marine Earth Science and Technology, Yokosuka, Kanagawa, Japan. tsubakir@jamstec.go.jp*

Sponges, porous filter-feeding organisms consisting of vast canal systems, provide unique substrates for diverse symbiotic organisms. The *Spongia* (*Spongia*) sp. massive sponge is obligately inhabited by the host-specific endosymbiotic bivalve *Vulsella vulsella*[1], which benefits from this symbiosis by receiving protection from predator. However, whether the host sponge gains any benefit from this association is unclear. Considering that the bivalves exhale filtered water into the sponge body rather than the ambient environment, the sponge is hypothesized to utilize water exhaled by the bivalves to circulate water around its body more efficiently. We tested this hypothesis by observing the sponge aquiferous structure and comparing the pumping rates of sponges and bivalves. Observations of water currents and the sponge aquiferous structure revealed that the sponge had a unique canal system enabling it to inhale water exhaled from bivalves, indicating that the host sponge adapted morphologically to receive water from the bivalves. In addition, the volume of water circulating in the sponge body was dramatically increased by the water exhaled from bivalves. Therefore, this sponge-bivalve association can be regarded as a novel mutualism in which two filter-feeding symbionts promote mutual filtering rates[2].

References

1. R. Tsubaki, M. Kato, Zool. Sci. 29 (2012) 585-592.
2. R. Tsubaki, M. Kato, Plos One (2014) e108885

Financial support by JSPS is gratefully acknowledged.

Environmental assessment of deep-water sponge grounds in relation to oil and gas activities: a Faroe-Shetland Channel case study

Johanne Vad [1, 2,] Theodore Henry[1], Sophie Green[3], Lea-Anne Henry[2] & J Murray Roberts[2]

[1] *School of Energy, Geoscience, Infrastructure and Society, Heriot-Watt University, Edinburgh, UK*

[2] *School of Geosciences, Grant Institute, University of Edinburgh, Edinburgh, UK*

[3] *British Geological Survey, Lyell Centre, Edinburgh, UK*

Deep-water sponge grounds constitute a major deep-sea habitat that support diverse benthic communities[1]. These habitats meet the criteria of Vulnerable Marine Ecosystems (VMEs) as recognised by the UN Food and Agriculture Organisation as well as Ecologically and Biologically Significant Areas (EBSAs) as recognised by the UN Convention on Biological Diversity[2]. In July 2014, a new Nature Conservation Marine Protected Area (NCMPA) was designated in the Faroe-Shetland Channel (FSC) to protect the deep-sea sponge grounds present in the area. Oil extraction and production activities have occurred within the FSC since the 1990s[3], with the development of Foinaven and Schiehallion oil fields located within the NCMPA. However, the current extent of the sponge grounds within the FSC and the impact oil extraction and production activities has on deep-sea sponges remains to be understood. This talk will present results (i) from our analysis of FSC seabed still images and (ii) from short-term weathered crude and/or dispersant toxicology experiments with shallow-water sponges as surrogate organisms. First, over 1, 500 still images of the FSC seabed acquired during successive Remotely Operated Vehicle surveys were examined and benthic organisms' presence were scored. The resulting dataset was analysed by Redundancy Analysis and Partial Redundancy Analysis to assess the proportion of community composition variability explained by abiotic or anthropogenic factors. Substrate type, depth and seawater temperature appear to be the main factors impacting benthic community composition in the FSC. Moreover, fish species, bryozoans and crinoids amongst other are found to be associated with the sponge grounds in the FSC. Second, short-term experiments in which shallow-water sponges exposed to weathered mixtures of Foinaven crude oil and/or Slickgone NS dispersants were conducted to assess toxicity and effects on respiration. Respiration and filtration rates were affected in some treatments and tissues were collected for assessment of molecular indicators of toxicity. These initial and our ongoing investigations will contribute to better understand the importance of deep-sea sponge grounds in the FSC and their sensitivity to oil production activities.

References

1. L.-A. Henry, J. M. Roberts, JNCC Report No. 508 (2014) 45pp.
2. M. M. Hogg, O. S. Tendal, K. W. Conway *et al.*, UNEP-WCMC Biodiversity Series No. 32 (2010) 88p.
3. J. R. Smallwood, W. J. Kirk, Geological Society London Petroleum Geology Conference series Vol. 6 (2005) 977-991.

Financial support by Heriot-Watt University, BGS, the Centre for Doctoral Training Oil and Gas, the Natural Environment Research Council and Oil & Gas UK is gratefully acknowledged. Research support by BP and Marine Scotland is gratefully acknowledged.

Additions to the biodiversity of the sponge fauna from Martinique (Fr.)

Esther van der Ent[1], Nicole J. de Voogd[1]

[1] *Naturalis Biodiversity Center, Leiden, The Netherlands. esther.vanderent@naturalis.nl*

Sponge biodiversity has been extensively studied in the Caribbean, but most scientific efforts have concentrated on the Greater Antilles, Western and Southern Caribbean, while the Eastern Caribbean Arc islands have been overlooked. Recently, Perez *et al.* (2017) provided a first inventory of sponge diversity on Martinique (Fr.). During their survey they found a minimum of 191 species, and of approx. 60 non-identified sponge species a substantial number was thought to be new to science. The survey was limited to South Caribbean shallow reefs, cryptic habitats and Caribbean and Atlantic mangroves, and sampling efforts among these habitats varied. They did not include North Caribbean and North Atlantic sites, nor deep reefs. Therefore this first inventory might still be an under- representation of the actual biodiversity of the sponges fauna of Martinique. We present additions to their record by presenting the results of the Madibenthos Expedition to Martinique, organized by the Muséum National d'Histoire Naturelle between September and October 2016. This six-week expedition aimed to make a complete inventory of benthic invertebrates from 0 to 100 meter depth around the entire island. The coast of Martinique shows distinct differences between the Atlantic and Caribbean side. Along the Atlantic coast strong ocean currents prevent the formation of 3D-structured reefs. The more sheltered reefs on the Caribbean side are built on hard volcanic rock in the north while the southern reefs and Baie de Fort-de-France are influences by sand and siltation. These influences create vastly different habitats, influencing sponge species distribution in space. We used classical morphological characteristics to ascertain sponge biodiversity. Molecular biodiversity was assessed utilizing mitochondrial and nuclear ribosomal markers from the Sponge Barcoding Project (Erpenbeck *et al.*, 2016). Approximately 650 sponge specimens were collected from 91 sites (9 intertidal and mangrove sites, 61 shallow reef sites, 21 dredging sites). Sponges were collected by snorkeling (0-3 m), SCUBA diving (3 – 50 m) and dredging (60 - 100 m). The abundance and diversity of sponge species was observed to be much higher on the Caribbean coast of Martinique compared to the Atlantic. Preliminary data from other benthic invertebrate organisms in this expedition show a similar pattern. The Atlantic coast of Martinique might be less hospitable as a reef ecosystem, although the impact of anthropogenic stressors on this side is also thought to have a longer history compared to the less disturbed Caribbean reefs. Interestingly, dredging in the deeper mesophotic zone yielded a high abundance of sponges, indicating that mesotrophic reefs in Martinique may be entirely 'sponge-reefs'. The Madibenthos expedition reflects the high abundance and diversity of sponges that is seen throughout the Caribbean, and highlights their functioning as habitat-formers now that stony coral cover is declining.

References

Erpenbeck, D., Voigt, O., Al-Aidaroos, A. M., Berumen, M. L., Büttner, G., Catania, D., Guirguisc, A.N., Paulaye, G., Schätzlea, S., & Wörheide, G. (2016). Molecular biodiversity of Red Sea demosponges. Marine pollution bulletin, 105(2), 507-514.

Pérez, T., Díaz, M. C., Ruiz, C., Cóndor-Luján, B., Klautau, M., Hajdu, E., Lobo-Hajdu, G., Zea, S., Pomponi, S.A., Thacker, R.W., Carteron, S., Guillaume Tollu, G., Pouget-Cuvelier, A., Thélamon, P., Marechal, J., Thomas, O.P., Ereskovsky A.V., Vacelet, J., Boury-Esnault, N. (2017). How a collaborative integrated taxonomic effort has trained new spongiologists and improved knowledge of Martinique Island (French Antilles, eastern Caribbean Sea) marine biodiversity. PloS one, 12(3), e0173859.

We gratefully acknowledge Philippe Bouchet for the invitation to join the expedition. See Madibenthos website http://madibenthos.mnhn.fr/

Sexual breeding of the red sponge *Mycale phyllophila* (Porifera: Demospongiae)

Dexiang Wang[1], Huilong, Ou[1]

[1] *State-Province Joint Engineering Laboratory of Marine Bioproducts and Technology, college of Ocean and Earth Sciences, Xiamen University, Xiamen, China, 361102.*

To solve the "supply problem" of sponge biomass for further investigation of drug and other biotechnological applications, sexual breeding of sponge from larvae to adult was carried out in this study. Compared with the intensive aquaculture of sponge explants, sexual breeding is more efficient and could avoid genetic resources degradation. The red sponge *Mycale phyllophila* are common species in coastal water of Fujian, China and found to be an excellent natural product provider. The whole procedure as following: Firstly, larvae were collected in site in June early morning using special manufacture silk sieve cloth. Secondly, larvae were brought back to laboratory and settle in a dark environment with gentle current. Thirdly, the effects of flow rate, food source and illumination intensity on survival and growth of juveniles of the sponge under control conditions were investigated. Finally, we investigated the appropriate time to transplant the juveniles to the sea and monitored survival and growth of juveniles in field. As result, we successful culture the larvae of the red sponge from laboratory to field and acquired the base protocol to culture sponge larvae in field. The results indicated that sponge sexual breeding is a promising method for sponge supply and that laboratory culture under controlled conditions is necessary before transplanting the juveniles to sea.

Fig.1 Sexual breeding of the red sponge *Mycale phyllophila* from larvae to adult

Is Saba Bank becoming a 'sponge reef'?

Mirthe Wiltink[1], Erik Meesters[2], Nicole J. de Voogd[3], Leontine Becking[1, 2, 3]

[1] *Marine Animal Ecology, Wageningen University & Research, The Netherlands*

[2] *Wageningen Marine Research, Den Helder, The Netherlands*

[3] *Naturalis Biodiversity Center, Leiden, The Netherlands*

The Saba Bank Nature Park, with an area of almost 2700 km^2, is the largest marine protected area in the Dutch Caribbean and recognized by the Convention on Biological Diversity as an "Ecologically or Biologically Significant marine Area". As the Saba Bank is removed from large landmasses, it provides an excellent case to study general processes that occur in coral reefs in the Caribbean. Our aim was to systematically quantify the diversity and health of the sponge assemblages on the Saba Bank. In addition, we monitored the change in sponge cover between the years 2013 & 2015 in order to assess whether the Saba Bank is following trends in other Caribbean reefs and becoming a 'sponge reef'.

Sponge assemblages were studied in 2013 and 2015 in 220 photo-quadrats in 11 different transects using the programme CPCe. To aid the identification in the photographs, an identification database was made based the collection of 87 sponge specimens, in situ photographs, morphological analysis and DNA-barcoding. Sponge diversity was subsequently compared with data from previous studies in 1972, 1986, and 2006.

Comparing our data to previous expeditions and surveys, we found at least 22 new records of sponge species for the Saba Bank, totalling at least 100 sponge species for the Saba Bank. More species may be present, as species accumulation curves are not saturated. Sponge cover was equal to coral cover and did not change between the years 2013 and 2015, indicating that Saba Bank at present does not appear to be turning into a 'sponge reef'. There was, however, a high prevalence of bleaching in Xestospongia muta, almost all large individuals showed bleaching in both years. There appears to be strong connectivity along the bank as we did not find a significant structure of species turnover across our sample sites. The Saba Bank is a hotspot of biodiversity and an important reservoir of diversity for other coral reefs in the region.

Funding: The Netherlands Ministry of Economic Affairs, project BO-11-019.02-008

Validation of recirculating *ex situ* aquaria systems for studying deep-water sponges: do individuals kept under *ex situ* conditions reflect physiological *in situ* performances?

Erik Wurz[1], Raymond Bannister[2], Hans Tore Rapp[3] & Ronald Osinga[1]

[1] *Wageningen University and Research, Marine Animal Ecology, De Elst 1, Wageningen, The Netherlands; contact: erik.wurz@wur.nl*

[2] *Institute of Marine Research, PO Box 1870, 5817 Bergen, Norway*

[3] *Department of Biology, University of Bergen, PO Box 7803, N-5020 Bergen, Norway*

Deep-sea sponge grounds in the North Atlantic recently came to the focus of the scientific community. These highly abundant sponges may be key players for benthic- pelagic-coupling processes. The physiological response of cold-water sponges to ongoing large scale environmental changes remains unstudied. Long-term *ex situ* incubation experiments have proven to be a tool to assess the metabolic response of marine invertebrates under actively manipulated seawater conditions. For the first time, physiological performances (respiration-, clearance-, and pumping rates) of the boreal Demosponge *Geodia barretti* (Bowerbank, 1858) will be examined in recirculating and flow-through aquaria systems. *Ex situ* performances will be compared to performances assessed under *in situ* conditions, to test the hypothesis that cultivated sponges held under different laboratory conditions will show comparable physiological performances. This allows an evaluation of eco-physiological *ex situ* responses to changing seawater properties and to implement these results in a broader ecological context.

SponGES has received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No. 679849.

The mariculture potential of the Philippine blue sponge *Xestospongia* sp. for the production of renieramycin

Clairecynth Yu[2], Geminne Manzano[1], Viviene Santiago[2], Lilibeth Salvador-Reyes[2] & Porfirio Aliño[1]

[1] *Community Ecology Laboratory, The Marine Science Institute, University of the Philippines, Diliman, Quezon City, Philippines 1101. geminnemanzano@msi.upd.edu.ph*

[2] *Marine Pharmacognosy Laboratory, Marine Science Institute, University of the Philippines, Diliman, Quezon City, Philippines 1101*

In the past two decades, several bioactive compounds have been isolated from Philippine marine organisms. This includes the renieramycin which have been reported to be cytotoxic to a variety of cancer cell lines. However, one of the obstacles faced in studying the bioactive compound is the limitation of the amount of the starting material and of the compound obtained from them. To address this problem, the mariculture potential of the Philippine blue sponge, *Xestospongia* sp. for supply of renieramycin was assessed through the pilot sponge culture in the open-sea at two different locations in the Philippines – in Puerto Galera, Oriental Mindoro (13.508404 N, 120.958230 E) and in Bolinao, Pangasinan (16.43958 N, 119.94475 E). The in situ culture site in Puerto Galera was located adjacent from where the donor sponges were collected and was characterized as a sheltered area with low exposure to wave action. Meanwhile the translocation site located in Bolinao was characterized by a high exposure to wave action. A total of 73 sponge explants were fragmented from sixteen different sponge donor colonies and were grown using the two farming methods employed in this study. Explants were assigned to different harvesting regimes and starting culture period to investigate the seasonality growth of the sponges as well as the effect of multiple harvesting in their growth rate. Environmental parameters such as the temperature and water quality were also recorded. Results showed that while the frequency of partial harvesting does not affect the growth of the explants, the season has significant effect in the growth rate of the sponges in Puerto Galera ($p<0.05$). Months between May and September recorded the highest specific growth rate (SGR) and the highest survival rate in Puerto Galera sponge explants. The said months recorded the highest water temperature as well. Meanwhile, there is no significant difference between the growth of the explants in Bolinao and Puerto Galera. High Performance Liquid Chromatography (HPLC) results confirmed the presence of renieramycin M on the sponges harvested from both the culture setup locations in Puerto Galera and Bolinao. Moreover, the extracts from these sponges were shown to be bioactive against the HCT116 (colon cancer cell lines).

This research study is part of the Discovery and Development of Health Products (DDHP-Marine) funded by the Department of Science and Technology – Philippine Council for Health Research and Development (DOST-PCHRD).

Posters Molecular, Cell and Organismal Biology

Gene expression dynamics accompanying the sponge thermal stress response

Christine Guzman & Cecilia Conaco

Marine Science Institute, University of the Philippines, Diliman, Quezon City 1101 Philippines cconaco@msi.upd.edu.ph

Marine sponges are important members of coral reef ecosystems. Thus, their responses to changes in ocean chemistry and environmental conditions, particularly to higher seawater temperatures, will have potential impacts on the future of these reefs. To better understand the sponge thermal stress response, we investigated gene expression dynamics in the shallow water sponge, *Haliclona tubifera* (order Haplosclerida, class Demospongiae), subjected to elevated temperature. Using high-throughput transcriptome sequencing, we show that these conditions result in the activation of various processes that interact to maintain cellular homeostasis. Short-term thermal stress resulted in the induction of heat shock proteins, antioxidants, and genes involved in signal transduction and innate immunity pathways. Prolonged exposure to thermal stress affected the expression of genes involved in cellular damage repair, apoptosis, signaling and transcription. Interestingly, exposure to sublethal temperatures may improve the ability of the sponge to mitigate cellular damage under more extreme stress conditions. These insights into the potential mechanisms of adaptation and resilience of sponges contribute to a better understanding of sponge conservation status and the prediction of ecosystem trajectories under future climate conditions.

