# A variety of interactions in the marine environment

# ABSTRACTS VOLUME FROM 49TH EUROPEAN MARINE BIOLOGY SYMPOSIUM

September 8–12, 2014
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Zoological Institute Russian Academy of Sciences

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Dear Participants,

Zoological Institute of Russian Academy of Sciences is pleased to welcome you in St. Petersburg, Russia at 49th EMBS. More than 200 scientists from 30 countreis take part in the Symposium presenting more than 70 oral talks and about 100 posters.

The aim of the meeting is to facilitate exchange of information, to stimulate new ideas, to promote collaborations and encourage new projects in marine biology. We hope you enjoy the 49th EMBS and keep a splendid memory of the wonderful city of Saint Petersburg.

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# KEY NOTE TALKS

## A COMPARISON ON THE DEGREE OF IMPLEMENTATION OF MARINE BIODIVERSITY INDICATORS BY EUROPEAN COUNTRIES IN RELATION TO THE MARINE STRATEGY FRAMEWORK DIRECTIVE (MSFD)

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[4]see footnote

In the last few years in the European countries of the EC the onset for the implementation of the Marine Strategy Framework Directive (MSFD) has been given which has to result in a description and plan for reaching Good Environmental Status (GES) of the European marine water bodies by 2020.

In a survey for 20 different European countries, the actual status and developments on Descriptor 1 of the MSFD (Biodiversity) or in related directives and legislation were determined by compiling and analyzing the documentation available for each country.

Criteria for the analysis were the ecological relevance of a proposed biodiversity indicator as being realistically representing biodiversity, and level of implementation of an indicator as being still under discussion or already in operation.

For the evaluation of the relevance of being a proper biodiversity indicator a value of 1 to 5 was given per indicator proposed by each country. Similarly, for the degree of implementation, i.e. the operationability, also a value of 1 to 5 was given.

Marked differences were found between countries in the description and in the development of the indicators for marine biodiversity as well as in the degree of implementation.

Although the MSFD descriptor for biodiversity seemed to be worked out rather exhaustively (itemized with many indicators) in many countries, at more detailed observation it became clear that most indicators are general statements and not fixed parameters nor specific species, as was often usual too in other official systems and classifications as the Water Framework Directive (WFD).

The conclusion from the available documentation was that no consistent and harmonized approach for describing marine biodiversity with concrete indicators at a pan-European level can be found. Most European countries are not well prepared to introduce the MSFD and most descriptors are not properly bottom-up science driven, nor well-described, biodiversity indicators.

The best prepared countries were UK and Latvia, the worst the Netherlands. The first two countries had involved many scientists in a bottom-up process to select relevant biodiversity indicators, the latter country used a top-down (political driven) approach resulting in hardly any relevant indicator for biodiversity at all.

A couple of countries outside the EC, as Turkey and Russia, showed a remarkable tendency for implementing a similar system as the MSFD in a more advanced way than their EC counterparts.

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## PARASITES ON THE EDGE: PATTERNS AND PROCESSES IN PARASITE TRANSMISSION IN ARCTIC COASTAL ECOSYSTEMS

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Parasites compose about 50% of the total biodiversity. It is becoming clear that they may influence the composition, structure and dynamics of populations and communities of free-living organisms. In particular, parasites dramatically affect coastal marine ecosystems. Parasite transmission there has recently received close attention but there studies have mostly been confined to the temperate zone, with only a few carried out in the Arctic and the Subarctic. The interest in the area, however, is steadily growing, not the least because of the global climate warming, which is especially pronounced there. Prolongation of the warm season, the reduction of the ice cover and the changing structure of currents are likely to modify the structure and dynamics of the Arctic marine ecosystems. Such modifications, which are already being recorded, are likely to involve the parasites as well. In my communication I will characterize the circulation of parasites in the coastal ecosystems of the Arctic seas, highlighting specific features in their species composition, life cycles and transmission ways. The focus will be on the parasites of seabirds from the coasts of Franz Josef Land, Svalbard, Novaya Zemlya and Vaigach. The role of biotic and abiotic factors, including anthropogenic ones, in the formation of parasitic infection of coastal marine invertebrates will be analyzed. I will show that this process is governed by a complex interaction of large-scale factors (e.g., surface seawater temperature) and local factors (the biotope, host species community structure at a given site etc.). Trematodes, the most common parasites in coastal communities, will serve as a background for highlighting the key role of temperature in the parasite transmission. A consequence of climate warming that will be considered is the widening of the “transmission window”, that is, the duration of the warm period when parasites can develop and infect new hosts. This widening may result in a cascade effect, with infection transmission intensifying along the chain of hosts involved in the parasite’s life cycle.

## REGIME SHIFTS IN MARINE BENTHIC ASSEMBLAGES

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Regime shifts involve abrupt and persistent changes in the structure and functioning of species assemblages and they are increasingly described in marine benthic ecology. Examples include the shift of coral reefs into macroalgal stands, the replacement of canopy algae by turf-forming species and the transformation of algal stands into barren habitat. These phenomena are typical of complex system with nonlinear dynamics and suggests common underlying causes leading to catastrophic transitions, such as positive feedbacks maintaining alternative states and tipping points. These transitions are often associated with significant losses in ecosystem services, so the ability to anticipate them has profound implications for ecosystem management and conservation. Generic indicators of incipient regime shifts have been derived building on the prediction from catastrophe theory that recovery from small perturbations – i.e. resilience – should slow down in the proximity of a tipping point, a phenomenon known as critical slowing down. As a consequence of critical slowing down, a system approaching a catastrophic bifurcation has a longer memory for perturbations and this results in characteristic fluctuations such as enhanced autocorrelation and variance. Real-world experiments of these predictions remain rare. I will provide an example using data from a long-term (7 years) ecological experiment in a rocky intertidal assemblage where reduced biomass of algal canopies promotes invasion of turf-forming algae, ultimately driving understory assemblages towards collapse. Results suggest that critical transitions can be anticipated in this system and pave the way for further experimental evaluation of critical slowing down in other marine benthic assemblages.

# BIOGENIC MODULATION OF ENVIRONMENTAL STRESS

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Most of our experiments do not adequately reflect what is going on in the natural environment. Apart from many other short-comings we tend to work with rigorously constant and tightly controlled conditions, whereas in nature many variables fluctuate at different frequency and amplitude. Thus, our results typically inform about the potential impact of a factor, but not the real one. Environmental fluctuations are generated by non-living mechanisms (upwelling, currents, seasons, NAO) interacting with biological processes such as photosynthesis and respiration. In addition, interactions among drivers and among the responding species may very substantially modulate the single factor/single species effects identified by most of our studies. Only if we up-scale simultaneously along several dimensions can we hope to produce results which advance our understanding of natural and anthropogenic change in ecosystems. Focussing on the presently popular field of ocean acidification I will highlight the scales of natural fluctuations in pH and/or $pCO_2$. I will then summarize the very sparse knowledge on the biological relevance of stressor fluctuations. Finally, I will conclude by some recommendations for a more holistic, less reductionist, and hopefully more realistic research.

# ORAL PRESENTATIONS

## *Organism – environment coupling*

### CARDIAC RESPONSES OF BLUE MUSSELS (*MYTILUS EDULIS*) AND HORSE MUSSELS (*MODIOLUS MODIOLUS*) TO SEASONAL IN TEMPERATURE AND PHYTOPLANKTON CONCENTRATIONS

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We monitored *in situ* over a full year cycle the physiological (heart activity), biological (reproductive status) and morphological (condition index) characteristics of the indicator species – blue mussels (intertidal and subtidal zones) and horse mussels of the White Sea – affected by specific physical (light, temperature, ice cover, salinity) and biological (food availability) conditions. We used cardiac activity of Bivalvia because it is usually fast and thus potentially suitable for a fast response in continuous biological monitoring. Moreover, it has been proven in experiments with animals that changes and variations in mussel heart rate correlate significantly with various natural factors (Marshall and McQuaid, 1993, 1994; Santini et al., 2000; Bakhmet et al., 2005). The heart rate was monitored by a non-invasive method derived from the technique of Depledge and Andersen (1990). The sensor consisted of an infra-red light-emitting diode axially coupled with a phototransistor. Each sensor was glued to the mussel shell in a position corresponding to the heart. The signals were filtered, amplified and automatically recorded at computer programmed intervals. During early spring the cardiac activity of all animals doesn't differ between each other. Winter season at the White Sea is characterized by low levels of temperature (ca. −1,5°C) and phytoplankton concentration (ca. 1000–2000 cells per l). Consequently the physiological condition of mollusks may be described as anabiosis and is supposed that during winter season the basic level of metabolism is similar at different species. Nevertheless the average heart rate remained at relative high level – 3–5 beats per min. Only from the middle of May – temperature about 4°C – the heart rate of subtidal blue mussels became significantly higher then other mussels. This situation is remains up to the middle of October when the temperature was about 6°C and heart rate of the animals is equaled. It was supposed that during active period of life this difference is due to the basic level of metabolism of those animals. The high significant correlation of temperature and cardiac activity (heart rate and amplitude of heart contraction) from February to January was shown. However, in some points – May and July–August – that relationship was not obviously. On the base of relative unchangeable level of temperature all indices of heart rate is decreased significantly. We assume that such changes in correlations may be based on the effect of food availability, i.e. phytoplankton concentrations. That biological index was changed drastically with two highest peaks (from 1000–2000 up to 130000–140000 cells per l) at the end of May and at the middle of July. One additional factor which may affect the heart rate is the reproductive status. But at the end of May all mussels have completely developed gonads and were ready for spawning. At the middle of June mussels have early developing stage of gonads. One time distance of our monitoring is especially interesting due to simultaneous changes of heart rate, temperature and phytoplankton concentration with different degree. We might see three points of those indices increasing during distance from 23rd of April to 25th of May. Main task was to estimate the factor which influenced at the cardiac activity more. To estimate the quality characteristics of heart rate changes the temperature coefficient Q10 was calculated. First increasing of cardiac activity has Q10 about 26,6 that unreal for blue mussels. It is well known that coefficient is about 2–4 for mussels. Just that time first increasing of phytoplankton concentration was shown. Thus we may conjecture that main reason for that cardiac activity change is the food availability. The second step of heart rate increasing has Q10 about 7,6. Again at the same time the quantity of diatoms increased significantly. Anyway due to relatively low index of Q10 the most reliable explanation may be the equal influence by temperature and food availability at the heart activity. At least in case of third increasing of heart rate the Q10 was equal to 2,3 that correspond with the known data. During that increasing any significant changes in phytoplankton concentration was not shown. So we may conclude that we have only temperature influence at that case. On the basis of our data we may suppose that, in spite of the mollusks are poikilotherm animals, some other factors besides temperature may show the dominant influence on the physiology of mollusks. In our experiment that factor was food supplying.

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## COMPARING OPTIMAL AND RULE-BASED BEHAVIOURAL STRATEGIES IN LARVAL FISH MODELS

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Coupling Individual-based models (IBMs) for fish larvae (or other living organisms with self-mobility) to hydrodynamic models requires an algorithm or a set of rules to describe the behaviour. How this is formulated is shown to have significant effects on dispersal and survival of modelled larvae. Ideally, the behavioural algorithm would be evolutionarily consistent, reflecting the flexible nature of behaviours such as habitat selection and foraging activity and preferably also their dependence on individual state. These algorithms should be constrained by the individual's limited ability to sense and predict and require little computation so they can be implemented in hydrodynamic models. This raises the questions: (1) How do simple rule-based algorithms compare with evolutionary optimal behaviour—the behaviour that maximises survival in a given environment? (2) How can behavioural algorithms be improved, while retaining simplicity, to capture adaptive behaviour? To address these questions, we developed an IBM to simulate the early life-history of a larval cod from 5 mm to 15 mm. We implemented a variety of simple algorithms that evaluate the tradeoff between ingestion and mortality rates. As ingestion may be prioritised at particular times of day and/or internal states of the individual, we assigned the larva a behavioural strategy vector. This provided the larva with information regarding the strength of stimulation to forage, and we incorporated three cues: (1) stomach fullness; (2) rate of change in light intensity; and (3) an individual boldness personality trait. Using survival per mm length interval as a measure of fitness, we carried out an exhaustive parameter search to find the values that maximised fitness throughout ontogeny for each cue. To assess the performance of each parameter combination, a state-dependent optimality model run in an identical environment was used as a benchmark. The best strategy utilised all cues, with parameter values changing through ontogeny. This strategy had an accrued probability of survival at 15 mm approximately 50% of the optimal behaviour, and an improvement of 30% over an ontogenetically fixed strategy and 17% over a strategy consisting of the best single length-dependent cue. A distinct difference in the strength of stimulation from behavioural cues was found between length intervals 5–7 mm and 8–15 mm, with the latter obtaining foraging stimulation from a near-empty stomach and the diel light cycle, whereas the former required only continual stimulation from its boldness personality trait. When comparing survival for each mm length interval, the best strategy vector achieved > 90% of the survival of the optimal behaviour with the exception of 5–6 mm (75%), suggesting there is additional information an optimal larva could potentially sense and use that is not captured in the simple behavioural rule. Incorporating multiple behavioural cues and their relative importance throughout ontogeny are shown to be important components of behavioural algorithms. When designing such algorithms for biophysical models, consideration of these traits is recommended, as the emergent behavioural responses are likely to lead to improved survival, which is particularly important for models examining recruitment hypotheses.

## MULTISCALE PATTERN OF VARIABILITY IN EARLY LIFE TRAITS OF A MEDITERRANEAN COASTAL FISH

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Pelagic larval duration (PLD) and spawning dates (SDs) are early life traits (ELT) fundamental for understanding fish life cycles and properly assessing patterns of dispersal and connectivity among populations. Although ELT are being used extensively for modelling larval dispersal, they are generally treated as fixed parameters or assessed in single locations or times, *de facto* neglecting their potential variability in space or time. This may get potentially biased valuations of dispersal and connectivity patterns. With the aim to better parameterize larval dispersal models, the spatial variability of PLD and SDs in the saddled sea bream *Oblada melanura* was investigated using otolith (ear stones) micro-structure. Three spatial

scales (from hundreds of metres to hundreds of kilometres) were considered along the coast of Murcia region (Spain, West Mediterranean Sea). PLD was found to vary significantly among areas located hundreds of kilometres from each other, but not at smaller spatial scales (~ 1 km), while an opposite pattern was observed for SDs. These results suggest that spatial variability of ELT should be considered when these parameters are used for running larval dispersal and connectivity models in different geographical contexts and to a range of spatial scales.

## ABUNDANCE VARIATIONS OF *CALANUS FINMARCHICUS* AND *C. HYPERBOREUS* IN THE NORTHERN NE ATLANTIC IN RELATION TO LOCAL AND LARGE-SCALE ENVIRONMENTAL FACTORS

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Zooplankton act as sentinel populations for climatic changes, as they respond quickly to variations in their environment, while they are not subject to fishing pressures. Since climate change has particularly dramatic consequences at high latitudes, we focus on two *Calanus* congeners (*C. finmarchicus* and *C. hyperboreus*) from three different locations in the northern NE Atlantic: a fjord in northern Norway, a transect north of Iceland and coastal stations off Svalbard. We describe and compare changes in the annual abundances of both congeners over the last two decades and demonstrate that they are affected both by local and large-scale environmental factors. The long-term variations in *Calanus* spp. abundances were related to local environmental factors such as temperature, salinity, chlorophyll *a* concentration (where available) and the start date of the spring bloom (available from 1998), and to large-scale climate indices, the North Atlantic Oscillation (NAO) and the Arctic Oscillation (AO). We found significant inter-annual variability in *Calanus* spp. abundances in all three locations. A significant decrease of *Calanus finmarchicus* abundances was observed in the north Norwegian fjord, contrasted by increasing numbers of *C. hyperboreus* over the same period. No temporal trend in *Calanus* spp. abundances was detected in Svalbard or in the waters north of Iceland. To identify environmental factors that significantly affected inter-annual variations of *Calanus* spp. we used a linear direct ordination method (redundancy analysis). Temperature, salinity, chlorophyll *a* concentration, the start date of the spring bloom, as well as annual NAO and AO were applied as variables constraining the ordination. In Svalbard, only temperature had a significant effect on *Calanus* spp. abundances and explained 5.1% of the total variance. North of Iceland temperature, salinity, NAO and AO were significantly related to *Calanus* spp. abundance anomalies and together accounted for 14.4% of the total variance. None of the tested environmental variables contributed significantly to the variability of *Calanus* spp. abundances in the northern Norwegian fjord. We suggest that local hydrography was a more important driver of *Calanus* populations than large scale climate states both in the northernmost location (Svalbard), where temperature was a dominating factor, and in northern Norway, where none of the tested environmental factors and *Calanus* abundances correlated. In the subarctic waters off north Iceland both local and large-scale factors seemed to be important. These findings enhance our understanding of long-term fluctuations in zooplankton abundances across the NE Atlantic basin as a whole.

## INVESTIGATION INTO THE SETTLEMENT PATTERNS OF *SERPULA VERMICULARIS*, TO INFORM FUTURE RESTORATION EFFORTS

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*Serpula vermicularis* can form dense aggregations in suitable conditions and are classified as biogenic reefs. These reefs are globally rare and of conservation importance, with the largest known extent occurring in Loch Creran. These reefs are known to be vulnerable to anthropogenic damage, particularly from physical disturbance such as dredging and anchoring. Due to their limited distribution and sensitivity, developing restoration techniques is of key importance. The aim of this study was to identify the time of year to deploy restoration materials to ensure the greatest recruitment and survival of recruits. Settlement tiles were deployed at 2 monthly intervals for a year (January to November 2012). Tiles were also deployed at 5 sites around the loch to investigate spatial variation in recruitment. Temperature and salinity loggers were also deployed at these five sites for the duration of the experiment. The tiles were photographed every 2–6 months, from the photographs abundance and size of recruits could be assessed. The results showed limited recruitment on all tiles until late summer, when there was a peak in recruitment on all tiles independent of their deployment duration. However these data also show significant spatial variation in recruitment between sites. These results suggest the timing of restoration efforts would not affect success. However, the location and subtle changes in environment between these locations would be important in the success of future restoration efforts.

## HABITAT CONDITIONS OF VARIOUS FISH SPECIES IN THE BARENTS AND KARA SEAS

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Based on PINRO investigations in the Barents Sea (2000–2013) and in the Kara Sea (2007–2013) main habitat conditions of most fish species are considered. Ranges and mean values of depth, bottom temperature and salinity were calculated for most species. Some groups of species with related to preferred depths, water temperature and salinity were separated. Species with wider range of habitat parameters are characterized by wider distribution areas in the investigated seas.

## LOOKING FOR THE MOST APPROPRIATE LOCATIONS FOR THE HARVESTING OF *PARACENTROTUS LIVIDUS* (LAMARCK, 1816)

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The rock sea urchin *P. lividus* constitutes a very valuable marine resource at many European regions. It has been intensively harvested for commercial purposes, leading to its depletion in some places. The objective of this work is to identify the most appropriate locations for the harvesting of *P. lividus* in the coast of Cantabria (Bay of Biscay) and to establish management measures for its sustainable exploitation. The study was carried out in five coastal areas (Pechón, Liñera, Oyambre, Laredo and Castro) distributed along 110 km of coastline. 41 rocky bottom transects were delimited and two depth ranges (<5m and 5-10m) were considered at each of these transects. Sea urchin abundance data, in terms of general semi-quantitative coverage and specific density (number of individuals per square metre), was recorded *in situ* and replicates of 10 individuals per depth range were collected at 21 transects. Total body size, fresh weight, gonadal fresh weigh and gonadal index data were obtained at the laboratory. For each variable, differences between coastal areas and depth ranges were analyzed using ANOVA or Kruskal-Wallis tests, according to normality and homoscedasticity results. When significant differences were detected, the analyses were complemented by Bonferroni and Mann-Whitney post-hoc tests for differences between pairs. Correlations between abundance data and biometrical variables were also studied by linear regression models. Finally, percentage frequency distributions of all the biometric variables were obtained and the fraction of commercial individuals (size>55mm) were calculated for each coastal area in order to estimate the available stock. The obtained results showed significant differences between areas but not between depth ranges. All the biometric variables, except the gonadal index, showed significant negative correlations ($-0.34<r<-0.51$; $p<0.05$) against abundance data. In general terms, three areas (Oyambre, Castro and Laredo) showed low densities with big individuals and the other two areas (Pechón and Liñera) showed higher densities but with smaller individuals. Despite the smaller size of the individuals on average, the latter two areas accumulated the 71% of the stock of commercial individuals, being the most suitable zones for the commercial harvesting of *P. lividus* in Cantabria.

## INTERANNUAL VARIATION OF THE ASEXUAL REPRODUCTION OF *AURELIA AURITA* FOLLOWED IN SITU (BAY OF KOPER, ADRIATIC SEA)

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Over the last decade we have witnessed increasingly frequent occurrences of gelatinous zooplankton masses, where the benthic polyp phase plays a key role in ensuring the long-term viability and success of jellyfish populations. Ecological tolerance of polyps and adaptation to environmental changes and anthropogenic factors are affecting the distribution of moon jellyfish (*Aurelia aurita* s. l.). Monitoring of polyps and their asexual reproduction under natural conditions is essential for understanding the problem of mass phenomena, i. e., jellyfish blooms. We studied the seasonal fluctuation of polyp abundance and their asexual reproduction dynamics from March 2010 to March 2013. The performed study was carried out in the Bay of Koper (northern Adriatic) where we monitored monthly the population of polyps attached to oysters at various depths and positions on one of the pillars located in Port of Koper. We recorded environmental parameters of temperature, irradiance PAR, salinity and pH. Maximum abundance was recorded in August (31 polyp/cm$^2$) and minimum abundance in December (8 polyp/cm$^2$). The abundance of polyps has a significant upward trend in correlation with increase in water temperature and a decreasing trend with increase in salinity. A high density of polyps has the effect of reducing asexual reproduction. Asexual reproduction in the form of budding and creation of stolons was present throughout the year with an increase in warmer periods. The strobilation process began in October (19.7 °C) and reached its peak in December (11.7 °C). The pattern of seasonal polyp dynamics abundance did not differ significantly between years, but it did change their density which could be caused by favourable environmental conditions.

## HABITAT USE BY THE BARENTS SEA COD UNDER RECENT WARMING CONDITIONS

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The Barents Sea cod is the northernmost cod stock in the world and currently the largest. Due to the combined effect of ocean warming and reduced fishing pressure the cod stock has recently increased to the same level as prior to the onset of industrialized fishery. At the same time, the distributional limit has shifted northwards. Here we characterize the cod's habitat according to important environmental factors and test if the change in cod distribution and density follows any of three previously proposed scenarios: "proportional density" – increased abundance lead to equal rate of density increase in all habitats, "constant density" - increased abundance is associated with constant density in preferred habitat and range expansion into less suitable habitat, and the "basin model" where the highest increase in density is in marginal habitats. We study density dependent and density independent changes in the habitat use of a record large cod stock under warming conditions.

## AMOEBOZOA IN DEEP-SEA ENVIRONMENTS

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We demonstrate the presence of unique, previously unknown phylogenetic lineages of Amoebozoa in the deep-sea bottom sediments. At the same time, some of these lineages are currently represented by multiple species, and their deep-sea members are closely related to the species isolated from shallower habitats. There are also examples of deep-sea amoebae lineages containing very closely related species isolated from distant areas of the ocean. In most cases, comparison between water column, bottom sediments, as well as deeper and shallower habitats allows a conclusion that the species composition in the sampled habitats is mainly determined by the habitat type (e. g., bottom sediments vs. water column), that may, in turn, determine the amount and type of substrates for amoebae to dwell on. The diversity of species on the bottom sediment surface decreases with increasing depth, which is likely to be determined by the factors, indirectly influenced by the depth, such as temperature, salinity and the amount of available organic matter.

