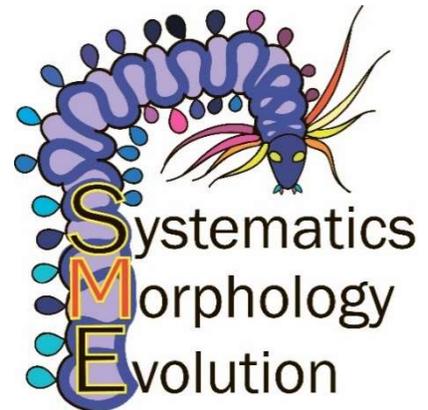


# ForBio and MEDUSA course: Systematics, Morphology and Evolution of Marine Annelids

14-16 April 2020, University Museum of Bergen

Virtual symposium

Time zone: GMT+2



## Keynote speakers:

**Alexander Tzetlin**, Moscow State University, RU

**Torsten Struck**, Natural History Museum, University of Oslo, NO

**Ken Halanych**, Auburn University, US

**Bruno Pernet**, California State University, Long Beach, US

**Andreas Hejnol**, Department of Biological Sciences, University of Bergen, NO

**Anna Zhadan**, Moscow State University, RU

**Vasily Radashevsky**, National Scientific Center of Marine Biology, Russian Academy of Sciences, RU

**Elena Kupriyanova**, Australian Museum, AU

**Luke Parry**, University of Oxford, UK

**Chema Martín-Durán**, School of Biological and Chemical Sciences, Queen Mary University of London, UK

**Conrad Helm**, University of Göttingen, GR

**Nataliya Budaeva**, University Museum of Bergen, University of Bergen, NO

**Nadezhda Rimskaya-Korsakova**, Moscow State University, RU

**Glafira Kolbasova**, Moscow State University, RU

[LOCAL TIME FOR EACH PRESENTER ADDED IN PARENTHESES IF DIFFERENT FROM NORWEGIAN TIME]

## 14 April **SYSTEMATICS & PHYLOGENY**

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- 08:50 **Nataliya Budaeva.** Welcome and short overview of the course.
- 09:00 Lecture: **Torsten Struck.** Phylogenetic position of Annelida and the problem to resolve the phylogeny of Lophotrochozoa.
- 09:50 Minibreak (10 min)**
- 10:00 (9:00) Lecture: **Luke Parry.** Fossil annelids.
- 10:50 Minibreak (10 min)**
- 11:00 (18:00) Student: **Chloé Julie Lois Fourreau.** Environmental features structure genetic diversity in the cryptic species complex of *Aricidea assimilis* (Tebble, 1959).
- 11:20 Student: **Miguel Meca.** Diversity of *Orbiniella* (Orbiniidae, Annelida) in the Nordic seas.
- 11:40 Lunch (1 h)**
- 12:40 (13:40) Lecture: **Anna Zhadan.** Methods of annelid collecting and fixation.
- 13:30 Minibreak (10 min)**
- 13:40 Lecture: **Torsten Struck.** Cryptic species and their evolutionary and ecological importance.
- 14:30 Minibreak (10 min)**
- 14:40 (15:40) Student: **Polina Borisova.** Phylogeny of Lumbrineridae (Annelida): a first molecular approach.
- 15:00 Student: **Martin Mejdell Hektoen.** Phylogeny and species delimitation of *Diopatra* (Annelida, Onuphidae) in the East Atlantic.
- 15:20 (16:20) Student: **Martha Everett.** Molecular and morphometric analyses reveal highly underestimated diversity in *Eteone* (Phyllodocidae, Annelida).
- 15:40 Break (20 min)**
- 16:00 (9:00) Lecture: **Ken Halanych.** Phylogeny of annelids.
- 16:50 Summary of the day

**15 April**

**MORPHOLOGY**

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09:00

Lecture: **Conrad Helm**. Comparative insights into the morphology of Annelida.

**09:50**

**Minibreak (10 min)**

10:00 (11:00)

Lecture: **Glafira Kolbasova**. Morphology and development of chaetae and mechanisms of chaetal replacement.