References

1. Guzman C and Conaco C. 2016. Gene expression dynamics accompanying the sponge thermal stress response. PLoS ONE. 11(10): e0165368

Financial support by the University of the Philippines System PhD Recruitment Grant (OVPAA-BPhD-2012-04) and L'Oreal-UNESCO For Women in Science National Fellowship is gratefully acknowledged.

Cellular Model of Sponge-Sponge Associations

Megan Conkling[1] & Shirley A. Pomponi[1]

[1]Florida Atlantic University, Harbor Branch Oceanographic Institute, Fort Pierce, Florida, USA. mconkli2@fau.edu

An *in vitro* model using high content imaging and protein microarrays was established to investigate sponge-sponge interactions at the cellular level. This study focused on *Amphimedon erina* and *Geodia* "*gibberosa*", a common epibiont-basibiont sponge association in Florida and the Caribbean. Primary cell cultures and co-cultures were established for each species. *Amphimedon compressa* and *Geodia neptuni*, which do not form such associations with other sponges, were used as controls. Cultures were stained with fluorescent markers and molecular probes and monitored using high content imaging to measure cellular responses related to cell cycling. Time-lapse imaging was conducted over a period of 24 hours. A protein expression microarray for apoptosis was used to validate the *in vitro* model and high content imaging results. Cellular responses of co-cultured cells of species that form sponge-sponge associations in nature differ from responses of co-cultured cells of species that do not form sponge-sponge associations. Protein expression data validate the *in vitro* model, specifically for apoptosis and cell proliferation. The *in vitro* model may not be appropriate to test hypotheses related to cellular interactions in natural sponge-sponge associations, but it is a meaningful platform to investigate cell-cell interactions between species and between individuals of the same species. The data revealed unexpected and potentially significant results related to DNA damage and repair that could lead to the establishment of a sponge cell line.

Transcriptomic reconstruction in *Spongia officinalis:* adjusting post- sequencing analyses to distinguish between host and prokaryotic symbionts

Tereza Manousaki[1], Jacques Lagnel[1], Vasiliki Koutsouveli[1, 2], Spyros Kollias[3], Costas Tsigenopoulos[1], Christos Arvanitidis[1], Costas Dounas[1], Antonios Magoulas[1] & Thanos Dailianis[1]

[1] Institute of Marine Biology, Biotechnology & Aquaculture, Hellenic Centre for Marine Research, Heraklion Crete, Greece. thanosd@hcmr.gr

[2] Life Sciences Department, Natural History Museum of London

[3] Norwegian Sequencing Centre, Centre for Ecological and Evolutionary Synthesis, University of Oslo, Norway

Transcriptome assembly, facilitated through next generation sequencing, emerges as an important requirement for consequent ecological studies. For non-model organisms, a *de novo* assembly approach is required due to the absence of a reference genome. However, since sponges commonly host complex communities of symbiotic prokaryotes, this type of analysis is challenging due to the presence of bacterial transcriptomes which might potentially interfere to the biological interpretation of the results introducing biases. Herein, we report for the first time a transcriptome acquisition for the common Mediterranean bath sponge *Spongia officinalis.* To this end, a new pipeline was developed that efficiently separates between bacterial expressed genes from those of eukaryotic origin, overcoming this challenge.

The pipeline involves standard read pre-processing steps and incorporates extra analyses to identify and filter prokaryotic reads out of the analysis. Following multiple quality control filters, the surviving reads were scanned for non-sponge sequences. First, we mapped the reads against the bacterial sequences of the NCBI RefSeq database with the tool ribopicker (ribopicker-standalone-0.4.3 version). Then, the unmapped reads were used for the transcriptome reconstruction. The resulted transcriptome assembly was annotated with standard annotation pipelines (BLAST2GO) and the resulted annotation was used to notify further on the contamination. As a final filtering step, the top blast hits of each contig were scanned and the taxon identity of the corresponding organisms were retrieved. Contigs with top hits taxon identities that matched bacterial sequences were eliminated to end up with a high-quality, prokaryote-free assembly.

The developed pipeline provides a roadmap for dealing with the technical RNASeq problems originating from contamination of symbionts – a non-trivial problem when dealing with sponge data. This work attempts to set the standards for subsequent transcriptome analyses in complex holobionts and produces baseline information to be used towards the effective assessment of gene expression in an economically and ecologically important sponge. Studies towards the latter can be especially valuable in face of current and anticipated stressors to the coastal marine habitat related to human activities and the ongoing climate change.

This work has been financially supported by the LifeWatchGreeceResearch Infrastructure (MIS 384676) and the Action «Proposals for Development of Research Bodies-KRIPIS», both funded by the Greek Government under the General Secretariat of Research and Technology (GSRT) and the National Strategic Reference Framework (NSRF).

A molecular study of the tissue regeneration in the Demospongiae: the role of the TGF/BMP protein family

Lorenzo Gallus[1], Marina Pozzolini[1], Sara Ferrando[1], Marco Giovine[1], Cristina Gagliani[2], Giorgio Bavestrello[1], Marco Bertolino[1] & Sonia Scarfi[1]

[1]Department of Earth, Environment and Life Sciences, University of Genova, Genova, Italy

[2]Department of Experimental Medicine, University of Genova, Genova, Italy

Sponges are amongst the most successful organisms on Earth. This is also due to their rapid regeneration capacity allowing the recovery from damage caused by predation as well as environmental stress. Until now, only some morphological and cellular data are available on the fragmentation/regeneration process in the Demospongiae [1], thus we decided to approach this important topic from a molecular point of view. One of the main mediators of tissue regeneration in higher organisms is the TGF-beta protein family. Thanks to the transcriptome, previously obtained in our lab, of the demosponge *C. reniformis*, and through various bioinformatics approaches, the sequences of several members of this family of proteins could be identified in this organism: a Gdf-like, a nodal-like, Bmp2, Bmp3, Bmp4 e Bmp7, besides the two subunits of the typical TGF receptor, the TGFR1 and TGFR2. Furthermore, two genes considered markers of staminality in other sponges were also identified, PIWI and Musashi, to shed some light on the possible differentiation processes taking place immediately after the sponge fragmentation. The expression profile of these genes was then analysed in quantitative PCR in fragmorphs withdrawn at various times from fragmentation (0, 3, 9, 24, 48 and 72 h). The analysis showed that most genes were significantly upregulated at 9 h (BMP2, BMP4, BMP7, GDF-like and TGFR1 and 2) from the cut. Contrariwise, for what concerns the staminality genes PIWI and Musashi they were both significantly downregulated from 24 h on, probably indicating the initiation of a differentiation process. We can conclude that, beside identifying the family of TGF-beta proteins in *C. reniformis*, we found that some of them are probably involved in the tissue regeneration process following the fragmentation. Further studies with the use of specific inhibitors are needed to confirm their role in this process.

Research supported by EU(FP7 grant agreement n: 266033 SPonge Enzyme End Cell for Innovative AppLication-SPECIAL)

References

1. Alexander BE, Achlatis M, Osinga R, van der Geest HG, Cleutjens JP, Schutte B, and de Goeij JM. PeerJ (2015), 3:e820

Histological and Ultrastructural Features of *Aplysina cauliformis* Infected with *Aplysina* Red Band Syndrome

Deborah Gochfeld[1], Maria Cristina Diaz[2, 3], Abigail Renegar[2] & Julie Olson[4]

1 National Center for Natural Products Research, University of Mississippi, Oxford, MS, USA
gochfeld@olemiss.edu
2 National Coral Reef Institute, Nova Southeastern University, Dania, FL, USA
3 Harbor Branch Oceanographic Institute-Florida Atlantic University, Fort Pierce, FL, USA
4 Department of Biological Sciences, University of Alabama, Tuscaloosa, AL, USA

Aplysina Red Band Syndrome is one of the most well characterized diseases affecting Caribbean sponges. ARBS affects sponges of the genus *Aplysina,* particularly *A. cauliformis,* one of the most widespread species across the Caribbean basin. Field characteristics of ARBS include a red band that progresses from an initial circular lesion in both directions along the branch of the sponge, leaving behind necrotic tissue. The red band is dominated by the filamentous cyanobacterium *Leptolyngbya* sp., which is responsible for the red coloration, although its role in the etiology of ARBS remains elusive. In the present study, we used a combination of histology and transmission electron microscopy to characterize the ultrastructural and cellular features associated with ARBS- affected sponges. Tissue adjacent to the lesion was compared to unaffected tissue on the same sponges and to healthy sponges. Damage to the structural integrity, overall cell density and cellular composition of the ectosome and choanosome adjacent to the lesion was observed. Whereas healthy tissue showed distinct cellular arrangement, this was disrupted near the ARBS lesion. Disintegration of choanocyte chambers was also observed. Archaeocytes and collenocytes were found in greater abundance in tissue adjacent to the lesion. Archaeocytes associated with diseased tissue appeared to be more active, as indicated by increased numbers and lengths of pseudopodia, and by a higher density of engulfed bacteria and symbiotic cyanobacteria, some of which were in various stages of disintegration. This latter observation supports previous work that found reduced densities of cyanobacterial symbionts in ARBS-affected sponges. *Leptolyngbya* sp. filaments tend to be associated only with the lesion itself, and were rarely observed penetrating into the adjacent tissue. These descriptions of anatomical and cellular responses to ARBS in *A. cauliformis* add to our understanding of the impacts of this widespread disease.

Financial support by the National Science Foundation is gratefully acknowledged.

Origin of animal cell homeostasis : new insights from a digestive cycle of carnivorous sponge *Lycopodina hypogea.*

Nelly Godefroy[1], Camille Martinand-Mari[1], Khalid Belkrir[1], Emilie Le Goff[1], Abdel Aouacharia[1], Jean Vacelet[2], Nicolas Galtier[1] & Stephen Baghdiguian[1]

[1] Institut des Sciences de l'Evolution (UM, CNRS UMR 5554), Université de Montpellier, France nelly.godefroy@umontpellier.fr

[2] Institut méditerranéen de biodiversité et d'écologie marine et continentale, Université Aix-Marseille, France

Lycopodina hypogea is a demosponge that belong to the deep sea family of Cladorhizidae. The interest in cladorhizidae has rapidly grown during the past twenty years since a unique feeding strategy, the carnivory, was described in *Lycopodina* (1, 2). Interestingly, carnivorous sponges gave up the classical filtering strategy to become exclusively carnivorous. They are totally devoid of both the choanocytes and the aquiferous system, which were considered to be diagnostic for sponges, and they are able to catch and to digest macroscopic living preys like artemia without any digestive cavity or specialized organ, which is a unique case in metazoans. Interestingly, all carnivorous sponges have evolved toward the same shape: erect morphology with axial polarity that is not classical for sponges. Then the shape seems to have played a important role in the acquisition of the carnivory. During the various stages of its nutrition cycle, *Lycopodina* is subjected to alternate cycles of retraction/extension of filaments (3). In a first study, we showed that programmed cell death and proliferation are involved in these spectacular morphological modifications induce by nutrition (4). Here, we extend this study at the molecular level in order to understand how complex are these mechanisms regulating tissue homeostasis. Since the shape is regulated either by mechanical constraints or by a fine regulation of the size and the localization of the cell populations, we extend our study on stem cells markers and proteins implicated in cell cycle control, cytoskeleton regulation, adhesion/migration, phagocytosis, autophagy and apoptosis. In this purpose, we did a transcriptomic study on two months unfed animals and on animals collected 15h, 40h or 216h after nutrition with artemia. Results show that: (i) the molecular networks that ensure cellular and morphogenetic homeostasis in *Lycopodina* possesses a molecular complexity comparable to that present in main modern Eumetozoans (excepted for intermediate filaments and associated junctions that were not found and extrinsic pathway of apoptosis that is minimal in *Lycopodina*); (ii) an important transcriptional regulation of all tested mechanisms is observed after nutrition. Most of regulated genes becoming to their initial level 9 days after nutrition. This study confirms that *Lycopodina* represents a unique opportunity to analyze the molecular and cellular homeostasis that control the shape homeostasis at the root of metazoans.

References

1. Vacelet, J., & N. Boury-Esnault. 1995. *Nature* 373 (6512): 333-35.
2. Vacelet, J, & N Boury-Esnault. 1996. *Med K Belg Inst Nat Wet.* 66(Suppl.): 109-15.
3. Vacelet, J, & E Duport. 2004. *Zoomorphology* 123: 179-90.
4. Martinand-Mari, Camille, Jean Vacelet, Michael Nickel, Gert Wörheide, Paul Mangeat, & Stephen Baghdiguian. 2012. *The Journal of Experimental Biology* 215 (Pt 22): 3937-43.

Financial support by CNRS and Univertsité de Montpellier is gratefully acknowledged.

Towards an insight into the metazoan gene regulation and development: genome draft of the endemic freshwater sponge *Eunapius subterraneus*

Helena Ćetković[1], Mirna Halasz[1], Maja Fabijanić[2], Bruna Pleše[1], Helena Bilandžija[1] & Kristian Vlahoviček[2]

[1] Division of Molecular Biology, Ruđer Bošković Institute, Bijenička cesta 54, 10000 Zagreb, Croatia

[2] Bioinformatics Group, Department of Molecular Biology, Faculty of Science, University of Zagreb, Horvatovac 102a, 10000 Zagreb, Croatia

Large scale –omics projects have provided valuable data across the animal kingdom and have revealed remarkable complexity and diversity of animal genomes. Given the rapid advances in genomic data collection and bioinformatics analysis methods, unique opportunity opens up towards the elucidation of early metazoan gene regulation and development. With their pivotal evolutionary position of arguably the simplest extant and earliest branching metazoans, sponges are rapidly gaining focus in genomic research, however, more genomic information within the sponge phylum is required.

We sequenced the genome of the freshwater sponge *Eunapius subterraneus* using a combination of next-generation sequencing technologies (Illumina and Oxford Nanopore) and assembled a draft version of its genome. *Eunapius subterraneus* is the only stygobitic sponge species[1], an endemic member of the suborder Spongillina (freshwater sponges) known from merely six caves near Ogulin, Croatia[2]. This endemic sponge was shown to possess numerous unique morphological, molecular and ecological features[3]. Using the -omics methodologies in combination with experimental approaches, we aim to dive more deeply into the understanding of some of the basic processes involved in multicellular development and differentiation.

References

1. Sket, B. Velikonja, M.. Stygologia 2 (1986) 254–266.
2. Bilandžija, H. Bedek, J. Jalžić, B. Gottstein, S. Nat. Croat. 16 (2007) 1-17.
3. Harcet, M. Bilandžija, H. Bruvo-Madarić, B. Ćetković, H. Mol. Phylogenet. Evol. 54 (2010) (3), pp. 1021-1027.

Financial support by the Croatian National Science Foundation (Project No. 6400) is gratefully acknowledged.

High Tolerance Of Hypoxia By The Deep-Water Boreal Sponge *Geodia barretti*

Amanda S. Kahn[1], Raymond J. Bannister[2] & Sally P. Leys[1]

[1] Department of Biological Sciences, University of Alberta, Edmonton, Alberta, Canada. kahn@ualberta.ca

[2] Institute of Marine Research, Bergen, Norway.

Geodia barretti is a major habitat-forming species in the North Atlantic that is under threat of trawl fisheries and drilling activities. A suite of experimental studies were undertaken to understand the metabolism of this sponge-bacterial holobiont under normal and reduced oxygen levels, which might be expected to occur during increased suspended sediments caused by trawl or drilling activities[1, 2]. Under normal, oxygenated conditions *G. barretti* has a finely balanced carbon budget and operates in a slight nitrogen deficit, taking up dissolved organic carbon, bacterial carbon, nitrite, and ammonium while releasing nitrate[3]. We designed continuous flow-through respiration and deoxygenation chambers to study the effect of hypoxia on the carbon and nitrogen budget of *Geodia*. We measured sponge excurrent flow rates, metabolism (as oxygen consumption), and feeding under normal and hypoxic conditions. Sponges continued to pump water through their aquiferous system, though at a reduced rate, down to oxygen concentrations of 40 µM. Ammonium uptake did not change under hypoxic conditions, suggesting no increase in anammox or other anaerobic metabolic processes. At oxygen concentrations of 10-20 µM, *G. barretti* entered a reduced metabolic state in which water pumping had ceased but resumed quickly after release from hypoxic conditions. Sponges maintained below 20 µM oxygen for 48 hours were still able to resume pumping after return to normal oxygen levels, indicating tolerance to low oxygen conditions. While these sponges are typically found in well-oxygenated waters, *G. barretti*'s potential to tolerate hypoxia may become increasingly relevant as hypoxic zones become a threat to deep-sea benthic communities, especially if hypoxia changes the metabolism of the holobiont.