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## DISTRIBUTION AND HABITAT PREFERENCES OF THE INVASIVE AND NATIVE PALAEMONID PRAWNS IN THE NORTH-EASTERN BALTIC SEA

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The rock pool prawn (*Palaemon elegans*) has rapidly expanded its distribution area throughout the entire Baltic Sea. The first rock pool prawns were determined in the southern Baltic Sea in 2002. The species was rare in the Northern Baltic Sea in 2010, but the number of new findings substantially increased in the following years. Standardized field sampling and laboratory experiments were conducted to clarify the distribution and habitat choice of the invasive rock pool prawn and native Baltic prawn (*Palaemon adspersus*) along the coastal waters of Estonia, north-eastern Baltic Sea. The field trap catches enabled to quantify the abundance of prawns in terms of catch per unit effort. In the habitat selection experiments radio-frequency identification system was used for tagging the animals. Based on the collected field data the invasive prawn was found throughout the study area while the native prawn was absent in the eastern Gulf of Finland. Ovigerous females were found only among the invasive species. The distributions of both species were most strongly related to vegetation cover, bottom substrate and transparency of water. Based on the laboratory experiments, the habitat preferences significantly differed between the native and invasive species. The invasive species prefered hard bottom habitats while the native species revealed no clear preferances and was observed equally in unvegetated hard bottom habitats and both vegetated soft and hard bottom habitats. The very fast dispersion and high abundance of breeding individuals of the invasive prawn suggest that the species has formed permanent populations in the northern Baltic Sea. In the areas where palaemonid prawns were previously absent (e.g. eastern Gulf of Finland), the invasive rock pool prawn represents a new ecological function and thus may have substantial impact on the benthic communities.

## THREE-SPINED STICKLEBACK IN THE WHITE SEA: LONG-TERM DYNAMICS AND SPATIAL DISTRIBUTION

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The three-spined stickleback *Gasterosteus aculeatus* now is the most numerous fish in the White Sea. Thus information on this species is important for understanding functioning of entire ecosystem of the sea. However, scientific data on its biology and spatial distribution, population structuring and population dynamics is quite scarce because this species did not attracted sufficient attention of researchers due to its negligible commercial significance and increase of its abundance only in recent years. This project is directed to describe long-term changes in abundance of three-spined sticklebacks based on historical and own data, distribution of the stickleback in different parts of the White Sea and their population differentiation. These studies are based on techniques of quantitative sampling of stickleback. To estimate densities of stickleback, we used a beach seine with wings of 7,5 m length and catching area about 150 $m^2$. Its catch efficiency was assessed by release of tagged stickleback in the catching area or by sampling in semi-isolated lagoon with known area and number of fish in it. Tagging of stickleback has been done by putting bright pieces of plastic on their dorsal spines. Number of fish in the lagoon has been assessed by release of tagged fish into the lagoon and counting their return at following sampling. In average, catch efficiency of the beach seine we used was approximately 0,7. Difference between replicate samplings in average were about 10%. Density of stickleback in different parts of the White Sea considerably varied with maximal values in the west-southern coast of the Kandalaksha Bay. According to our estimates, total number of spawning fish in 2010–2011 approached 300 mln individuals or 750 mt. Estimates of total biomass based on available data on fecundity and survivorship of early life stages in Kandalaksha Bay resulted in about 9000 mt of stickleback in the White Sea. 76% of them occur in Kandalaksha Bay, 17% in Onega Bay and 7% – in Dvina Bay. The first genetic analyses studied the variation of mitochondrial gene coding cytochrome b showed spatial differences in distribution of haplotypes of this locus of mtDNA in the White Sea. Comparison of obtained data with own and literature data from the Baltic Sea basin suggests that the southern part of the White Sea was inhabited by stickleback related to the Baltic population of this species. Historical analyses and own data on abundance collected during last years showed very large changes in stickleback abundance during the last century. The species was extremely numerous in the 1930s gradually declined and had very low abundance during 1960s–90s. Population started to grow in the late 1990s, but till now they are not so numerous as in the 1930s. Comparison of this dynamics with climate data in the area suggests that high abundance of stickleback is associated with warmer periods whereas in colder periods this species was not numerous in the White Sea.

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## REPRODUCTIVE SUCCESS OF THE BOREAL BARNACLE *SEMIBALANUS BALANOIDES* AT ITS SOUTHERNMOST DISTRIBUTION LIMIT (GALICIA, SPAIN)

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The boreal barnacle *Semibalanus balanoides* has been used to test several biogeographic hypotheses in a climate change framework. The winter cold limitation hypothesis states that the southern geographic limit of a northern species is set by adult intolerance of warm winters, mediated by reproductive failure and reproduction success in cold winters. This hypothesis has been corroborated for *S. balanoides* based on modeling and observation data; higher recruitment and an expansion of the distribution range to the south has been observed in cold winters. The reasons for this success in cold winters (higher fecundity, smaller larval mortality, higher settlement, less juvenile mortality), remain unclear. We studied the reproduction of *S. balanoides* in the southernmost populations of its distribution range in Galicia (NW Spain). Three sites were selected in two estuaries for a two year reproductive cycle study (2013–2014). Fecundity, reproductive period, embryogenesis success and size at maturity were compared with northern European populations. Synchronized fertilization and embryogenesis take place in Galicia where sea water temperatures remain over 12°C throughout the year, while in northern populations reproduction fails if temperatures remain above 10°C in winter. *S. balanoides* in Galicia has one brood per year in January–February that hatches after 1–1.5 months incubation. A small proportion of individuals never hatched their larvae despite full development; in these cases the embryos remained inside the body cavity and rotted. All of the new settlers (March–April) reproduced the following winter when 10 months old and between 2–3 mm opercular length. Our results show that *S. balanoides* is able to reproduce in its southernmost distribution limit in Galicia, although failures were detected in fecundity, but also show adaptation of reproduction to environmental conditions that would likely cause total reproductive failure in more northern populations.

## BIOPHYSICAL COUPLING OF CHL-A AND ENVIRONMENTAL DRIVERS USING RECONSTRUCTED SATELLITE DATA FIELDS; THE POTENTIAL FOR FISHERIES INDICES USES IN HIGHER LATITUDE WATERS

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Remote sensing data provides high resolution information on a variety of biological and environmental variables that can be utilised for identifying potential links between the environment and higher trophic level organisms (e.g. – drivers of fisheries recruitment). However despite their obvious advantages, data gaps appear quite regularly particularly in the higher latitudes where frequent cloud cover and low irradiance in the winter can limit the satellites spatial coverage significantly. We explored the potential to interpolate data gaps in remote sensing fields by using the DINEOF filling procedure on the chl-*a*, SST and PAR fields for Icelandic waters. Eight day composites of the variables were used and the accuracy of the interpolation was verified by comparing with in-situ data. The Root Mean Square error was <1 for all variables when at least 40% of the pixels were valid.

The reconstructed datasets were used to explore the biophysical coupling and spatio-temporal variability between chl-*a* and potential environmental drivers using maximum covariance analysis while generalised additive models were used to explore the spatial variability in the dominant drivers of the spring bloom phenology of chl-*a*. The findings are discussed in the context of producing indices for fisheries management in higher latitude ecosystems.

## IF THE TEMPERATURE CHANGE INDUCES PRODUCTION OF MEDUSAE IN THE WHITE SEA?

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Pelagic coastal community in the sea is the complicated mosaic of alternate populations. Many meroplankton species send their larvae to the plankton. But also gelatinous carnivore (hydrozoan and scyphozoan medusae) appear in the periods of abundant zooplankton to feed and sexual reproduction. What are the environment cues which regulate this nature mosaic? In this research, I checked if the temperature affects production of medusae in the White Sea. Nineteen hydromedusan and two scyphozoan species inhabit the White Sea and most of them can be collected near the Pertsov Biological Station (Rugozerskaya Inlet, Kandalaksha Bay). Hydromedusae predate mainly on crustacean preys (Prudkovsky, 2013). In average they are usually insufficient to reduce the prey populations. But predation rate is highest in the rare areas or in the rare periods with high medusae abundance. Most hydromedusae species in the Rugozerskaya Inlet appear in the spring when the ice is melting and only two species appear in the middle of the summer. Hydroid colonies *Bougainvillia superciliaris* and *Sarsia tubulosa* with medusa buds were collected in the sea at the end of March 2011–2013 when the sea was covered by the ice and the temperature was negative. Hydroids *Coryne producta* and *Obelia geniculata* produced medusae in July or August 2012–2013 when the temperature of the sea had achieved 10–15°C. Because of rarity of the accurate observations of medusa budding process, we know a little about the environment cues, which regulate hydroids life cycles. In the rearing experiments, I estimated the hypothesis of regulation of the life cycle of hydroids and scyphozoan polyps by temperature. In experiments five hydroid species (*Bougainvillia superciliaris*, *Halitholus cirratus*, *Catablema vesicarium*, *Rathkea octopunctata*, *Obelia longissima*) and scyphozoan polyp *Cyanea capillata* produced medusae in different seasons of year out of the usual periods. The repeated successful experiments in different seasons were carried out for *Rathkea octopunctata* and *Catablema vesicarium*. The schemes of experiments were the same for different species. The "temperature shift experiments" were carried out in 2013 after prolonged cultivation of species in the constant temperature conditions (0°C, 5°C or 10°C). Several species (*R. octopunctata*, *C. vesicarium*, *H. cirratus*) produced medusae as a result of fall the temperature till 0–5°C. On the contrary several species (*O. longissima*, *C. capillata*) produced medusae as a result of rise the temperature till 5–10°C. Hydroid *B. superciliaris* produced medusa buds both after fall and after rise the temperature to the value 4–6°C. I have not achieved the evident results for *Sarsia tubulosa* and *Coryne producta*. In experiment hydroid *S. tubulosa* produced medusae in the end of July or in September with invariable temperature 4–6°C or 10–12°C. These results are in contradiction with usual temperature at which hydroid produce medusae in the sea. Hydroid *C. producta* produced medusae for several months with invariable temperature 4–6°C or 10–12°C. It was occurred in the same period as in the sea. Some results pointed to complexity of life cycle regulation. The colonies *O. longissima* released medusae both in September after rise the temperature and in June with invariable temperature conditions. It is probably the shift in the food ration could induce the medusae generation in the last case. Also in the process of experiments I elucidated the life cycles of two Pandeidae species *H. cirratus and C. vesicarium*.

## GENETIC VARIATION IN PHOTOSYNTHETIC PERFORMANCE AND TOLERANCE TO EMERSION STRESS IN *FUCUS VESICULOSUS*

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Some ecosystems such as the Baltic Sea are comprised of a single dominant foundation species (*Fucus vesiculosus*). Thus genetic diversity of *F.vesiculosus* may play an analogous role to species diversity, and is likely to affect the function and resilience of the ecosystem. However, the contribution of genetic variation among individuals of the foundation species to these effects is seldom documented. Genetic variation is of particular importance when analyzing key traits of the foundation species such as photosynthesis or stress responses. It will determine their local persistence in a changing environment. Therefore, we grew replicate clones of *F. vesiculosus* collected from the Finnish southwestern Archipelago Sea, in a common garden environment in summer 2012 & 2013. We quantified their genetic variation using photosynthetic parameters, growth, and stress responses (exposing the tips to dessication and freezing regimens). Genetic variation within physiological responses such as photosynthesis and growth were observed after tips of *F. vesiculosus* were held for 10 weeks in common garden environments. Short dessication resulted in high photosynthesis, whereas *F. vesiculosus* did not recover from freezing regimens. Our data indicate that different genotypes of *F. vesiculosus* can respond physiolocically to a broad range of environmental conditions. We suggest that the observed genetic variation in key physiological traits might be highly favorable for the persistence of *F. vesiculosus* in the face of climate change.

## BRYOZOAN FEEDING – STENOLAEMATES' POINT OF VIEW

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Among other taxa of invertebrates, marine bryozoans (Bryozoa: Gymnolaemata) are active suspension feeders. They use simple ring of ciliated tentacles surrounding their mouth to create water currents, retain and transport food particles. In ctenosome and cheilostome species each tentacle possesses 5 longitudinal ciliary bands: 2 lateral, 2 laterofrontal and one frontal; in stenolaemates frontal ciliary band is absent. Particle capture mechanism was a subject of many studies and it were suggested that (i) the transport of most particles is assisted by tentacle flicks, (ii) in ctenostomates and cheilostomates it is accompanied by frontal ciliary band, (iii) laterofrontal cilia function as a sieve, (iv) laterofrontal cilia are sensory ones and trigger local stoppage or reversal of lateral cilia with following retaining and transportation of food particles by frontal cilia. According to many data, the first mentioned way is suggested to be the most probable and accepted as universal one also for phylactolaemates bryozoans, phoronids and brachiopods. Since marine bryozoans consume small food particles (about 20-40 micron) with limited nutrient they must accomplish several hundreds flicks per minute. But our results on feeding behavior of marine bryozoans were quite contrary and, besides, one can assume that numerous flicks demands more energy then it might be obtained from captured food. We aimed to reveal whether transport of food particles in stenolaemates lacking frontal cilia is assisted mostly of tentacle flicks, and whether such a behavioral reaction is depended on physiological shape of the animal.

We analyzed feeding behavior and water currents in 20 colonies of 3 stenolaemate species (*Crisia eburnea*, *Crisiella producta*, *Tubulipora flabellaris*) and 2 ctenostomates (*Buskia nitens* and *Flustrellidra hispida*). All colonies were studied in isothermic room at 11°C in the flow tank in still (0 mm/s) and flowing (0.2 mm/s) water. Flow velocity and particle concentration were kept similar to that ones in natural habitats. For visualization of water currents we added small amount of $TiO_4$ suspension (particle diameter << 50 mkm). Ten colonies of each species were studied directly after sampling ('feed up') and 10 colonies were maintained in filtered sea water during 24 hours before observation ('starved'). We made 20 recordings (10 minutes long) of individual polypides of each colony, 10 from still, and 10 from flowing water. Several colonies were fixed and treated according to standard electron microscopy methods.

We found that average number of flicks per minute did not exceed 4 in stenolaemates and *B. nitens*, and 7.5 in *F. hispida*. Difference in average flick number in 'feed up' and 'starved' polypides was insignificant in all species studied in both still and flow water and hence does not depend on physiological shape of the polypide or flow condition. To understand how stenolaemates transport food particles (since they lack frontal cilia and perform only few flicks per minute) we made computer-based reconstruction of feeding current and estimated velocity of moving food particles. All stenolaemate species possess tube-shaped zooids and polypides during feeding never protrude introvert and expose tentacles from the orifice only up to 4/5 of their length, thus their mouth is situated below the peristome level. Within feeding current we distinguished central part (1.45 ± 0.15 mm/s, in flowing water) and peripheral (0.80 ± 0.06 mm/s) zone where water leaves tentacle crown. Since the diameter of central zone corresponds the border of cystid wall this part of feeding current inevitably goes down toward the mouth. In ctenostomates filtered water easily goes out between tentacle bases but in stenolaemates high peristome prevents from this. But stenolaemate polypide possess particular ciliary tufts between tentacle bases (lacking in other marine bryozoans) probably providing moving of filtered water towards peristome edge. Thus, we suggest that in stenolaemates the main factor assisting in particle transport is peculiarity in spatial arrangement of tentacles during feeding and cystid shape.

## LIFE CYCLE AND GAMETOGENESIS OF THE CHEILOSTOME BRYOZOAN *CRIBRILINA ANNULATA* (GYMNOLAEMATA) ON THE SUBSTRATA WITH DIFFERENT LONGEVITY IN THE WHITE SEA

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Study of the reproductive ecology of the cheilostome bryozoan *Cribrilina annulata* living on the substrata with different life time (fronds of *Laminaria sp.* or some species of red algae) revealed that the average colony lifespan lasts approximately one year. During reproductive season (May-August) the population is represented by three generations: (1) mature overwintered colonies, (2) their progeny (daughter generation) consisting of (a) 'early' colonies formed in May-June and reproducing in June-July, and (b) 'late' colonies which are formed in July-August and propagate next spring, and (3) granddaughter generation – descendants of the 'early' daughter colonies – which were formed in the mid-summer and will be reproducing next year. Some of the overwintered 'early' colonies of the daughter generation can reproduce twice during two successive seasons.

In the Chupa Inlet (Kandalaksha Bay, White Sea), spawning of *Cribrilina annulata* occurs from May to July (only few colonies with embryos were found on red algae fronds in the beginning of August). Beginning of the reproduction is not determined by the colony size as embryos were noticed in the specimens consisted of only about ten zooids. Also it was noticed, that overwintered colonies in May predominantly bud dwarf fertile zooids thus possibly accelerating and intensifying the larval production in the population. Maximal number of embryos in colonies was reached at the end of June and the peak of newly formed colonies was recorded in the beginning of August for the given population. Production of sperm occurs during spring-early summer in male and hermaphroditic zooids. Ovarian structure does not change significantly during reproductive season, and in August female gonads degenerate.

Oogenesis in the colonies living on two different algal substrata showed some slight differences: (1) on red algae oogonia divide till the end of summer while on *Laminaria sp.* most germinal cells are formed in May and then their division stop; (2) on red algae formation of hermaphroditic zooids was terminated earlier (in June) than on *Laminaria* (in July); (3) lifespan of *Cribrilina*'s colonies on red algae is longer than on *Laminaria sp.* (on average 1 year 4 months versus 1 year 1 month). Old colonies of *Cribrilina annulata* die off together with breaking of *Laminaria* sp. fronds during the autumn storms. On red algae colonies are getting older and die on undamaged fronds that states that the colony life-time is determined by factors which not depend on substratum longevity.

## SUSTAINABILITY, ECONOMIC VALUE, ECOLOGICAL IMPACT OF MUSSEL FARMS IN NORTHERN ADRIATIC SEA UNDER DIFFERENT ANTROPOGENIC AND CLIMATIC SCENARIOS

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We assess ecological impact, economic value and sustainability of a mussel farm along a coastal area of the adriatic sea, by combining field campaings, lab experiements, socio economic survey and numerical modelling. We monitored on monthly basis mussel growth and several water quality parameters in 6 sampling sites along the gulf, differing for salinity, hydrodynamic and trophic condition. Potential impacts of farming activity on water quality and upper sediment have been investigated by comparing sediment properties among areas below farms in which mussel production started 5 and 10 years ago, area in which mussel farming stopped 5 years ago, and area in which farming never took place. Laboratory experiments were set up to investigate feeding preference and faeces/pseudofaeces production. Results were used to calibrate a bioenergetic model representing the mussel physiology and growth in relation to environmental conditions, and the impact of mussel aquaculture on water column. The model was then coupled to an hydrodynamic, a bigeochemical and a food web models for system level computation of mussel potential production, related energetic requirements, and nutrients budget. Information on socio economic aspects of this activity has then been integrated, in order to evaluate ecological footprint, emergy balance and social carrying capacity of the activity. Results represent a relevant contribution to coastal zone management, allows for evaluating possible interactions of mussels farms with other uses of the basin and permit the assessment of the ecological role of farming in the ecosystem. Results support the conclusion than mussel farming in this area is a paradignmatic example of sustainable exploitation of a renwable resource. Simulations also indicate the possibility to enlarge this activity without significant impacting ecosystem status.

## SHELL SHAPE VARIATION IN *LITTORINA SAXATILIS* (MOLLUSCA, CAENOGASTROPODA) ALONG ENVIRONMENTAL AND GEOGRAPHIC GRADIENTS

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Marine gastropod *L. saxatilis* is an important component of the North Atlantic intertidal communities, occupying a wide range of ecologically various habitats and represented phenotypically different ecotypes. Thus, *L. saxatilis* is an attractive model object for microevolutionary studies and the mechanisms of speciation.

In this study adult *L. saxatilis* were sampled from four geographically distinct sites, where the ecotype populations occupy exposed and sheltered shores, upper and lower littoral horizons. Our investigation aims to study how the morphological phenotypes (specimens with different shell shape) vary between shore types and levels and to estimate their plasticity. Shell shape variation of *L. saxatilis,* fixed in certain habitat, indicates a correlation with environmental factors (wave exposure, predation, isolation, etc) and probably related to the effect of selection.

The samples of *L. saxatilis* were collected from 13 populations ($N = 783$) of four distinct regions: 1) the White Sea, the Kandalaksha Bay (Russia); 2) the Barents Sea, Eastern Murman (Russia); 3) the Barents Sea, the Telegraph Bay (Norway); 4) the Skagerrak, the Swedish west coast, Sweden. Shell shape of both exposed and sheltered ecotypes from the White and the Barents Seas (Russia) were examined. Only samples from exposed rocky shore were investigated in the Barents Sea (Norway) and the Swedish west coast. Samples from the upper and lower horizons of the shore (upper and lower littoral) were obtained for all studied populations.

Landmark-based geometric morphometric techniques were applied to analyze shell shape of *L. saxatilis* from ecological different habitats and geographic locations. For two-dimensional morphogeometric analysis each shell, oriented to a standard position, was imaged by digital camera. To estimate differences of the shell shape 18 landmarks were placed on each image. Using the software TPS developed by Rohlf (1998) shell shape variables (centroid size, uniform components and relative warps) were obtained for further statistical analysis. The variables were also analyzed with multivariate techniques and MANOVA.

The morphometric analysis showed the exposed populations from the White Sea to be different in shape from all examined sheltered populations ($F = 11{,}58$; $p \leq 0{,}01$), whereas snails of the sheltered populations from all locations had similar shape ($F = 2{,}84$; $p \geq 0{,}5$). Only specimens from the upper littoral of exposed populations differ from sheltered populations; lower littoral populations are quite similar all over. At the Barents Sea (Russia) significant differences between shell shapes of upper and lower littoral snails were detected for two exposed populations ($F = 26{,}11$; $p \leq 0{,}01$). There is no morphological differences of sheltered populations and between its littoral horizon location ($F = 4{,}10$; $p \geq 0{,}5$). Significant differences in shell shape were found between upper and lower littoral in exposed population from the Barents Sea (Norway) ($F = 12{,}11$; $p \leq 0{,}01$). Both upper and lower littoral variation in the shell shape of the two exposed populations in the Swedish west coast were shown ($F = 32{,}57$; $p \leq 0{,}01$). A general trend was that all differences between shell shape specimens from upper and lower littoral habitats mostly detected in exposed populations.

In complex analysis, including all examined specimens from four different geographical locations significant differences in shell shape were found out between upper and lower littoral ecotypes only in Swedish west coast populations ($F = 24{,}98$; $p \leq 0{,}01$). Specimens from the upper littoral horizon are more variable in shape under the environment factors and less variable between geographical regions (according to transformational grids). Whereas individuals from the lower littoral being significantly less (Wilks' $\lambda = 0{,}32$, $\chi^2 = 112{,}5$, df = 15, $p < 0{,}001$) variable both under environment conditions and geographic regions. We found morphological differentiation between ecotypes from the exposed and sheltered populations towards down to the shore and according to the environmental gradient. The strength of selection causing differentiation between upper and lower littoral specimens is variable depending of geographic regions. For example, crab activity and stone damage are considered important in selecting of different *L. saxatilis* ecotypes in Sweden (Johannesson, 2004). In other regions environment factors act not so narrowing and differentiation appears negligible. Despite of it similar selective regimes influencing on *L. saxatilis* populations along the northern Atlantic coast may have rather similar shell morphology. Ecotypes of the different geographical regions found in the same environmental conditions and habitats are very similar in shell form and shape.