**10:50**

**Minibreak (10 min)**

11:00 (12:00)

Lecture: **Nadezda Rimskaya-Korsakova**. Segment formation in annelids. Lessons of siboglinids' studies.

**11:50**

**Lunch (1 h 10 min)**

13:00 (14:00)

Student: **Timofei Pimenov**. Structure of the brain in sabellid species (Annelida, Sabellidae) *Euchone analis* and *Bispira manicata*.

13:20 (14:20)

Student: **Dmitry Fedorov**. Ultrastructure of the myzostomid parenchyma: an advice from *Myzostoma echinus* Graff, 1884 and *Hypomyzostoma jasoni* Summers & Rouse, 2014 (Myzostomida, Annelida).

**13:40**

**Minibreak (10 min)**

13:50

Lecture: **Nataliya Budaeva**. Diversity and morphology of annelid jaws.

**14:40**

**Break (20 min)**

15:00 (16:00)

Lecture: **Alexander Tzetlin**. Diversity of annelid diets.

**15:50**

**Minibreak (10 min)**

16:00

Student: **Paul Kalke**. May the Palps be with you - Morphology and innervation of head appendages in Terebelliformia.

16:20

Summary of the day

**16 April**

**DEVELOPMENT AND LIFE HISTORIES**

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- 9:00 (17:00) Lecture: **Elena Kupriyanova**. Diversity of annelid life histories.
- 9:50 Minibreak (10 min)**
- 10:00 (15:00) Lecture: **Vasily Radashevsky**. Evolution of life histories in Spionidae.
- 10:50 Minibreak (10 min)**
- 11:00 (18:00) Student: **Nur Fazne Ibrahim**. Taxonomy and reproductive biology of Nypa worms, *Namalycastis* spp. (Nereididae: Namanereidinae) in Setiu Wetlands, Terengganu, Malaysia.
- 11:20 (12:20) Student: **Alexandra Shalaeva**. FGF signaling pathway during regeneration of the polychaete worm *Alitta virens*.
- 11:40 Student: **Ole Brodnicke**. Cryptobenthic diversity changes in coral sand due to coral reef degradation.
- 12:00 Long lunch break (3 h)**  
**Discussion of student award (lecturers only)**  
**15 min in the beginning of the lunch break**
- 15:00 Lecture: **Andreas Hejnal**. Early development in annelids.
- 15:50 Minibreak (10 min)**
- 16:00 (15:00) Lecture: **Chema Martín-Durán**. A developmental and genomic perspective on the evolution of Annelida.
- 16:50 Minibreak (10 min)**
- 17:00 (8:00) Lecture: **Bruno Pernet**. Functional morphology and evolution of larval feeding in annelids.
- 17:50 Closing remarks and student awards

# Student presentations

## Abstracts:

### **Environmental features structure genetic diversity in the cryptic species complex of *Aricidea assimilis* (Tebble, 1959)**

Joachim Langeneck <sup>1</sup>, Chloé Julie Loïs Fourreau <sup>2</sup>, Alberto Castelli <sup>1</sup>

<sup>1</sup> University of Pisa

<sup>2</sup> University of the Ryukyus

*Aricidea assimilis* (Tebble, 1959) is a species of Paraonidae inhabiting soft bottoms of the Mediterranean sea. It has been regarded as a potential cryptic species since Laubier and Ramos noted wide morphological variations in the branchiae and antennae. To test this hypothesis, the molecular diversity of specimens morphologically assigned to *A. assimilis* has been investigated. 85 specimens have been collected in the Tyrrhenian and Adriatic seas, ranging from 0.5m to 225 m depth. Two mitochondrial markers (16S, COI) and one nuclear marker (ITS2) have been amplified. Haplotype networks and concatenated Bayesian phylogenetic tree retrieved two highly divergent lineages. There was no clear relationship between molecular and morphological variations. However, the lineages were clearly distinguished by depth; one “deep” lineage corresponded to specimens of 70-225 m, and one “shallow” lineage to 0.5-10 m depth. Within the shallow lineage, specimens were furthermore differentiated between brackish and marine environments. PTP and ABGD species delimitation tests supported the two main lineages separation into a shallow and a deep species. The shallow brackish and shallow marine lineages are considered incipient species. Additionally, the haplotype networks showed a high genetic connectivity within each lineage, with haplotypes shared between Adriatic and Tyrrhenian sea, suggesting *A. assimilis* may have a larval stage. Thus, this study suggests that environmental features play a much more important role than biogeography in structuring genetic diversity of *A. assimilis*. Molecular data shows that depth and correlated factors can ultimately drive speciation in Paraonidae, and also gives novel insight into the elusive development of this group.