References

1. T. Kutti, R. J. Bannister, J.-H. Fosså, C. M. Krogness, I. Tjensvoll, G. Søvik, J. Mar. Biol. Ecol. 473 (2015) 64-72.
2. I. Tjensvoll, T. Kutti, J.-H. Fosså, R. J. Bannister, Aquat. Biol. 19 (2013) 65-73.
3. S. P. Leys, A. S. Kahn, J. K. H. Fang, J.-H. Fosså, T. Kutti, R. J. Bannister, Limnol. Oceanog. (under review).

Financial support from the Norwegian Research Council to RJB and NSERC Discovery Grant to SPL is gratefully acknowledged.

Inter-individual variability in the physiological state of *Geodia barretti*: differential expression and ultrastructural studies

Vasiliki Koutsouveli[1], Paco Cárdenas[2], Maria Conejero[3] & Ana Riesgo[1]

[1] Life Sciences Department, Natural History Museum of London V.Koutsouveli@nhm.ac.uk.

[2] Department of Medicinal Chemistry, Division of Pharmacognosy, BioMedical Center, Husargatan 3, Uppsala University, 751 23 Uppsala, Sweden

[3] Royal Botanic Gardens Kew, Richmond, Surrey TW9 3AE, United Kingdom

Geodia barretti is one of the dominant sponge species of the deep-sea sponge grounds in the boreal North Atlantic. The value of this species is not only of ecological significance but also of biotechnological importance. Secondary metabolites with antifouling activity have been previously identified from this species [1, 2] showing its further potential in natural products.

In this study, we combined RNA-seq and ultrastructural observations via Transmission Electron Microscopy (TEM) to understand inter-individual variability in the physiological state in *G. barretti* by identifying differentially expressed genes and cellular and histological features. Samples from three individuals of *G. barretti* were collected at 94 m from Kosterfjord in Sweden on the 4th of May 2016 and were preserved accordingly for each analysis. RNA-seq was conducted with NextSeq 500 illumina. Twenty million reads for the first, 30 million reads for the second and 6 million reads for the third individual were used for the *de novo* assembly. In total, 550 thousand transcripts were produced of which only 102 differentially expressed between the individuals 1 vs 2, while 3175 and 2667 million contigs were differentially expressed between the individuals 1 vs 3 and 2 vs 3 respectively.

In TEM, the mesohyl of *G. barretti* was characterized by a respectable amount of bacteria and large spherulous cells with inclusions (~20µm). The latter have been previously described in this species and are considered to possess nutritive-metabolic or storage functions and to be connected to growth and secretion processes [3]. In both analyses, inter-individual variability was detected. The third individual was found to contain larger quantities of shperulous cells and a lesser content of bacteria compared to the other two individuals. The future plan is to identify the chemical content of these spherulous cells in order to understand their role inside the life cycle of *G. barretti* and discover their biotechnological potential. We are going to include more specimens of the same species, collected at different periods and also compare with other boreo-arctic North Atlantic *Geodia* species (e.g. *Geodia antlantica*) collected from similar habitats.

References

1. M. Sjögren, U. Göransson, P. Johnson, M. Dahlström, R. Andersson, J. Bergman, P.R. Jonsson, L. Bohlin. *J. Nat. Prod. 67* (2004), pp 368–72.
2. L. Bohlin, U. Göransson, C. Alsmark, C. Wedén, A. Backlund 2010. Phytochem Rev. 9 (2010): 279-301.
3. F. Hoffmann, H. T. Rapp, T. Zöller, J. Reitner. *J. Biotechnol.* 100 (2003): 109-118.

Financial support by EU-SponGES H2020 project is gratefully acknowledged.

Reproductive features of Antarctic demosponges from the orders Dendroceratida, Poecilosclerida and Haplosclerida (Porifera)

Vasiliki Koutsouveli[1], Sergio Taboada[1], Juan Moles[2], Javier Cristobo[3], Conxita Avila[2], Andrea Bertran[2], Joan Solà[2] & Ana Riesgo[1]

[1] Department of Life Sciences (Invertebrate Division), The Natural History Museum of London, Cromwell Road, SW7 5BD, London, UK. V.koutsouveli@nhm.ac.uk

[2] Department of Evolutionary Biology, Ecology and Environmental Science, Faculty of Biology, University of Barcelona, Avda. Diagonal 643, 08028 Barcelona, Spain

[3] Instituto Español de Oceanografía, Avenida Príncipe de Asturias, 70 bis, 33212, Gijón, Spain

Sponges comprise a dominant element of the Antarctic benthic communities, posing both high species richness (more than 300) and large population densities [1, 2]. Despite that, reproduction events in Antarctic sponges have been rarely reported [3-5]. In our study, we surveyed the tissue of 6 species of the orders Dendroceratida (*Dendrilla antarctica*), Poecilosclerida (*Phorbas areolatus, Kirkpatrickia variolosa,* and *Isodyctia* *kerguelenensis*) and Haplosclerida (*Hemigellius pilosus* and *Haliclona penicillata*) for reproductive elements. Samples were collected by SCUBA diving on rocky outcrops at 15 m depth in Deception Island (62°59'31.20" S, 60°33'5.07" W, South Shetland Islands, Antarctica) during 2011 and 2013, and they were preserved and processed for light and transmission electron microscopy.

All species were found to contain only female reproductive elements and brooded their embryos within their mesohyl. In general, their reproductive features were similar to those in their counterparts of other latitudes [6], although several features were observed for the first time in some species, such as bifurcate follicle cells in *P. areolatus*, embryonic gigantism in *I. kerguelenensis* and spongin fibers within the embryos of *D. antarctica*. Our study contributes to the scarce knowledge of reproduction in benthic Antarctic invertebrates and provides the grounds for the study of their specific adaptations to the environment to understand their ecological and biological resilience.

References

1. M. Campos, B. Mothes, I.L.V Mendes, Revista Brazil. Zool., 24(2007) 687-708.
2. J.B. McClintock, C.D. Amsler, B.J. Baker, R. van Soest, Integr. & Compar. Biol., 45(2005) 359-368.
3. M. Burton, M. Further Zool. Res. Swedish Antarctic Exped. 1901-1903 3(1934) 3-54.
4. A. Sarà, C. Cerrano, M. Sarà. Polar Biol. 25(2002) 425-31.
5. A. Riesgo, S. Taboada, L. Sánchez-Vila, J. Solà, A. Bertran, C. Avila. PloS one. 10(2015) e0118805.
6. A.V. Ereskovsky. The comparative embryology of sponges. Springer Science & Business Media; (2010).

Funding by DISTANTCOM project (CTM2013-42667/ANT; Ministry of Economy and Competitiveness of Spain), and SDF14032 Departmental Internal Funds of the NHM is gratefully acknowledged.

External and internal anatomy of *Cladocroce caelum* (Haplosclerida, Demospongiae)

Jéssica da Hora & Emilio Lanna

Universidade Federal da Bahia, Instituto de Biologia, Salvador, Brazil.
[jessiedahora@gmail.com; emiliolanna@gmail.com]

Morphological characters are essential for the understanding of phylogenetic trees, being of pivotal importance those studies focusing on the anatomy of organisms. Most Demospongiae have choanocytes in contact with the mesohyl, while in the majority of the sponges of Haplosclerida, the choanocytes are separated from the mesohyl by pinacocytes. The haplosclerid *Cladocroce caelum* is found along all the Brazilian coast, but little is known about their biology. It is an abundant sponge at Salvador city coast and it has several associated organisms, being important for the maintenance of local biodiversity. In addition, to understand the anatomy of *C. caelum* can help to uncover gaps in the phylogeny of Haplosclerida and even Demospongiae. Thus, the objective of this work was to describe the organization and body structure of *Cladocroce caelum* aiming to understand whether the organization of the aquiferous system is similar to other studied Haplosclerida. Fragments of specimens were collected through skin dive at different localities in Salvador, NE, Brazil. The fragments were subjected to standard histological techniques and transmission and scanning electron microscopies. It was noted that *C. caelum* has, in general, repent or repent-branched habits. The species had an exopinacoderm composed of a monolayer of pinacocytes, which also delineates the inhalant and exhalant canals. The mesohyl is poorly developed and is formed by collagen fibrils, spongin fibers of the multiespicular tracts, and few cell types, such as archeocytes and collencytes. The choanocyte chambers occupy a large portion of the sponge tissue, forming a dense choanosome. The choanocyte chambers of *C. caelum* present an apopyle delimited by flattened apopylar cells, differently from others haplosclerids that usually have cone cells delimiting the apopyles. Analyzing the main cells and structures of *C. caelum* it can be observed that they agree with what has been observed in demosponges. However, the choanocyte chambers of *C. caelum* are not in agreement with the classifications proposed for others demosponges, existing the possibility that it has a different (new) pattern of organization of choanocyte chambers, besides presenting some peculiarities probably relevant for the phylogeny of Haplosclerida. The description of the external and internal morphology of *Cladocroce caelum* can contribute to a better knowledge of the evolution of Porifera.

Financial support by CNPq, FAPESB, PROPCI-PRODOC/UFBA are gratefully acknowledged.

Sexual reproduction of *Dysidea janiae*, a tropical Dictyoceratida in association with a calcareous alga

Bruno Cajado & Emilio Lanna

Universidade Federal da Bahia, Instituto de Biologia, Salvador, Brazil. emiliolanna@gmail.com

The dyctioceratid *Dysidea janiae* lives with the endozoic calcified red alga *Jania adhaerens* that supports its skeleton. It is one of the most abundant sponges at Todos os Santos Bay, Northeastern of Brazil, but basic aspects of its reproductive biology remains unknown. Therefore, we conducted a 2-year long study (June 2013 to September 2015) to describe the gametogenesis and embryogenesis of this species and to analyse the influence of algae thalli on reproduction. We collected ten samples per month and analysed them through histological methods. *Dysidea janiae* is viviparous and gonochoristic with a continuous but small reproductive effort, ratifying the pattern detected in others shallow-water tropical sponges. Spermatogenesis and oogenesis were asynchronous among individuals, with different cohorts co-occurring in both males and females. Spermatogonia maturation was also asynchronous at the spermatic cyst level, with three different stages occurring at the same time in the same cyst. Spermatic cysts [56.6 (±11.92) µm (mean±SE) in diameter] were typically ovoid, surrounded by a thin follicle of flattened cells and were larger than oocytes [43.8 (±14.45) µm]. A layer of nurse cells appeared at the beginning of oocytes maturation and remained until the embryonic stage. Initially the nurse cells formed a monolayer, but we observed an increase in the number of layers until the early-embryonic stage. At late-embryonic stage there was a decrease in the number of nurse cells layers and an increase on the size of the embryo [162.1 (±20.55) µm]. Cleavages were chaotic, generating cells with different sizes with no clear pattern of distribution. The cells of the embryo acquired the yolk granules from the nurse cells apparently by their transient pseudopodia. Embryonic development leaded to a parenchymella larva [181.7 (±17.09) µm], as well as in others Dictyoceratida. The mature parenchymella was solid and bullet-shaped with amoebocytes-like cells with evident nucleus internally; there were basophils and compact amoebocytes-like cells below the mono-stratified cylindrical-shaped epithelium. The asynchrony within the spermatic cyst is unusual in Demosponges, but their size and the female reproductive elements are similar to others Dictyoceratida. This alga-sponge symbiosis is apparently obligatory and it seems that there were a high specificity in the settlement of the larva, because the reproductive elements were not always near to the algae thalli, despite it occupied a large area at the sponge tissue. As no algae propagule are found within the larvae, the acquisition of the algae by the sponge is probably caused by a trial and error relationship of the larvae, surviving only those that find *J. adhaerens* after being spawned.

Financial support by PROPCI-PRODOC/UFBA, CNPq and FAPESB are gratefully acknowledged.

The Global Invertebrate Genomics Alliance: Keeping Pace with Evolution and Technology

Jose V. Lopez[1] & the GIGA Community of Scientists

[1] *Halmos College of Natural Sciences and Oceanography, Nova Southeastern University, Ft Lauderdale FL*

The Global Invertebrate Genomics Alliance (GIGA) supports genomics research on aquatic or non-model invertebrates. A 2015 GIGA workshop in Munich Germany focused on gathering international collaborators, highlighting current milestones, discussing bioinformatics resources, and delineating potential sources of funding. The Alliance continues to uphold an inclusive, grassroots "bottom up" approach, though more coordinated efforts may arise from significant influxes of funding, collaborations with large sequencing centers, enhanced technologies and the concomitant decreasing costs of DNA sequencing. GIGA coordination of research efforts may follow along taxonomic lines, pressing research questions, and the creation of new synergies. For example GIGA is now part of a large Earth BioGenome Project (EBP) to sequence all extant eukaryotic species. News items can be posted on the GIGA homepage - http://GIGA-cos.org. High throughput DNA sequencing technologies will likely boost the number of published whole invertebrate genomes, which is still far less than vertebrates, insects or model organisms. GIGA remains timely for several reasons: Invertebrate taxa are underrepresented in the current tally of whole genome projects, comprising no more than 30% of currently completed genomes. (There is currently only one published sponge genome). The marine realm holds representatives of all but two animal phyla, and many of these are not found in terrestrial or limnic ecosystems.

Sequencing and characterizing more invertebrate genomes provides a valuable and rich data resource for building better hypotheses. These can eventually lead to better understanding important physiological processes, insight into species resistance and resilience, and the expression of a wide variety of phenotypes – development of diverse body plans and morphology, regenerative capacities, longevity, bioluminescence, secondary metabolites and the evolution of immunity, symbiosis, vision and complex neural networks. The breadth of potential invertebrate targets for genome sequencing remains wide open for discovery. Prioritization and increasing urgency of genome projects may stem from threats to habitats (e.g. coral reefs) and the resident biological diversity. GIGA has agreements to host large sequence datasets with http://Compagen.org, and http://Reefgenomics.org, since easy accessibility are tantamount for successful comparative genomics approaches which provide context and meaning to the broad phylogenetic spectrum. New efforts should continually look to increase data sharing capacities, assist in sampling and taxonomic inventories, expanding international outreach to areas in S. America and Asia, and investing in extensive computational biology and bioinformatics training of young scientists and their ability to interpret sequence data.

Proteasome mechanism of adaptive plasticity of sea cold-water sponges

Yulia Lyupina[1], Andrey Lavrov[2], Pavel Erokhov[1], Svetlana Abaturova[1], Nikolay Gronostaev[1], Oksana Kravchuk[1], Victor Mikhailov[1] & Igor Kosevich[2]

[1] *Laboratory of biochemistry of ontogeny processes, N.K. Koltsov Institute of Developmental biology of Russian Academy of Sciences, Moscow, Russian Federation yulial@bk.ru*

[2]*Department of Invertebrate Zoology, Moscow State University, Moscow, Russian Federation*

The key role in the proteome homeostasis in eukaryotic cells plays the ubiquitin- proteasome system (UPS) which determines the adaptive plasticity of multicellular organisms. Marine invertebrates of intertidal zones, in particular, Sponges (Porifera) are the unique model for studying the molecular mechanisms of adaptation. The aim of this research is to clarify the role of the proteasome pathway in regulating cellular proteome under dissociation and reaggregation processes in the sea cold-water sponges *Halichondria panacea* and *Halisarca dujardini* (Demospongiae, Pallas, 1766). Proteasomes of marine cold-water Sponges have not previously explored. Sampling was carried out in the Kandalaksha Bay of the White Sea (66 ° 34 'N, 33 ° 08' E). It was first investigated the chymotrypsin-like (ChLA) and caspase–like (CLA) proteasome activities by the level of hydrolysis of fluorogenic oligopeptide Suc-LLVY-AMC and Z-LLG-AMC, respectively, and proteasome subunits in clarified homogenates of cells and tissues of sea cold-water sponges *Halichondria panacea* and *Halisarca dujardini*. The oligopeptide hydrolysis rate is determined at 10 C and 37C. The specificity of the reaction established in experiments with the proteasome inhibitor MG-132 and lactacystin. The increase of the temperature (from 10 to 37 ° C) resulted in an increase of ChL of *Halisarca dujardini* tissues by 3.5 times, and in *Halichondria panacea* by 2 times, while in the ChLA of *Halisarca dujardini* dissociated cells by 7 times higher than *Halichondria panacea* dissociated cells. Under dissociation of tissue in the sponge cells heat shock protein HSP70 content and proteasome subunit alpha type and beta 5 and proteasome ChL are reduced. We found that chaperone system is activated, as well as changes in the structure and activity of the proteasome occur in the cell reaggregation processes in the studied cold-water marine sponges. In the process of reaggregation the relative abundance of proteins HSP70 chaperones and proteasome subunit alpha type varies significantly only in the period of intensive transformations and / or differentiation / dedifferentiation of cells in aggregates. We first established that a feature of proteasome of marine cold-water sponges *Halichondria panacea* and *Halisarca dujardini* is low of 26S proteasome forms, which indicates that their proteasome system focuses primarily on hydrolysis of non-ubiquitinated proteins. We used the method of the modified native electrophoresis to study not only the proteasome fractions and changes in the proteasome activities in clarified homogenates, but also to identify changes in the electrophoretic mobility of the 20S proteasome. In the dissociated cells and tissues of sponges are not detected 26S proteasome. The dissociated sponge cells increases the electrophoretic mobility of 20S proteasome forms, indicating that structural changes in the 20S proteasomes. The obtained results allow us to consider the induction of chaperone HSP70 and changes in the structure of the 20S proteasome as key mechanisms for adaptation and for the development of protective responses in Sponges and, possibly, other marine cold-water invertebrates. For the first time we received the original information proteasome system of multicellular organisms in the early stages of evolution.