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## ESTUARINE POPULATION OF *SEMIBALANUS BALANOIDES* IN GRADIENT OF LIMITING FACTORS IN THE KOLA BAY

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Acorn barnacle *Semibalanus balanoides* (L. 1766) is a common dominant species of the littoral in the Barents Sea. Extreme effects of the environment in the intertidal zone considerably increased in the estuarine areas. We explored the population of *S. balanoides* in the Tuloma river estuary of the Kola Bay. There were no data on the barnacle abundance and survival in this estuary. Surveys were conducted in summer and winter-spring time from 2003 to 2011 along seven cross profiles (transects) of littoral basins and littoral streams (a drain of littoral waters from littoral basins). Typically, barnacles inhabit all levels of intertidal zone, but they were not found here. First of all, there were no *S. balanoides* in the upper littoral level. Barnacles were found out only in the mid- and low horizons of the intertidal zone, and solely within beds of littoral streams and littoral basins adjoining them. As the second feature of the population, barnacle abundance increased exponentially along the littoral from the river's estuary to the sea. Certainly, the main revealed feature was very narrow localization of *S. balanoides* colonies in the estuary: they were strictly limited within beds of littoral streams with some adjacent littoral basins. Barnacles were not found beyond the margin of these streams. It was the result of extreme conditions affecting barnacle's survival in the estuary zone. Low water salinity, desiccation, temperature and the abrading effect of ice were the most important factors determining distribution of *S. balanoides* in the estuary littoral. Under these stressful conditions *S. balanoides* were altogether absent in the upper littoral level. Obviously, exposure to limiting factors is minimal within littoral basins and littoral streams. However, in one littoral horizon, the environmental impact is almost the same in all transects, except for salinity. It was defined that the population density and biomass of *S. balanoides* increased along the salinity gradient from the Tuloma River mouth to the sea. On the other hand, with regard to long-term observations, abundance of barnacles gradually decreased along the total increase in water salinity of the estuary from 2003 to 2011. Possibly, *S. balanoides* were depressed at higher and lethal air temperatures during air exposures in summer because of the climate change.

## SENSITIVITY OF SYMBIOTIC AND ASYMBIOTIC LARVAE OF BROADCAST SPAWNING CORALS TO ULTRAVIOLET RADIATION

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The eggs and embryos of scleractinian corals are thought to be the most sensitive life stages with respect to ultraviolet radiation (UVR). It concerns especially the broadcast spawned coral larvae, which are positively buoyant and spend many hours near the surface under conditions of high solar radiation. Here we experimentally tested how UVR in the environmentally relevant range effects survival and cellular damage (the level of malondialdehyde equivalents, an indicator of lipid peroxidation) in the larvae of two broadcast spawning corals *Montipora digitata* and *Acropora intermedia*, and whether sunscreens, mycosporine-like amino acids (MAAs), reduce UV-induced stress. Larvae of *M. digitata* contained symbionts (zooxanthellae), while the larvae of *A. intermedia* were asymbiotic. Experiments were conducted over 2 days following the release of fertilized gametes. The exposure to UVR induced more rapid and pronounced mortality, as well as higher lipid peroxidation in the larvae of *M. digitata* compared to those of *A. intermedia*. The latter had a higher (2-fold) initial concentration of MAAs and were able to sustain continues synthesis of these substances under UVR exposure. In contrast, while the concentration of MAAs in *M. digitata* larvae showed a pronounced increase after 1d exposure to UVR, it dropped markedly by the end of the experiment. In all, short-term exposure to UV radiation might have small impact on planktonic stage of broadcast spawning coral species with horizontal transmission of symbionts due to the absence of additional source of oxidative stress, probably originating within the symbiotic algae. The ability of asymbiotic broadcast larvae to maintain continues MAA synthesis triggered by UV radiation might also contribute sufficiently to their low UV sensitivity. In the light of the predicted UVR increases in the tropical regions next decades, our results may be helpful for an assessment the coral recruitment success if UVR climate changes.

## HABITATS, POPULATION COMPOSITION, BEHAVIOR AND DIET OF AN INTRODUCED CRAB *RHITHROPANOPEUS HARRISII* IN THE RUSSIAN WATERS OF THE BLACK SEA AND THE TAMAN BAY

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Harris mud crab (*Rhithropanopeus harrisii*) has been first time collected in the Black Sea in the Dnieper and Bug estuaries in 1936 or 1937 (the collection of the Zoological Institute of Russian Academy of Sciences; Makarov, 1939). It is an alien species that has been possibly transported to the Black Sea as a hitchhiker on ships from Europe where it has been found for the first time in Netherlands in 1873-1876 (Miers, 1886). Since then it has been found in the North-western Black Sea (Reznichenko, 1967), Azov Sea (Mordukhai-Boltovskoi, 1952), Baltic Sea (Murina, 1952), Caspian Sea (Nebolsina, 1959), and Aral Sea (Andreev et al, 1988). No data existed in the literature regarding the Kerch Strait area and the Caucasian coast of the Black Sea.

Our update and field survey indicate that the Harris mud crab is currently wide spread in the Sea of Azov, and Caspian Sea. It is well established and reaches density of up to 120 specimens per 100 m$^2$ in the Taman Bay (Kerch Strait area of the Sea of Azov). Along the Russian Caucasian coast of the Black Sea and in Kaliningrad area of the Baltic Sea it is rarely found in open salty waters, but rather in some isolated locations along the coasts and in river estuaries.

The crab has been studied by the author in the Taman Bay, Sea of Azov and river estuaries of the Black Sea over a period of 3 years. Its population structure and densities have been assessed. Extensive observations of its behaviour and habitat preferences have also been noted. *R. harrisii* food chain position and preferences have been studied. There is a substantial difference in the crab behaviour, coloration, habitat preferences and population structure between the shallow semi-enclosed Taman Bay and narrow small river estuaries on the Russian coast of the Black Sea.

Previously abundant native mud crab *Brachynotus sexdentatus* has not been observed in these waters soon after the introduction of invasive *Rhithropanopeus harrisii*. A population of *B. sexdentatus* has been found in the Black Sea off the coast near Anapa where its invasive counterpart is absent. These observations may suggest their direct competition and lead to a better understanding of the sudden decline on the native *B. sexdentatus*.

This study was supported by the Russian Foundation for Basic Research grant 13-04-01127.

## MULTISCALE MODELLING OF PORTOFINO'S MPA COMMERCIAL FISH POPULATION. TOWARDS A NEW ECOSYSTEM-BASED MANAGEMENT APPROACH

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The protection of the so-called essential fish habitat (EFH: habitats where fish concentrate for recruitment, spawning or feeding) from the negative impacts of human activities -including fishing activities- is one of the most important concerns throughout the Mediterranean basin. A key challenge in the effective management of marine resources is translating from small scale studies of distribution and dynamics to the regional scale of management action. In order to address these challenges scientists and managers are exploring innovative ways, such as remote sensing techniques, to address issues related with fishing activities detrimental to coastal resources. Modelling of species distribution provides better understanding of the ecosystem services, functions, and patterns of biodiversity, as well as the interactions between species and environment. Consequently, the specific aims of this study were to test the potential of remote sensing techniques and distribution modelling approaches to map and to identify the environmental variables that influence the distribution of fish population at Portofino Marine Protected Area (MPA) in the Ligurian Sea. The last years the management of fish stocks in the MPA has been challenging due to the fact that there is an uneven distribution of coastal fishing activity around the Park. We analysed benthic terrain variables such as depth, rugosity, slope, curvature, and bathymetric position index derivate from echosounder multibeam bathymetry information, which we combined with visual census and video observations to concurrently map and quantify the location, in terms of density and size of five fish genders (*Diplodus* spp., *Serranus* spp., *Epinephelus* spp., *Sparus* spp. and *Scorpaena* spp.) that have been previously recognized in the area and related to coralligenous and with fishing activities. The underwater visual census (50 m transects, in three replicates per depth of 5m width) was carried out in two defined depths, 15 and 35 m depth on boulders and coralligenous habitats respectively, to identify the most suitable habitat structure for fish. Additionally during the diving activities we collected information regarding lost gear, litter and key species that represent the habitats under consideration. We assessed their distribution together with the seafloor characterization and at different levels of protection within the MPA. In addition, Maximum Entropy approach (Maxent software) was used in order to model small scale fish species distribution and obtain a probability estimate of occurrence in the entire MPA. Moreover we also used the random forests technique to generate predictive models, as a comparison to Maxent. The results include maps of the fish population evaluated as well as detailed description of the benthic terrain characterization that provide suitable habitat for their distribution. Our results provide a better understanding on the extent of available fishing grounds and stock population structure within the MPA providing critical results, which inform ecosystem-based management at Portofino MPA.

# *Predator – prey, parasite – host, and other inter- or intraspecific interactions*

## INVESTIGATION OF SAITHE (*POLLACHIUS VIRENS*) AND HAKE (*MERLUCCIUS MERLUCCIUS*) POTENTIAL COMPETITION IN THE NORTH SEA

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We investigated the potential competition between saithe and hake in a large marine ecosystem: the North Sea. Indeed, these two commercial gadoids present opposite abundance trends since 2005. Saithe spawning stock biomass is decreasing in the area while hake abundance increases. These opposite population trajectories fulfill the first condition inferring a potential competition between the two species in this area. In addition, we highlighted in a previous study an increasing spatial overlap between saithe and hake in the North Sea and pointed out the positive correlation of this overlap with temperature and Norway Pout (*Trisopterus esmarkii*) presence. Based on the previous assumptions and in a context of global warming, we focused on competition for food resource investigating the feeding habits of both saithe and hake in the area. In this aim, we realized stomach content analyses to identify both species diet. The diets have been described using four different types of information: (i) prey occurrence, (ii) prey abundance, (iii) prey biomass and (iv) prey relative importance. Saithe and hake diet compositions have been compared using each type of information and Kruskall-Wallis test. We calculated the Schoëner index using average prey biomass composition to estimate diet overlap between the two species. Finally the diversity of the diet has been estimated for both saithe and hake using Shannon index in order to determine whether or not one species is more generalist than the other. The results obtained complete the previous results obtained while studying saithe and hake spatial overlap and allow us to progress in the investigation of the competition between these two species in the North Sea.

## DIET OF THE BARENTS SEA COD AS INDICATOR OF ECOLOGICAL CHANGES IN MARINE ECOSYSTEM

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Diet of cod, the most abundant piscivorous fish and key predator in the Barents Sea ecosystem, consists of more than 150 prey species, including macrozooplankton and commercially important fish and invertebrates. Abundance/biomass of commercial fish stocks and their juveniles assess by analytical methods as well as surveys estimates of northern shrimp, hyperiids and euphausiids abundances were compared with their importance in cod diet in 1949–2013. Statistically significant relations between abundance of some species (e.g. capelin, juvenile cod and haddock etc.) and their importance in cod diet were revealed. At the same time some prey species were consumed by cod irrespective of their stock state. Long-term data on prey dynamics in the key predator diet can reflect current state and changes of the Barents Sea ecosystem structure under fisheries pressure and climatic fluctuations.

## PARASITE SPILL-OVER, SPILL-BACK AND DILUTION EFFECTS OF INVASIVE OYSTERS IN THE WADDEN SEA

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Invaders are able to affect native parasite-host dynamics via a variety of ways. New established hosts can act as reservoirs by co-introducing a parasite that also infects native hosts (*spill-over effect*). In addition, invaders may act as an alternative host for native parasites, thus increasing the parasites' population sizes and subsequently intensifying parasite burdens in native hosts (*spill-back effect*). Alternatively, invasive species can reduce the disease risk for native hosts, e.g. by preying on infective stages *(dilution effect).* Here we present the results of observational and experimental studies that show evidence for these three effects in the intertidal of the Wadden Sea, in which the Pacific oyster, *Crassostrea gigas*, is one of the most prominent invaders that interacts with native blue mussels, *Mytilus edulis*. In the field we found evidence for a spill-over effect of the parasitic copepod *Mytilicola orientalis* from oyster to mussels, however evidence for spill-back and dilution effects on shell-boring polychaetes and trematodes were less apparent. In addition, we found the infection levels of parasites in both mussel and oyster hosts to be more similar within beds than among beds, indicating that the effect of the invader on native-parasite host systems mainly acts on local spatial scales. The implications of the observed spill-over to native hosts are further illustrated with pre-liminary results of studies on the impact of infections on native hosts

## ON THE FOOD OF THE ANTARCTIC SEA ANEMONE *URTICINOPSIS ANTARCTICA* CARLGREN, 1927 (ACTINIIDAE, ACTINIARIA, ANTHOZOA)

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During the study of variability of the taxonomically important anatomical features of *Urticinopsis antarctica*, remains of some invertebrate animals and fishes were found in gastral cavity. Some of them were quite digested, others were, to the contrary, quite intact.

The species belongs to the most common and plentiful sea anemones of the Antarctic coast, therefore it is good represented in the collection of Zoological Institute. Our research and data published before show that the species is widespread in Antarctic and Sub Antarctic waters. It was recorded from McMurdo Bay (Verrill, 1922; Carlgren, 1927), South Shetland Islands, Prudz Bay (Sodruzhestva Sea), Cosmonauts Sea, Haswell Archipellago (Davis Sea) (Grebelny, 1975). But only few specimens of *Urticinopsis antarctica* contained eaten animals. Three anemones had in gastric cavity the remains of invertebrate animals and one had the remains of a fish, rather damaged by digestion. To all appearance they could be considered as food items for our sea anemone. To this group we should refer two mollusks *Laevilacunaria pumilia* Smith, 1879 и *Eatoniella caliginosa* Smith, 1875 (Gastropoda; 56 RAE, King George Isl., 4 m), a single specimen of crinoids (Crinoidea; “Polarstern” 39-th cruise, Weddell Sea, 504–529 m), spines of the sea-urchin *Sterechinus neumayeri* Meissner, 1900 (Echinoidea, 56 RAE, King George Isl., 4 m), a small ophiuroid *Ophiurolepis ?brevirima* Mortensen, 1936, a piece of arm of larger brittle star *?Ophiuroglypha carinifera* (Koehler, 1901) (Ophiuroidea; “Polarstern” 39-th cruise, Weddell Sea, 504–529 m), and fish bones (probably *Trematomus* sp., Nototheniidae; 54 RAE, Prudz Bay, 4–5 m).

In contrast to all foregoing animals, three specimens of side-swimmers or scuds ?*Conicostoma* sp. (Amphipoda; “Polarstern” 39-th cruise, Weddell Sea, 504–529 m) were not in the least spoiled by digestion. It is possible that they are not object of feed, but may be they are symbionts or commensals, or even parasites, that live in gastric cavity of the anemones. It is the specialists on amphipods who emphasize the attention on the unusual structure of their mouth organs and expressed assumption about symbiotic nature of these amphipods (Lowry and Stoddart, 1983).

The predatory feeding habits of *Urticinopsis antarctica* was confirmed by observations of research-drivers, participants of Soviet Antarctic expeditions. Reportedly B. I. Sirenko, series of sea-urchin shells frequently surround large specimens of *Urticinopsis antarctica*. Moreover, direct experiments of A. F. Pushkin confirm, that anemones can digest big sea-urchins in few days. Study of the stinging capsules set of *U. antarctica* showed, that sometimes the capsules typical for scyphozoan medusas, which are for sea anemones kleptocnids (stolen nematocysts), occur in endodermal epithelium of the pharynx (Grebelny, personal communication). According to data of the British researchers 21% of *Urticinopsis antarctica* diet constitute medusas (Dayton, Robiilliard and Paine in Holdgate, 1970). These authors also ascertained that the sea stars *Perknaster fuscus antarcticus*, *Odontaster validus, Diplasterias brucei* often fall a prey to this sea anemone.

All data available show that the most common and abundant in Antarctic shallow waters sea anemone *Urticinopsis antarctica* doesn’t show any manifest preferences in feed, and eats any benthic animals and jellyfishes. Moreover, according to British researchers, cannibalism is also usual for this species (Dayton, Robiilliard and Paine in Holdgate, 1970, fig. 4).

The following taxonomists of Zoological Institute RAN, St. Petersburg, have readily helped us identify animals: E. N. Egorova, Mollusca; A. V. Smirnov, Crinoidea and Echinoidea; I. S. Smirnov, Ophiuroidea; S. A. Malyavin, Amphipoda; and A. V. Neelov, Pisces.

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## HYBRIDIZING MUSSELS *MYTILUS EDULIS* AND *M. TROSSULUS* IN THE WHITE SEA: GENETICS, DISTRIBUTION, ECOLOGY AND MORPHOLOGY

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The originally Pacific temperate blue mussel *Mytilus trossulus* and its Atlantic congener *M. edulis* are closely related, widespread benthic species. They can be routinely distinguished by molecular markers while reliable diagnostic morphological markers are lacking. Whenever areas of the two species overlap they fall into introgressive hybridization Historically in Northern Europe populations of *M. trossulus* were known to be confined to the Baltic Sea. Recently *M. trossulus* was found in some other regions of the Northern Europe, in particular in the White Sea it coexists with *M. edulis*. Here we use a set of four semi-diagnostic allozyme loci to perform a detailed survey of *Mytilus* populations in the Kandalaksha Bay of the White Sea. We use genetic data to map the distribution of *M. trossulus* and *M. edulis* in the region (i); to evaluate the extent of hybridization between the two species (ii); to determine the micro-biotopic (substrate) preferences of genotypes; vi) study size distributions of genotypes. We also perform a morphological analysis to assess the applicability of the species discrimination by the shell character suggested earlier – the extension of the nacreous layer under the ligament on the inner shell surface. *M.edulis* predominated in most populations of Kandalaksha Bay, but in the very top of the Bay, in Kandalaksha harbor and surrounding waters *M. trossulus* prevailed. In other regions *M. trossulus* genotypes appeared sporadically, mainly in the area of Umba harbor. Analysis of hybridization confirmed earlier observations on bimodality of mixed populations – domination of parental species genotypes over hybrids. Mosaic distribution at the regional level is supplemented with micro-biotopical mosaicism: *M. trossulus* genotypes were found to be more frequent on algae substrates, while *M. edulis* were more common on bottom substrates. Genetic study of different size classes showed a shortage of *M. trossulus* among bigger mussels in mixed populations. We also found a good congruence between genetics and morphology: *M. trossulus* on average had a reduced nacreous layer and, hence, a persistent prismatic stripe under a ligament, while *M. edulis* didn't have this stripe due to developed nacreous layer. This morphological marker thus could be used for preliminary identification of *M. trossulus* in the White Sea populations and for mapping two species distributions. As a conclusion, our data indicate that in the White Sea *M. edulis* and *M. trossulus* stand out as rather isolated gene pools and as morphological and ecological distinct entities.

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## MOTILITY OF *SIEDLECKIA NEMATOIDES* (APICOMPLEXA): STRUCTURAL CHANGES OF CYTOSKELETAL ELEMENTS AFTER DRUGS APPLICATION

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Apicomplexans belong to the most monitored group of Protista, comprising exclusively parasites of vertebrates and invertebrates. Members of the phylum Apicomplexa are characterised by typical apical complex of organelles and a complicated cell cortex consisting of cortical alveoli, i.e. dual membrane layer (= inner membrane complex, IMC) underlying the plasma membrane. The IMC is connected with numerous cytoskeletal elements such as actomyosin complex, microtubules and a network of intermediate filamentous proteins. Numerous studies report that the motile apicomplexan invasive stages, the so-called zoites, use a unique mechanism of substrate dependent gliding motility facilitated by a conserved form of actomyosin motor (the so called "glideosome" concept). This concept was described in *Toxoplasma gondii* and *Plasmodium falciparum,* important human pathogens responsible for dangerous diseases (malaria and toxoplasmosis). Actin filaments (F-actin) in these parasites are, in contrast to their microtubules, very unstable and overwhelming majority of actin is present in its globular form. Their actin filaments can be observed only after treatment with jasplakinolide (JAS, a drug that drives actin polymerization). The gliding motility relies on dynamic turnover of actin, unpolymerized form of which seems to have an increased potential to form filaments relative to vertebrate actin. Similarly their myosins are considered unconventional and form a new class (XIV) of small myosin motors lacking typical regulatory domains. This actomyosin motor is localized in between the parasite plasma membrane and IMC, and the gliding motility is based on the locomotion of myosin along actin filaments together with the transport of adhesins to the parasite’s posterior end. It is well documented that this machinery is based and limited by a formation of transient actin filaments and their fixation to the IMC, and requires a stabile subpellicular network of microtubules. Nevertheless, there exist early emerging groups of Apicomplexa, comprising lower coccidian and gregarines, in which the exact mechanism of motility still remains unknown. These organisms seem to use several mechanisms of motility that correlate with various modifications of their cell cortex (in gregarines named epicyte), and their locomotion usually differs from the substrate-dependent gliding observed in apicomplexan zoites. These different modes of motility, such as bending, rolling, coiling or waving, gliding, metaboly or peristalsis, could represent specific adaptations to parasitism in different environment. Deeper understanding of cell motility in basal lineages of Apicomplexa will improve our knowledge on the apicomplexan evolutionary history and in this way it could help to explore new practical possibilities, such as treatment for diseases caused by them. Here we present our preliminary data on *Siedleckia nematoides* Caullery et Mesnil, 1898, belonging to blastogregarine family Siedleckiidae. This intestinal parasite of polychaete *Scoloplos* (*Scoloplos*) *armiger* Müller, 1776, was collected at the Nikolai Pertsov White Sea Biological Station of Moscow State University (Velikaya Salma straight, Kandalaksha Gulf of the White Sea). It develops attached to the host cell via mucron with a well-developed apical complex and feeding mode is apparently myzocytosis. The elongated, flattened individuals of *S. nematoides* perform wavy movement and are covered by a pellicle, consisting of the plasma membrane and IMC. Their surface appears smooth lacking any grooves or folds. Interestingly, subpellicular microtubules are organized in several layers; one of them is continual and located just beneath the IMC, while the other discontinuous layers are to be found deeper in the cytoplasm. Drugs proved to influence polymerization of cytoskeletal proteins, actin and tubulin, were used to evaluate the presumptive involvement of specific subcellular components in gregarine motility. For monitoring the subpellicular microtubules, incubation of living parasites in oryzalin (a drug causing the disruption of the microtubules) was performed. To verify the essential role of continuous assembly and disassembly of actin microfilaments in motility of *S. nematoides*, drugs with contradictory effect, i.e. JAS and cytochalasin D (inhibits polymerization of actin) were applied on living parasites. Behavioural and morphological changes of parasites induced by drugs’ application were monitored, and individuals used in experiments were subsequently fixed for further analyses. Incubation in all mentioned drugs resulted in partial or complete blocking of parasites’ motility, but their motility recovered after returning them to the natural habitat (seawater). The distribution of actin, myosin and α-tubulin was investigated using the direct and indirect fluorescent labelling for confocal laser scanning microscopy (CLSM). The application of oryzalin for prolonged period completely blocked the parasites’ motility, and the putatively unpolymerized α-tubulin (visualized using specific antibody and CLSM) seemed to be more dispersed throughout the cytoplasm in contrast to control parasites incubated in the sea water. Increasing of oryzalin doses resulted in further decrease of fluorescence signal and formation of rosette-like tubulin structures. Similarly, changes in presence and distribution of F-actin were observed using the TRIC-phalloidin staining for CLSM; i.e. prolonged incubation of parasites in high doses of JAS caused significant increase of fluorescent signal, while their incubation in cytochalasin D resulted in its obvious decrease. Results of this study proved that the actin and tubulin polymerized forms play essential role in the movement of *S. nematoides* and the motility mechanism is comparable to the “glideosome” concept described in apicomplexan zoites.