## Diversity of *Orbiniella* (Orbiniidae, Annelida) in the Nordic seas

Miguel A. Meca<sup>1\*</sup>, Jon Anders Kongsrud<sup>1</sup>, Katrine Kongshavn<sup>1</sup>, Tom Alvestad<sup>1</sup>, Karin Meißner<sup>2</sup>,  
Anna Zhadan<sup>3</sup>, Nataliya Budaeva<sup>1</sup>

<sup>1</sup>Department of Natural History, University Museum of Bergen, University of Bergen, Bergen,  
Norway

<sup>2</sup>Senckenberg Forschungsinstitute und Naturmuseum, German Centre for Marine Biodiversity  
Research, Hamburg, Germany

<sup>3</sup>N.A. Pertsov White Sea Biological Station, Biological Faculty, M.V. Lomonosov Moscow State  
University, Russia

*Orbiniella petersenae* Parapar, Moreira and Helgason, 2015 was described based on formalin fixed material from two different areas in a large depth range. Most of the specimens (including the holotype) were collected on the slope northeast of Iceland, in Arctic cold, deep waters (-0.7 to -0.8°C; 1490 to 1915 m), whilst the rest of them were found on the shelf and slope (133 to 1007m depth) southwest of Iceland, in the north-eastern Atlantic, warmer waters (4.8 to 7.4°C). Ethanol preserved material of *Orbiniella* collected between 2010 and 2016 during the Norwegian and German scientific expeditions and monitoring programs allowed analysing genetic divergence and phylogenetic relationships among several populations inhabiting different depths (shelf, slope and abyssal) and water masses (north-eastern Atlantic, Norwegian and Greenland Seas). Our analyses based on two mitochondrial (COI and 16S) and one nuclear marker (ITS2) showed the presence of at least five well supported clades in the studied area. One clade was from shallow waters (171-781m) along the Norwegian and the South Iceland shelves and the Faeroe-Iceland ridge, whilst the other four clades were from the deep waters (1574-3356 m). Two of the deep-sea clades demonstrated overlapping distribution in the deep Norwegian Sea. The other two deep clades were from southwest of Iceland and from the northern Greenland Sea. Our preliminary morphological analysis showed minor differences in the shape of prostomium, peristomium, parapodia and hooks between the five clades, which could be used to discriminate and characterize them. However, the two deep clades with overlapping distribution exhibited some intermediate forms with no clear differentiation among them. The type locality of *O. petersenae* overlaps with the distribution of two deep clades from the Norwegian sea which makes it difficult to assign one of the genetic clades to the species name *O. petersenae*. Examination of the holotype might aid in finding morphological characters differentiating *O. petersenae* from the rest of the recovered clades.

# Phylogeny of Lumbrineridae (Annelida): a first molecular approach

Polina Borisova<sup>1</sup>, Nataliya Budaeva<sup>2</sup>

<sup>1</sup> P.P. Shirshov Institute of Oceanology, Russian Academy of Sciences, Russia

<sup>2</sup> Department of Natural History, University Museum of Bergen, University of Bergen, Norway

Lumbrineridae comprise over 200 described species grouped in 19 genera. The most important diagnostic characters for genera and species are found in the maxillary structures. To date, no molecular studies specifically on lumbrinerid phylogeny have been conducted, many genera completely lack molecular data. In the present study, we reconstructed phylogeny of the family and test the monophyly of currently accepted genera based on combination of nuclear 18S and 28S rDNA and mitochondrial 16S rDNA and COI genes. We also studied morphology of jaw apparatuses in eight species using micro-CT. Our results contradict the previously published morphology-based phylogeny in relationships between the genera. Type genus, *Lumbrineris*, appeared paraphyletic, while *Ninoe* and *Gallardoneris* were monophyletic. Several characters of jaw morphology previously seen as synapomorphies of large clades were shown to be homoplastic.