This work partly supported by RFBR grant 16-04-00454.

Optimization of Cryopreservation Methods for the Marine Sponge *Dysidea etheria*

Stephanie Munroe[1, 2], Dirk E. Martens[1], Detmer Sipkema[3] & Shirley A. Pomponi[2]

[1]*Wageningen University & Research, Bioprocess Engineering*

[2]*Harbor Branch Oceanographic Institute, Florida Atlantic University*

[3]*Wageningen University & Research, Microbiology*

Cryopreservation is commonly used method for the long-term storage of cell lines. Despite years of research, no cell lines have been created from marine invertebrates yet. Cryopreserved stocks of cells eliminate environmental changes, allow researchers to study species that are not geographically nearby, and will be useful to study cell biotechnology or bioactive compound production in the future. The marine sponge Dysidea etheria was chosen as our model organism to establish a cryopreservation method. By testing a range of concentrations of commonly used cryoprotectants, such as 3-10% DMSO and 10-50% glycerol, we determined the optimal cryoprotectant for D. etheria based on its ability to preserve cell viability and minimize cell loss during the cryopreservation process. Viability and total number of live cells were measured after an initial cell dissociation, after an incubation period in the cryoprotectants, and after cryopreservation for 24 hours. Cells cryopreserved in 8%-10% DMSO maintained a similar viability to that of freshly dissociated cells (approximately 75%-90% of viable cells). Cells cryopreserved in 3.75%-18.75% glycerol (final concentration) had much lower numbers of live cells, lower viabilities, and the cells were irregular in shape. During this study, we determined that 10% DMSO is the optimal cryoprotectant for D. etheria cells. This approach can be used to optimize cryoprotectants for cells of other marine invertebrate species.

Exploring Specialized Metabolites in the Deep-Sea Arctic Sponge *Geodia hentscheli*

Patryk Nilsson [1], Ulf Göransson[1], Paco Cardénas[1]

[1] *Department of Medicinal Chemistry, Division of Pharmacognosy, BioMedical Center, Husargatan 3, Uppsala University, 751 23 Uppsala, Sweden.. patryk.nilsson@gmail.com*

New marine natural compounds are necessary to replace toxic chemicals to the marine environment such as organotin, a heavy-metal based coating used to paint the hull of ships to keep them free from fouling. In this project the aim was to explore the compounds of the poorly known arctic sponge *Geodia hentscheli.* With extraction methods, HPLC-UV and LC-MS/MS the results showed that the sponge had many different compounds, many hydrophilic compounds that need alternative separations methods, for example HILIC columns. The chromatographic profile showed that there is no obvious major compound(s), which indicates that further exploration needs to be done. A bioassay on barnacle larvae suggested that one or more compounds have antifouling activity; this activity was strongest in the less hydrophilic fractions. A crude isolation of *m/z* 940 indicates that this compound could be the one with antifouling activity by itself or in synergy with other compounds.

References

[1] Hedner, E., Sjogren, M., Hodzic, S., Andersson, R., Göransson, U., Jonsson, P,R., Bohlin, R. Antifouling Activity of a Dibrominated Cyclopeptide from the Marine Sponge *Geodia barretti*. J Nat Prod. 2008;71;330-333.

Financial support from the EU Horizon 2020 programme SponGES under grant agreement No. 679849.

Recombinant Production of Hydroxylated Collagen Polypeptides derived from the Demospongia *C. reniformis*: A new Biotechnological Source of Marine Collagen

Marina Pozzolini[1], Sonia Scarfì[1], Annalisa Salis[2], Gianluca Damonte[2] & Marco Giovine[1]

[1]*Department of Earth, Environment and Life Sciences, University of Genova, Genova, Italy*

[2]*Centre of Excellence for Biomedical Research, University of Genova, Genova, Italy*

Collagen from marine sources is a very attractive alternative to bovine collagen. In biomedicine, several applications of collagens derived from sponges have been described, many of which from the demospongia *Chondrosia reniformis*. The production of these molecules in recombinant form would allow to obtain well-defined molecular types and to limit the expensive procedures of sample recovery and purification. Here we report the realization of a yeast strain able to produce hydroxylated collagen polypeptides derived from *C. reniformis*.

First the cDNAs coding for the a and b subunits of the sponge enzyme prolyl-4-hydroxylase (P4H) were identified by PCR approach, then they were cloned in pPink and in pPIC6a vectors respectively and finally they were stably integrated in the genome of the methanotrophic yeast *Pichia pastoris*. The strain with the highest P4H activity was then transformed with a third expression vector (pPICZ) containing the coding region of a sponge collagen polypeptide in frame with an Histidine-TAG at the 3'-end. Recombinant protein expression was then induced and collagen polypeptides were purified by affinity chromatography and analysed by SDS-PAGE followed by Mass Spectrometry, in order to confirm the sequence and the presence of hydroxy-proline residues. The biocompatibility of the recombinant proteins was evaluated by MTT test in human neonatal fibroblasts and furthermore, tissue culture plates were treated with 10 mg/ml recombinant protein solution to test its cell adhesion properties. In conclusion, a first recombinant hydroxylated marine collagen polypeptide was produced in the Pichia system, resulting biocompatible and suggesting its use as porcine gelatin substitute for cell culture.

Research supported by EU (FP7 grant agreement n: 266033 SPonge Enzyme End Cell for Innovative AppLication-SPECIAL)

Recycling is the key: multi-analysis of incorporated silica from digested diatom frustules in Antarctic sponges

Ana Riesgo[1], Sergio Taboada[1], Nadia Santodomingo[1], Nathan J. Kenny[1], Juan Moles[2], Vasiliki Koutsouveli[1], Eileen Cox[1], Manuel Maldonado[3], Conxita Avila[2], Luis Cardona[2]

[1] Department of Life Sciences (Invertebrate Division), The Natural History Museum of London, Cromwell Road, SW7 5BD, London, UK. A.Riesgo@nhm.ac.uk

[2] Department of Evolutionary Biology, Ecology and Environmental Science, Faculty of Biology, University of Barcelona. Avda. Diagonal 643, 08028 Barcelona, Spain

[3] Department of Marine Ecology, Center of Advanced Studies of Blanes, CSIC, Accés a la cala St. Francesc 14, 17300, Blanes, Spain

Sponges and diatoms rely on biogenic silica to build their internal and external skeletons, respectively. However, the mechanisms by which they construct them are remarkably different. While diatoms polymerize their silica within intracellular silicic acid deposition vesicles [1], sponges are able to do this both intracellular and extracellularly [2, 3]. Biogenic silica present in sponge spicules is usually considered to derive from seawater uptake and posterior polycondensation using enzymes called silicateins. Interestingly, sponges can feed upon a wide variety of microorganisms, including diatoms from the phytoplankton. In the Southern Ocean, the rate of diatom uptake in sponges has been shown to be higher than in other latitudes, mainly due to their exceptional abundance in the seawater. Whether sponges can actually recycle the silica contained in the digested diatom frustules currently remains untested. We collected 5 demosponge species (*Mycale acerata, Isodictya kerguelensis, Phorbas areolatus, Hemigellius pilosus* and *Haliclona penicillata*) from Deception Island (Antarctica) and fixed their tissues for TEM, SEM and electron probe microanalysis (EPMA), as well as silicon isotope analysis, alongside seawater and diatom samples.

Our results show multiple indications of demosponge silica uptake from the digested frustules of diatoms. First, within the mesohyl of the demosponges we observed many diatoms, some of them being intracellularly digested by archaeocyte-like cells. Second, we detected many vesicles in archaeocyte-like cells containing silica (analyzed by TEM and EPMA) that were not spicule-forming sclerocytes. Third, our SEM observations showed evidence of digestion also in the diatom frustules obtained from sponge tissues, also observed in their counterparts from tropical latitudes. And fourth, our silicon isotopic analysis showed that spicules are more depleted in ^{30}S than diatoms frustules, which in turn are more depleted than seawater. This is consistent with a two-step absorption process, i.e., from seawater to diatoms and from diatom frustules to sponges, although it is also observed in other sponges with little or none diatom feeding. Our results open a new avenue to explore silica deposition in sponges, and suggest a new method of biogenic silica uptake, at least in environments with high abundance of diatoms, such as Antarctica.

References

1. M. Hildebrand, R. Wetherbee. In: Progress in Molecular and subcellular biology 33 (2003) 11-57.
2. M.J. Uriz, X. Turon, M. Becerro. In: Progress in Molecular and subcellular biology 33 (2003) 163-193.

3. M. Maldonado, A. Riesgo. Cell Tiss Res. 328(2007) 639-50.

Funding by DISTANTCOM project (CTM2013-42667/ANT; Ministry of Economy and Competitiveness of Spain), and SDF14032 Departmental Internal Funds of the NHM are gratefully acknowledged.

Bibliometric Analysis Elucidates Historical Trends of Molecular, Cellular, and Genetics Research in Poriferan Taxa

Jeffrey Robinson

National Institutes of Health. Bethesda MD, 20892. USA. jeff.robinson.evol@gmail.com

The Porifera have served as model organisms for molecular and cellular research throughout the 20th century, yet the use of Porifera models for specific research questions has varied depending on research question and the state of technology. During the mid-1900's for example, sponge taxa enjoyed a spotlight in studies on cell-cell recognition and adhesion, and other topics of cellular biochemistry including cellular differentiation. Increased availability and research focus of mammalian cell culture and other model systems resulted in Porifera having less general relevance as a model system for cellular studies. In the genomics era, affordable and efficient application of genomics and transcriptomics allowed the Porifera experienced a resurgence. Porifera have become particularly important for research on the origin and evolution of key developmental genes and developmental regulatory pathways relevant to the early evolution of Metazoan bodyplans, related to their key position in the tree of life. Molecular data has also resulted in significant reorganization (and controversy) in Porifera taxonomy and systematics. In order to better understand the historical patterns of the use of Poriferan taxa in molecular and cellular research, I took a bibliometrics analysis approach. Using the Web of Science™ database, I queried to obtain a comprehensive list of publications of molecular and cellular research which used Poriferan taxa as a research subject. Text categorization, topic analysis, and bibliographic coupling were then performed using the Science of Science (Sci2) Tool[1]. Historical trends molecular and cellular research topics were examined and graphed, clustering analysis was performed to show patterns of use of specific Poriferan taxa, and citation networks were visualized in 'bubble graph' format using Gephi[2] network visualization software. Results provide a broad overview of research trends in the use of Porifera for molecular, cellular, and genetics research.

References

1. Sci2 Team. (2009). Science of Science (Sci2) Tool. Indiana University and SciTech Strategies, https://sci2.cns.iu.edu.
2. Bastian M., Heymann S., Jacomy M. (2009). Gephi: an open source software for exploring and manipulating networks. International AAAI Conference on Weblogs and Social Media.

A cost-efficient method of DNA barcoding of sponge communities with Illumina MiSeq Next Generation Sequencing

Tim A. Schol[1] and Leontine E. Becking[1,2,3]

[1] Marine Animal Ecology, Wageningen University & Research, The Netherlands, tim.schol@wur.nl

[2] Department of Environmental Science, Policy, and Management, University of California, Berkeley, CA, USA

[3] Naturalis Biodiversity Center, Leiden, the Netherlands

Until recently most molecular biodiversity assays with sponges have been conducted using traditional per sample Sanger sequencing. The method is straightforward, though the costs remain high and Sanger sequencing does not allow sequencing of multiple intra- specific variants within a sample, such as with ITS. We tested the advantages of using a more cost reducing Next Generation Sequencing (NGS) approach of Shokralla et al. (2015) and Lange et al. (2014) towards amplicon sequencing and revealing sponge biodiversity within different environments using the Illumina MiSeq V3 sequencing platform. As a test set we sequenced sponge communities from coral reefs, mangroves and marine lakes from Kalimantan and Papua, Indonesia. The aim is to assess the phylogenetic relatedness among these communities and to elucidate the evolutionary history of the putative endemic species in the marine lakes. We designed primers to obtain products of ± 400 bp. We sequenced 800 specimens for two markers (COI & 28S), totaling 1600 samples and at least 10000 reads per sample. Taxonomic assignment was performed by blasting acquired reads against the NCBI non-redundant database. Often sequence reads proved to be of a non-sponge origin, possibly resulting from within sponge sample contamination. Preliminary results of genetic variation demonstrate that sponges from marine lakes are genetically more closely related to sponges from mangrove forests than those of coral reefs. Phylogenetic analyses suggest recent divergences of lake-specific species providing possible indications of radiations within Indonesian marine lakes. While our study applied NGS to generate COI and 28S barcodes for sponges, our method can also be implemented with other markers and phyla. Likewise, although our workflow was aimed towards building a DNA barcode database by multiplexing individual specimens, sequencing of environmental bulk samples is also applicable with the presented workflow.

References

1. S. Shokralla, T. M. Porter, J. F. Gibson, R. Dobosz, D. H. Janzen, W. Hallwachs, G. B. Golding, M. Hadjibabaei, Sci. Rep. 5 (2015) 9687.
2. V. Lange, I. Böhme, J. Hofmann, K. Lang, J. Sauter, B. Schöne, P. Paul, V. Albrecht, J. M. Andreas, D. M. Baier, J. Nething, U. Ehninger, A. H. Schmidt, BMC Genom. 15 (2014) 63.

Financial support by The Netherlands Organisation of Scientific Research ALW-VENI # 863.14.020 is gratefully acknowledged.

Influence of temperature on reproduction of temperate *Tethya* spp.

Megan R. Shaffer, Simon K. Davy, James J. Bell

School of Biological Sciences, Victoria University of Wellington, PO Box 600, Wellington, New Zealand
Megan.Shaffer@vuw.ac.nz

Sponges exhibit a variety of patterns of reproduction. With a lack of consistency in reproductive timing across the phylum (i.e. some reproduce continuously, others seasonally), it is often difficult to distinguish common drivers of reproduction for sponges. Trends in the literature indicate that temperature may influence reproduction, which has future implications for sponge population growth and connectivity under predicted warming oceans. Here, we sought to describe the previously unknown reproductive biology of *Tethya* spp. on the South Coast of Wellington, New Zealand in relation to water temperature. Twenty sponges were collected monthly from two locations over the course of two years (February 2015-2017) and processed for histological analyses. In addition, the occurrence of asexual buds was recorded. The observed oocytes and the lack of hermaphroditic sponges (e.g. tissue containing both male and female gametes) supported previous evidence that *Tethya* are oviparous and gonochoristic reproducers. In both locations, oocytes were only present in the tissue of sponges collected in summer months, from December to February, when water temperature reached 14°C and above (as recorded from temperature loggers). Buds were found on sponges during every month of collection. These results suggest *Tethya* spp. in New Zealand have only one seasonal sexual reproductive event each year, potentially coinciding with warmer water temperatures. In addition, they exhibit continuous asexual reproduction with seemingly no relation to temperature. The reproductive activity of *Tethya* spp. may potentially be altered with future thermal stress from climate change, which could have consequences on the genetic construct and overall fitness of the population.

Barcode first, identify later? Testing the use of a reverse taxonomic approach to assess the demosponge community composition in an Arctic seamount

Tone Ulvatn[1], Hans Tore Rapp[1], Joana R Xavier[1]

[1] Department of Biology and K.G. Jebsen Centre for Deep-Sea Research, University of Bergen, PO Box 7803, N-5020 Bergen, Norway. Tone.Ulvatn@student.uib.no

Often, the amount of samples and the pace at which they are collected largely surpasses our capacity to process, let alone identify, them. This is particularly so for groups that require substantial taxonomic effort and expertise, such as sponges. Recently, a reverse taxonomic approach (sequence first, identify later) has been proposed as a cost-effective method that enables assessment of diversity and biogeographic patterns without *a priori* knowledge of the community under study.

The aim of this project was to test the use of such an approach in the assessment of the demosponge community composition of different sections (summit, slope and deep basin) of an Arctic seamount - the Schultz massif. Its benthic habitats have been investigated in recent years showing several sponge-dominated communities differing in density and species composition. These communities have been partly studied from a morphological point of view, however a large number of collected specimens remained to be identified and morphologically cryptic and/or new species were expected to be found. We have therefore produced COI barcodes for as yet unidentified collected demosponges and assigned them to molecular operational taxonomic units (MOTUs). Sequences publicly available on GenBank and on the Sponge Barcoding Project database were used as a phylogenetic backbone to assign our sequences to higher taxonomic levels (clades); and previously identified specimens collected from nearby areas were sequenced and used as "regional anchors". A subset of the samples within each MOTU was also examined by traditional taxonomic methods to ascertain the validity of our molecular assignments. Here we present the obtained results and discuss the promises and pitfalls of this reverse approach in terms of the accuracy and sensitivity as well as overall resources required (time, money and technical-scientific expertise) for its implementation.