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## DEVELOPMENTAL TRENDS IN BACTERIAL SYMBIOSES AND THEIR NUTRITIONAL CONSEQUENCES IN TWO DEEP-SEA MUSSELS

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Repeated discoveries of communities thriving upon hydrothermal vents, hydrocarbon seeps and organic falls initiated a new era in deep-sea biology, and altered conventional understanding of deep-sea ecosystems. In these habitats, chemosynthetic bacteria occur both as free-living primary producers and as symbionts, supporting the often-endemic communities by deriving metabolic energy from the electron donors and electron acceptors available at anaerobic-aerobic interfaces. As hosts, the Bathymodiolinae mussels represent one of the most diverse and pervasive taxa to colonise these reducing environments. Distributed amongst the gill filaments of adult Bathymodiolinae are symbiotic thiotroph and methylotroph Gammaproteobacteria, whose presence reflect the availability of sulphides and/or reduced one-carbon compounds (e.g. methane) in the surrounding environment. To better understand how these mussels are able to survive and prosper, this research sought to identify 1) the smallest size at which these species reach maturity; 2) trends in symbiont acquisition and proliferation during early stages of development; 3) whether symbiont patterns are influenced by habitat type and; 4) the nutritional consequences of these various scenarios. The developmental biology and symbioses of *Idas modiolaeformis* and *Nypamodiolus* (formerly *Idas*) *simpsoni* were examined using molecular approaches, histology and microscopy. *Idas modiolaeformis* mussels were retrieved from hydrocarbon seeps and vegetative organic substrata deployed in the Eastern and Western Mediterranean, while *Nypamodiolus simpsoni* were collected from the same organic matter in the Western Mediterranean and from the bones of mammal carcasses deployed in the Atlantic (Setúbal Canyon, Western Portuguese Margin). Differences and similarities in the developmental biology of the two genera and patterns of infection by their environmentally-acquired bacterial symbionts are described for the first time. Post-larval plantigrades are asymbiotic in both species regardless of habitat type, indicating strict heterotrophy in larvae and early post-larvae. A nutritional transition then takes places towards predominantly-chemosymbiotic mixotrophy in adults, following the environmental acquisition of symbionts as juveniles. Extracellular infection is initially non-specific occurring on nearly all non-ciliated epithelia, with increasing specificity on non-ciliated gill epithelia in adult individuals. Habitat types, rather than species-specific factors, appear to dictate the compliment of symbionts and their densities at a given size. These results are discussed in the biogeographic context of these species and their apparent evolutionary success in adapting to ephemeral, chemically-reduced habitats in the deep sea.

## DISTANT MIGRATIONS OF CRINOID ASSOCIATES. HOW DO THEY DO THIS?

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Fragmented communities which consist of isolated patches are common in marine environment. Individual hosts, either solitary organisms or colonies, inhabited by symbiotic animals can be considered as fragments of a meta-community which consists of sub-communities of symbionts.

The community fragments which are based either on non-living or living objects interact via two processes: settlement of plankton larvae, and migrations of post-settled juveniles and adults. The main difference between free-living and symbiotic animals is that obligatory symbionts are poorly adapted to survive outside the hosts. Their host-to-host migrations are very risky due to high predation pressure, suggesting the strong isolation between symbiotic sub-communities. Our previous experiments with the comatulid crinoid hosts *Himerometra robustipinna* demonstrated intensive migration of adult and sub-adult symbionts from one host to another within host aggregations (short – distance migrations, tens cm). We have also found immigrants on the crinoid hosts separated by several meters. The aim of this study was to test hypotheses on the main routes of colonization of spatially separated crinoid hosts. Two sets of *in situ* experiments with the crinoid *H. robustipinna* were performed. In the first one, tagged and free of symbionts crinoids were distributed among four groups of boulders, which were mounted on the sand bottom 2.5–5.0 m away from the rocks with native assemblages of crinoids. Experimental crinoids were exposed for one, two, three, and four weeks. In the second set, individual crinoids were placed inside plastic cages, which were suspended in the water 1.0–1.5 m above the bottom. The aim was to check whether symbionts are able to disperse with currents. As the control we considered symbiotic assemblages washed out from the crinoids used in the experiments. It included four main taxa: polychaetes, galatheids, shrimps, and ophiuroids (listed according to their abundance). The prevalence in the control was 100%, intensity varied from 9.5 to 12.9 individuals per one infested host, and species richness from 2.3 to 2.9 species per host. The first experimental set demonstrated colonization of crinoids by adult and sub-adult polychaetes, galatheids and shrimps, while ophiuroids were not found. The prevalence was close to that in the control (87.5–100%), while intensity and species richness were substantially lower (1.8–5.0, and 1.1–1.5 respectively). Polychaetes had the highest abundance among colonizers. They were followed by shrimps; galatheids were rare. In the experimental set 2, the prevalence after 11–12 days of exposure was slightly lower than in the control (85.7 vs 100%), species richness was the same as in the control (2 species per individual host), while mean intensity was more than twice higher (11.7 and 4.25 individuals per host respectively). Polychaetes, shrimps, galatheids, and gastropods were found among colonizers. The most numerous group of colonizers were non-specialized species of shrimps *Periclimenes diversipes*. Our results proved the ability of symbionts to colonize spatially remote hosts even if they were suspended in the water column. Species composition of symbionts colonizing crinoids exposed on the boulders (dominated by polychaetes) differed from those suspended in the water (dominated by shrimps). This suggests two possible ways of symbionts dispersion: crawling on the substrate (polychaetes), and transportation by currents (shrimps).

## SEASONALITY AND HOST-PARASITE INTERRELATIONSHIP OF *MYTILUS GALLOPROVINCIALIS* LAMARCK, 1819 PARASITES IN TURKISH BLACK SEA COASTS

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This is the first comprehensive research study on the parasites of *Mytilus galloprovincialis* Lamarck, 1819 collected from the Sinop coast of the Black Sea and their relationships with several environmental and biotic factors. A total of 1740 mussels were collected monthly at 3 sampling stations representing different ecosystem in the period between August 2012 and July 2013 and examined for parasites using standard investigation procedures. Five parasite species were identified: two protozoan *Nematopsis legeri* de Beauchamp, 1910 and *Peniculistoma mytili* (Morgan, 1925) Jankowski, 1964, one turbellarian *Urastoma cyprinae* (Graff, 1882), one trematode *Parvatrema duboisi* (Dollfus, 1923) and one polychaeta *Polydora ciliata* (Johnston, 1838). Infection prevalence (%), mean intensity and abundance values of each parasite species were calculated according to season, sampling localities and length of mussel. *Nematopsis legeri* was the dominant species in terms of both infection prevalence and intensities. *Nematopsis legeri* and *Parvatrema duboisi* occurred more in sampling locality III to complete their life cycle in secondary hosts. Larger sized mussels had higher parasite intensities. Statistically significant differences in the occurrence values of each parasite species were discussed in detail using figures and tables.

## PARASITE FAUNA OF THE RED MULLET, *MULLUS BARBATUS PONTICUS* ESSIPOV, 1927, AND ITS DYNAMICS IN RELATION WITH SOME HOST AND SEASONAL FACTORS

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The red mullet, *Mullus barbatus ponticus*, is a commercially important food fish in the Black Sea region. In this comprehensive research study, a total of 330 fish specimens caught at the Black Sea coasts in Sinop, Turkey were investigated for its parasite fauna. Sixteen parasite species were identified, comprising three protozoa, one Microsporidia, two digenea, three cestoda, six nematoda and one acanthocephala and they were *Trichodina domerguei*, *Trichodina* sp., *Paratrichodina* sp., *Loma* sp., *Proctotrema bacilliovatum*, *Galactasomum lateum*, *Grillotia dasyatidis*, *Nybelinia* sp., Tetraphyllidae gen. sp. pleurocercoid, *Hysterothylacium fabri*, *H. aduncum*, *Ascarophis valentina*, *Capillaria* sp. *Contraceacum* sp., unidentified larval nematode (L2) and *Acanthocephaloides irregularis*. The overall infection prevalence and mean intensity values were 96.77% and 49.37 ± 8.69 parasites per infected fish, respectively. *Proctotrema bacilliovatum* was the dominant species among all with its highest prevalence value (70.61%). Both infection indice values for each parasite species in relation to fish length and sex and season were also determined and discussed.

## WHEN MUSSELS ARE MOST TASTY: SEASONAL VARIATION OF CALORIC VALUE AND TISSUE BIOCHEMICAL COMPOSITION OF *MYTILUS* IN THE NORTH

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Mussels of genus *Mytilus* are widely distributed in boreal and subarctic seas serving as a major food item for many benthos feeding birds, such as eider ducks and others. The pressure of waterfowl on local *Mytilus* populations may be very heavy especially in the North where mussels reaching the edge of their distribution range are characterized by slow growth and reduced population recruitment. The impact of predation depends on the trophic requirements of the birds and the nutritional value of mussels. The aim of the present study was to trace seasonal changes in biochemical composition of mussel tissues, to evaluate their energy content and to estimate the potential impact of eider ducks on mussel populations in the White Sea, Sea of Okhotsk and the Pechora Sea (SE part of Barents Sea).

The ratio of body parts (shell, soft tissues, mantle fluid) and tissue biochemical composition in mussels largely depends on their reproductive cycle, which is associated mainly with seasonal course of water temperature. Mussels from the Sea of Okhotsk and the Pechora Seas had higher content of soft tissues (25–30 %) compared to the White Sea mollusks (15–20%). Proteins made up 50–60% of dry weight tissue in White Sea mussels and 70 % for those from the Sea of Okhotsk. Glycogen content in the White Sea mussels was significantly higher than that of mussels from the Pechora Sea and Sea of Okhotsk. Maximum values were observed in summer in post-spawning period when available food concentration was maximal followed by a slow spending of glycogen reserves in autumn and winter. Seasonal variation in lipid content was opposite to glycogen levels in tissues. On average, mussel dry tissues contained about 8–12% of lipids. In the period of active gonad maturation and preparation for spawning glycogen concentrations decreased rapidly accompanied by a sharp increase in the proportion of lipids, indicating the conversion of glycogen to lipids in oocyte maturation.

We determined the average number and size of mussels in the crops of king eiders *Somateria spectabilis* and common eiders *S. mollissima* and calculated the total energy content of mussels consumed at once by actively feeding birds. Taking into account the caloric value of mussels in the studied areas it appeared that the birds feeding in the White Sea should consume about 40% more mussels than in the Sea of Okhotsk for getting the same amount of energy. We assume that differences in nutritional value and energy content of mussels from different waters may account for the degree of impact of migratory birds on mussels coastal populations.

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## ATTACHMENT STRATEGY OF *ELEUTHEROSCHIZON DUBOSCQI* (APICOMPLEXA): A PROTOCOCCIDIAN SHARING FEATURES OF GREGARINES AND CRYPTOSPORIDIA

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Apicomplexa represent very successful group of unicellular parasites that evolved unique adaptations for invading and surviving within their hosts. In contrast to well-studied etiologic agents of significant human diseases (e.g. malaria, cryptosporidiosis), apicomplexans restricted to invertebrates remain poorly understood. Nevertheless, they appear to be very important in the comprehension of evolutionary pathways and phylogenetic relations within the phylum Apicomplexa. It is assumed that ancestral apicomplexans parasitized marine annelids, and their adaptation to the parasitic life style and further radiation took place before the era of vertebrates. At the beginning they spread to other marine invertebrates, then to freshwater and terrestrial invertebrates, and finally to vertebrates. Their zoite exhibits a high degree of polarity in that it has an apical pole equipped with a unique complex, comprising specialized secretory organelles, polar rings, and a conoid. This invasion apparatus traditionally used as the best defining feature for Apicomplexa, can be also found in other Myzozoa. Apicomplexan evolution most likely progressed from myzocytotic predation to myzocytotic extracellular parasitism (e.g. gregarines, cryptosporidia), and finally to intracellular parasitism typical for coccidia. The origination of extracellular parasitism in gregarines resulted in improvement of their attachment apparatus, which exhibits an enormous diversity in architecture. Recent studies pointed out the unique epicellular localization of cryptosporidia within extraordinary host cell-derived parasitophorous sac, and the similarity in their attachment and feeding strategy with gregarines; i.e. both groups form a specialized host-parasite interface and reflect analogous modes of adaptation to similar environment within host. Based on phylogenetic analyses reporting close affinity of gregarines and cryptosporidia, speculation that cryptosporidia represent a ‘missing link’ between the gregarines and coccidia is frequently discussed. This study focuses on attachment strategy, cell cortex and cytoskeleton of protococcidian *Eleutheroschizon duboscqi* Brasil, 1906, a representative of marine deep-branching apicomplexans, which shares features of both the gregarines and coccidia. Littoral samples of host polychaete *Scoloplos* (*Scoloplos*) *armiger* Müller, 1776 were collected at the Nikolai Pertsov White Sea Biological Station of MSU (Velikaya Salma straight, Kandalaksha Gulf, White Sea). The helmet-shaped stages attached to the host cell show more or less distinct metabolic activity. Attached parasites are covered by a parasitophorous sac (PS) resembling that of cryptosporidia. The caudal part of the PS forms a short tipped appendage, a tail. The attachment apparatus consists of several short projections (lobes) arranged in circles, surrounded by another circle of filamentous fascicles. No organelles of apical complex were observed. Cell surface exhibits shallow grooves with micropores at their bottom. The parasite pellicle seems to be trilaminar, but the membranes are difficult to discern. The phalloidin labelling for confocal laser scanning microscopy (CLSM) confirmed the high accumulation of filamentous actin (F-actin) in a brush border of host epithelium and in two layers at the parasite periphery; the outer one seems to correspond to the PS that is considered of host cell origin (including the attachment site) and the inner less distinct layer that could correspond to the layer of short filaments underling the parasite pellicle observed under electron microscopy. The tail formed from the caudal part of the PS exhibited signal of medium intensity for F-actin. The cytoplasm of parasites exhibited F-actin signal of lower intensity, similarly to cytoplasm of epithelial cells. The staining with Evans Blue viewed under CLSM revealed a relatively high concentration of unspecified proteins in the PS tail and in the area of attachment site. During experiments with membrane-permeable probes influencing the polymerization of cytoskeletal proteins, G-actin into actin filaments (jasplakinolide, cytochalasin D) and α-tubulin in microtubules (oryzalin), parasites not only survived incubation in very high doses of these drugs and but also showed signs of motility within their sacs for next couple of hours. After treatment with jasplakinolide (stabilizes actin filaments, induces actin polymerisation) the F-actin staining became brighter in the area of the PS, while specimens treated for long period in cytochalasin D (disrupts actin filaments, inhibits actin polymerisation) exhibited almost no F-actin labelling. Parasites labelled with the specific anti-actin antibody (known to recognize *Toxoplasma* actin) exhibited only indistinct fluorescence signal. The immunolocalization of actin differed from phalloidin labelling in that the antibody did not label the PS, but labelled the host tissue with the same intensity as parasite inside the PS. A weak staining of the PS tail was observed in all individuals. The myosin labelling was restricted to the periphery of the PS. The immunolabelling with an anti-α-tubulin antibody used for visualization of subpellicular microtubules and related structures was strongly positive for brush border of host intestinal epithelium. Despite the fact that under electron microscopy no typical microtubules were observed, both the surface of the parasite itself and the PS exhibited relatively distinct labelling. After prolonged incubation of living parasites in oryzalin (disrupts microtubules), the peripheral labelling gradually decreased through more diffuse to very weak as if putatively unpolymerised form of α-tubulin dispersed throughout the cytoplasm. Detailed electron microscopic analysis revealed that *E. duboscqi* attachment strategy shares features of cryptosporidia and gregarines, i.e. it conspicuously resembles an epicellularly located gregarine embraced by PS, which seems to develop in similar manner as shown in cryptosporidia. Interestingly, the membranes of parasite pellicle become disorganized during its early development, and the interface between PS and parasite remains unclear. In advanced developmental stages, the space between PS and parasite pellicle appears translucent with tiny filamentous structures and it resembles the cortical vesicle of gregarine epimerite, even though it envelopes the entire parasite up to the PS tail. We also speculate that attached individuals preserve their PS until the end of development, even if they eventually detach from host tissue.

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## ATLANTIC HERRING FRESH FROM THE CELTIC SEA – THE CHEF'S SUGGESTION ON TODAY'S WHALE MENU

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Atlantic herring (*Clupea harengus*) is an important pelagic key species within the Celtic Sea ecosystem. It is favourite prey for sea birds and cetaceans, and of high value for the Irish fishery industries. Over the last years, the Celtic Sea herring stock has been increasing, and simultaneously increased the number of land-based sightings for fin and humpback whales (*Balaenoptera physalus* and *Megaptera novaeangliae*). It is difficult to differentiate between an increase in abundance, or a higher rate of resightings of the same whales. Both whale species have been observed lunge feeding in herring spawning grounds and dietary studies indicate a high importance of herring within their diet. Here, we simulate trajectories of whales in the Celtic Sea during herring spawning migration. A dynamic model was developed to investigate the co-occurrence of predator and prey and the model output was compared to eight years of visual observations in the field. First, the distribution of energy provided by herring was analysed and quantified as a forcing factor. Then, the movement of predators, including behaviour changes, i.e. diving and feeding, has been simulated, using an oriented random walk process. The model represents a theoretical distribution of a top predator and its prey and includes predation interactions. Predation is governed by processed derived from dynamic energy budgets in a framework of optimal foraging, although the loss of energy during foraging was seen as a deterministic feature and energy gain remained a stochastic component important to include in the simulation process. Results of the simulations provide valuable information about prey exploitation, which is difficult to obtain in the field. It can give an indication, if predator abundance has been increasing, or if whales remain for a longer period within their feeding area and therefore increase the rate of resightings. This model was designed to assess the impact of cetacean predation on the herring population, which can feed into the fishery management plan and the development towards an ecosystem approach to fisheries management.

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## BIODIVERSITY AND DISEASE RISK: DOES DIVERSITY ACTUALLY REDUCE DISEASE RISK?

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It has been suggested that an increase in biodiversity results a decrease in disease risk via the so called dilution effect. However, this idea which initially derived from Lymes disease has been challenged as being too simplistic. Here, we extend this skepticism to non-host dilutors and macroparasites. Using a marine trematode parasite and organisms known to reduce its free-living cercarial stages we designed mesocosm experiment that manipulated both the density and the diversity of the dilutors. Our results indicate that the effects of biodiversity on disease risk are actually very complex and not only depend on the identity of the dilutor but generally result in complex interactions between dilutors that can both reduce or enhance the disease risk for a target host. Hence, the relationship between diversity and disease risk seems much more idiosyncratic than the 'biodiversity reduces disease risk' hypothesis suggests.

## STRUCTURE OF SYMBIOTIC ASSEMBLAGES ASSOCIATED WITH PLANTED CORALS DIFFERS FROM THAT OF NATURAL ONES

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All scleractinian corals are inhabited by diverse symbiotic animals from different taxa, while the most abundant group among them is decapods. These symbionts play an important role in protecting hosts from predators and maintaining them clean and healthy. Due to the fast coral reef degradation numerous successful attempts of planting coral fragments on artificial constructions have been performed in the Southeast Asia countries (Latypov 2006, Quan et al. 2008). However, it is unknown whether the symbiotic assemblages associated with planted corals have the same species composition and structure as natural ones. The main goal of our report was to respond on this question. For comparison of planted and natural colonies we cultivated fragments of *Pocillopora verrucosa* colonies on triangle iron frames elevated above the ground on 30 – 40 cm and exposed them during 6 and 12 months, and collected colonies from the natural environment in the vicinity of cultivation site. We treated 42 planted coral colonies and 28 wild coral colonies. Totally 34 species were found on natural and planted corals, 26 of which were decapod crustaceans (crabs *Trapezia* spp., shrimps Alpheidae, Palaemonidae, etc.). We recognized among them 18 species of obligatory symbionts (15 species of decapods, 2 species of gastropod and 1 of bivalve mollusks), and 16 species of facultative symbionts (decapods, gastropod, sipunculans, flat worms and ophiuroids). Abundance and mean number of species per coral colony were significantly higher for both obligatory and facultative symbionts in natural colonies than in planted ones (12.00 ind. per colony, 5.90 species per colony and 6.05 ind. per colony, and 3.89 species per colony, respectively). There are two possible explanations of impoverishment of planted colonies. 1. Coral colonies elevated above the ground on frames are inaccessible for symbionts migrating from colony to colony. 2. Symbionts inhabiting planted coral colonies suspended in the water are more accessible for predators, than symbionts in the colonies adjoining to hard substrate. These observations have and important consequence for the strategy of coral reef re-cultivation, since employment of frames for planting fast growth coral colonies have to be supplemented by protection of natural colonies or/and planting corals on the consolidated substrates.

# THE IMPACT OF *AURELIA* SP. DEGRADATION ON THE MICROBIAL COMMUNITY DYNAMICS IN THE BLACK SEA

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Due to their high protein content, jellyfish might represent high quality organic substrate for microbial community. In order to study the impact of *Aurelia* sp. degradation on the ambient microbial community in the Black Sea, where this jellyfish reoccurs yearly, two set of short-term degradation experiments were conducted. One of the central objectives of our research was to examine the aspect of jellyfish substrate as selective force that either inhibits and/or stimulates the growth of specific bacterial groups. In both sets of experiments, the ambient microbial community was supplemented with the same amount of jellyfish biomass, however in the first experiment (ExpI) the enclosures were filled with the coastal seawater, while in the second experiment (ExpII) the offshore seawater was used. Each experimental set up comprised of a triplicate of jellyfish-enriched bottles and a bottle without jellyfish addition that served as control. The experimental enclosures were incubated *in situ* to ensure natural conditions. The daily dynamic of bacterial community structure was followed using DNA fingerprinting technique – the *denaturing gradient gel electrophoresis* (DGGE). Furthermore, to obtain the information on the dynamics of the dominant bacterial families, the 16S rRNA bacterial gene clone libraries were constructed at the beginning and at the end of both experiments. These data were supplemented with particulate and dissolved organic and inorganic nutrient analyses as well as stable $^{13}C$ and $^{15}N$ isotope analyses of particulate organic matter (POM, ≥ 0.8 μm fraction), which provided an insight into the processes of organic matter transformations. The jellyfish biomass addition triggered a rapid response of ambient bacterial community; during the exponential growth phase the bacterial community had considerably higher specific growth rates in the jellyfish-enriched bottles ($0.38\ d^{-1}$ and $0.31\ d^{-1}$ in ExpI and ExpII, respectively) compared to the control ($0.29\ d^{-1}$ and $0.24\ d^{-1}$ in ExpI and ExpII, respectively). In the first 24 hours, the concentration of POM decreased for about 50% in both experiments, followed by an increase and accumulation of POM at the end of both experiments (day 3). As depicted from C to N ratio and stable isotope analysis the quality of POM changed over time in both experiments. The $\delta^{15}N$ of POM gradually increased in both experiments, suggesting that the lighter isotope was taken up and transformed by bacteria thus either becoming volatile or dissolved and therefore transferred into the <0.8μm fraction, leading to the accumulation of the heavier isotope in the particulate (>0.8μm) fraction. This was further supported by the measurements of inorganic nutrients that showed the accumulation of dissolved nitrogen and ammonium ($NH_4^+$) in the < 0.8μm fraction at the end of the experiments. The analyses of bacterial community using DGGE fingerprinting method revealed that the structure has changed already after 24 hours in all experimental bottles, which could be due to the bottle effect, and already after 48 hours, the jellyfish-enriched and the control communities formed distinct clusters, in both experimental set ups. The analyses of bacterial 16S rRNA gene clone libraries showed that coastal (ExpI) and offshore (ExpII) communities were different at the start. The coastal community was prevailed by *Alphaproteobacteria* (27%, which were dominated by SAR11 clade) and *Cyanobacteria* (23%), followed by app. equal contribution of *Gammaproteobacteria* and *Bacteroidetes* (from which only *Flavobacteriales*) and some minor and unclassified taxa. On the other hand, the offshore community comprised mostly of *Gammaproteobacteria* (51%), followed by *Bacteroidetes* (17%, from which only *Flavobacteriales*) and *Alphaproteobacteria* (14.3%, dominated by SAR11) as well as some minor taxa and lower percentage of unclassified groups. The community composition within the jellyfish-enriched treatment was largely altered at the end of both experiments. A common response of both coastal and offshore community to jellyfish substrate was a decrease of *Alphaproteobacteria* (within which SAR11 clade diminished the most). In the coastal community the prevailing *Alphaproteobacteria* were outnumbered by known degraders of complex organic substrates – *Gammaproteobacteria* that constituted more than half (52%) of the total community at the end of the experiment. On the other hand, in the offshore community a shift from prevailing *Gammaproteobacteria* to *Flavobacteriales* (*Bacteroidetes*) (50% of the total community), which are also know to be capable of degrading high molecular weight organic compounds, was recorded. Our preliminary data suggest that the jellyfish biomass stimulated the growth of bacterial community, which efficiently re-mineralized this rich organic substrate that led to the accumulation of dissolved inorganic nutrients. In general, the jellyfish substrate inhibited the growth of *Alphaproteobacteria* (in particularly SAR11 clade) and stimulated the growth of *Gammaproteobacteria* in the coastal and *Flavobacteriales* in the offshore experimental enclosures.