# Phylogeny and species delimitation of *Diopatra* (Annelida, Onuphidae) in the East Atlantic

**Martin Mejdell Hektoen<sup>1,2</sup>, Nataliya Budaeva<sup>3</sup>, Endre Willassen<sup>3</sup>**

<sup>1</sup> Åkerblå AS, Trondheim, Norway

<sup>2</sup> NTNU University Museum, Norwegian University of Science and Technology, Trondheim, Norway

<sup>3</sup> Department of Natural History, University Museum of Bergen, University of Bergen, Bergen, Norway

*Diopatra* Audouin & Milne Edwards, 1833 is the most species-rich genus of onuphid bristle worms with 65 currently recognized species worldwide, 24 reported from the East Atlantic. They are widely distributed in tropical and subtropical waters and are important habitat engineers in the intertidal zone due to their robust tubes. The genus has several distinct autapomorphies such as spiral shaped branchiae and serrated limbate chaetae, but the systematics and taxonomy within the genus is still relatively poorly understood. The aim of this study was to review the species occurring in the East Atlantic. Approximately 900 specimens from 133 stations collected from the West African coast between Morocco and Angola between 2005 and 2012 were studied, as well as historic material described by Augener (1918) and Kirkegaard (1988). A phylogeny based on the mitochondrial markers COI and 16S rDNA, and the nuclear marker 28S rDNA was constructed. 110 specimens were selected for molecular analysis, and 76 specimens had at least one genetic marker successfully amplified. *Diopatra*, including the synonymized genus *Epidiopatra* Augener, 1918, was retrieved as monophyletic with five distinct subclades all delimited by clear morphological synapomorphies. Morphology and molecular species delimitation (bPTP and BPP) were used to estimate species diversity. We recognize 31 species from our material, 18 of which are new to science. In addition, a cryptic species complex comprising between one and 12 species showing pedomorphic characteristics was left unresolved due to poor sampling leading to ambiguous delimitation results.

# Molecular and morphometric analyses reveal highly underestimated diversity in *Eteone* (Phyllodocidae, Annelida)

**Martha Everett<sup>1</sup>, Glafira Kolbasova<sup>1</sup>, Nataliya Budaeva<sup>2</sup>, Tatiana Neretina<sup>3</sup>**

<sup>1</sup>Department of Invertebrate Zoology, M.V. Lomonosov Moscow State University, Russia

<sup>2</sup>Department of Natural History, University Museum of Bergen, University of Bergen, Norway

<sup>3</sup>N.A. Pertsov White Sea Biological Station, Biological Faculty, M.V. Lomonosov Moscow State University, Russia.

Genetic diversity of the genus *Eteone*, Savigny, 1820 (*Phyllodocidae*) was studied using mitochondrial (COI, 16S) and nuclear (18S) markers. The material was obtained mostly from the White Sea but also included specimens from the Sea of Okhotsk, the Barents Sea, the Norwegian Sea, the North Sea, the Greenland Sea, and the West coast of Africa. Our study discovered five monophyletic clades of *Eteone* from the White Sea and more than 16 clades altogether among the examined material. The morphological study revealed five morphotypes in the White Sea differing in the shape of the prostomium, parapodia and dorsal and ventral cirri, and in the structure of the proboscis. Previously only two species of *Eteone* (*E. flava* and *E. longa*) were reported from the White Sea. The relation between *Eteone* and genera *Mysta*, Malmgren, 1865 and *Hypereteone*, Bergstrom, 1914 was investigated. *Mysta* and *Hypereteone* ended up inside the *Eteone* clade, which casts doubt on their separation. Our results suggest that further revision of *Eteone*, *Mysta*, and *Hypereteone* utilizing genetic data should be performed in the study area and world-wide.