Financial support: this study is part of the SponGES project funded by the European Union's Horizon 2020 research and innovation programme (grant agreement 679849).

Spermatogenesis of the poecilosclerid *Tedania ignis* (Porifera, demospongiae)

Vivian Vasconcellos & Emilio Lanna

Universidade Federal da Bahia, Instituto de Biologia, Salvador, Brazil. vivianvasconcellos@gmail.com

In Poecilosclerida (Demospongiae), the sperm cells differentiate from choanocytes, except for carnivorous sponges, in which sperm cells are originated from archeocytes. Within this group, the spermatogenesis is carried out within the spermatic cysts, a structure that envelops, with follicle cells, the spermatic cells. In general, Poecilosclerida species have primitive spermatozoa, with a comparatively large cytoplasm volume and several small michondria. However, a study with *Crambe crambe* showed that this species has a very peculiar spermatogenesis resulting in a V-shaped spermatozoon. This finding implies in the reproductive and evolutionary aspects in Porifera and shows the necessity to study other species of Poecilosclerida, aiming to find patterns on the spermatogenesis of Porifera. Therefore, the goal of this study was to describe the spermatogenesis of the poecilosclerid *Tedania ignis*. *Tedania ignis* is found along the East coast of America, from Mexico Gulf to southern of Brazil, it is orange or red and have an encrusting habit. Tissue fragments of several specimens were obtained in Salvador, Bahia, Brazil. These samples were processed for light and electron microscopy (SEM and TEM).

Tedania ignis is a simultaneous hermaphrodite, with spermatogenesis occurring during all year long. The spermatogenesis was carried out in the spermatic cysts, with no synchronism among cysts, but, inside each cyst the spermatic cells matured at the same time. Spermatic cysts were spread in the choanosome. Spermatogonia were characterized as large (diameter 2.8 ± 0.7 μm) and spherical cells with hyaline cytoplasm and large nucleus. Golgi apparatuses and a group of spherical mitochondria were present near to the nucleus but opposite of the flagellum. The following step generated the spermatocytes. These cells were characterized by a volume reduction (diameter 2.0±0.5μm), due to cell divisions, resulting in sister cells that remained interconnected by cytoplasmic bridges. Golgi apparatus are found next to the nucleus and the mitochondria could be found spread into the cytoplasm. Then, to become the spermatids there was a significant reduction of the cytoplasmic material, due to the exocytosis of the most cytoplasm that form the residual body. The Golgi apparatus was the single organelle present in this stage and it was found ahead of the nucleus and the mitochondria were not found. Mature spermatozoa were filiform and the flagellum was not inserted in the base of the main body, but alongside of it. This characteristic can be related to the V-shaped sperm cells, like those of *Crambe crambe*. Somatic cells were also found inside de spermatic cysts. This cell was round, the nucleus was centrally and only mitochondria were recognized. The spermatogenesis in *T. ignis* is similar to the others poecilosclerids. However, the mature spermatozoa are more similar to the *Crambe crambe* (in which the spermatozoa are of the modified type) than the other species of Poecilosclerida. The shape of the sperm could be related to physiological or functional reproduction and, could be explained by convergent evolution.

Financial support was provided by the Brazilian agencies: CAPES, FAPESB, PROPCI/PRODOC UFBA, and CNPq

Transatlantic Cooperation on Deep-sea Research within the Atlantic Ocean Research Alliance (AORA)

Margaret Rae, Joana R. Xavier, Ana Teresa Caetano

In 2013, Canada, the European Union and the United States of America signed the **Galway Statement on Atlantic Ocean Cooperation** launching an Atlantic Ocean Research Alliance (AORA)[1]. The overarching objectives of the cooperation are to improve ocean health and stewardship, promote sustainable management of resources, improved ecosystem assessments and forecasts and deeper understanding of vulnerabilities and risks, including climate change as well as to generate new tools to increase resilience, conserve rich biodiversity, manage risk and determine social, environmental, and economic priorities.

The priority areas of the cooperation identified thus far will be presented.

1. In working together to advance results in the identified areas of research cooperation, the parties seek to improve efficiencies and effectiveness by:
2. Organizing and leveraging research activities in a way that takes advantage of opportunities for synergies in work already underway and the use of infrastructure or installations
3. Better coordination of data sharing, interoperability and coordination of observing infrastructure
4. Promoting researcher mobility
5. Coordinating the planning and programming of relevant activities and resources
6. To date, four AORA Working Groups have been established:
7. Atlantic Seabed Mapping International Working Group
8. Ocean Literacy Working Group
9. Aquaculture Working Group
10. Ecosystem Approach to Ocean Health & Stressors

In this Townhall event, an overview of the AORA will be presented focusing on the progress made since the signing of the Galway Statement. The work proposed by the Ecosystem Approach to Ocean Health & Stressors Working Group will be summarized and the two EU Horizon 2020 research projects SponGES and ATLAS will summarize their work and experience regarding transatlantic cooperation. A Panel Session on a Future Outlook on Science/Research Cooperation in the Atlantic will follow and include links to an informal network called Atlantic Seafloor Partnership for Integrated Research and Exploration (ASPIRE) and also links with other deep-sea working groups such as the Atlantic Seabed Mapping International Working Group (ASMIWG).

[1] www.atlanticresource.org

Attending Delegates

Dr.	Muhammad Azmi	Abdul Wahab	Australian Institute of Marine Science
Ms.	Michelle	Achlatis	The University of Queensland
Mr.	Jose Maria	Aguilar-Camacho	National University of Ireland Galway
Dr.	Louise	Allcock	NUI Galway
Dr.	Belinda	Alvarez	Lund University (Sweden)
Ms.	Adriana	Alvizu	University of Bergen
Mr.	David	Amptmeijer	University of Groningen
Dr.	Stephanie	Archer	Fisheries and Oceans Canada
Mr.	Joerg	Arnscheidt	Ulster University
Ms.	Liv	Ascer	University of São Paulo
Ms.	Fernanda	Azevedo	UFRJ
Prof.	Tatjana	Bakran-Petricioli	University of Zagreb, Faculty of Science
Mr.	Jake Ivan	Baquiran	University of the Philippines-Diliman
Mr.	Martijn	Bart	University of Amsterdam
Mr.	Giampiero	Batani	GEOMAR, Helmholtz Centre for Ocena Research Kiel - University of New South Wales, Sydney
Prof.	Christopher	Battershill	University of Waikato
Dr.	Kristina	Bayer	GEOMAR-Helmholtz Centre For Ocean Research
Ms.	Lindsay	Beazley	Government of Canada
Ms.	Lisa	Becking	Wageningen University & Research
Dr.	James	Bell	Victoria University of Wellington
Ms.	Holly	Bennett	Victoria University of Wellington
Dr.	Marco	Bertolino	Università degli Studi di Genova
Mr.	Nicklas	Bisbo	Aarhus University
Ms.	Carole	borchiellini	AMU/CNRS
Dr.	Nicole	Boury-Esnault	Université d'Aix-Marseille/CNRS
Dr.	Patrick	Cabaitan	University of the Philippines
Ms.	Alexandra	Campbell	Cardiff University
Mr.	Paco	Cardenas	Uppsala University
Dr.	Cesar	Cardenas	Chilean Antarctic Institute
Dr.	Frine	Cardone	University of Bari
Ms.	Francisca	Carvalho	University of Bergen
Dr.	Cristiano	Carvalho Coutinho	Universidade Federal do Rio de Janeiro
Ms.	Cristiana	Castello Branco	Museu Nacional /UFRJ
Dr.	Andia	Chaves Fonnegra	University of the Virgin Islands
Dr.	Pierre	Chevaldonne	CNRS
Dr	Báslavi Marisbel	Cóndor Luján	Universidade Federal do Rio de Janeiro
Dr.	Cecilia	Conaco	University of the Philippines
Ms.	Megan	Conkling	Florida Atlantic University
Mr.	Gabriele	Costa	UNIGE
Prof.	Phil	Crews	University of California
Dr.	Bill	Crowe	Institute of Technology Sligo
Mr.	Azraj	Dahihande	CSIR-National Institute of Oceanography-Goa

Dr.	Thanos	Dailianis	Hellenic Centre for Marine Research (HCMR)
Mr.	Joshua	Davison	Plymouth University
Mr.	Desiderius	de Bakker	NIOZ/WMR
Mr.	Jasper	de Goeij	University of Amsterdam
Mr.	Christiaan	De Leeuw	Wageningen University & Research
Ms.	Dora	de Moura Barbosa Leite	Museu Nacional - UFRJ
Mr.	Lennart	de Nooijer	NIOZ
Dr.	Nicole	de Voogd	Naturalis Biodiversity Center
Prof.	Bernard	Degnan	University of Queensland
Dr.	Sandie	Degnan	University of Queensland
Ms.	Marie-Claire	Demers	University of Wollongong
Ms.	Ariyanti	Dewi	University of Queensland
Dr.	Maria Cristina	Diaz	Florida Atlantic University
Mr.	Curtis	Dinn	University of Alberta
Prof.	Alan	Dobson	University College Cork,
Ms.	Karen Sarmento	Dos Santos	Museu Nacional do Rio de Janeiro - Universidade Federal do Rio de Janeiro
Ms.	Rachel	Downey	Australia National University
Dr.	Cole	Easson	Nova Southeastern University
Prof.	Hermann	Ehrlich	Institute of Experimental Physics
Dr.	Merrick	Ekins	Queensland Museum
Dr.	Alexander	Ereskovsky	CNRS, Aix-Marseille university
Dr.	Dirk	Erpenbeck	Ludwig-Maximilians-Universität München
Dr.	Patrick	Erwin	University of North Carolina Wilmington
Dr.	Karen	Evans	University of Liverpool
Mr.	Alper	Evcen	Ege University
Prof.	Fernanda	F. Cavalcanti	UFBA
Ms.	Luisa	Federwisch	Alfred-Wegener-Institut Helmholtz-Zentrum für Polar- und Meeresforschung
Dr.	Eliana	Ferretti	Studio Associato Gaia snc
Dr.	Cara	Fiore	Appalachian State University
Ms.	Daria	Firsova	NUIG
Mr.	Humberto	Fortunato	Universidade do Estado do Rio de Janeiro - UERJ
Ms.	Maïa	Fourt	IMBE
Ms.	Benedetta	Fradusco	Ludwig Maximilians Universität
Mr.	Warren	Francis	LMU Munich
Dr.	Christopher	Freeman	Smithsonian Marine Station
Dr.	Viviana	Frisone	Comune di Montecchio Maggiore
Dr.	Jane	Fromont	Western Australian Museum
Dr.	Lorenzo	Gallus	University of Genova
Ms.	Leyre	Garate	Center of Advanced Studies of Blanes (CEAB-CSIC)
Ms.	Erika	Garcia-Bonilla	Microbiomas
Dr.	Anita	George	Queensland Museum
Dr.	Vasilis	Gerovasileiou	Hellenic Centre for Marine Research (HCMR)
Prof.	Marco	Giovine	University of Genova
Dr.	Deborah	Gochfeld	University of Mississippi

Dr.	Nelly	Godefroy	Montpellier University
Dr.	Claire	Goodwin	Huntsman Marine Science Centre
Mr.	Nathan	Grant	University of Alberta
Ms.	Marie	Grenier	CNRS
Ms.	Sarah	Griffiths	Manchester Metropolitan University
Ms.	Johanna	Gutleben	WUR
Ms.	Christine	Guzman	
Prof.	Eduardo	Hajdu	Museu Nacional/UFRJ
Dr.	Mirna	Halasz	Ruder Boskovic Institute
Ms.	Ulrike	Hanz	NIOZ
Ms.	Mary Kay	Harper	University of Utah
Mr.	Nickolas James	Hawkes	Institute of Biology
Prof.	Ute	Hentschel Humeida	GEOMAR Helmholtz Centre for Ocean Research Kiel
Ms.	Kylie	Hesp	Wageningen University
Dr.	Jon Thomassen	Hestetun	University of Bergen
Mr.	Malcolm	Hill	University of Richmond
Ms.	Kate	Hill	Florida State University
Mr.	April	Hill	University of Richmond
Dr.	John	Hooper	Queensland Museum
Dr.	Kerry	Howell	Plymouth University
Ms.	Tal	Idan	Tel Aviv University
Dr.	Chris	Ireland	University of Utah
Mr.	Shriraj	Jakhalekar	CSIR - National Institute of Oceanography, Goa, India.
Dr.	Dorte	Janussen	Senckenberg Research Institute and Nature Museum
Ms.	Karla	Jaramillo	ESPOL-CENAIM / NUI Galway
Dr.	Amanda	Kahn	University of Alberta
Ms.	Kathleen	Kaiser	Florida State University
Ms.	Liisi	Karlep	Tallinn University of Technology
Mr.	Ehsan	Kayal	Station Biologique de Roscoff
Mr.	Joseph	Kelly	Stony Brook University
Mr.	Nathan	Kenny	The Natural History Museum
Mr.	Daniel	Kersken	Senckenberg Research Institute Frankfurt
Prof.	Michelle	Klautau	UFRJ
Ms.	Vasiliki	Koutsouveli	Natural History Museum
Ms.	Gabriella	Krogius	Uppsala University
Ms.	Shelly	Krueger	University of Florida
Mr.	Lars	Kumala	University of Southern Denmark
Ms.	Anaíra	Lage	Museu Nacional of Universidade Federal do Rio de Janeiro
Dr.	Claire	Laguionie Marchais	NUIG
Dr.	Emilio	Lanna	Universidade Federal da Bahia
Mr.	Andrey	Lavrov	Lomonosov Moscow State University, Biological Faculty
Mr.	Dennis	Lavrov	Iowa State University
Ms.	Lauren	Law	University of Alberta
Dr.	Colin	Lawton	NUI Galway

Dr.	Emilie	Le Goff	Montpellier University
Ms.	Camille	Leal	UFRJ
Mr.	Carlos	Leiva	University of Barcelona / Natural History Museum of London
Dr.	Michael	Lesser	University of New Hampshire
Prof.	Sally	Leys	University of Alberta
Prof.	Zhiyong	Li	Shanghai Jiao Tong University
Mr.	Swee Cheng	Lim	
Dr.	Gisele	Lobo-Hajdu	UERJ
Ms.	Maria Belinda	Longakit	National University of Ireland Galway
Prof.	Jose	Lopez	Nova Southeastern University
Ms.	Maria	Lopez Acosta	CEAB-CSIC
Dr.	Magdalena	Lukowiak	Polish Academy of Sciences
Dr.	Heidi	Luter	Victoria University of Wellington & Australian Institute of Marine Science
Dr.	Yulia	Lyupina	N.K. Koltsov Institute of Developmental Biology
Ms.	Diede	Maas	Wageningen University & Research
Mr.	Keir	Macartney	University of New Hampshire
Ms.	Jasmine	Mah	University of Alberta
Dr	Manuel	Maldonado	Centro de Estudios Avanzados de Blanes (CSIC)
Mr.	Renarta	Manconi	
Ms.	Geminne	Manzano	Community Ecology Laboratory
Mr.	Joe	Marlow	Victoria University of Wellington
Ms.	Maria Vittoria	Marra	Martin Ryan Institute, NUI Galway
Dr.	Kenan	Matterson	Smithsonian National Musuem of Natural History
Mr.	Sam	McCormack	University of Waikato
Prof.	Grace	McCormack	NUI Galway
Mr.	Fernando	Moraes	Instituto de Pesquisas Jardim Botanico do Rio de Janeiro
Mr.	Mario	Moreno	Universidad mayor
Dr.	Teresa	Morganti	Marine Science Institute of Barcelona (ICM-CSIC)
Dr.	Christine	Morrow	NUIG
Mr.	Sambhaji	Mote	CSIR-National Institute of Oceanography
Dr.	Benjamin	Mueller	University of Amsterdam
Ms.	Stephanie	Munroe	Wageningen University
Dr.	Guilherme	Muricy	Museu Nacional - Universidade Federal do Rio de Janeiro
Mr.	Michael Angelou	Nada	University of the Philippines
Ms.	Catherine	Numa	IUCN Centre for Mediterranean Cooperation
Ms.	Lauren	Olinger	University of the Virgin Islands
Dr.	Julie B.	Olson	University of Alabama
Ms.	Alice	Oprandi	University of Genoa
Dr.	Ronald	Osinga	Wageningen University and Research
Dr.	Maria del Mar	Otero	IUCN Centre for Mediterranean Cooperation
Dr.	Huilong	Ou	Xiamen University
Mr.	Cristian	Pacheco	
Mr.	Andrea	Padiglia	University of Genova
Mr.	André	Padua	