# PREDATOR-PREY RELATIONSHIPS AT BATHYAL DEPTHS: A CASE STUDY USING CHEILOSTOME BRYOZOANS

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From below the depths reached by scuba diving, information on, and direct observations of, predation and predator-prey relationships are extremely scarce. In most cases, our knowledge is obtained from the predator's gut contents or from indirect clues such as, for instance, the presence of potential predator and prey species in a single grab or epibenthic sledge sample, or from predation marks left behind in the skeleton of the attacked organism. The effect of predation pressure in evolutionary terms can be deduced from morphological adaptations such as the formation of defensive skeletal structures in prey organisms. Bryozoan colonies producing calcified skeletons reach their greatest diversity and abundance at middle to outer shelf depths, and are therefore presumed to form a significant food source for a variety of predatory taxa. We here present a comparative study of cheilostome bryozoans from shallow-water to bathyal depths in the northeastern Atlantic. The presence and frequency of a range of skeletal structures that are interpreted as anti-predator defences, such as avicularia or oral spines, are assessed. Moreover, damages to the skeletons of single zooids that were presumably caused by partial predators are taken into consideration. Our preliminary results show that, when compared with congeneric species from shallow waters, bathyal species show a surprisingly high investment into defensive structures, and that reparation of zooids following partial predation is fairly common. This suggests that predation pressure at bathyal depths may be significantly greater, and a more important driving force in the evolution of deep sea organisms, than previously acknowledged.

# Marine communities and food webs

## INTERTIDAL ZOOCENOSES OF THE KOLA BAY

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Intertidal macrobenthic communities, being the complex of species, have a large number of interspecific relationships, able to well-coordinated response to changes in environmental parameters and species-specific response to external stimuli, that makes them of interest to researchers. Zoobenthos is able to be responsive to changes in environmental parameters, while remaining stable and adapted to even extreme influences.

The goal of the research is to study the structure of intertidal zoocenoses of the Kola Bay of the Barents Sea.

The seasonal dynamics of species composition; biomass, abundance of macrobenthos communities and dominant species in the Kola Bay; zoocenoses distribution in intertidal areas, differing in hydrological characteristics, particle size composition and the level of anthropogenic pressure, were studied.

Bivalves *Mytilus edulis* and barnacles *Semibalanus balanoides* are dominants in the studied zoocenoses. Bivalves *Macoma balthica* dominate on soft-bottom areas.

Biomass and abundance of benthic communities and dominant species is increasing from the innermost part of the bay to the bay mouth, that is caused by the turn of intertidal substrates to greater heterogeneity and changes in hydrological conditions. Population parameters of dominating species are changing similarly.

Cluster analysis of benthos data sets allowed to reveal three faunal complexes. The innermost part of the bay, characterized by low salinity, high intensity water movement, muddy intertidal substrate, forms the estuarine species complex. Faunal complex of the Kole Bay mouth represents the maritime community. The third group consists of species complexes, inhabiting the middle part of the bay.

## EFFECT OF THE FILTER-FEEDING BIVALVE *CERASTODERMA GLAUCUM* ON BENTHIC METABOLISM; A MICROCOSM EXPERIMENT

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Benthic invertebrates play a key role in biogeochemical processes due to their sediment reworking and bioirrigation activities thus affecting biological, physical and chemical fluxes across the sediment-water interface. The aim of this study was to assess the effect of the filter-feeding bivalve *Cerastoderma glaucum* (Bruguière, 1789) on the benthic metabolism of lagoonal sediments impacted by a waste water treatment plant. Short-term whole-core experiments were performed under close to in-situ conditions in winter and spring, with sediment and bivalves collected inthe vicinity of the water treatment plant of Aetoliko in Messolonghi lagoon (Greece). Six undisturbed sediment cores were brought to the laboratory. In half of the cores, *C. glaucum* (1 cm average length) were added at a density of 1600 ind $m^{-2}$. Oxygen consumption and inorganic nutrient ($NH_4^+$, $NO_x$, $SiO_4^{4-}$ and $PO_4^{3-}$) fluxes were studied, under dark and light conditions, 7 days after adding the bivalves. Chromophoric Dissolved Organic Matter (CDOM) was also measured by Excitation-Emission Matrix (EEM) fluorescence both in the water column and the porewater. During the course of the experiments, negative fluxes were found for all the nutrients and oxygen. The uptake of nutrients in the cores with *C. glaucum* was 1.5 times higher than the control, suggesting that the animal activities contributed to the removal of nutrients from the water column. In the same cores the nutrients present in the first layers of the sediment (0-1.5cm) were lower suggesting that the cockles are affecting the removing of nutrients. PARAFAC modeling identified 6 main components within the CDOM, three protein-like components and three humic-like components. CDOM components were directed towards the sediment and showed the same profile pattern in porewater as for inorganic nutrients.The high negative fluxes in the presence of cockles suggest that *C. glaucum* is a key species regarding the functioning of lagoonal habitats and that, when present in high densities, it may play an important role in lowering the levels of eutrophication in these ecosystems.

## STUDY OF *POSIDONIA OCEANICA* CANOPY IN THE AREA AFFECTED BY COSTA CONCORDIA WRECK

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Epiphytic community and phenology of *Posidonia oceanica* (L.) Delile leaves in the area affected by Costa Concordia wreck were studied. Three sampling sites were selected along a gradient of increasing distance from the wreck and according to an asymmetric hierarchical experimental design. Percentage cover of algal and animal taxa observed on the leaves was estimate and phenological parameters were measured seasonally from March 2012 to July 2013, from shortly after the sinking of the ship to the overturning step of the wreck. Despite a high local natural spatio-temporal variability, results showed significant modifications especially on the epiphytic community living in the site close to Costa Concordia wreck if compared to the two control sites, likely due to the shipwreck event. This research provides both first information about impact caused by the presence of the Costa Concordia wreck and preliminary data on influence of the yard for the ship removal on benthic marine ecosystem.

## VAGILE MEIOFAUNA FROM ROCKY WALLS OF A SUBMARINE CAVE

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The vagile meiofauna from the rocky walls of the submarine cave *il Ciolo* (Otranto Channel, South East Italy) has been considered for a pilot study on this disregarded component of the submarine cave biodiversity. The cave is a blind tunnel of about 125 m length, all in the first 5 m below the sea level. The meiofauna has been studied with the collection of vagile organisms from artificial substrates (panels) and natural rocky walls. This double approach allowed the description of the community starting point (on artificial substrata) and of its mature composition (on rocky walls). The collected samples (deriving from different seasons and years) gave a list of more than 100 taxa in total, notwithstanding the the identification of specimens did not go under the taxonomic level of family. Harpacticoida (Crustacea, Copepoda) represented the most important taxon in terms of numbers of individuals, and taxa. A detailed study on the distribution of Harpacticoida showed the presence of two different communities at the extremes of the cave length. Seasonal differences were marked, and acted differently from the positional ones on the community composition.

## INFLUENCES OF HABITAT COMPLEXITY ON BENTHIC MACROINVERTEBRATES COMMUNITIES; DOES BIOLOGICAL TRAIT COMPOSITION RESPONDS REGULARLY ACROSS SEASONS?

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The structure and organization of macroinvertebrates assemblages are known to be variable in spatial and temporal scales, being influenced by a variety of biotic and abiotic factors. In the present study we analyzed the response of eight macroinvertebrates biological traits (i.e., body size, mobility, habitat location, feeding mode and apparatus, food type, habitat modification and bioturbation) to habitat complexity within the three main habitat types found at Messolonghi lagoon (i.e., bare sediment, *Valonia aegagropila and Cymodocea nodosa/ Rytiphlaea tinctoria*). The analysis was focused on identifying the effect of these habitats acting as biological trait filters in a temporal scale. To account for the complexity of these habitats phytal biomass, volume and fractal dimension at different scales were measured. Results show a positive correlation of the habitat complexity measurements with the distribution of feeding mode, mobility and habitat location. A less solid correlation over body size and food type was determined. Seasonality was not found to shift the representativeness of the studied biological traits across the habitats. In terms of abundance the bare sediment habitat denoted higher seasonal variation with a huge decline in summer. This study shows the contribution of the habitat complexity in structuring the distribution of the studied biological traits on macroinvertebrates communities at Messolonghi lagoon.

## SOFT-BOTTOM MACROBENTHIC COMMUNITIES IN SHALLOW-WATER BAYS OF MURMAN COAST OF BARENTS SEA

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Surprisingly little is known about soft bottom macrobenthic communities in shallow and highly isolated bays. Big ships with typical marine grabs (0,1 $m^2$+) could not work here since that bays are shallow or isolated. Small grabs work here badly, they can collect coarse marine sediments hardly and unreliable. Diver operated sampling tools are likely the most reliable choice for that type of sampling, although not an ideal one. We collect and analyzed diver-operated grab (0,004) samples from Dalnezelenetskaya Inlet (shallow water bay, protected from Sea by islands, sampled in 2002 and 2008) and from Linjalampi and Sisjaarvi salty lakes (actually – a highly isolated lagoon with marine salinity and regular water exchange with open sea due to tidal current through an shallow strait (sampled in 2010, 2011, 2012)) to understand spatial and temporal dynamic of benthic assemblages. Based on abundance data, 3 communities were identified in lakes, which correspond to specific abiotic condition: “shallow” (which include stations above summer thermocline),”deep” (below thermocline), and “mixed bottom” (on gravel/shelly bottom). Benthic communities of Dalnezelenetskaya Inlet in general resemble “shallow” community of the lakes. All the variant of “shallow” community in both bays are regarded to be a variant of Macoma calcarea community. Although, the community of Dalnezelenetskaya Bay in 2002 and in 2008 differs significantly. An average abundance of polychaeta *Polydora quadrilobata* increased in 2 orders of magnitude, abundance of polychates *Spio arctica, Spio armata, Harmothoe imbricata, Scoloplos armiger* and *Apistobranchus tunbergi* also increased in several times. These changes are likely a result of eutrophication in Dalnezelenetskaya Bay, which can be caused by experimental aquaculture of red king crab in cages here. What is interesting, we have found unpublished data about benthos under experimental aquaculture kelp farm in Dalnezelenetskaya Inlet (sampled in 1988), and abundance of *Polydora quadrilobata* was also high here. The major feature of benthos from salt lakes is the high abundance of polychaeta *Scalibregma inflata* and mollusk *Nucula tennuis*. Dalnezelenetskaya Inlet differs from lakes in generally high abundance of *Opelia limacina, Opiura robusta* and *Capitella capitata*. Such a diverse data allowed us to distinguish temporal changes from spatial heterogeneity and differences in abiotic regime between these two bays.

## DIET OF NON-TARGET FISHES – COMPARISON BETWEEN THE NORTHERN BARENTS AND KARA SEA

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Based on investigations of PINRO and sampling of stomach data in the northern Barents and Kara Sea in 2007-2013 diet composition and feeding intensity of more than 15 non-target fish species is analyzed. Most species were benthivorous, while portions of lanctivorous and piscivorous were considerably low. Feeding intensity and diet composition of many species (e.g., *Artediellus atlanticus*, *Icelus bicornis*, *Cottunculus microps*, *Triglops nybelini*, etc) were different in the areas investigated. The Kara Sea can be considered as an advantageous area for some species with high food sources and lack of predators. Possible food competition with commercially important fishes (Greenland halibut, capelin, polar cod) is also evaluated.

## STEREO CAMERAS AT STATION M; UNDERSTANDING THE CARBON UTILIZATION OF EPIBENTHIC MEGAFAUNAL COMMUNITIES

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Data continues to be collected at Station M, ~4000m at the Monterey Deep-sea Fan, adding to a 24 year time-series that has substantially improved understanding of the connections between surface food supply and deep-ocean benthic communities and the role of the deep-ocean benthic environment in the global carbon cycle (Sherman and Smith, 2009). The role of carbon bioturbation, remineralization and sequestration by deep-ocean benthos in the global carbon cycle is however, relatively unknown (Smith et al., 2013). Deep-sea epibentic megafauna (animals ≥ 1 cm) play a role in carbon sequestration through the redistribution of organic material, oxygen and other nutrients in the sediment surface layers (Smith et al., 1993). Megafauna community composition, abundance and size distribution vary in response to climate induced changes in particulate organic carbon supply to the sea floor (Ruhl and Smith, 2004) and have been suggested as an indicator group to understand the effects of climatic variation on abyssal benthos and long-term carbon sequestration (Ruhl, 2007). It is important to understand the abundance, size distribution and biomass of megafaunal communities to further define this role. Gathering data on the megafauna community body size, biomass, spatial distribution and movement patterns will be essential to understand both the community response to changes in food supply and the communities impact on carbon sequestration (Lauerman et al., 1996). A deep-sea stereo camera has been developed that has enabled significant advances in the ability to make precise and accurate length measurements of fauna from images (Harvey et al., 2012). This presentation will outline how stereo camera techniques are being used to measure the body size and biomass of epibenthic megafauna at Station M. Biomass estimates are required to calculate the organic carbon utilization of epibenthic megafauna using wet-weight specific oxygen consumption rates of individual species (Smith, 1989; Smith et al., 1993). Estimates of organic carbon utilization of the epibenthic megafaunal community will be combined with time-series data on surface food supply, sediment community oxygen consumption (a measure of the total benthic community oxygen utilization) and community composition. This will enable significant advances in the understanding of the role of epibenthic megafauna in deep-sea carbon sequestration.

## PREDATION, A FUNDAMENTAL PROCESS IN MACROFAUNA COMMUNITY ASSEMBLING

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It exists several theories (*e.g.* neutrality, species sorting or patch dynamics) that describe processes of assembling communities in natural environment but there is no consensus. The phase of colonization *per se* (emphasizing patch dynamics), preceding the phase of negative interactions (emphasizing species sorting) and the phase of regulation (emphasizing neutrality), remains the less well-studied experimentally, and the less well-quantified by mathematical models. In order to fill this gap of knowledge, an approach combining an *in situ* experiment and a stochastic model was proposed to study arrivals and settlement of individuals of different species (benthic macrofauna) in a pristine environment (sets of cages) containing what was assumed to be non-limiting resources (a large quantity of allochtonous organic matter). The time frame of the colonization study was set for 3 months. Data analyses of the diversity permitted to identify five species (*Capitella capitata*, *Gammaropsis maculata*, *Erichthonius punctatus*, *Pyllodoce mucosa* and *Harmothoe mariannae*) that structured the assemblage process around the trophic resource. During the experiment, the stochastic component (inter-microcosm variability) increased. In addition, a large group of rare and occasional species created a random noise in the dynamics. The population dynamics of each of the 5 interacting species were simulated; the model accounted for functional traits that structure individual interactions. The colonization was characterized by the rapid emergence of a trophic network. Predation regulated early arrival of primary consumer species, hence controlling a potential mass effect, which may have led to the dominance of *Capitella capitata*. *C. capitata* disappeared from the final assemblage before the end of the experiment, switching dominance with *G. maculata*. The theoretical paradigms were contradicted by these results suggested that new hypotheses will have to be tested in order to propose a more realistic framework to describe the assembling of benthic macrofaunal communities in coastal ecosystems.

## CHANGE OF BOTTOM COMMUNITIES IN THE TIKHAYA BIGHT (GUKER ISLAND FRANZ JOSEF LAND, ARCTIC)

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After 21 years of investigations of our precursors (Weslawski, Zajaczkowski, 1992; Averincev, 1993) we have renewed studies off the Guker Island. We made one transect from 0 to 30 m using the diving quantitative method and up to 70 m using VanVeen grabs.

As a result several bottom communities were found:

Seasonal community of amphipods *Onisimus littoralis* and brown and green algae which grew in water without ice cover. The community is arranged at depth from 3 to 5 m on gravel and slightly muddy sand. There are five species in its composition. Abundance and biomass of the community are 20 spm/m$^2$ and 26 g/m$^2$ respectively. The availability of the community during summer season at the same depths is typical of the Arctic.

Community of bivalves *Serripes groenlandicus* and *Mya truncata* and bryozoans *Alcyonidium disciforme* occupies a wide space of muddy bottom with stones and clay at depths from 7 to 30 m. There are more than 36 taxa in this community. Abundance and biomass in the community are 809 spm/m$^2$ and 155 g/m$^2$ respectively. Previously the community of algae *Saccharina latissima+Alaria esculenta+ Desmarestia aculeata* was arranged at this depth on hard substrates. At present time in the community of bivalves and bryozoans small fragments of drifted algae *S. latissima* and *D. aculeata* were found.

Community of bivalves *Musculus niger* and *Yoldia hyperborea* was found at depths 67–72 m on clayey silt. There are 18 taxa in the community. Abundance and biomass in the community of bivalves are 727 spm/m$^2$ and 356 g/m$^2$ respectively. This is first information about the community in the Tikhaya Bight.

The comparison of previous data with up-to-date distribution of bottom communities in the Tikhaya Bight allow us to say that considerable changes of benthic communities took place. They could be explained by siltation in the investigated area. The most striking succession appears in the change from the algae community distributed on stony substrate to the bivalve community distributed on soft substrate.

## FROM CORMORANTS TO ALGAE: TROPHIC CASCADES IN THE BALTIC SEA

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The Great Cormorant (*Phalacrocorax carbo sinensis*) has been present in the Baltic Sea since the 1990s, with the population increasing to 18 000 breeding pairs in 2013. Cormorants nest in large densities on small islands and are voracious fish predators,with each breeding pair consuming 1 kg fish·day$^{-1}$, thus they may affect benthic communities by inducing trophic cascades. In addition, nitrogen enrichment from guano runoff can also fertilize benthic communities near colonies. In this study, we sampled community assemblages, biodiversity and abundance of fish, invertebrates and algae from colony and control islands to determine how cormorant predation and nitrogen enrichment from guano is affecting these communities.

While cormorants did not seem to affect overall biodiversity and species diversity, there were important differences in species composition between colony and control islands. Most notably, there significantly less perch (*Perca fluviatilis*), and ruffe (*Gymnocephalus cernuus*) near colony islands than near control islands, indicating that these were preferred prey for cormorant. Invertebrate communitiess varied widely between sites, but isopods (*Idotea* spp.) and gammarid amphipods were more abundant in colony sites, potentially indicating lower predation on these invertebtrates due to lower fish abundance. This was further supported by the fact that the macroalga *Fucus vesiculosus* is less abundant near colony islands, likely due to both increased grazing from isopods and increased competition from opportunistic filamentous algae due to nitrogen enrichment.

## UNDERSTANDING ECOSYSTEM INTERACTIONS: CONCEPTUAL ECOLOGICAL MODELS IN BENTHIC HABITATS MONITORING

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Conceptual ecological models (CEMs) are visual representations of a target system (e.g. ecosystem, habitat, protected site) which summarise complex ecological interactions. They facilitate the selection of monitoring indicators by identifying key biological components, environmental drivers and aspects sensitive to human pressures. Although CEMs are recognised as an important step in terrestrial monitoring programmes, they are rarely used in the marine environment due to greater ecosystem complexity and a lack of information for many habitat types. However, with increased legislative demands to assess and report on benthic habitat condition, the need to develop CEMs for effective marine monitoring has never been greater. As part of the UK Marine Biodiversity Monitoring Programme, the Joint Nature Conservation Committee (JNCC) has developed a methodology for creating habitat CEMs. This is based on a thorough literature review and incorporates knowledge gap analysis, confidence assessment and peer-review stages. A hierarchical set of models is produced which includes a general model to represent the entire habitat and various sub-models which investigate constituent biotopes or biological communities in more detail. The models describe environmental drivers at global, regional and local scales and how these drivers influence the biological assemblage groups. Faunal interactions, ecosystem functions and feedback systems are also expressed. Ecosystem complexity is captured by displaying the impact and magnitude of each interaction and the degree of natural variability for each model component. The species and ecological groups included within the models relate to sensitivity assessments, highlighting aspects of the habitat important for monitoring both natural variation and human-induced change. The models are used as a qualitative tool to identify potential relevant indicators and inform recommendations for future research. The greater understanding of habitat ecology provided by the models will aid subsequent data interpretation and models may be used as a communication tool among partners when developing management options. This CEM methodology can be applied to various habitat types and adapted to meet the conservation objectives of a particular monitoring programme.

## IMPACT OF THE BLUE MUSSEL (*MYTILUS EDULIS*) ON THE PELAGIC FOODWEB STRUCTURE IN THE WESTERN WADDEN SEA, THE NETHERLANDS

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Many studies have addressed the potential effects of bivalve filter-feeders on the surrounding ecosystem, mostly using phytoplankton biomass as a parameter. So far little attention has been given to the impact of filter-feeders on the structure and composition of the microbial foodweb. In 10 lab experiments between June and September natural sea water from the Dutch Wadden sea was exposed to mussels. Subsequently, both mussel filtered and unfiltered (control) water was used in dilution experiments to establish specific growth rates and grazing mortality rates for bacteria, pico-and nanophytoplankton, while for their main predators, HNAN's and ciliates, net growth rates were calculated.

Results from this study show that mussel grazing removed on average 60% of the available nanophytoplankton, HNAN and ciliate carbon, while bacterial and picophytoplankton carbon was removed to a much lower extent. The reduction in HNAN and ciliate predators by mussels significantly reduced grazing mortality rates on both pico-and nanophytoplankton, but not on bacteria. Specific growth rates increased for bacteria (from 0.67 to 1.16 day$^{-1}$), most likely due to mussel excretion products.

In the Dutch Wadden Sea, during the experimental period, HNAN and ciliates predators almost completely grazed the production of bacteria and picophytoplankton, while for nanophytoplankton the percentage of production grazed varied between 33 and 113%. Mussel filtration severely reduced the flux of carbon from pico- and nanophytoplankton to their main predators.