# Structure of the brain in sabellid species (Annelida, Sabellidae) *Euchone analis* and *Bispira manicata*

Timofei Pimenov<sup>1</sup>, Nadezhda Rimskaya-Korsakova<sup>1</sup>

<sup>1</sup> Department of Invertebrate zoology, Lomonosov Moscow State University

Sabellidae are the peculiar sedentary annelid tubeworms inhabiting wide range of marine environments, such as shallow water soft-bottoms or crevices of rocks and corals. They use the unique highly specialized radiolar crown for sedimentation of suspended particles. Sabellid radiolar crown and the phylogenetic position of the whole group at the base of sedentary annelid clade make fan worms a potential key to unravel the organization of the common sedentary annelid ancestor and the functional morphology patterns of the innervation of the anterior appendages in the family. The studied species *Euchone analis* and *Bispira manicata* represent two main sabellid clades which differ morphologically and ecologically. We investigated the structure of the brain and innervation of the anterior appendages by means of histology, light microscopy and 3D reconstructions. The brains and anterior nerves of both species possess the same gross patterns of organization but the particular differences in form of clusters of perikarya and neuropiles and in location of the roots of the anterior nerves relative to the skeleton and muscles of the radiolar crown. The brains of both species consist of three pairs of main clusters of perikarya. The brain neuropile include three commissures of two roots of circumesophageal connectives. The radiolar crown is innervated by three pairs of nerve bundles, two of which fuse at the base of radioles and then divide into pairs of longitudinal nerves of the oral side of each radiole. Another pair of nerve bundles gives rise to the paired longitudinal nerves running along the aboral side of each radiole. The elements of the brain and anterior nerves are more compact and distinct in *E. analis*, than in *B. manicata*. Found variations in the brain and the anterior nerves' organization are caused by features of the gross anatomy of the anterior end of the body, configuration of the branchial crown skeleton and mouth cavity. Thus, the feeding diet and habitats of the investigated species determine the variation of the brain structures and innervation of the anterior appendages in *E. analis* and *B. manicata*.

**Ultrastructure of the myzostomid parenchyma: an advice from *Myzostoma echinus* Graff, 1884 and *Hypomyzostoma jasoni* Summers & Rouse, 2014  
(Myzostomida, Annelida)**

**Dmitry A. Fedorov<sup>1</sup>, Glafira D. Kolbasova<sup>2</sup>, Alexandr B. Tzetlin<sup>2</sup>**

<sup>1</sup>Skolkovo Institute of Science and Technology, Moscow, Russia

<sup>2</sup>Lomonosov Moscow State University, Biological Faculty, Moscow, Russia

Among all the known annelids, Myzostomida have a very unusual body plan, being incompletely segmented, acoelomate and parenchymous. Nevertheless, the fine anatomy and development of myzostomids is still poorly studied. The most of available data on their ultrastructure has been obtained on only species *Myzostoma cirriferum* Leuckart, 1836 that is a small-sized myzostome with thin parenchymal layer. In *M. cirriferum* the myoepithelium was detected only within the epidermal tissue. We studied two large species *Myzostoma echinus* Graff, 1884 and *Hypomyzostoma jasoni* Summers & Rouse, 2014, that may have the parenchymal layer up to 0.5 cm thick. According to our data, parenchyma in *M. echinus* and *H. jasoni* is formed by the mesodermal myoepithelium. The parenchymal cells are connected via desmosomes and form numerous meandering protrusions. In general, the structure of parenchyma in *H. jasoni* and *M. echinus* is similar with the mesoderm structure in some Phyllodocidae and Cossuridae, that have vascular system reduced. The new data on the myoepithelial origin of the parenchyma allow us to take a fresh look on the organization of the reproductive and excretory systems in Myzostomida.