Dr.	Sabrina	Pankey	University of New Hampshire
Prof.	Maurizio	Pansini	University of Genoa
Ms.	Cecilia	Pascelli	AIMS
Prof.	Joseph	Pawlik	University of North Carolina Wilmington
Ms.	Robyn	Payne	University of the Western Cape
Ms.	Raquel	Pereira	Uppsala University
Ms.	Jeannette	Perez	Universidad Simon Bolivar
Dr.	Thierry	Perez	
Dr.	Alicia	Perez-Porro	Smithsonian Institution - National Museum of Natural History
Mr.	Iaroslav	Petrenko	Freiberg University of Mining and Technology
Dr.	Mari-Carmen	Pineda	Australian Institute of Marine Science
Mr.	Ulisses	Pinheiro	UFPE
Prof.	Andrzej	Pisera	Polish Academy of Sciences
Dr.	Lucia	Pita Galán	GEOMAR Helmholtz Centre for Ocean Research Kiel
Dr.	Bruna	Plese	IRB
Dr.	Shirley	Pomponi	Florida Atlantic University
Mr.	Luis	Porras	Ludwig-Maximilians-Universität
Mr.	Igor	Pozdnyakov	St. Petersburg State University
Dr.	Marina	Pozzolini	Genova University
Mr.	Roberto	Pronzato	
Dr.	Autun	Purser	Alfred Wegener Institute
Dr.	Fran	Ramil	Universidade de Vigo
Dr.	Ana	Ramos	Instituto Español de Oceanografía
Mr.	Blake	Ramsby	James Cook University
Prof.	Hans Tore	Rapp	University of Bergen
Dr.	Emmanuelle	Renard	AMU/CNRS
Dr.	Abigail	Renegar	Nova Southeastern University, Halmos College of Natural Sciences and Oceanography
Dr.	Miriam	Reverter	NUI Galway
Ms.	Bárbara	Ribeiro	Universidade Federal do Rio de Janeiro
Dr.	Marta	Ribes	ICM-CSIC
Dr.	Ana	Riesgo	The Natural History Museum of London
Dr.	Laura	Rix	GEOMAR Helmholtz Centre for Ocean Research Kiel
Dr.	Sven	Rohde	University of Oldenburg
Ms.	Christine	Rooks	University of Bergen
Dr.	Rebecca	Ross	Plymouth University
Dr.	Nisit	Rueangsawang	Rajamangala University of Technology Krungthep
Ms.	Juliet	Ruggiero	
Mr.	Cesar	Ruiz	AMU
Ms.	Joana	Sandes	UFRJ
Mr.	Andreu	Santin Muriel	Institute of Marine Science (ICM-CSIC)
Dr.	Nadia	Santodomingo	Natural History Museum
Prof.	Sonia	Scarfi	University of Genova
Dr.	Laura	Schejter	Instituto Nacional de Investigacion y Desarrollo Pesquero
Dr.	Marie-Lise	Schläppy	University of the Highlands and Islands
Dr.	Christine	Schönberg	The University of Western Australia
Prof.	Peter	Schupp	Institute for Chemistry and Biology of the marine Environment
Ms.	Astrid	Schuster	Ludwig-Maximilians-Universität München

Dr.	Amy	Scott-Murray	Natural History Museum
Ms.	Alexia	Setti	Università degli Studi di Genova
Ms.	Megan	Shaffer	Victoria University of Wellington
Dr.	Sigal	Shefer	Tel Aviv University
Dr.	Detmer	Sipkema	Wageningen University
Ms.	Cèlia	Sitjà	CEAB-CSIC
Ms.	Beate	Slaby	GEOMAR-Helmholtz Centre For Ocean Research
Dr.	Marc	Slattery	University of Mississippi
Mr.	Hiren	Solanki	NUIG
Ms.	Shirley	Sorokin	SARDI Aquatic Sciences
Ms.	Karin	Steffen	Uppsala University
Dr.	Georg	Steinert	Laboratory of Microbiology
Mr.	John	Stevely	University of Florida
Ms.	Hilde	Strand Dybevik	University of Bergen
Mr.	Brian	Strehlow	University of Western Australia
Mr.	Thomas	Swierts	Naturalis Biodiversity Center
Dr.	Sergio	Taboada	The Natural History Museum
Dr.	Robert	Thacker	Stony Brook University
Dr.	Mikael	Thollesson	Uppsala University
Prof.	Torsten	Thomas	University of New South Wales
Prof.	Olivier	Thomas	NUI Galway
Ms.	Holly	Trew	University of the West Indies
Dr.	Remi	Tsubaki	Japan Agency for Marine Earth Science
Prof.	Xavier	Turon	Centre for Advanced Studies of Blanes (CEAB-CSIC)
Ms.	Marta	Turon Rodrigo	CEAB
Dr.	Sarah	Tweedt	Yale University
Ms.	Tone	Ulvatn	University of Bergen
Dr.	Mat	Upton	Plymouth University
Dr.	Maria J.	Uriz	Consejo Superior de Investigaciones Cientificas
Mr.	Jean	Vacelet	IMBE
Ms.	Johanne	Vad	Heriot-Watt University
Ms.	Marla	Valentine	Old Dominion University
Ms.	Esther	Van der Ent	Naturalis Biodiversity Center
Dr.	Fleur C.	van Duyl	Royal NIOZ
Ms.	Vivian	Vasconcellos	Universidade Federal da Bahia
Mr.	Joost	Verhoeven	Memorial University of Newfoundland
Mr.	Jan	Vicente	Hawaii Institute of Marine Biology
Ms.	Sonia Marcela	Villegas Plazas	Microbiomas Foundation
Dr.	Oliver	Voigt	Ludwig-Maximilans-Universität München
Dr.	Dexiang	Wang	Xiamen University
Ms.	Vonda	Hareham hayes	Fisheries and Oceans Canada
Ms.	Alice	Webb	NIOZ
Dr.	Philippe	Willenz	Royal Belgian Inst of Natural Sciences
Ms.	Mirthe	Wiltink	Wageningen University
Prof.	Dr. Gert	Woerheide	Ludwig-Maximilians-Universität München
Mr.	Michael	Wooster	Kaust
Dr.	Janie	Wulff	Florida State University

Mr.	Erik	Wurz	Wageningen University & Research
Dr.	Marcin	Wysokowski	Poznan University of Technology
Dr.	Joana R	Xavier	University of Bergen (UiB)
Ms.	Clairecynth	Yu	Community Ecology Laboratory
Mr.	Wei	Zhang	Flinders University
Dr.	Jing	Zhao	Xiamen University
Prof.	Carla	Zilberberg	Universidade Federal do Rio de Janeiro

Index

Authors

Poster list

Poster Session 1 - Tuesday, 27 June 2017

[Systematics/Evolution - Symbiosis - Biomaterials/Biomolecules]

Systematics/Evolution

Poster No.	Title	First Name	Last Name	Organisation	Abstract Title
P1	Ms.	Adriana	Alvizu	Universitetet i Bergen	A revised molecular phylogeny of the subclass Calcaronea
P2	Dr.	Fernanda	Azevedo	Federeal University of the Rio de Janeiro (UFRJ)	Biodiversity and biogeography of tropical Western Atlantic Calcarea (Porifera)
P3	Dr.	Marco	Bertolino	Università degli Studi di Genova	A Messinian Paleo-Sponge Community from Northwestern Italy
P4	Mr.	André	Bispo	Museu Nacional/UFRJ	A new species of *Haliclona* (Haplosclerida: Chalinidae) from sandstone reefs in Ceará (NE Brazil)
P5	Dr.	Carole	Borchiellini	AMU/CNRS	What about PCP pathway in sponges?
P6	Ms.	Francisca	C Carvalho	University of Bergen	Diversity, distribution and phylogenetic relationships of the North Atlantic lithistid sponges
P7	Ms.	Raisa	Campos Rizzieri	Universidade Federal do Rio de Janeiro	Integrative taxonomy for the genus *Ernstia* (Porifera, Calcarea, Calcinea) in the lesser antilles, caribbean sea
P8	Mr.	Paco	Cardenas	Uppsala University	Phylogenetic relationships of the Thrombidae and suggestion of a new Tetractinellida sub-order
P9	Ms.	Cristiana	Castello-Branco	Museu Nacional /UFRJ	First record of *Bolosoma* (Hexactinellida, Euplectellidae) for the Atlantic Ocean and new species
P10	Dr.	Andia	Chaves Fonnegra	University of the Virgin Islands	*Cliona laticavicola* is an ecophenotype and an ontogenic life stage of the coral excavating sponge *Cliona delitrix*
P11	Ms.	Báslavi Marisbel	Cóndor Luján	Universidade Federal do Rio de Janeiro	On-going speciation of the amphiamerican calcareous sponge *Clathrina aurea*
P12	Dr.	Fernando	Coreixas de Moraes	Instituto de Pesquisas Jardim Botânico do Rio de Janeiro	Sponge bottoms off the Amazon River mouth revisited
P13	Dr.	Javier	Cristobo	Spanish Institute of Oceanography (IEO)	Diversity of Porifera in the Aviles Canyons System: COCACE project
P14	Dr.	Nicole	de Voogd	Naturalis Biodiversity Center	Calcareous sponges of the Western Indian Ocean and the Red Sea
P15	Dr.	Nicole	de Voogd	Naturalis Biodiversity Center	The deep water sponge fauna of Guadeloupe
P16	Mr.	Daniel	Drew	Yale University Peabody Museum	The Sponge Collection of the Yale Peabody Museum of Natural History
P17	Ms.	Hilde	Dybevik	University of Bergen	Taxonomic Revision of the Family Heteropiidae (Porifera, Calcarea) in Norwegian Waters
P18	Dr.	Alexander	Ereskovsky	CNRS, Aix-Marseille university	Three new *Halisarca*-like sponges (Porifera, Verongimorpha) from tropical seas
P19	Dr.	Dirk	Erpenbeck	Ludwig-Maximilians-Universität München	Molecular Biodiversity of Iranian Persian Gulf Sponges
P20	Dr.	Dirk	Erpenbeck	Ludwig-Maximilians-Universität München	Molecular Taxonomy of African Freshwater Sponges
P21	Prof.	Fernanda	F. Cavalcanti	UFBA	New Species And A New Record Of The Genus *Leucilla* (Calcarea, Calcaronea) To The Tropical Brazilian Coast.
P22	Prof.	Fernanda	F. Cavalcanti	UFBA	Taxonomy Of Calcareous Sponges (Porifera, Calcarea) Sampled On Artificial Substrates In A Recreational Marina From The Tropical Brazilian Coast.
P23	Ms.	Tayara	Fontana	Universidade Federal do Rio de Janeiro	Biodiversity of calcineans (Porifera, Calcarea) from Martinique, Lesser Antilles, Caribbean Sea
P24	Mr	Humberto	Fortunato	Universidade do Estado do Rio de Janeiro	A new species of Hymeniacidon from Brazil and redescription of Halichondria (Halich.) melanadocia de Laubenfels, 1936
P25	Ms.	Christine	Guzman	University of the Philippines, Dillman	Comparative Transcriptome Analysis Reveals Insights Into The Streamlined Genomes Of Haplosclerid Demosponges
P26	Dr.	Kathryn	Hall	Queensland Museum	Beyond the sponge barcode: testing the taxonomic utility of microbial diversity analysis using 16S rRNA gene sequences among tetillid sponges
P27	Ms.	Mary Kay	Harper	University of Utah Asia Campus	Taxonomy of Theonellidae in the Indo-West Pacific
P28	Mr	Eduardo	Hadju	Universidade do Estado do Rio de Janeiro	Two new species of Hemimycale (Hymedesmiidae: Poecilosclerida: Demospongiae) from Southeastern Brazil
P29	Mr.	Zvi	Hoffman	Universidad Autónoma de Baja California Sur	Six new species of verongiid sponges from southern region of Baja California Peninsula, Mexico
P30	Dr.	Valeria	Itskovich	Limnological institute SB RAS	Toward integrative taxonomy of endemic Lake Baikal sponges Lubomirskiidae.
P31	Ms.	Hina	Jabeen	University of Karachi	Two new records of marine sponges (Demospongiae: Haplosclerida) from the coast of Karachi, Pakistan
P32	Ms.	Karla	Jaramillo	CENAIM - ESPOL Ecuador and NUI Galway	A first assessment of the sponge biodiversity off the coast of mainland Ecuador
P33	Mr.	Joseph	Kelly	Stony Brook University	Molecular taxonomy and phylogeography of the sponge genus Ircinia from northern Australia
P34	Dr.	Nathan J	Kenny	The Natural History Museum, London	Deeper understanding of deep sea Axinellida: mitochondrial sequencing of a novel abyssal sponge
P35	Mr.	Camille Victória	Leal	Universidade Federal do Rio de Janeiro	Divergence between molecular and morphological data in Brazilian *Arenosclera* sponges (Haplosclerida, Demospongiae)
P36	Ms.	Dora	Leite	Museu Nacional (UFRJ)	Integrative Systematics of Tropical Western Atlantic *Mycale* of the "*immitis*-group"
P37	Mr.	Swee Cheng	Lim	National University of Singapore	Taiwan deep-water sponge collection at the National Museum of Natural Science at Taichung (Taiwan)
P38	Dr.	Gisele	Lobo-Hajdu	UERJ, Universidade do Estado do Rio de Janeiro	Phenotypic Plasticity in Sponges: a case study on *Callyspongia* sp. from Northeastern Brazil
P39	Prof.	Jose	Lopez	Nova Southeastern University	*Cinachyrella* as a model sponge genus for evolution, microbial symbiosis and experimental biology
P40	Ms.	Maria Belinda	Longakit	National University of Ireland Galway	Evolution of haplosclerid sponges: insights from kinetid structures
P41	Dr.	Magdalena	Łukowiak	Polish Academy of Sciences	Spicular Analysis for Reconstructions of Sponge Communities in Modern Coral Reefs
P42	Dr.	Magdalena	Łukowiak	Polish Academy of Sciences	Siliceous Sponges from the Upper Eocene of Eastern Central Ukraine
P43	Ms.	Diede	Maas	Wageningen University and Research	Varied environments drive rapid divergence in sponge (*Suberites diversicolor*) populations
P44	Mr.	Renata	Manconi	Universita' di Sassari	The freshwater sponge fauna of Madagascar: a first assessment
P45	Mr.	Sam	Mc Cormack	University of Waikato	Systematics of marine sponges from the Bay of Plenty, New Zealand
P46	Dr.	Christine	Morrow	NUIG	Progress with Poecilosclerida (Demospongiae: Porifera) – more molecular insights into poecilosclerid phylogeny
P47	Dr.	Christine	Morrow	NUIG	A new species of *Hymeraphia* Bowerbank, 1864 from the cold water coral reefs off the south west coast of Ireland.
P48	Dr.	Christine	Morrow	NUIG	Stir it Up! - Support for the movement of the 'Bob Marley' sponge, *Pipestela candelabra* from Axinellidae to Bubarida
P49	Dr.	Christine	Morrow	NUIG	Clarifying the status of *Raspaciona aculeata* versus *Raspailia aculeata*
P50	Dr.	Christine	Morrow	NUIG	The peculiar spicules in *Tethyspira*: an apomorphy for *Tethyspira* or a synapomorphy with Raspailiidae?
P51	Dr.	Guilherme	Muricy	Museu Nacional - Universidade Federal do Rio de Janeiro	Taxonomy of *Corticium* (Porifera: Homoscleromorpha) from Western Australia
P52	Dr.	Guilherme	Muricy	Museu Nacional, Universidade Federal do Rio de Janeiro	Taxonomy of the genus *Plakinastrella* (Porifera: Homoscleromorpha: Plakinidae) from Western Australia
P53	Dr.	Guilherme	Muricy	Museu Nacional - Universidade Federal do Rio de Janeiro	High richness of sponges at the mouth of the São Francisco river, in Northeast Brazil: another barrier falls in the Tropical Western Atlantic