Comparing the initial numbers in natural sea water with the net increase after 24 hours revealed that mussel filtration resulted in an increase of bacterial and HNAN biomass. The results from this study reveals a potentially important effect of mussels on the pelagic foodweb not revealed by considering phytoplankton biomass alone.

## DEFENSIVE ROLE OF PHLOROTANNINS RESOLVED: CONSTITUTIVE AND INDUCED RESISTANCE TO HERBIVORY IN BLADDER WRACK

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We manipulated the access of herbivores to the brown alga *Fucus vesiculosus* in a field experiment and measured the losses to grazing, induction of resistance, and the contents of phlorotannins when exposed to or protected from herbivory. Highly synchronized reproduction of the herbivores resulted in vast seasonal variation in grazing with severe grazing on the algae observed in autumn. Resistance to herbivory, measured as losses to herbivory, showed considerable variation among bladder wrack genotypes, and so did the content of phlorotannins. Consumption of algae by herbivores decreased and the probability of survival increased with the increasing content of constitutive phlorotannins. Induced resistance was triggered by strong grazing in the autumn. The magnitude of the induced resistance was the higher the more the algae were consumed. Phlorotannins increased 18 % in the algae exposed to natural herbivory and explained over 60 % of the induced resistance. There was a trade-off between the contents of constitutive and induced phlorotannins: the algae with higher constitutive levels showed smaller induced increase in phlorotannins implying phlorotannin production being costly. The trade-off may partly explain the large genetic variation of phlorotannins. Thus, phlorotannins provide both constitutive and induced resistance against herbivory. Induced resistance may be a response to strong seasonality in grazing and very important for minimizing mortality risk during the periods of high grazing pressure.

# SPATIO-TEMPORAL CHANGES OF OB BAY MACROBENTHOS AS AN INDICATOR OF PEAK SALINITY VALUES

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Studies of animal distribution along the salinity gradient have a long history (Remane, 1934; Khlebovich, 1974; Telesh, Khlebovich, 2010). However, estuaries of the northern rivers are of particular interest in this respect. Exceptional within-year variability and enormous extent of Arctic estuaries makes them interesting objects to study the effect of salinity on the distribution of benthic organisms. In this regard, especially interesting is the Gulf of Ob (also known as Ob Bay), having length of more than 700 km and a width of 40–50 km. Detailed surveys of macrozoobenthic assemblages in Ob Bay and adjacent sea areas were conducted in 1993, 1994, 2007, 2010 and 2013 by IO RAS (68° to 73° N). Sampling was done at more than 50 stations, using grabs "Ocean" with sampling area 0,1 m$^2$ and 0.25 m$^2$ in compliance with standard techniques. All works were accompanied by measurements of hydrological and hydrochemical parameters and grain size analysis. During surveys conducted in 2007–2013 a distinct latitudinal zonality along the estuarine gradient of the Ob Bay was described. The most southern part of the bay (southward of 69°30' N) was inhabited with typical freshwater fauna with a predominance of chironomids and bivalves *Pisidium sp.* Northward of 69°30' N and up to 71°30' N was an area inhabited by a typical brackish fauna represented by euryhaline species: amphipoda *Pseudalibrotus birulai*, isopoda *Saduria entomon*, polychaete *Marenzellaria wireni* and polychaetes *Capitellidae* spp. Between 71°30' N and 72°30' N was a transitional community, typical representatives of which were polychaete *Ampharete vega* and bivalvia *Portlandia aestuariorum.* Some species found in this area, penetrated further north than the indicated boundary, but maximum values of their biomass were observed at the transition zone stations (amphipoda *Pontoporeia femorata* and priapulida *Halicriptus spinulosus*). Between 72°30' and 73° N a sufficiently narrow frontal zone (in comparison with the rest of the estuary) was situated, characterized by abrupt changes in hydrological parameters. Near-bottom salinity varied from 10 to 30 ‰, a number of hydrochemical parameters and the type of soil varied similarly. *Portlandia arctica, Pectinaria hyperborea, Macoma* spp., *Thyasira* spp. and several other species formed the basis of the population of aforementioned area. Then followed a typical Kara sea marine shallow water community with the dominance of *Astarta borealis, Macoma calcarea, Stegophiura nodosa.* If we have a look at the changes in species richness of Ob estuary macrobenthos from south to north, we can see, that increase in diversity in the area of brackish and transitional communities dissemination is not associated with changes of near-bottom salinity. Number of species varies from 4 to 10 in a salinity range 0.03–0.5 ‰, whereas an increase in salinity from 0.5 ‰ to 16 ‰ leads to an increase in species richness from 10 to 11 species. Almost complete absence of coincidence between faunistic boundaries and near-bottom water salinity also should be mentioned. The boundary between freshwater and brackish communities is located 250 km southward of 1 ‰ isohaline. V. V. Khlebovich (pers. comm.) described a similar pattern of brackish polychaete *Marenzellaria wireni* distribution in the fresh waters of the Yenisei estuary, where its habitat marked the area of winter inflow of saline waters. Long-term changes of Ob Bay macrobenthos (1993–2013 years) also showed relative sustainability of the boundaries of species assemblages, despite the significant interannual variations in runoff, as well as seasonal changes in the basic hydrological parameters, especially salinity, which can reach values of the order of 10 ‰. Nevertheless, these changes are likely to be synchronous throughout the estuary, which allows us to suggest that spatial distribution of benthic communities is stable, while maintaining the boundaries of changes in physicochemical parameters, and along with the stable position of frontal zones. However, comparison with the data obtained in 1993–1994, shows that within a period of 20 years there have been changes in community structure. In particular, this can be attributed to the massive development in the brackish area of polychaetes *Capitellidae* spp., in 2007–2013 they reached a density of 16 000 ind/m$^2$, whereas in 1993 they were not found here at all. Such an increase in the number of opportunistic species may occur as a result of the organic enrichment. Thus, we can assume that the distribution of macrozoobenthic communities in the Ob Bay does not reflect a momentary hydrological situation, but is a measure of maximum extension of saline or desalinated water inflows.

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## ICE ALGAE OF VELIKAYA SALMA STRAIGHT OF THE WHITE SEA: COMPOSITION, ABUNDANCE, VERTICAL DISTRIBUTION

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Ice biota plays an important role in the fluxes of matter and energy in Arctic ecosystems. Primary production of the ice algae and cyanobacteria is used by planktonic and benthic animals. In the latest decades changes in the Arctic ice cover are seen due to the climate change, for example, the fraction of one-year ice is growing. Such a change of the environment can cause changes in composition, abundance and productional characteristics of the ice biota and matter fluxes in food chains in Arctic ecosystems. That's why studies of the biota of first-year ice, and the seasonal ice of the White Sea is of this type, grow in importance.

At present, quite a lot of data exist on the White Sea ice biota (e.g., Sazhin et al., 2012). Species composition and abundance of ice alge is subject to considerable spacial and temporal variability, which determines the necessity of annual monitoring of ice algal communities in different parts of the sea.

In this study we present the data on the species composition and biomass of ice algae in March in the Velikaya Salma Straight of Kandalaksha bay of the White Sea. Vertical distribution of algae in the ice cores, species composition and abundance of under-ice phytoplankton were also studied.

Research was conducted in Velikaya Salma straight from the 20th of March to the 2nd of April 2012 and from the 17th to the 23rd of March 2013. The work was based at the Moscow State University White Sea Biological Station (WSBS). In 2012, four stations were done: in the bays Kislaya, Rugozerskaya, Ermolinskaya and at the WSBS. In 2013 two stations were done: at Kindo Cape and in WSBS bay. At each station two or three ice cores were sampled, together with the under-ice water. Cores were drilled with a SPIRE-type corer with inner diameter of 15 cm. Each core was divided into several parts according to the visually distinguishable ice structure. These parts were placed into plastic vessels, no less than 1 liter of sea water (filtered through a membrane filter with 2 µm pore diameter and then sterilized) was added, and the samples were melted in normal temperature. From these samples of melted water sub-samples (20–50 ml) were taken to evaluate the numbers of picophytoplankton and small (less than 8 µm) flagellates. The remaining water was concentrated by the means of the backwards filtration and fixed with Lugol's solution. Cell counting of different-sized phyto- and zooplankton was conducted according to methods described earlier (Belevich, Ilyash, 2012; Ilyash et al., 2012).

## ZOOPLANKTON COMMUNITIES OF FRANZ JOSEF LAND: A GAP OF THE ARCTIC

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Franz Josef Land is one of the most unstudied area of the Arctic in terms of its pelagic realm. Although this Arctic region was discovered 140 years ago, rare data exist describing the peculiarities of its hydrological structure and the plankton communities. In July – August 2013, the complex expedition has studied this area, using the new real-time approach in collecting the plankton samples in accordance to the hydrological profiles. The studies were performed both in the large and small straits, as well as in the neritic zone closeby the islands. The analysis of the zooplankton samples revealed good correspondence of the plankton community to the major water layers (masses), exhibiting the presence of the key copepod species in particular waters in regard to their biogeographical characteristics. In addition, the areas of high hydrological activity (coastal zone of the islands) were characterized by high diversity of the zooplankton fauna comparing to the layers representing the stable water masses, where much of the biomass was comprised by a small number of copepod species. These areas of active hydrological processes may serve not only as the expatriation zones, but also as the source areas of the plankton biodiversity. The vertical and spatial distribution of three *Calanus* species (*C. glacialis, C. finmarchicus*, and *C. hyperboreus*) has shown a good evidence of their correspondence to the water masses of different origin (Arctic or Atlantic). Moreover, the deep-dwelling Arctic species, *C. hyperboreus,* has been found in relatively unusual environment (near-surface layers) disregarding its dormancy that have started already. We suppose that the influence of the hydrological regime may have more impact for the zooplankton community in the hydrologically active areas than it was assumed before.

Our gratitudes go to the project "Pristine Seas" and the organizers of the expedition, National Park "Russian Arctic" (Russia) and National Geographic Society (USA).

## SEMI-ISOLATED FJORDIC LAGOONS IN THE BARENTS SEA AND THE STUDIES OF IMPACT OF THE INTRODUCED RED KING CRAB (*PARALITHODES CAMTSCHATICUS*) ON BENTHIC COMMUNITIES

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Inner parts of some fjords of Scandinavia and Kola Peninsula are separated from their outside parts by narrow and shallow sills forming thus semi-isolated fjordic lagoons. Such lagoons in the Ambarnaya Bay (Varanger-fjord, Barents Sea), or “salt lakes” (as local people call them) Linjalami and Sisajarvi (total area about 1 km$^2$, maximum measured depth 41 m, depth of outer entrance at low tide less than 1 m) host peculiar benthic communities. All age groups of red king crab (*Paralithodes camtschaticus*), a species introduced to the Barents Sea in the 1960s are present in these lagoons round year. This contrasts to most coastal areas in the Barents Sea where adult crabs are leaving shallow inshore zone in autumn and come back by late winter or spring. The predation pressure of king crabs in the lagoon appears to be relatively constant throughout the year and this makes them an interesting model area to study the impact of introduced crabs on benthic communities. Long term observations (since 2001) indicated, that interannual changes in crab density and population composition depends on the type of climatic conditions of the year and success of crab reproduction. In the years 2010 – 2012 we conducted a survey of benthic communities in the lagoons. A notable characteristic of the benthic fauna is deficiency of echinoderm species which are considered as a prey selectively consumed by red king crabs (especially in their life history periods associated with molting). In particular sea urchins *Strongylocentrotus droebachiensis* are virtually absent in the kelp zone (being abundant in kelps in the outside part of Varanger-fjord) but are common in blue mussel (*Mytilus edulis*) banks in the strait connecting Linjalampi and Sisajarvi lagoons. Both biotopes are however used as foraging grounds by king crabs so that a hypothesis explaining the absence of sea urchins in the kelp zone by crab predation faces difficulties. Iceland scallop (*Chlamys islandica*) population in the lagoon is relatively stable in spite it is also a known common prey of adult king crabs. Neither composition nor biomass of macrobenthos showed significant changes over three years of observations. Abundance – Biomass curves (ABC) which are often used as a test for presence some stressors indicated that at some places benthic communities consisted of numerous small sized species that is typical for the impact of eutrophication, hypoxia, pollution, active predation or another factors of organism mortality. As the presence of the first three factors is unlikely, this may be a result of unselective consumption of infaunal organisms by king crabs. However there is no consistent ABC pattern in space and time. Predation impact (if present) of crabs on infauna is thus at least moderate and reversible. It can be concluded that king crabs now are a normal component of the coastal ecosystem even though its present condition may be different from the one at time prior to red king crab introduction.

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## SPRING SEA-ICE ALGAL AND ICE-EDGE PHYTOPLANKTON COMMUNITIES FROM THE LAPTEV SEA POLYNYA IN 2012

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Climate system of the Arctic is currently undergoing evident changes. The retreat of sea ice from the Arctic regions during the last 30 years has been receiving considerable attention. The wind-forced Laptev Sea polynya is a major area of sea-ice production in the Arctic, and it is one of the key elements of environmental system of the Laptev Sea. It is therefore essential to improve our knowledge of the Laptev Sea polynya system, as the crucial shelf area with high level of biological activity, and significant contributor to primary production. To investigate the influence of polynya on hydrological and hydrobiological properties of the Laptev Sea shelf waters, oceanographic station sites were generally confined to the location of the polynya area during Russian-German expedition TRANSDRIFT XX. To reveal temporal variability of these characteristics, the measurements were repeated several times at the same sites between March 19 and April 24 of 2012. The ENVISAR ASAR satellite imagery shows the evolution of the coastal polynya during this time. Therefore, our phytoplankton and sea-ice algal records allowed us to trace the development of biological processes in the polynya area during the early spring.

Results of microalgae study revealed, that diatoms, represented mainly by sea-ice species are the predominant group of algae both in sea-ice communities and phytoplankton in the Laptev Sea during the time observation. The single cells of heterotrophic dinoflagellates were reported mainly in the phytoplankton communities. Detail investigations of microalgae allowed us to infer the distinctive regional features of algae assemblages and theirs development during the time observation: At the stations located in the southernmost part of the Laptev Sea polynya, in the vicinity of the Lena River Delta sea-ice bottom diatom communities characterized by the greatest algal abundances and biomass, which gradually increased during the observation period and reached the maximum at the end of this period. The lowest biomass value observed under the fast-ice conditions.

## RELATIONSHIPS BETWEEN DEPOSIT FEEDING ACTIVITY AND MICROPHYTOBENTHIC BIOMASS ACROSS A SEDIMENTARY GRADIENT

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The density, structure and functional roles of macrofauna and microphytobenthic (MPB) communities are known to change across sedimentary gradients, yet how relationships between deposit feeders and MPB scale-up across such transitional environments, is poorly understood. Here, sediment chlorophyll-*a* concentration (a proxy of MPB biomass) was measured in relation to the occurrence of feeding traces made by the tellinid bivalve *Macomona liliana* together with macrofaunal densities and sediment properties within 55 plots (0.12 m$^2$) across a sediment mud content gradient. Correlative relationships between recent deposit feeding activity and MPB biomass were scale dependent, significant only at the site scale. Generalised Least Squares regression was used to determine the relationships between mean MPB biomass and measured predictor variables between plots. MPB biomass declined by 28 % as coverage of feeding traces increased from 2 to 28 %, with feeding trace area contributing significantly to variation in chl-*a* (std. coef. = −0.24, $p = 0.01$). However, the interaction term between mobile suspension feeding cockles *A. stutchburyi* and sediment mud content explained a larger amount of the variability (std. coef. = 0.72, $p < 0.001$). Therefore, we need to consider the potential for interactive effects involving non deposit-feeding species on MPB across abiotic gradients.

## MICROPLANKTON COMMUNITIES IN THE ICE AND UNDER-ICE WATERS OF THE WHITE SEA (KANDALAKSHA BAY)

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Composition and production characteristics of the microplankton community of the ice and under-ice water of the White Sea are analyzed in the study. Concentrations of chlorophyll "*a*", prokariots and bacteriovorus protists (mainly heterotrophic nanoflagellates), as well as primary and bacterial production were measured at different sites of the Kandalaksha bay. Chlorophyll "*a*" concentrations in the period preceding the ice formation were extremely low (0.066–0.085 mg/m$^3$). It was evenly distributed in the upper 25-m layer. Phaeophytin composed 60% of the total concentration of phytopigments. Primary production was also very low, less than 0.065 mgC m$^{-3}$h$^{-1}$ in the upper 5 m layer and less than 0.01 mgC m$^{-3}$h$^{-1}$ in the deeper layer. In the early spring the primary production were essentially higher: up to 1.66 mgC m$^{-3}$h$^{-1}$ in the upper 0.5-m layer. However the most active growth of microalgae was recorded in the ice, the values of primary production achieved 12 mgC m$^{-3}$h$^{-1}$. Bacterial abundance in the period before ice formation increased from surface to the thermocline layer at 20 meters (165±28 – 217±18 ×10$^3$ cells/ml). In winter concentrations of microorganisms was extremely low both in the water and in the ice (about 80×10$^3$ cells/ml), however in February a significant difference was registered in the abundance of prokaryotic cells in the ice and in the under-ice water (650±214 and 289±44 ×10$^3$ cells/ml respectively). In the early spring the maximal values of bacterial abundance were observed in the 1-meter layer of the under-ice water. They exceeded the concentration of microorganisms in the ice 1.5–3 times (132–282 and 43–105 $\times 10^3$ cells/ml respectively). At the deeper water horizons bacterial abundance was about 178–189$\times 10^3$ cells/ml. Biomass of bacteriovorus protists in the period before the ice formation increased with depth (down to the thermocline) from 1.02 to 1.85 mgC/m$^3$. In winter this parameter was about 1.3±0.06 ±0.16 in the ice and 1-meter under-ice water layer and 0.92±0.16 ±0.16 deeper (up to 30 meters). Bacterial production during the period preceding the ice formation varied from 0.88 to 1.58 mgC m$^{-3}$ d$^{-1}$. Bacterial specific growth rate was 0.26 d$^{-1}$. The share of actively respiring (CTC+) bacterial cells in plankton in this season was 8–17%. The mean value of bacterial grazing by heterotrophic nanoflagellates was 0.86 mgC m$^{-3}$ d$^{-1}$; that equals 70% of bacterial production. In the early spring the maximal prokaryotic activity was observed in the ice and 0.5-meter layer of the under-ice water. Average bacterial specific growth rate there was 0.93±0.3 d$^{-1}$, while in the deeper layers (up to 10 m) it achieved only 0.43±0.2 d$^{-1}$. The share of actively respiring bacterial cells in spring was lower than in the late autumn: 6±2%. However the values of bacterial production and specific growth activity in the water exceeded significantly that obtained in the period preceding the ice formation (2.05–2.86 mgC m$^{-3}$ d$^{-1}$ and 0.68–1.21 d$^{-1}$ respectively). In the ice these values were even higher: 2.05–4.1 mgC m$^{-3}$ d$^{-1}$ and 1.12–1.3 d$^{-1}$ respectively. Considerable difference was observed in the values of bacterial grazing by heterotrophic nanoflagellates: in the ice it was estimated only 3–18%, while in the under-ice water its values were 5 times higher and achieved 80–88%. Therefore in the period before the ice formation the activity of all microplankton community components (both phytoplankton and heterotrophic organisms) is fading. In the early spring the growth of microorganisms breaks out primarily in the ice. This biotope is characterized by maximal values of bacterial and primary production in the early spring. Only in the ice the calculated bacterial carbon demand (Meon, Amon 2004) is completely satisfied by microalgae production. In the water both during the period before ice formation and in the under-ice water bacterial carbon demand is likely compensated by other sources of organic matter. The part of bacterial production grazed by heterotrophic nanoflagellates regardless of its value averages 80%.

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## SPATIAL AND TEMPORAL VARIATION OF ARCTIC MEROPLANKTON IN NORTHERN NORWAY

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The early development of many benthic invertebrates involves some form of planktonic larval stage. This enables them to disperse over large distances, to utilize food from the productive upper water layers, and perhaps to escape predation by abundant and diverse benthic omnivores. Although the importance of this period in the benthic life cycle has been recognized, our knowledge of larval distribution in time and space is still very limited, especially for arctic regions with their pronounced seasonal variability in environmental conditions. This study presents seasonal and spatial variation in abundance and composition of arctic meroplankton over the continental shelf in northern Norway. The study system, the Lofoten-Vesterålen region, is characterized by an alternating pattern of shallow banks and deep troughs, as well as a complex current system, which most likely affects larval dispersal and distribution patterns. Meroplankton was sampled seasonally from September 2013. The spatial pattern of larval distribution showed an accumulation over the shallow banks and a decline of larval abundance with distance from shore. Furthermore, a strong seasonality was recorded for all major taxonomic groups, with generally low abundance during the winter months after a sharp autumn peak. The autumn community was numerically dominated by larvae of molluscs and bryozoans, but representatives of all major benthic taxa were found frequently. This is one of the first studies to provide results on spatio-temporal distribution of arctic meroplankton and will contribute to the understanding of timing and transport pathways of benthic larvae in a highly seasonal shelf ecosystem.

## BENTHIC FAUNA OF THE BLAGOPOLUCHIYA BAY (THE KARA SEA)

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Study of coastal communities off the Novaya Zemlya archipelago receives great importance in the last decades. This is largely due to the fact that the coastal zone of the Novaya Zemlya is exposed to high technological risk associated with the underwater disposal of large quantities of waste here, including radioactive waste and vessels of various types, for example the nuclear submarine K-27. The consequences of these risks are not always predictable, and the environmental assessment of the benthic communities in the waste disposal sites is necessary. Previously, such work was performed just near the Stepovoy and Abrosimova Bays at the Southern Island (Galtsova et al, 2004; Pogrebov et al., 1997), and they were rather incomplete. Inside the bays benthic samples were absent.

Macrofaunal samples were collected in the inner part of the Blagopoluchija Bay (Kara Sea, Northern Island of Novaya Zemlya Archipelago, 75°40'N, 63°40'E) and at the slope of Novozemelsky Trough by RV "Proffesor Shtokman" in September–October 2013. 10 stations (30 samples) were collected by the standard method using 0,1 m$^2$ Okean grab. Moreover, the intertidal description was made.

Blagopoluchija Bay is the deep fiord with the average depth 70–160 m. The bay is separated from the open sea by the threshold with depths up to 30 meters. A deep hollow with the 200 m depth is located in the middle of the bay.

The shore consists of the black shales. Several intertidal types were revealed-rocky shore, rocky coarse-grained, exposed sandy beach. Only in the upper lagoon the small fragment of muddy-sand intertidal were discovered. The intertidal and upper subtidal zones are deprived of higher plants and macrophytes because of the severe climatic conditions. The only inhabitants of the intertidal zone are the benthic amphipods *Gammarus setosus*, due to their ability to migrate from the intertidal to the deeper subtidal zone during the coldest months. During the summer the density of these amphipods can reach several dozen per 1 m$^2$.

Sediments in the central part of the bay (at the depth of 40–180 m) are represented by the unstratified gray silts without any oxygen depletion. Numerous small stones are present in the silt, possibly due to the ice gouging. The density of the macrobenthos in the central part of the bay varied from 440 to 2700 ind/m$^2$ (in average 1054 ind/m$^2$). The bivalves *Ennucula tenuis, Thyasira* cf. *sarsi*, polychaetes *Tharyx* sp., *Micronephtys minuta,* and sipunculans *Golfingia margaritacea* were the main dominants in this area. The main contribution to the macrobenthic biomass was made by the sipunculans *G. margaritacea,* their density reached 20–30 ind/m$^2$ and their biomass reached 51 g/m$^2$. At the shallowest parts of the bay the bivalve *Portlandia arctica* dominated, its density reached 154 ind/m$^2$ and its biomass reached 12 g/m$^2$.