# **May the Palps be with you - Morphology and innervation of head appendages in *Terebelliformia***

**Paul Kalke<sup>1</sup>, Patrick Beckers<sup>2</sup> and Conrad Helm<sup>1</sup>**

<sup>1</sup>Department of „Animal Evolution and Biodiversity“, Helm Lab, Institute for Zoology and Anthropology, University of Goettingen, Untere Karspuele 2, 37073 Goettingen

<sup>2</sup>Institute for Evolutionary Biology and Ecology, University of Bonn, An der Immenburg 1, 53121 Bonn

Annelids are worldwide distributed and could be found in nearly all conceivable habitats. As their lifestyles and biotopes, their morphology shows a vast range of diversity. A key structure explaining the evolutionary success of this old group and having a strong impact on the understanding of systematic questions are the head appendages of annelids. We can find grooved feeding palps, several numbers of antennae, cirri and tentacles, feather crowns and branchiae to whole groups without any. These diversity of sometimes unique sometimes widely spread morphological features are distributed along the often old groups and families of annelids, which make it difficult to homologise them. One of these highly discussed groups are the Terebelliformia comprising e.g. Ampharetidae, Terebellidae and Pectinariidae which all bears for example numerous tentacles originating at different parts of the head. The classification of these and a lot more of head appendages spread around the annelid tree is still unclear and need further investigations. For that reason we use an integrative morphological approach including immunohistochemical stainings and subsequent clsm analyses, serial azan sections as well as  $\mu$ -CT data to analyse the morphology and innervation patterns of the anterior appendages in Terebelliformia. Our data give an overview of neuroanatomical characteristics of the appendages of interest, and provide new insights for our understanding of the evolution of annelid head appendages and the evolution of Annelida in general.

# Taxonomy and reproductive biology of Nypa worms, *Namalycastis* spp. (Nereididae: Namanereidinae) in Setiu Wetlands, Terengganu, Malaysia

Nur Fazne Ibrahim<sup>1</sup>, Yusof Shuaib Ibrahim<sup>2</sup>, Izwandy Idris<sup>1</sup>

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<sup>2</sup> Faculty of Science and Marine Environment (FSME), Universiti Malaysia Terengganu, 21030, Kuala Nerus, Terengganu, Malaysia.

Nypa worms, or polychaete are among the dominant invertebrate communities in the mangrove ecosystems and are important as bioturbator and keystone species. However, research regarding this species is still meagre in Malaysia. Therefore, this study of one-year duration was conducted to gather the information on taxonomy, reproductive biology and distribution of the nypa worms, *Namalycastis* spp. in Setiu Wetlands, Terengganu. A total of 508 individuals of the nypa worms was collected and identified as *Namalycastis multiseta* (n= 495), *N. rhodochorde* (n= 1) and *N. sp. 1* (n= 12). *Namalycastis multiseta* differs from *N. rhodochorde* by having Type A neurochaeta, while *N. rhodochorde* has Type C. In addition, the number of sesquigomph spiniger of the *N. multiseta* is up to 30 at the mid to posterior body, as compared to the *N. rhodochorde* which has 2–6 sesquigomph spiniger at the whole body. The *Namalycastis sp. 1* is distinguished from other species by lack of notochaeta and of whitish whole dorsal body color. In reproductive aspect, the results of the dominant species of *N. multiseta* revealed that the gonochoric species was comprised of immature, sub-matured and nearly matured individuals, with the female and male ratio closely 1:1. They practice semelparous reproductive pattern with one spawning season detected at the end of year 2015. The fecundity data was in range of 380±100 to 21000±100 eggs per 10 chaetigers, with the mean oocyte diameter between 32–120 µm. In terms of the habitat preference, all species were found in the rotten nypa fronds where the area was characterized by medium sand type (1–2 φ), with moderately sorted (0.78–1.16 φ) and negatively skewed sediment. The worms also showed a preference towards the mangrove area of high total organic matter content (7–75 %). The present study highlighted the *N. multiseta* as a new record in Malaysia and the second record worldwide. The species is also documented as the third species under the Genus *Namalycastis* in Malaysia.