P54	Dr.	Guilherme	Muricy	Museu Nacional - Universidade Federal do Rio de Janeiro	*Rhabdastrella fibrosa* Hechtel 1983 and Geodia corticostylifera Hajdu et al. 1992 are junior synonyms of *Geodia tylastra* Boury-Esnault, 1973 (Demospongiae: Astrophorina)
P55	Mr.	Viraj	Muthye	Iowa State University	Diversity in inferred mitochondrial proteomes in Phylum Porifera
P56	Mr.	Cristian	Pacheco	Universidad Nacional Autónoma de México	Excavating sponges of Central America Pacific and evidence of a complex of species in *Cliona mucronata*
P57	Ms.	Raquel	Pereira	Uppsala University	Suberites From The North Atlantic: Taxonomic Tribulations And Spicule Similitude
P58	Dr.	Thierry	PEREZ	CNRS	The International Associated Laboratory MARRIO (France, Brazil, Ireland): Patterns of sponge biodiversity and chemical diversity from Martinique to Rio de Janeiro
P59	Mr.	Ulisses	Pinheiro	Universidade Federal de Pernambuco	New cleistocheliferous species of *Clathria (Thalysias*) Duchassaing & Michelotti, 1864 (Microcionidae; Poecilosclerida; Demospongiae) of intertidal zone from Brazil
P60	Mr.	Ulisses	Pinheiro	Universidade Federal de Pernambuco	Two new species of *Oceanapia* Norman, 1869 (Phloeodictyidae; Haplosclerida; Demospongiae) from slope area of oil and gas exploitation in Rio Grande do Norte State, Northeastern Brazil
P61	Prof.	Andrzej	Pisera	Polish Academy of Sciences	The Sponge Genus *Laocoetis* Pomel 1872 (Hexactinellida, Hexactinosida): a Case of Extreme Morphological Conservatism
P62	Prof.	Andrzej	Pisera	Polish Academy of Sciences	New Minchinellid Sponge (Calcarea, Lithonida, Minchinellidae) from the Oxfordian (Late Jurasssic) of Russia
P63	Mr.	Luis	Porras	GeoBio-Center, Ludwig-Maximilians-Universität München	A new morphological approach to sponge phylogeny: Homoscleromorpha as a case study
P64	Mr.	Igor	Pozdnyakov	St. Petersburg State University	Evolutionary transformations of choanocyte kinetid in the phylum Porifera and their significance for phylogenetic reconstructions
P65	Dr.	Miriam	Reverter	National University of Ireland	Chemosystematics as a complementary tool for *Haliclona* species (Class Demospongiae, Order Haplosclerida)
P66	Dr.	Ana	Riesgo	The Natural History Museum of London	Integrative taxonomy reveals a new genus and new species of an Antarctic calcinean sponge (Porifera, Calcarea, Clathrinida)
P67	Dr.	Pilar	Rios	Spanish Institute of Oceanography (IEO)	New records of *Iotroata acanthostylifera* (Stephens, 1916) and *Janulum spinispiculum* (Carter, 1876) (Porifera) in Flemish Cap (NW Atlantic)
P68	Dr.	Pilar	Rios	Spanish Institute of Oceanography (IEO)	A new sponge-dominated ecosystem found in the Aviles canyon(Cantabrian Sea)
P69	Ms.	Lívia	Rocha	National Museum of the Federal University of Rio de Janeiro	Taxonomy of Brazilian Petrosiidae deposited at Museu Nacional/UFRJ
P70	Ms.	Sula	Salani	Museu Nacional do Rio de Janeiro, MN	Biodiversity of Hymedesmiidae (Porifera, Poecilosclerida) of the Brazilian Coast
P71	Ms.	Astrid	Schuster	Ludwig-Maximilians-Universität München	The Western Tropical Atlantic ‘ring’ of rock sponges – A molecular phylogenetic approach using four different markers (28S, 18S, ITS and CO1)
P72	Ms.	Astrid	Schuster	Ludwig-Maximilians-Universität München	Dating Demosponge Divergences –New Mitogenomes from ezRAD And The Fossilized Birth-Death Clock Model
P73	Ms.	Astrid	Schuster	Ludwig-Maximilians-Universität München	Deep-water tetractinellid sponges from the Galápagos Islands: first molecular and morphological analysis reveals seven new species
P74	Dr.	Mikael	Thollesson	Uppsala University	Gossip – tapping the taxonomic grapevine
P75	Dr.	Oliver	Voigt	Ludwig-Maximilans-Universität Munich	Evolution of key biomineralization genes in calcareous sponges
P76	Ms.	Qi	Yang	Flinders University	Development of A Multilocus-Based Approach for Sponge (Phylum Porifera) Identification: Refinement and Limitations
P77	Mr.	Alper	Evcen	Ege University	Sponge Species Associated With Posidonia Oceanica Meadows Along The Coast Of The Aegean Sea (Turkey)
P78	Dr.	Julio Cesar		Universidade do Estado do Rio de Janeiro	First records of shallow-water sponges (Demospongiae) from the largest marine no-take zone in South America, the Nazca-Desventuradas Marine Park (SE Pacific)
Sponges and microbes					
P79	Ms.	Michelle	Achlatis	University of Queensland, Australia	Single-cell measurement of metabolic interactions between a bioeroding sponge and its endosymbiotic dinoflagellates using nanoscale secondary ion mass spectrometry.
P80	Mr.	Jake Ivan	Baquiran	University of the Philippines-Diliman	Influence of eutrophication pressure on the resilience and sensitivity of sponge-associated microbial community
P81	Mr.	Giampiero	Batani	University of New South Wales - GEOMAR Helmholtz Centre for Ocean Research	Visualization of eukaryotic-like-proteins as ring-like structures within bacteria-containing sponge cells
P82	Dr.	Yosr	Benredjem Romdhane	Institut National des Sciences et Technologies de la Mer I.N.S.T.M	Anti-tumoral activities of the sponges *Sarcotragus* gender and their associated bacteria
P83	Ms.	Alexandra	Campbell	Cardiff University	Microbial Community Dynamics of the Mangrove Fire Sponge, *Tedania ignis*, Following Time in a Sustained Mariculture Setup
P84	Dr.	Thanos	Dailianis	Hellenic Centre for Marine Research	Comparative study of the microbial diversity in four Mediterranean irciniid sponges
P85	Dr.	Cara	Fiore	Appalachian State University	Specialization of Microbiomes in Sponge and Coral Hosts
P86	Ms.	Leire	Garate	Centre d'Estudis Avançats de Blanes (CEAB-CSIC)	Searching for bacterial genes involved in the symbiosis between sponges and calcifying endosymbiotic bacteria
P87	Ms.	Erika	Garcia-Bonilla	Microbiomas	Insights into the microbial diversity of the Mediterranean marine sponge *Haliclona fulva* (Demospongiae: Haplosclerida)
P88	Mr.	Sarah	Griffiths	Manchester Metropolitan University	Does a Sponge’s Genotype Influence its Microbiome?
P89	Ms.	Kate	Hill	Florida State University	Spatiotemporal Variation and the Invasibility of Mesofaunal Communities Associated with *Tedania ignis*
P90	Dr.	Carla	Huete-Stauffer	Centre d'Estudis Avançats de Blanes (CEAB)	Do sponge microbiomes depend on past water prokaryotic assemblages?
P91	Ms.	Nora	Kandler	Victoria University of Wellington	In Situ Responses of the Sponge Microbiome to Ocean Acidification
P92	Prof.	Zhiyong	Li	Shanghai Jiao Tong University	Functional transcripts indicate phylogenetically diverse active ammonia-scavenging microflora in sympatric sponges
P93	Dr.	Heidi	Luter	Victoria University of Wellington and Australian Institute of Marine Science	Microbiome changes in diseased *Geodia barretti*
P94	Mr.	Mario	Moreno	University	Metabolic profiles of microbiota from Antarctic sponges revealed by metagenomics
P95	Mr.	Michael Angelou	Nada	University of the Philippines-Diliman	Microbial community composition of the demosponge *Haliclona amboinensis* (Order Haplosclerida) in Bolinao, Philippines
P96	Dr.	Joanne	Preston	University of Portsmouth	Phase shifts in microbial symbiont community associated with compromised immunity and death in Cliona celata from Skomer Marine Conservation Zone, UK.
P97	Mr.	Thomas	Swierts	Naturalis Biodiversity Center	Biogeography of prokaryote communities in Indo-Pacific giant barrel sponges.
P98	Dr.	Robert	Thacker	Stony Brook University	Genetic variability of sponge-cyanobacteria symbioses across the Caribbean

P99	Mr.	Joost	Verhoeven	Memorial University of Newfoundland	Microbiome Comparison Suggests Differential Involvement of Bacterial Associates in the Carnivorous Sponges *Chondrocladia grandis* and *Cladorhiza oxeata*
P100	Ms.	Marcela	Villegas-Plazas	Microbiomas foundation	Microbial Communities of the Marine Sponge *Xestospongia muta* at Microhabitat Transitions show Increased Diversity with Depth, a Core Stable Microbiome across Different Seasons and Concurrent Metabolomic Profiles
P101	Ms.	Vonda	Wareham Hayes	Fisheries and Oceans Canada	Egg deposition by *Rossia palpebrosa* (Cephalopoda: Rossiinae) in deep-sea sponges, in temperate Northwest Atlantic and fringes of polar Canadian Arctic
P102	Prof.	Wei	Zhang	Flinders University	Multi-primers Targeting 16S rDNA Variable Regions Essential for Sponge (Porifera) Microbiome Study
P103	Dr.	Jing	Zhao	Xiamen University	Structure and Dynamics of Microbiomes Associated with Marine Sponge *Tedania* sp. During Life Cycle
Biomaterials / Biomolecules					
P104	Mr.	Paco	Cardenas	Uppsala University	Isolation and identification of sterols from *Haliclona* sp. from Taiwan
P105	Dr.	Javier	Cristobo	Instituto Español de Oceanografía	Deep-sea sponge grounds associated with canyons and seamounts of the Cantabrian Sea
P106	Dr.	Nicole	de Voogd	Naturalis Biodiversity Center	Metabolic characterization of marine sponges, genus *Xestospongia* using NMR-based metabolic profiling techniques.
P107	Ms.	Ariyanti	Dewi	University of Queensland	Sponge-derived compounds from Australian chromodorid nudibranchs
P108	Ms.	Gabriella	Krogius	Division of Pharmacognosy	Visualizing the spatial distribution of barettins and barrettides in the deep-sea sponge *Geodia barretti* using MALDI-TOF mass spectrometry imaging
P109	Dr.	Claire	Laguionie Marchais	NUIG	Exploiting and conserving deep-sea genetic resources
P110	Mr.	Philip	Nemoy	University of Haifa	Sustainable cultivation of sponges in the Eastern Mediterranean Sea: Integrated aquaculture with fish farms
P111	Mr.	Iaroslav	Petrenko	Freiberg University of Mining and Technology	Bioelectrometallurgical Application of Poriferan Chitin
P112	Prof.	Andrzej	Pisera	Polish Academy of Sciences	The Giant Basal Spicule of *Monorhaphis* Sponge Revisited
P113	Dr.	Nisit	Ruengsawang	Rajamangala University of Technology Krungthep	Value-Added in Thai Pottery by Biological Materials from Freshwater Sponges
P114	Prof.	Sonia	Scarfì	University of Genova	Identification, Purification and Characterization of Proteins with Cytotoxic/Antitumor Activity from Chondrosia reniformis
P115	Ms.	Astrid	Schuster	Ludwig-Maximilians-Universität München	Morphological descriptions of the 'lithistid demosponge' fauna (Porifera, Tetractinellida and Sphaerocladina) from the Western Tropical Atlantic
P116	Mr.	Hiren	Solanki	National University of Ireland Galway	Two new sesterterpenes isolated from the Antarctica sponge *Phorbas bergmontae* Hajdu & Teixeira, 2011
P117	Dr.	Mathew	Upton	Plymouth University	Deep-sea discovery – deep-sea sponges as a source of novel biologics

Poster Session 2 - Wednesday, 28 June 2017

[Ecology/Molecular, Cell & Organismal Biology]

Ecology					
P1	Dr.	Muhammad Azmi	Abdul Wahab	Australian Institute of Marine Science	North-western Australia: a sponge biodiversity hotspot
P2	Dr.	Belinda	Alvarez	Lund University (Sweden)	Silica concentration influence on sponge spicule dimensions
P3	Dr.	Stephanie	Archer	Fisheries and Oceans Canada	Sponge distribution and community-habitat associations in nine glass sponge reefs in the Strait of Georgia
P4	Prof.	Tatjana	Bakran-Petricioli	University of Zagreb, Faculty of Science	Diversity of sponge species in the coralligenous community along the eastern Adriatic
P5	Mr.	Martijn	Bart	University of Amsterdam	Carbon cycling by the deep-sea glass sponge *Vazella pourtalesi*
P6	Ms.	Lindsay	Beazley	Government of Canada	Cohort Analysis and Kinship of the Hexactinellid Sponge *Vazella pourtalesi* on an Artificial Substrate
P7	Dr.	Marco	Bertolino	Università degli Studi di Genova	Changes in a Mediterranean coralligenous sponge assemblage at a pluri-millennial temporal scale
P8	Dr.	Marco	Bertolino	Università degli Studi di Genova	A survey of the shallow water sponge fauna of the Cyprus island (Eastern-Mediterranean)
P9	Dr.	Patrick	Cabaitan	University of the Philippines	Fine-scale population structure of tetillid sponges in a tropical reef lagoon
P10	Dr.	Cesar	Cardenas	Instituto Antártico Chileno	Assessing the relationship between sponge assemblages and canopy-forming algae in shallow-water rocky reefs in the Western Antarctic Peninsula
P11	Dr.	Cesar	Cardenas	Instituto Antártico Chileno	New Ice-Free Areas in Antarctic shallow-waters: an Opportunity for Sponge Colonization?
P12	Dr.	Frine	Cardone	University of Bari	Deep-Sea sponges from the Cape Verde archipelago collected during RV Meteor cruise M80/3
P13	Ms.	Caroline	Cordonis	University of Wollongong	Diversity and abundancy of intertidal zone sponges on rocky shores of NSW, Australia: patterns of species distributions, abundance and diversity.
P14	Dr.	Fernando	Coreixas de Moraes	Instituto de Pesquisas Jardim Botânico do Rio de Janeiro	Space-time evaluation of the composition and abundance of boring sponges on Abrolhos Bank shallow reefs, Bahia, Brazil
P15	Mr.	Gabriele	Costa		Mediterranean *Cystoseira* forests vs. barren: the case of sponges
P16	Ms.	Marie F.	Creemers	Charles Darwin Foundation, Santa Cruz, Galápagos Islands, Ecuador.	First characterization of the deep-sea sponge communities on seamounts of the Galapagos Marine Reserve
P17	Mr.	Azraj	Dahihande	CSIR- National Institute of Oceanography	Understanding Functional Morphology of the Sponge Aquiferous System by Using Computed Tomography (CT) Scan Technique
P18	Mr.	Didier	De Bakker	Royal Netherlands Institute for Sea Research (NIOZ	Better estimates of chemical and mechenical excavating rates of coral boring sponges in the caribbean
P19	Mr.	Christiaan	De Leeuw	Wageningen University & Research	What processes shape sponge biodiversity patterns?
P20	Ms.	Marie-Claire	Demers	University of Wollongong	Seagrass attributes and seascape patterns as drivers of sessile invertebrate distribution in a coastal biogenic environment
P21	Mr.	Curtis	Dinn	University of Alberta	New Species Records for Sponges of the Eastern Canadian Arctic and Subarctic
P22	Ms.	Rachel	Downey	Australia National University	Re-examining the under-explored NW Pacific abyssal sponge assemblages of the Kuril-Kamchatka and Okhotsk Sea
P23	Ms.	Rachel	Downey	Australia National University	New insights into the temporal and spatial impacts of the Larsen AB ice shelf collapse on sponge assemblages
P24	Dr.	Alexander	Ereskovsky	CNRS, Aix-Marseille university	Sponges in semi-submerged caves of the North of Bulgaria (Black Sea)
P25	Prof.	Alexander	Ereskovsky	CNRS	Integrative investigation of an unprecedented epizootic event affecting endemic sponges of Lake Baikal
P26	Prof.	Fernanda	F. Cavalcanti	UFBA	Evaluating The Influence Of Abiotic Factors On The Recruitment Rate Of Calcareous Sponges (Porifera, Calcarea) In Salvador, Bahia State, Tropical Brazilian Coast.
P27	Ms.	Luisa	Federwisch	Alfred-Wegener-Institut Helmholtz-Zentrum für Polar- und Meeresforschung	Glass Sponge Distribution in Relation to Abiotic Factors and Predators – A Large-Scale Regional Study in the Weddell Sea, Antarctica
P28	Mr.	Pedro Victor	Ferreira	Universidade Federal do Rio de Janeiro	Past and present scenario of the western atlantic sponge Clathrina aurea (Porifera, Calcarea)
P29	Mr.	Humberto	Fortunato	Universidade do Estado do Rio de Janeiro	Biological habitat preference of the exotic ophiuroid *Ophiothela mirabilis* on marine sponges from Brazil
P30	Ms.	Maïa	Fourt	IMBE	Mediterranean Deep-Sea Sponges From The MedSeaCan And CorSeaCan Cruises