The macrobenthic community at the threshold was significantly different from the community inside the bay. The sediments in this area were represented by the silts with numerous manganes nodulels, pebbles and small stones. The main dominants in the area of the thredhold were the gastropodes *Lepeta coeca*, polyplacophorans *Tonicella marmorea* and *Stenosemus albus*, polychaetes Spirorbidae, large ostracodes *Philomedes globulosus* and different bryozoans. The most of macrobenthic organisms here inhabitated the surface of the stones and nodules.

The macrobenthic fauna of the Novozemelsky Trough slope differed from the bay fauna strongly. At the shallower part of the slope (65 m depth) the bivalves *Astarte crenata* dominated. At the deeper part of the slope (125 m depth) the ophiuroids *Ophiocten sericeum* and *Ophiacantha bidentata* dominated.

Our data suggest that the macrobenthic community in the fjord-type bays in the Novaya Zemlya Archipelago, separated from the Kara Sea by the threshold, differs from the community in the trough slope located at the same depth.

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## SUBLITTORAL MACROBENTHIC ASSEMBLAGES IN THE GORLO STRAIT (WHITE SEA): MOSAIC PATTERN AND LOW BIOMASS IN AN AREA OF ACTIVE HYDRODYNAMICS

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Gorlo is a relatively narrow (about 40 km wide) and shallow (average depth 37 m) strait connecting the outer part of the White Sea with its inner part. It is known for the non-stratified water column and strong tidal currents. The targeted survey in the Gorlo Strait designed according to historical records of the shrimp species *Crangon allmanni* (an indicator species for sublittoral areas with strong near bottom currents) made possible comparison of macrofaunal communities inhabiting mobile sandy substrates as well as more stable coarse substrates. Recognition of these two types of communities was supported by statistical tests and classification of species lists according to Braun-Blanque's methodology. The communities on mobile sand and those on coarser sediments differed in the number of species (in average 47.2 species per station on coarser substrates vs. 16.7 species on sand), and biomass (21 – 171 g m$^{-2}$ vs. 0.5 –

1.5 g m$^{-2}$). Several common species were characteristic for both types of communities, in particular *Hydrallmania falcata*, Astartidae, *Nephtys pente* and *Chaetozone setosa*. *Crangon allmanni* was the only shrimp species, which occurred at nearly all stations. Typical species reported for the community of coarser substrates included *Ophiocantha bidentata*, *Ophiura robusta*, *Hemithyris psittacea*, *Hiatella arctica*, *Tonicella marmorea*, *Verruca stroemia*, *Anobothrus gracilis*, *Melinna elisabethae*. Taxa that characterized benthic community on sand were mostly polychaetes: *Ophelia limacina* was recorded in significant number nearly exclusively at the stations of this group. Strong negative correlation was observed between the sediment sorting coefficient and the species richness or various measures of heterogeneity diversity. This indicated that poor sorting of sediments (owing to specific oceanographic and lithodynamic processes) and increasing of the relative contribution of gravel and stones enhance carrying capacity of benthic habitats and, respectively biodiversity. In general, mosaicity, unclear dominance patterns and low biomass of the sublittoral macrobenthos in the Gorlo Strait are most probably influenced by strong and changing direction near bottom currents which transport significant amount of sand, limit accumulation of organic particles in sediments, determine complex lithodynamics thus creating in turn fine scale mosaics of substrates.

## PHENOLOGICAL SHIFTS IN THE SEASON DYNAMICS OF DOMINANT ZOOPLANKTON SPECIES IN THE WHITE SEA

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We hypothesize that shifts in the annual pattern of the environmental parameters may affect the phenology of the zooplankton. The long-term dynamics of phenological indices of dominant zooplankton species have been analyzed in the White Sea to test this hypothesis. We have used the 50-year data series (1961–2010) of the long-term zooplankton monitoring at D-1 monitoring station (the White Sea, Kandalaksha Bay, Chupa Inlet). Long-term changes in phenology of five mesozooplankton species (cold-water *Calanus glacialis*, warm-water *Centropages hamatus*, *Temora longicornis*, *Acartia longiremis* and *Evadne nordmanni*) were studied in regard to the seasonal dynamics of the water temperature. The duration of the summer period has increased by 8 days during the last 50 years due to the early warming up of 0–10 m water layer in spring. *Calanus glacialis* responded to these changes by the earlier (by 18-days) appearance of CI copepodites. We assume that early start of the ice melt and, consequently, earlier phytoplankton bloom may promote *Calanus* reproduction and development of the young stages to start before the multiannual average. Alongside with that, higher temperatures may directly affect the early development of this species, as it was shown by Daase et al. (2011). In contrast to cold-water C. glacialis, the phenology and abundance of warm-water copepods has not changed significantly. Both the timing of autumn cooling and the average summer temperatures were nearly the same during the last 50 years, resulting in relatively stable conditions during the reproductive period of warm-water species. Prolongation of the summer period duration had no effect on warm-water species reproduction.

## PREDATORS MEDIATE THE EFFECT OF FOUNDATION SPECIES IN SUBTIDAL BARNACLE CLUSTERS

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Foundation species facilitate dependent organisms directly or alter their interactions with others (for instance, consumers or prey). Although both processes may back up similar community structure, they must be distinguished to understand community functioning. Barnacles *Balanus crenatus* commonly dominate epibenthic patches on mixed sediments in the White Sea subtidal. Their clusters on empty bivalve shells and small stones develop a mobile macrobenthic assemblage different from the one associated with the surrounding unstructured soft sediment. To examine the direct and indirect effects of this foundation species on mobile benthic macrofauna, we conducted field caging experiments using predator-exclosures, enclosures with crabs *Hyas araneus* and shrimps *Spirontocaris phippsi*, and open cages (control). Each cage contained initially defaunated clusters of live barnacles and their empty shells (hereafter "dead barnacles"). We also sampled natural epibenthic patches and the adjacent sediment.

After a year of exposure live barnacles in open cages developed a mobile assemblage almost matching the one in natural epibenthic patches. Dominant species displayed different responses to the treatments. Specifically, the abundance of the polychaete *Pholoe minuta* and the clam *Hiatella arctica* was similar in the clusters of live and dead barnacles but decreased in presence of predators. In contrast, the polychaetes *Cirratulis cirratus*, *Pygospio elegans* and the mytilids *Musculus discors* strongly preferred live barnacles over dead regardless of predator presence. Overall, the assemblages in open cages resembled predator treatments rather than exclosures. Consistent with our predictions, the dependent assemblage was functionally heterogeneous and composed of taxa apparently sensitive either to biogenic (like feces production or flow alteration) or indirect architectural (like shelter provision) effects of the foundation species.

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# POSTER PRESENTATIONS

## *Organism – environment coupling*

### SPATIAL MICRO-DISTRIBUTION OF SHOOTS IN *POSIDONIA OCEANICA* (L.) DELILE MEADOWS

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*Posidonia oceanica* (L.) Delile meadows contain huge numbers of shoots and their dynamics is strictly related to spatial distribution patterns of those shoots. In order to investigate the structure of *P. oceanica* meadows at very small spatial scale (i.e. in the $10^{-2}$–$10^{0}$ $m^2$ range), patterns in shoot distribution were analyzed. Spatial distribution of shoots was recorded by cutting all the leaves and by digitizing shoot location from images of 10 square frames (1 $m^2$), sampled in seemingly uniformly dense meadows at two sites in Southern Italy. Spatial point patterns have been explored using Clark & Evans nearest neighbour distance index. Advantages were highlighted, as well as the potential implications of this type of data set. The raw data, provided by the authors as supplementary material, are currently the first and the only information available about shoot spatial micro-distribution. In this regard, although our data set cannot represent the whole spectrum of variability in *P. oceanica* meadows, it certainly shed some light on the small scale patterns of *P. oceanica* meadows and it prompts us many questions, some of which are still unanswered.

### GLUTATHIONE SYSTEM RESPONSE UNDER THE INFLUENCE OF TEMPERATURE IN TISSUES OF MUSSELS *MYTILUS EDULIS* L

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Effects of temperature alterations on the content of reduced glutathione (GSH) and the activity of glutathione S-transferase (GST) in the gills and digestive gland of sublittoral mussels *Mytilus edulis* L. from the White Sea was studied. During the experiment, the mussels subjected to an elevated temperature (+8°C) within 24 hours with following 72 hours recovery to initial conditions (0 – +2 °C). It is shown that both increase and subsequent decrease of temperature alters the reduced glutathione content and activity of glutathione of S-transferases. Glutathione transferase activity decreased during the whole experiment, whereas significant changes in glutathione levels were detected only after 48 hours after the start of the experiment. Studied biomarkers in gills and digestive gland changed in the similar manner, while the level, force and time of response were tissue-specific.

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### FEEDING OF JUVENILES OF TREE-SPINED STICKLEBACK *GASTEROSTEUS ACULEATUS* L. IN THE COASTAL ZONE OF THE WHITE SEA

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The tree-spined stickleback *Gasterosteus aculeatus* is the most studied species of family Gasterosteidae. This species is usually numerous and often dominates in freshwater and coastal ecosystem. Sticklebacks form various types of relationships with various organisms in the ecosystem. In the White Sea tree-spined stickleback are the most numerous species now. After hatching stickleback during several weeks live in the near shore area. The main goal of this study is to provide qualitative and quantitative description of diet, feeding resources and food selectivity of tree-spined stickleback juveniles in the White Sea during their inshore stage of life cycle. Samples were collected during August – September 2011–2013 with ten day intervals in Seldanaya Inlet, the north-western part of Kandalaksha Bay. This is the shallow inlet with dense seagrass *Zostera marina* bed where stickleback intensively spawn, and convenient habitat for juveniles. Sampling was performed by the 7,5 m beach seine during the low-tide. We measured the body length, total weight and gutted weight. 30 juveniles per sample were analyzed for content of their stomachs. They were subdivided into four size classes with intervals 5 mm. Simultaneously, zooplankton and zoobenthos samples were collected to analyze feeding resources. Zooplankton was collected by planktonic net towed vertically or by filtering of 100 l of surface water. Zoobenthos was collected by three angular scraper towed for 0,5 m. Diet of juveniles of all size classes included 20 taxa in 2011 and 18 taxa in 2012–2013. The taxa belonged to Copepoda, Cladocera, Harpacticoida, Orthocladiinae, Gammaridae, Bivalvia and Gastropoda. In 2011 the main part of diet contained of following organisms: *Microsetella norvegica* (Boeck, 1865) found in average in 80% of stomachs per sample, *Helicostomella subulata* (Ehrenberg, 1833 Jörgensen, 1924) – 40%, Orthocladiinae – 45%, other Copepoda – 30%. In 2012 the main part of diet contained of *Temora longicornis* (Müller, 1792) и *M. norvegica* – were represented in average 57 and 73% of stomach respectively. Also *H. subulata* and Harpacticoida comprised 57 and 43% of stomachs. In 2013, the main part of juvenile diet was composed of *T.longicornis* и Oligochaeta – 65 and 45%. Some food components were important during only short periods of time, for instance Oligochaeta in mid-August of 2011 and Orthocladiinae in early August of 2013 were represented in 93% and 86% of stomachs. Therefore the diet of stickleback juveniles was quite similar in different years, although some variation in composition and dominant groups of food organisms in different years and seasons has been observed. Based on comparison of stomach content juveniles and abundance of planktonic and benthic organisms in the sea, we can conclude that small juveniles (body length 10–17 mm) prefer to feed on Oligochaeta. When Oligochaeta are present in the sea, they, as a rule, dominate in stomachs as well. When Oligochaeta are absent, small juveniles prefer to feed on *H. subulata.* Larger juveniles mostly prefer Orthocladiinae. Their representation in stomachs is significantly correlated with abundance in the sea and does not depend on abundance of other food organisms. The next organism in terms of preference is *T. longicornis.* Usually this is one of the most common organism in stomachs and can be only pushed out by abundant Orthocladiinae. Such food objects as Copepoda naupli, *Podon leuckarti* (G. O. Sars, 1862), Ostracoda, Gastropoda, Hyas larva, *M.norvegica* and others are normally are present in the diet, but in total do not exceed 30–50% of stomach content. We did not find correlation between representation of these organisms in stomachs and their abundance in the sea.Therefore in general juvenile tree-spined stickleback feed on relatively large organisms of zooplankton and zoobenthos. At the same time, some potential food organisms which are common in the sea such as a boreal species *Centropages hamatus* (Lilljeborg, 1853) abundant in the surface waters, and *Oithoha similis* (Claus, 1866) usual for more open parts of the sea are actively avoided by stickleback juveniles.

## VARIATION IN FEEDING INTENSITY OF THE COLONIAL HYDROID *OBELIA LONGISSIMA* (PALLAS 1766) DEPENDING ON THE PHASES OF THE WHITE SEA TIDAL CYCLE

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As demonstrated by laboratory experiments, the patterns of feeding intensity in colonial hydroids that prey on zooplankton depend on hydrodynamics (Marfenin, Malyutin, 1995). Given expressed periodicity of tidal currents, food intake may depend on the phase of the tidal cycle. This assumption was tested on specimens of *Obelia longissima* collected near the White Sea Biological Station of the Moscow State University during eight semi-diurnal tidal cycles between the 21st and 25th of July, 2013. The tidal cycle was divided into 14 phases, about one per hour. Specimens of *O. longissima* were gathered from a platform floating 50 meters from shore and preserved in 4% formaldehyde solution. Feeding intensity was determined based on the share of food containing hydranths. Five samples were obtained from each specimen, 100 hydranths (gastrozooids) per sample. When a hydranth captures food, it changes color. «Starved» (whitish) and «satiated» (rufous colored) hydranths were counted in each 100-hydranth sample, and the percentage of «full» and «empty» hydranths was thus determined. Environmental conditions at the time of specimen collection: calm, water temperature 12—15°C, northeast wind at 3–7 m/s, 60% cloud cover, atmospheric pressure 760.7 mm Hg. Velocity of tidal currents around and inside the hydroid thickets is non-homogeneous, which made it an unsuitable parameter for the purposes of this study.

The percentage of food containing gastrozooids (FG) varies depending on the stage of the tidal cycle. Minimum values are observed at slack water stages: 22% at low tide and 24% at high tide. During tidal flow the share of FG increases, reaching 74% three hours before high tide and 84% three hours after high tide. The share of FG declines as the tide approaches high or low water.

Food lumps in the stomach of *O. longissima* have been found to contain: *Oithona similis* (Claus 1866), *Centropages hamatus* (Lilljeborg 1853), *Acartia longiremis* (Lilljeborg 1853), *Temora longicornis* (Müller 1785), *Pseudocalanus minutus* (Krøyer 1848) and *Microsetella norvegica* (Boeck 1865); *Podon leuckarti* (Sars 1862) and *Evadne nordmanni* (Loven 1835); nauplii and cypris larvae of the cirripedian species *Verruca stroemia* (Müller 1776). We also discovered nauplii of other non-cirripedian crustaceans, as well as unidentified remains including crustacean fragments and «slurry» of unclear origin.

The content of *O. similis* in the gastrozooids of *O. longissima* measures between 9% (an hour after high tide) and 27% (an hour before low tide) (Table 1). The content of *C. hamatus* can reach 4% at the stages «one hour before low tide» and «two hours before high tide», and the content of *A. longiremis* — from 5% two hours after low tide up to 21% three hours before high tide. The content of *V. stroemia* nauplii in the diet of *O.longissima* amounts to 30% at the stages «two hours before low tide» and «two hours before high tide», and the share of unidentified remains may add up to 48% an hour after high tide. *M. norvegica* is barely present in the stomach contents (1—3% of the total amount of food), however at the stages «one hour after low tide» and «two hours after high tide» its share reaches 9% and 13%, accordingly. *P. calanus*, *T. longicornis,* and cypris larvae of *V. stroemia* do not prevail in the diet of *O. longissima*, but individual members of these species were occasionally found in the food lumps.

The share of food containing gastrozooids and the composition of food lumps in the hydranths of the colonial hydroid *O. longissima* varies considerably depending on the stage of the tidal cycle.

## BURROWING SHRIMPS IN THE FAUNA OF PETER THE GREAT BAY (SEA OF JAPAN)

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Investigations of macrozoobenthos in Russian waters of the Sea of Japan during about 100 years provided only fragmentary view in the taxonomical composition of burrowing shrimps of the infraorders Gebiidea and Axiidea.

Our study conducted in 2010–2013 showed that fauna of burrowing shrimps in Peter the Great Bay numbers 8 species: *Trypaea petalura, T. japonica* and *T. makarovi* (Callianassidae), *Upogebia major, U. issaeffi* and *U. yokoyai* (Upogebiidae), *Boasaxius princeps* and *Leonardaxius amurensis* (Axiidae). *T. makarovi* is a new species, *U. yokoyai* – a species new for the Russian fauna. The using of original sampling device allowed to show for the first time that burrowing shrimps are common representatives in vast shallow waters making up from 2 to 33% from total biomass of macrozoobenthos. The densest populations (from 13 to 200 ind/m$^2$) are found from 0 to 1–3 m depth near protected coasts, including estuaries. It was shown that larval development of shrimps includes 3 or 4 zoeal stages in Upogebiidae, 5 stages in Callianassidae and 8 stages in Axiidae. The breeding season of shrimps in Peter the Great Bay lasts from May to September, the highest density of upogebiid larvae was recorded in June, callianassid and axiid larvae – in July. *U. major* и *T. petalura* hatch larvae several times during reproductive season, the rest species only once a year. The density of upogebiid larvae was higher in Amursky Bay, callianassid larvae were more abundant in Ussuriisky Bay. Axiid larvae were not numerous in both bays. Early larval stages of all shrimp species concentrated in the northern shallow-water parts of both bays owing to the cyclonic gyrations, late stages were probably carried out seawards by runoffs.

## LIPID COMPOSITION RESPONSE TO TEMPERATURE CHANGES IN BLUE MUSSELS *MYTILUS EDULIS* L. FROM THE WHITE SEA

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Temperature is the most important factor for marine ectotherms whose metabolism rate is determined by its variables. Different physiological, biochemical and molecular regulation mechanisms provide ectotherm adaptation/acclimation to various temperature fluctuations. Membranes play diverse and essential roles as physical barriers, controlling the transport of molecules, establishing ion gradient, and acting in membrane-based cell signaling. Various kinds of environmental stress including temperature cause alterations in cell membrane lipids physical properties reflecting in the membrane dynamic (mainly fluidity). The membrane fluidity activates the adaptive response of the organism to environmental stresses through a regulating the activity of membrane-bound enzymes, ion channels and pumps, receptors and others. Mechanisms of ectotherm acclimation at temperature fluctuations include “homeoviscous adaptation” of membrane fluidity which is accompanied by enlarged unsaturated fatty acid content resulting in increased fluidity at low temperature. The time frame of “homeoviscous adaptation” is unclear, although it has been shown that intertidal mussel membranes can be restructured within hours in response to temperature fluctuations during the tidal cycle. The aim of this work was to study the gill lipid composition response in blue mussels Mytilus edulis L. (living in stable aquaculture environment with no tidal effects) to acute (24 hours) and long-term (14 days) temperature effects. Sampling and experiments were carried out at the “Kartesh” Biological Research Station of the Zoological Institute RAS (Chupa Bay, Gulf of Kandalaksha, White Sea). The first temperature effect aquarium experiment consisted of two stages: 1. ambient water temperature rise from 0 – +3°C to +8°C (24 hours) or drop from +8°C to 0 – +3°C (24 hours); 2. subsequent return water temperatures to the initial values (0 – +3°C or +8°C, respectively). The second temperature experiment involved the acclimation (14 days) of blue mussels to different water temperatures (5, 15 (as a control) and 20°C). After the experimental exposure periods were over, the mussel gills (n=5) were fixed in 96% ethanol for further analysis. Thin-layer, high performance liquid and gas chromatography methods were used for analysis of total lipids, membrane phospholipids and fatty acids composition, respectively. The research was carried out using the facilities of the Equipment Sharing Centre of the Institute of Biology, Karelian research center of RAS. It was shown the mussel gill lipid composition response to a rapid temperature changes (24 hours) is a consequence of non-specific bivalve physiological reaction to environmental stress (such as shell valves closing and metabolic depression state development). It’s known the mechanism of metabolic depression is one of the basic adaptive strategies of intertidal animals to various kinds of environmental stress. Moreover, it was demonstrated rapid temperature change (24 hours), as well as long-term temperature acclimation (14 days) lead to mussel gill fatty acid composition changes (for instance, unsaturated fatty acids content increased in mussel gill phospholipids under the low temperatures influence), indicating a use of “homeoviscous adaptation” mechanism to maintain the membrane integrity and permeability in mussels gills under temperature fluctuations. Thus, it was suggested the mussel gill lipid composition changes in response to acute temperature effect represent its physiological adaptive mechanism and involve the protection of cell membranes whereas the lipid composition reaction to the long-term temperature influence is to maintain and restore the cell membrane homeostasis within new environmental conditions.

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## INTERANNUAL VARIATION OF THE ASEXUAL REPRODUCTION OF *AURELIA AURITA* FOLLOWED *IN SITU* (BAY OF KOPER, ADRIATIC SEA)

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Over the last decade we have witnessed increasingly frequent occurrences of gelatinous zooplankton masses, where the benthic polyp phase plays a key role in ensuring the long-term viability and success of jellyfish populations. Ecological tolerance of polyps and adaptation to environmental changes and anthropogenic factors are affecting the distribution of moon jellyfish (*Aurelia aurita* s. l.). Monitoring of polyps and their asexual reproduction under natural conditions is essential for understanding the problem of mass phenomena, i.e., jellyfish blooms. We studied the seasonal fluctuation of polyp abundance and their asexual reproduction dynamics from March 2010 to March 2013. The performed study was carried out in the Bay of Koper (northern Adriatic) where we monitored monthly the population of polyps attached to oysters at various depths and positions on one of the pillars located in Port of Koper. We recorded environmental parameters of temperature, irradiance PAR, salinity and pH. Maximum abundance was recorded in August (31 polyp/$cm^2$) and minimum abundance in December (8 polyp/$cm^2$). The abundance of polyps has a significant upward trend in correlation with increase in water temperature and a decreasing trend with increase in salinity. A high density of polyps has the effect of reducing asexual reproduction. Asexual reproduction in the form of budding and creation of stolons was present throughout the year with an increase in warmer periods. The strobilation process began in October (19.7 C) and reached its peak in December (11.7 °C). The pattern of seasonal polyp dynamics abundance did not differ significantly between years, but it did change their density which could be caused by favourable environmental conditions.

## WHICH ENVIRONMENTAL FACTORS CONTROL THE COMPOSITION OF MIXED MUSSEL POPULATIONS (*MYTILUS EDULIS*, *M. TROSSULUS*) IN THE WHITE SEA?