## **FGF signaling pathway during regeneration of the polychaete worm *Alitta virens***

**Alexandra Yu. Shalaeva, Roman P. Kostyuchenko, Vitaly V. Kozin**

Saint Petersburg State University, Russia

Epimorphic regeneration is a complex process consisting of multiple stages, the most intriguing of which is blastema formation. Blastema initiation in vertebrates is known to depend on fibroblast growth factors (FGF) signaling. However for invertebrates, which show outstanding regenerative abilities, there are only a few such works, interestingly enough none of which are dedicated to spiralian. Our research for the first time shows not only a variety of FGF ligands and receptors but provides valuable insight into their spatiotemporal expression and functions in this process in *Alitta virens* (Spiralia, Annelida). We found in *A. virens* two genes encoding FGF ligands and two genes of their receptors. Phylogenetically both ligands are placed into FGF8/17/18 subfamily and receptors' sequences are associated with such of other Spiralian animals. In situ hybridization on both ligands and receptors demonstrate an early response to the amputation as soon as during the first day of regeneration. For the ligands, tissue specificity varies and the signal decreases as regeneration progresses over time. Noteworthy, their expression dynamics correlates with those found for receptors. The critical requirement of FGF signaling, especially on early stages, is also supported using inhibitors of this pathway followed by proliferation assay which demonstrates that blastemal cells are dependent on those molecules. Our results suggest it is FGF signaling, which enables regenerative response, while the ventral nerve cord and some mesodermal cells around the gut could be the place where the signal for it originates. This mechanism seems similar to vertebrates assuming such a response to the injury could be ancestral for bilaterians.

# Cryptobenthic diversity changes in coral sand due to coral reef degradation

Ole Brodnicke<sup>1</sup>, Kim Præbel<sup>2</sup>, Michael Sweet<sup>3</sup>, Katrine Worsaae<sup>1</sup>

<sup>1</sup> Marine Biological Section, Copenhagen University, Denmark

<sup>2</sup> Norwegian College of Fishery Science, University of Tromsø, Norway

<sup>3</sup> College of Science and Engineering, University of Derby, England

Healthy coral reefs harbour a staggering diversity of fishes and invertebrates. The function of fishes and some meiofauna has been well described. However, most of them are rarely seen and surveyed, as many species are small, camouflaged and hidden. These unseen, elusive 'cryptobenthic' fishes have been shown to be pivotal in sustaining the high productivity of coral reefs and they in turn feed on meiofauna. In this project, we therefore propose to document in detail for the first time the diversity of benthic fauna on coral reefs throughout the Maldives archipelago. Furthermore, we assess how reef health results in variations in the number and diversity of meiofauna (mainly annelids) and cryptobenthic reef fish. An effort likely yielding several new species. Another novel aspect of this project is our proposed use of environmental DNA (eDNA) to document the diversity of these otherwise elusive species. eDNA has already shown promise in many ecosystems to describe and catalogue rare, endangered or elusive species. Development of such a tool in collaboration with local governmental stakeholders extends the toolbox available to marine biologists and conservationists at lower cost, higher accuracy and with relatively little effort compared to traditional coral reef diversity surveys. Based on eDNA samples and physical specimen collection we will through phylogenetic analysis identify changes in connectivity of selected meiofaunal and cryptobenthic reef fish populations constituting a range of dispersal strategies such as reproductive strategies (spawning, brooding etc). Furthermore, a recent approach to assess trophic interactions has been trailed in which fish guts have been sampled for eDNA to establish diet preferences. By applying this approach to fish collected from reefs with various degrees of degradation we will be able to document the importance of meiofauna in their diet as well as diet plasticity. Contrasting diet plasticity, dispersal capabilities and habitat preferences of the keystone species investigated with the environmental measures of reef degradation will reveal how prone these are to climate change and ultimately local extinction. Conclusively, this study will enable us to evaluate how important species in the benthic community of coral reefs are impacted by climate change.