P31	Mr.	Maïa	Fourt	IMBE	Spatial and temporal adaptation of a traditional mediterranean fishery facing regional change: combining history and ecology to study past, present and future of sponge harvesting
P32	Dr.	Vasilis	Gerovasileiou	Hellenic Centre for Marine Research	World Register of marine Cave Species (WoRCS): a tool for evaluating sponge diversity in marine caves and anchialine systems of the world
P33	Dr.	Vasilis	Gerovasileiou	Hellenic Centre for Marine Research	The availability of map resources for the distribution, degradation status and threats to sponge assemblages in the European Seas – initial baselines in the MERCES project
P34	Dr.	Deborah	Gochfeld	University of Mississippi	Geographic Variability in Antibacterial Chemical Defenses Among Branching Morphotypes of Caribbean *Aplysina*
P35	Dr.	Claire	Goodwin	Huntsman Marine Science Centre	Sponge Biodiversity of the shallow sublittoral Antarctic Peninsula
P36	Dr.	Claire	Goodwin	Huntsman Marine Science Centre	Engaging recreational SCUBA divers in recording sponge biodiversity
P37	Mr.	Nathan	Grant	University of Alberta	In situ arrests of glass sponge (Hexactinellida) feeding currents in response to suspended sediments
P38	Ms.	Marie	Grenier	CNRS	Prince Albert's underwater caves: Sponge fauna of unusual artificial reefs at Monaco
P39	Ms.	Sarah	Griffiths	Manchester Metropolitan University	Genetic Population Structure of *Ircinia campana* and *Spheciospongia vesparium* in the Greater Caribbean
P40	Ms.	Johanna	Gutleben	WUR	Integrating (Meta)genomics data into sponge symbiont cultivation
P41	Ms.	Ulrike	Hanz	NIOZ	Environmental drivers of deep-sea reefs
P42	Dr.	Kerry	Howell	Plymouth University	The distribution of Ostur in relation to physical variables within the Faroe-Shetland Channel
P43	Ms.	tal	idan	Tel Aviv university	Oases of diversity: East-Mediterranean mesophotic sponge grounds
P44	Mr.	Shriraj	Jakhalekar	CSIR National Institute of Oceanography, Goa, India.	Studies on sexual reproduction and secondary metabolite profile of the sponge *Ircinia fusca* (Carter) (Demospongiae: Dictyoceratida)
P45	Ms.	Liesl	Janson	Department of Environmental Affairs	Time to revisit the Western Indian Ocean Ecoregions and Hotspots: A Numerical Zoogeographical analysis using sponges as a case study
P46	Dr.	Dorte	Janussen	Senckenberg Research Institute and Nature Museum	Sponge communities of the Antarctic Peninsula: influence of environmental variables on species composition and richness
P47	Dr.	Amanda	Kahn	University of Alberta	How Do Glass Sponge Reefs Get Enough Food? Feeding And Excretion By The Glass Sponge *Aphrocallistes vastus*
P48	Ms.	Kathleen	Kaiser	Florida State University	Ecology of *Halichondria corrugata*, a Common Endemic species in the Northern Gulf of Mexico
P49	Dr.	Vyacheslav	Khalaman	Zoological Institute of Russian Academy of Sciences	Achilles' heels and trojan horse of the ecologically aggressive sponge *Halichondria panicea* (Pallas, 1766)
P50	Ms.	Shelly	Krueger	University of Florida	Shallow-Water Sponge Restoration in Florida Bay
P51	Dr.	Emilio	Lanna	Universidade Federal da Bahia	Today's environmental conditions influence in the tomorrow's reproduction of five tropical demosponges
P52	Dr.	Emilio	Lanna	Universidade Federal da Bahia	Reproductive cycle and fecundity of *Heteropia* sp. (Calcarea, Porifera): a putative non-indigenous sponge in the Atlantic Tropical Ocean
P53	Ms.	Lauren	Law	University of Alberta	Distribution, diversity, and function of glass sponge (Porifera, Hexactinellida) reefs in Hecate Strait, British Columbia, Canada
P54	Dr.	Michael	Lesser	University of New Hampshire	Using Compound Specific Isotopic Analysis of Amino Acids to Discern Trophic Mode in Sponges From Shallow to Mesophotic Depths
P55	Mr.	Sambhaji	Mote	CSIR-National Institute of Oceanography	*Cliona* aff. *viridis* as a possible bioindicator on a tropical coral reef experiencing multiple sources of stress
P56	Mr.	Joe	Marlow	Victoria University of Wellington	Bleaching recovery of a phototrophic bioeroding sponge
P57	Mr.	Joe	Marlow	Victoria University of Wellington	Photographic bioeroding sponges in turbid environments
P58	Ms.	Emily	McGrath	Victoria University of Wellington	Adaptive mechanisms and physiological effects of suspended and settled sediment on barrel sponges
P59	Dr.	Teresa	Morganti	Consejo Superior de Investigaciones Cientifica	A Trophic Niche Separation May Explain the Tight Coexistence of High (HMA) and Low (LMA) Microbial-Abundance Sponges
P60	Dr.	Benjamin	Mueller	University of Amsterdam	Coral cavities – Stable habitats with zero growth? Assessing potential growth rates and community changes in cryptic sponges
P61	Dr.	Gary	Murphy	University of Exeter	New approaches to quantifying bioerosion by endolithic sponge populations: applications to the coral reefs of Grand Cayman
P62	Dr.	Alice	Oprandi	Università degli Studi di Genova	Using siliceous spicules in the *Posidonia oceanica* "matte" to discover past dynamics of the sponge community
P63	Mr.	Huilong	Ou	Xiamen University	Research on Annual Growth and Large-scale Transplantation of The Marine Sponge, *Mycale phyllophila*
P64	Mr.	Andrea	Padiglia	University of Genova	Keratosa sponges stranded on the Sardinia coasts: a long term study
P65	Ms.	Robyn	Payne	University of the Western Cape	Demospongiae taxonomy and diversity at two sites within the Western Indian Ocean region
P66	Ms.	Jeannette	Perez	Universidad Simón Bolivar	Experimental manipulation in interspecific interactions among 3 species of sponges associated with roots of *R. mangle*.
P67	Ms.	Jeannette	Perez	Universidad Simón Bolivar	Spatial-temporal variation of natural sponge interactions associated with *R. mangle* roots in Morrocoy National Park, Venezuela.
P68	Mr.	Ulisses	Pinheiro	Universidade Federal de Pernambuco	Hatchability of gemmules in Spongillidae and Metaniidae (Porifera: Spongillida) at different inland waters
P69	Dr.	Autun	Purser	Alfred Wegener Institute for Polar and Marine Science	Sponges of the Langseth Ridge: Mapping sponge distributions under ice with a towed camera / sonar platform
P70	Ms.	Tia	Rabsatt	University of the Virgin Islands	An Analysis of the Relationship between Sponge Cover and Coral Recruitment
P71	Dr.	Ana	Ramos	Instituto Español de Oceanografía	Is the Gibraltar Strait the real southern boundary for Northeast Atlantic sponges?
P72	Prof.	Hans Tore	Rapp	University of Bergen	Sponge grounds of seamounts along the Arctic Mid-Ocean Ridge – Diversity, distribution patterns and oceanographic setting
P73	Prof.	Hans Tore	Rapp	University of Bergen	SponGES - Deep-sea Sponge Grounds Ecosystems of North Atlantic: an integrated approach towards their preservation and sustainable exploitation.
P74	Prof.	Claudio	Richter	Section Bentho-Pelagic Processes	Solitons shape Antarctic hexactinellid sponge communities
P75	Dr.	Pilar	Rios	Instituto Español de Oceanografía	Large-scale distribution of bird's nest sponge *Pheronema carpenteri* (Thomson, 1869) along Northwest African slope
P76	Dr.	Sven	Rohde	University of Oldenburg	Light dependent allelopathic activity of the tropic sponge *Pseudoceratina* sp.
P77	Dr.	Christine	Rooks	Centre for Geobiology, University of Bergen	Deep-sea sponges under stress: from nutrient sources to nutrient sinks?
P78	Mr.	Alberto	Rovellini	Victoria University of Wellington	Decadal dynamics of Indonesian sponge assemblage: roles of endogenous and exogenous drivers
P79	Dr.	Nisit	Ruengsawang	Rajamangala University of Technology Krungthep	Value-Added in Thai Pottery by Biological Materials from Freshwater Sponges
P80	Ms.	Juliet	Rugiero	University of the Virgin Islands	Effect of temperature stress on survival, pigmentation and regeneration of three Caribbean sponges
P81	Mr.	César Augusto	Ruiz Pinzon	Institut M&diterranéen de Biodiverité et d'Ecologie Marine et Continentale	Combining Metabarcoding and Metabolomics to better understand the ecological succes of Homoscleromorpha sponges in underwater caves

P82	Dr.	Laura	Schejter	Instituto Nacional de Investigacion y Desarrollo Pesquero - Consejo Nacional de Investigaciones Científicas y Técnicas	South Orkney Islands: a poorly sponge-studied region of the White Continent. Results of Argentinean Antarctic Cruises 2012 and 2014
P83	Dr.	Laura	Schejter	Instituto Nacional de Investigacion y Desarrollo Pesquero- Consejo Nacional de Investigaciones Científicas y Técnicas	Contribution to the description of *Fibulia myxillioides* (Burton, 1932) and new records of the species at Burdwood Bank, after 90 years of its unique collection date
P84	Dr.	Christine	Schönberg	University of Western Australia	Sponge science culture and demography
P85	Dr.	Christine	Schönberg	University of Western Australia	*Coelocarteria singaporensis* – an unexpected bioeroding sponge?
P86	Prof.	Peter J.	Schupp	Carl-von-Ossietzky University Oldenburg	Sponges don't like pumice, they like hard rock!
P87	Ms.	Megan	Shaffer	Victoria University of Wellington	Limited connectivity promotes cryptic speciation in *Tethya* spp.
P88	Dr.	Sigal	Shefer	Tel Aviv University	How to Protect a Mesophotic Sponge Ground – A Case Study
P89	Dr.	Anshika	Singh	National Inst. of Oceanography	Trade-off between growth, reproduction and spatial competition of the intertidal marine sponge *Cinachyrella* cf. *cavernosa*
P90	Prof.	Marc	Slattery	University of Mississippi	Biogeographic Connectivity of Sponge Communities in the Tropical Atlantic
P91	Ms.	Shirley	Sorokin	Primary Industries and Regions South Australia	Calcarea on the shelf edge of the Great Australian Bight, Australia
P92	Ms.	Shirley	Sorokin	Primary Industries and Regions South Australia	Dominance and diversity of deep-water sponges on the shelf edge and slope of the Great Australian Bight, South Australia
P93	Ms.	Tanja	Stratmann	NIOZ – Royal Netherlands Institute for Sea Research	Oxygen consumption and nutrient fluxes of deep-sea sponges
P94	Ms.	Holly	Trew	University of the West Indies	Patterns of *Cliona delitrix* prevalence in a near-shore artificial reef system
P95	Dr.	Remi	Tsubaki	Japan Agency for Marine Earth Science	Mutualistic relationship between host sponge *Spongia (Spongia)* sp. and its endosymbiotic bivalve *Vulsella vulsella*
P96	Ms.	Johanne	Vad	Heriot-Watt University	Environmental assessment of deep-water sponge grounds in relation to oil and gas activities: a Faroe-Shetland Channel case study
P97	Ms.	Marla	Valentine	Old Dominion University	Functional Redundancy in Tropical Marine Sponge Communities
P98	Ms.	Esther	van der Ent	Naturalis Biodiversity Center	Taxonomic, phylogenetic, microbial and ecological assessment of two coral-killing cyanobacteriosponges in the Spermonde Archipelago, Indonesia
P99	Ms.	Esther	van der Ent	Naturalis Biodiversity Center	The Biodiversity of the Sponge fauna from Martinique (Fr.)
P100	Dr.	Fleur	Van Duyl	Royal Netherlands Institute for Sea Research	Spatiotemporal variations in stable isotope signatures (delta13C and delta15N) of sponges on the Saba Bank, Caribbean Sea
P101	Dr.	Dexiang	Wang	Xiamen University	Sexual breeding of the red sponge *Mycale phyllophila* (Porifera: Demospongiae)
P102	Ms.	Mirthe	Wiltink	Wageningen University	Is Saba Bank becoming a 'sponge reef'?
P103	Mr.	Michael	Wooster	King Abdullah University of Science and Technology	Defense by association: sponge-eating fishes alter the small-scale distribution of Caribbean reef sponges

P104	Mr.	Erik	Wurz	Wageningen University and Research	Validation of recirculating *ex situ* aquaria systems for studying deep-water sponges: do individuals kept under ex situ conditions reflect physiological in situ performances?
P105	Ms.	Clairecynth	Yu	Marine Science Institute	The mariculture potential of the Philippine blue sponge *Xestospongia* sp. for the production of renieramycin
Molecular, Cell & Organismal Biology					
P106	Dr.	Patrick	Cabaitan	University of the Philippin	Gene expression dynamics accompanying the sponge thermal stress response
P107	Dr.	Cecilia	Conaco	University of the Philippines	Gene expression dynamics accompanying the sponge thermal stress response
P108	Ms.	Megan	Conkling	Florida Atlantic University	Cellular Model of Sponge-Sponge Associations
P109	Dr.	Thanos	Dailianis	Hellenic Centre for Marine Research	Transcriptomic reconstruction in *Spongia officinalis*: adjusting post- sequencing analyses to distinguish between host and prokaryotic symbionts
P110	Dr.	Lorenzo	Gallus	University of Genova	A molecular study of the tissue regeneration in the Demospongiae: the role of the TGF/BMP protein family
P111	Dr.	Deborah	Gochfeld	University of Mississippi	Histological and Ultrastructural Features of Aplysina cauliformis Infected with *Aplysina* Red Band Syndrome
P112	Dr.	Nelly	Godefroy	Université de Montpellier	Origin of animal cell homeostasis : new insights from a digestive cycle of carnivorous sponge *Lycopodina hypogea*.
P113	Ms.	Liv	Goldstein Ascer	University of São Paulo	Plastic additive changes contraction patterns in *Hymeniacidon heliophila*: a changepoint analysis.
P114	Dr.	Mirna	Halasz	Ruder Boskovic Institute	Towards an insight into the metazoan gene regulation and development: genome draft of the endemic freshwater sponge *Eunapius subterraneus*
P115	Dr.	Amanda	Kahn	University of Alberta	High Tolerance Of Hypoxia By The Deep-Water Boreal Sponge *Geodia barretti*
P116	Ms.	Vasiliki	Koutsouveli	The Natural History Museum of London	Inter-individual variability in the physiological state of *Geodia barretti*: differential expression and ultrastructural studies
P117	Ms.	Vasiliki	Koutsouveli	The Natural History Museum of London	Reproductive features of Antarctic demosponges from the orders Dendroceratida, Poecilosclerida and Haplosclerida (Porifera)
P118	Mr.	Lars	Kumala	University of Southern Denmark	Osculum dynamics and filtration activity studied in small single-osculum demosponge (*Halichondria panicea*) explants
P119	Dr.	Emilio	Lanna	Universidade Federal da Bahia	External and internal anatomy of *Cladocroce caelum* (Haplosclerida, Demospongiae)
P120	Dr.	Emilio	Lanna	Universidade Federal da Bahia	Sexual reproduction of *Dysidea janiae*, a tropical Dictyoceratida in association with a calcareous alga
P121	Prof.	Jose	Lopez	Nova Southeastern University	The Global Invertebrate Genomics Alliance: Keeping Pace with Evolution and Technology
P122	Dr.	Yulia	Lyupina	N.K. Koltsov Institute of Developmental Biology	Proteasome mechanism of adaptive plasticity of sea cold-water sponges
P123	Ms.	Stephanie	Munroe	Wageningen University	Optimization of Cryopreservation Methods for the Marine Sponge *Dysidea etheria*
P124	Mr.	Patryk	Nilsson	Division of Pharmacognosy	Exploring Specialized Metabolites in the Deep-Sea Arctic Sponge *Geodia hentscheli*
P125	Dr.	Julie	Olson	University of Alabama	Infection with *Aplysina* Red Band Syndrome results in biochemical and bacterial community changes to the holobiont
P126	Dr.	André	Padua	Universidade Federal do Rio de Janeiro	In vitro formation of chimaeric individuals after cell dissociation in a calcareous sponge
P127	Dr.	Marina	Pozzolini	Università delgi Studi di Genova	Recombinant Production Of Hydroxylated Collagen Polypeptides Derived From The Demospongia *C. reniformis*: A New Biotechnological Source Of Marine Collagen
P128	Dr.	Ana	Riesgo	The Natural History Museum of London	Recycling is the key: multi-analysis of incorporated silica from digested diatom frustules in Antarctic sponges
P129	Dr.	Jeffrey	Robinson	National Institutes of Health	Bibliometric Analysis Elucidates Historical Trends of Molecular, Cellular, and Genetics Research in Poriferan Taxa

P130	Mr.	Tim	Schol	Wageningen UR	A cost-efficient method of DNA barcoding of sponge communities with Illumina MiSeq Next Generation Sequencing
P131	Ms.	Megan	Shaffer	Victoria University of Wellington	Influence of temperature on reproduction of temperate *Tethya* spp.
P132	Ms.	Karin	Steffen	Uppsala University	Getting started with the whole genome sequencing project of the demosponge *Geodia barretti*
P133	Ms.	Tone	Ulvatn	University of Bergen	Barcode first, identify later? Testing the use of a reverse taxonomic approach to assess the demosponge community composition in an Arctic seamount
P134	Ms.	Vivian	Vasconcellos	Universidade Federal da Bahia	Spermatogenesis of the poecilosclerid *Tedania ignis* (Porifera, Demospongiae)
P135	Ms.	Alice	Webb	NIOZ	The mechanisms underlying carbonate dissolution by excavating sponges: pH reduction and cell differentiation