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*M. edulis* (Me) and *M. trossulus* (Mt) are sister species routinely distinguished by molecular markers. They form mixed populations and hybridize in the White Sea. Factors regulating the proportion of two species in mixed populations are unknown. We genotyped 1049 mussels from 26 populations by 4 semi-diagnostic allozyme loci. For each individual we calculated the "structure score" which assesses the probability of a mussel to be Mt (STRUCTURE software, Pritchard et al 2000). Hybrids were scarce and we did not consider them as a separate group. We distinguished two morphotypes: mussels: with reduced and with developed nacreous layer under the ligament. We found this character to be in good correspondence with genotype: Mt usually possesses the reduced nacreous layer while Me – the developed one. The proportion of mussels with reduced nacreous layer (Prnl) was positevely correlated with the mean structure score (MSS) calculated for populations ($MSS = 0.994*Prnl + 0.069$; R-square=0.89; F=199.1; $p<0.001$). Thus Prnl could be used as a proxy for taxonomic structure of mixed population. To reveal the environmental factors controlling taxonomic structure we investigated 16 sites with different salinity and wave exposure. Each site was classified as exposed or sheltered. Sites with salinity (S) < 17 psu (mean S = 7.9) were classified as sites with reduced salinity, others – as sites with "normal" salinity (mean S=18.1). In an each site 3 samples of mussels were collected from two types of substrate: the bottom and the fucoid's canopy. In each sample the Prnl was assessed. The mixed linear model with substrate type, exposition level and salinity level (as fixed predictors) and Prnl as dependent variable was fitted. As random effects in the model we used the intercept for region and site as well as by site random slope for the effect of substrate type. We found Prnl to be significantly dependent on substrate type and exposition level but not on salinity level The highest Prnl were found on fucoid's canopy comparing to bottom substrate and in sheltered sites in comparison with exposed ones. We conclude that Me and Mt are segregated by substrate and wave exposure in the Whits Sea: Mt is confined to the algal substrate and sheltered localities.

## VERTICAL DISTRIBUTION OF PHOTOTROPHIC MICROORGANISMS BASED ON OPTICAL MEASUREMENTS IN SEPARATING LAKES OF KANDALAKSHA GULF

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As a result of a recent years study on the Karelia shore of the White Sea more than ten lakes in different stages of separation from the sea have been discovered. Five of them are located close to the Nikolay Pertsov White Sea Biological Station of Moscow State University. The process of converting a marine environment into a lake encompasses changes in numerous water basin properties: its temperature and salinity, pH and other hydrochemical parameters, fauna and flora varieties. In such reservoirs very important role play different microorganisms, including various bacteria destructing organic matter, creating hydrogen sulphide, hydrogen and methane; phototrophic bacteria, able to photosynthesise without oxygen; and also protozoa that utilise organic matter created by bacteria during chemo- and photosynthesis.

In this work, five reservoirs with symptoms of meromixis have been studied in July-September 2013: lake Kislo-Sladkoe (the Polupresnaya lagoon), lake Trehtsvetnoe in the Pekkelinski Gulf, a lagoon at Zeleniy cape, lake Niznee Yershovskoe, lake Yelovoe near the Yeloviy island of the Kusokotski archipelago. To sample water at different depths with 5 cm step we used a submersible pump. It gave an opportunity to compare vertical profiles of oxygen and hydrogen sulphide concentration with the number and distribution of oxygenic and anoxygenic phototrophic microorganisms. Spectral properties of water samples (absorption and fluorescence spectra) were recorded using Unico spectrophotometer and Solar CM2203 luminescence spectrometer. The concentrations of microorganisms derived from spectral data were correlated with physicochemical water properties: temperature, salinity, oxygen distribution, pH value, light level, abundance of biogenic elements. The brightly coloured layers at the interface of aerobic and anaerobic zones were of specific interest in our work. In the summer 2013 in two reservoirs a persistent red layer was present, formed by cryptophytic algae Rhodomonas and in three other reservoirs green layers were present. Observations of the position of the red cryptophytic layer showed that it can be used as an indication of stable environmental conditions. Spectroscopic data showed that green layers in the anoxygen zone get their colour from a mass development of green sulphur bacteria. Green-coloured bacterial layers were not disturbed in September, meaning they are steady and more characteristic for water basins at further stages of isolation from the sea that are less affected by sea tides.

## DISTRIBUTION OF SOME SPECIES OF *BUCCINUM* DEPENDING ON HABITAT CONDITIONS IN THE NORTHWESTERN PART OF THE SEA OF OKHOTSK

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The Gastropods are a large group of benthic organisms that is significantly presented in the benthos of the Sea of Okhotsk. In 2013 a bottom trawl survey was conducted in the northwestern part of the Sea of Okhotsk. It included implementation of cuts from 142 °52′ and 152 °50′E and 56°30′ and 58°55′N, with distance 20-30 miles. About 50 species of gastropods were identified in particular species of the *Buccinum* genus: *B. osagawai, B. ectomocyma, B. pemphigus, B.miyauchii, Lussivolutopsius marinae, Neptunea lamellose* and others. There are shown the areas of distribution, the preferred depth, soils and temperature ranges. According to the preferred temperature the investigated species are divided into stenothermic moderately cold water and stenothermic cold-water. Data on the temperature range of *B. osagawai* occurrence has been refined. According to the preferred soils can be distinguished species living on aleurite and clayey silts; sandy, silty soils and silts and eurytopic sp. *N. lamellosa.* In relation to the depths species can be divided into elitoral - bathyal, sublitoral-upperbathyal, bathypelagical - abyssopelagical *sp.B. pemphigus* and sublitoral *sp. B. ectomocyma*. According to Savilov distribution (1961) of the benthic fauna of the Sea of Okhotsk the main area within the boundaries of the survey is the zone of the prevailing development collecting detritus, which approximately corresponds to zones of clay and silty-clayey silts according to Bezrukov (1960). According to Kuznetsov (1980), a large part of this zone is occupied be the *Ophiura sarsi* ecosystem, smaller part – by biocoenosis Yoldia *thraciaeformis*, there are also areas occupied by biocoenosis *O. leptoctenia*, *Ctenodiscus crispatus*. This fact is confirmed by large catches of these species, especially *Ophiura sarsi*. Within this area *L. marinae*, B. *ectomocyma, B. rossicum, B. kinukatsugai, B.miyauchii, N. beringianus* occur. Much smaller part occupies an area of solid soils sestonophages around the Kashevarov bank. It is an area of *B. pemphigus* distribution. The areas of *B. osagawai* and *N. lamellosa* distribution are larger than one ecological zone, so these species can be attributed as eurytopic.

## SPATIAL DISTRIBUTION OF POPULATIONS OF "*SAXATILIS*" SPECIES COMPLEX (MOLLUSCA: LITTORINIDAE) ON THE EAST MURMAN ROCKY SHORE (BARENTS SEA)

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The periwinkles populations of "*saxatilis*" sibling species complex – *Littorina saxatilis (*Olivi, 1792), *L. arcana* Hannaford Ellis, 1978, *L. compressa* Jeffreys, 1865 – are sympatric and widely distributed along North East Atlantic shores. They inhabit both boulder shores and different types of the rocky coasts. The species specimens are characterized by the poor external species-specific features and can be distinguished only by the internal characters of their reproductive system. It is therefore, there are limited data on the species-specific ecological features including population's spatial distribution. Distribution of periwinkles on vertical rocky surface may be considered as a model for the zonal distribution of these species (approximated "two-dimensionally" as opposed to "three-dimensionally" on the boulder intertidal or sloping rocky shores). The main purpose of this paper is to test the hypothesis of ecological features of three sibling species (that is their ecological niche separation) using criterion of their vertical shore distribution in the model of "two-dimentional" spatial distribution of the vertical rock surface.

Periwinkles were collected 5–7.08.2013 from 4 vertical rocky surfaces of intertidal zone in two sheltered shore sites (2 surfaces in each site) of Dalnezelenetskaya Bay, Barents Sea (69°07'N and 36°05'15"E). The mollusks were collected from three horizons: "low" (from the bottom up to the middle of *Semibalanus balanoides* belt); "middle" (from the middle of S.balanoides belt to the upper border of its settlements) and "high" (above *S. balanoides* settlements). We performed five quantitative samples of

$0{,}025 m^2$ in low and middle horizons of every rocky surface in every site (40 samples totally). Besides that, we collected qualitative samples in high horizons of every location (4 samples totally) due to the low density of the upper zone mollusks.

All collected mollusks were measured by ocular micrometer to the nearest 0.1 mm under a stereomicroscope. Periwinkles with shell width more than 2.5 mm were dissected; their sex and species were determined according to the morphology of the reproductive system. There were totally collected 1396 periwinkles, 428 of which were identified to species. Species-specific distribution of mollusks was approximated using logistic regression; size-dependent correlations were determined using general linear models.

We found that regardless of collection site there is marked increase in the size of shell with increasing height of the mollusk location ($N=274$; $F=22{,}14$; $p<0{,}05$). The largest mollusks were found on high horizon. Important to note, that size of shell is not depend of periwinkle's gender. *L. saxatilis* and *L. arcana* are no differ in size, but the specimens of these species both are comparatively lager than *L. compressa*. There is general feature of the species distribution. Regardless of a collection site, the proportion of *L. arcana* specimens is increased with horizon from low to high. In contrast, the proportion of *L. compressa* is drastically decreased from low to high horizon. Virtually almost all the population of *L. compressa* is connected with the low parts of the model sites. The distribution of *L. saxatilis* was shown to be more density uniform along the zonal gradient.

Therefore our data support the hypothesis of ecological differentiation of the sibling species of "*saxatilis*" species complex. The zonal patterns of its distribution show clear evidence of species peculiarities. That is apparently support their ecological niche specificity and may be regarded as an important information to assess its sympatric speciation.

## ABUNDANCE AND DISTRIBUTION OF FISH EGGS IN THE COLOMBIAN PACIFIC OCEAN DURING SEPTEMBER 2007

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Evaluations of ichthyoplankton (fish eggs and larvae) are important in ecological studies and fisheries prospections, since help to define periods and breeding areas, and because such early stages are a key link within the trophic web of zooplankton and upper levels. For assessing the distribution and abundance of fish eggs in September 2007 along the Colombian Pacific Ocean (CPO), zooplankton was collected by oblique tows to 184 m mean depth with a 60-cm bongo sampler (294- and 520-μm mesh). The abundances reached $53382/100 m^3$ in the first net and $631/100 m^3$ in the second one. The largest aggregations in the neritic south area of the CPO can be associated with spawning of fish stocks, high productivity, and the proximity of mangrove swamps, which are spawning and nursery grounds. The highest abundances in ocean waters could be partially explained by transport and retention processes, as an effect of the complex system of currents in the CPO. Considering both nets, diel variation was not wide (day $2476/100 m^3$ *vs.* night $2200/100 m^3$), suggesting continuous spawning, although many fish have higher spawning at night to avoid predators. Surface water temperature and salinity did not appear to play a significant role on distribution and abundance of eggs. This scenario can change, depending on the sampling month, fish species and the reproductive mode and location and extent of spawning grounds, and because fish spawning behavior is dictated by photoperiod (length of daylight).

## WATERBORNE COPPER AND CADMIUM AFFECT CALCIUM-DEPENDENT PROTEOLYSIS IN MUSSEL: LABORATORY SIMULATION AND FIELD SURVEYING

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Coastal environments of Kandalaksha Gulf in the White Sea (Russia) despite nature conservation efforts are heavily influenced by human activities. It results in a considerable increase in the levels of pollutants, such as heavy metals, particularly in estuarine areas. Biochemical markers of heavy metal toxicity were assessed in widely distributed marine invertebrates, *Mytilus edulis* (Mollusca, Bivalvia), collected from a series of anthropogenically-impacted areas within Kandalaksha Gulf and distanced towards the open sea reference sites. The data on biomarker responses were support by precise assessment of the physic-chemical parameters of the sampling area. The other part of the experiment has been consisted in laboratory modelling of dose- and time-responses to dissolved $Cu^{2+}$ and $Cd^{2+}$ on mussels. Some molecular parameters such as intracellular calcium-dependent proteases, or calpains, are considered to be the biochemical markers of heavy metal accumulation due to their metal-dependent functional proteolytic activity and conformational changes under metal chelating. Calpains are known to be responsible for

1) degradation of abnormal proteins enriched cellular milieu at metal accumulation as well as for

2) regulation of multiple cellular functions required in adaptation to pollutant load in vertebrate and invertebrate species.

Heavy metal accumulation primarily affects intracellular molecular machinery inducing non-specific responses required to adapt metabolism to pollutant load. Besides that the specific interaction between biopolymers and metal ions enabling to penetrate cytoplasm compartment has been revealed. The regulation mechanisms govern calpain activity are complex and two different mechanisms of calpains and heavy metals direct interaction besides non-specific stimulation were supposed:

1) metal ions such as mercury directly bind catalytic SH-groups in the calpain active site; as a result calpains are irreversible inactivated; or

2) metal ions interact with $Ca^{2+}$-binding sites in the structure of calpain molecule leading both in complete or partial inactivation of calpains as well as in partial $Ca^{2+}$ ions substitution allowing calpain activity.

The in vivo effect of heavy metal ions on calpains has been investigated in blue mussel organs such as hepatopancreas, gills, and mantle. Calpain was purified from the tissues by gel-chromatography, then proteolytic enzyme activity was measured; besides that calpain gene expression was estimated by RT-PCR. The model experiment have shown that the exposure of $Cu^{2+}$ in a dosage 5, 50, or 150 mkg/l and $Cd^{2+}$ in a dosage 10, 100, or 500 mkg/l within 24 and 72 h affect calpain activity and expression in dose- and time-dependent manner. In order to quantitate the observations the metal tissue distribution and accumulation dynamics were estimated. The in vitro effect of copper and cadmium ions on partially purified enzyme enabled us to identify their interaction mechanism. It turned out that $Cu^{2+}$ has induced in vitro calpain activity on 24% in comparison with $Ca^{2+}$, while $Cd^{2+}$ has shown marked inhibitory effect through calpain SH-group binding. Our results provided insights into the biomarker potential of intracellular protease activity besides the new data on the molecular mechanisms of heavy metal toxicity.

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## LONG-TERM AND TRANS-GENERATIONAL EFFECTS OF OCEAN ACIDIFICATION: A STUDY OF BENTHIC SPECIES UNDER NATURALLY-FLUCTUATING CONDITIONS

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Arctic and subarctic marine ecosystems are very sensitive to climate-related changes, but they remain poorly studied in this respect. It is particularly difficult to ascertain whether cold-water marine organisms will be able to adapt to ocean acidification in the long term. Studies tend to show that environmental conditions that occur during the reproductive cycle of adults can influence offspring fitness and survival. However, to our knowledge, few studies have investigated multigenerational effects (i.e. from adults to progeny) of ocean acidification. The present study assessed both direct and trans-generational effects of near-future pH decrease in cold-water benthic invertebrates over 15 weeks of exposure under flow-through, naturally-fluctuating conditions (i.e. seasonal variations in photoperiod, temperature and pH). It examined the effects of ocean acidification (0.4 units below ambient pH) on both adult biology (feeding, calcification, growth, fecundity, fertilization success) and subsequent offspring biology (embryonic/larval development, settlement, morphology, survival). Feeding, calcification and growth rates of sea urchins and whelks were not markedly affected over the course of the study. However, gonad development in both species was lower under low pH conditions. Furthermore, fertilization success, developmental kinetics and larval size and survival in sea urchins decreased in the following order: control conditions (adults and progeny in ambient seawater) to crossed conditions (adults in ambient seawater, progeny in acidified seawater) to acidified conditions (adults and progeny in acidified seawater). Successful settlement was restricted to the progeny of control adults. These findings emphasize the importance of conducting realistic trans-generational studies to measure the potential impacts of ocean acidification on organisms that live in seasonally fluctuating environments.

## SPATIAL AND BIOLOGICAL INFORMATION OF THREE UNCOMMONLY FISHED DEEP-WATER SPECIES IN THE EASTERN IONIAN SEA

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Data for three uncommonly fished deep-water species, *Mora moro, Molva dipterygia macrophthalma* and *Epigonus telescopus*, were collected from experimental long line fishing in a coral and a no-coral area in the Eastern Ionian Sea. Sampling was carried out in depths ranging between 300 and 800 m in June and October 2010 in the framework of CoralFISH project. A total of 18 long-lines were deployed in each area. In total, 51 *M. moro*, 19 *M. d. macrophthalma* and 6 *E. telescopus* were collected. Number, length, total weight, net weight, sex, maturity, gonad weight and liver weight were recorded from almost all specimens. Spatial and bathymetric distribution, biological information concerning size, W-L relationship, sex ratio, maturity, GSI and HIS indices and diet were examined. A similar number of *M. moro* were caught in both areas, more *M. d. macrophthalma* were fished in the coral area, whereas *E. telescopus* were found only in the no-coral area. *M. macrophthalma* was found in shallower depths (448–660 m), *M. moro* in deeper waters (605–857 m), while *E. telescopus* was found between their depth range (580–727). *M. moro* specimens were all females; their size ranged between 353–445 mm TL in the coral area, whereas 276–441 mm TL in the no-coral area. *M. d. macrophthalma* size ranged between 452–616 and 532–741 mm TL in the coral and no-coral area, respectively. *E. telescopus* were all males with size range 431–482 mm TL. Maturity stages of *M. moro* indicated a wide reproductive period. A winter reproduction can be hypothesized by the presence of maturing *M. d. macrophthalma* female gonads in October. *E. telescopus* male gonads indicated a summer-autumn reproductive period. Stomach and intestine analysis showed that Osteichthyes, Natantia and Cephalopoda were the most important prey categories for *M. moro*; the former two categories dominated *M. d. macropthalma* diet, whereas the last two were preferred by *E. telescopus*.

## PARALYTIC SHELLFISH POISONING (PSP): EFFECTS ON FEEDING, GROWTH AND LIPID STORAGE IN JUVENILE *OSTREA CHILENSIS*

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Frequent blooms of the dinoflagellate *Alexandrium catenella* in southern Chile encouraged undertaking the present study which uses the bivalve *Ostrea chilensis* as a model for evaluating the oyster feeding, growth and lipid storage responses to diets containing paralytic shellfish poison (PSP) produced by *A. catenella*. Medium-term (30 days) physiological responses of two groups of juvenile oysters (contaminated and control) were measured every 10 days. Five replicates (each one with 25 individuals) were exposed to diets containing *A. catenella* (70% *A. catenella* + 30 % *Isochrysis galbana*) and other five replicates were fed with a diet containing the non-toxic algae *Isochrysis galbana* (100 %). Diets were continuously supplied at a concentration of 2 mg/l, in which the feeding and metabolic activity was measured, and the scope for growth index was calculated. Lipids storage and mortality were also measured every 10 days. The results showed that the toxic diet has dramatic negative effects on feeding and metabolism of the juvenile individuals of *Ostrea chilensis*, with high reduction of the lipid storage and growth. Mortality was also increased in individuals fed with the contaminated diet. This study supports the conclusion that the presence of the toxic dinoflagellate *A. catenella* in the diet imposes significant restrictions in obtaining energy to juvenile individuals of *Ostrea chilensis*, a fishery resource of great importance in southern Chile.

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## ABUNDANCE AND SPATIAL DISTRIBUTION OF TWO INFAUNAL BIVALVES, *MACOMA BALTHICA* AND *CERASTODERMA EDULE*, IN THE BARENTS SEA INTERTIDAL ZONE

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Species usually shows unique features of population structure at biogeographic extremes, among which is a remarkable difference in abundance as compared to the central part of the species range.

In present study we were focused on the Barents sea populations of two widespread infaunal species of bivalves – *Macoma balthica and Cerastoderma edule. M. balthica* is an amphiboreal species; northern part of its range in East Atlantic spreads up to Spitsbergen in north, and up to the Kara Sea in east. This species also is very common in the White Sea. On the contrary, northeastern distribution limit of the common cockle *C. edule* belongs to the Barents Sea. Samples were collected at 11 sites of Murman coast of the Barents Sea for *M. balthica* (1 at the West Murman, 4 in the Kola Bay and 6 at the East Murman), and at 17 sites for *C. edule* (2 at the West Murman, 4 in the Kola Bay and 11 at the East Murman).

*M. balthica* abundance at the West Murman and the Kola bay sites varied from hundreds to thousands individuals per square meter. Maximun abundance (more than 3000 ind./m$^{-2}$) was observed in the Kola Bay at cape Abram. Such dense populations are typical for *M. balthica* in neighboring range parts: the White Sea, the Pechora Sea, and even the North Sea. At the East Murman *M. balthica* abundance was lower (less than 100 ind./m$^{-2}$ at most sites). The lowest abundance (about 30 ind./m$^{-2}$) was observed in Dalnezelenetskaya bay. All poplations were stable during observation period. Alive *C. edule* were found in 11 out of 17 sites. Its abundance was extremely low at all sites (less then 10 ind./m$^{-2}$ at most sites). Cockle abundance increased up to 20 ind./m$^{-2}$ only in some years. We found *Cerastoderma* shells at some sites without alive cockles. We suppose that *C. edule* inhabit Murman coast as a metapopulation. Cockle populations became extinct during our monitoring (2002 – 2013) at some sites (for example, at Shelpino in 2009). The easternmost cockle population was found in Tryashina bay. We observed neither alive nor dead *C. edule* further to east (bays Drozdovka and Ivanovskaya).

In the North Sea, both *C. edule* and *M. balthica* populations typically have «nurseries» at the high intertidal floor. We did not observe such vertical distribution pattern in the Barents Sea. Therefore, we studied local distributions within one intertidal floor. We chose the middle intertidal floor as the most typical habitat for both species. We used random-regular sample net and Moran's spatial autocorrelation for 2 East Murman (Dalnezelenetskaya and Yarnyshnaya bays) and 1 Kola bay (Pala bay) sites. We found aggregation patches only in Pala bay. For both bivalves patch diameter was about 4 meters.

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## FIRST DATA ON THE SEXUAL REPRODUCTION IN THE MEDITERRANEAN CHEILOSTOME BRYOZOANS *MYRIAPORA TRUNCATA* AND *ADEONELLA CALVETI*

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We studied seasonal aspect of the sexual reproduction in two Mediterranean cheilostome bryozoans – *Myriapora truncata* (Myriaporidae) and *Adeonella calveti* (Adeonidae), which form erect perennial colonies. Sampling was undertaken monthly by SCUBA near Marseille, during 2013–2014.

Colonies of these species have similar structure and retain active all year-round, living on similar substrata (on the rocky bottom in crevices, and caves and semi-caves). Each colony consists of zooidal buds developing on the tips of branches, autozooids with feeding polypides as well as autozooids with degenerating or regenerating polypides.

The structure of their ovaries coincides. Mature ovary bears macrolecital vitellogenetic oocyte with its nurse-cell, surrounded by flattened follicular cell layer. Ovarian wall in its basal part is formed by columnar cells which encircle oogonies and previtellogenetic oocyte duplets and subovarian zone with basal cells and intercellular spaces. However, dynamics of oogenesis differs between the species. Irrelevant of the season female zooids of *M. truncata* comprise ovaries which contain from one to four oocyte/oogonial duplets, one being vitellogenetic. *A. calveti* do not maintain ovaries in autumn and winter time (from September till February). During spring its ovaries contain few small germ sells whereas the number of oogonial/previtellogtenic oocyte duplets varies from one to seven. In June previtellogenetic oocytes start to grow but yolk granules were not seen till late summer.

Accordingly, *M. truncata* produces larvae through the entire year while *A. calveti* seems to reproduce seasonally as the mature larvae were detected in the beginning of September only. It is necessary to mention that earlier these species were studied by Gautier (1962), but his data strongly differ from ours. Gautier observed embryos in the ovicells of *Myriapora* only in March and did not found them in zooids of *Adeonella*.

As to the patterns of reproduction *A. calveti* is characterized by the II reproductive pattern (macrolecithal oogenesis followed by non-placental brooding) and *M. truncata* was previously attributed to the species with IV pattern (macrolecithal oogenesis followed by matrotrophic brooding by means of placental analogue – embryophore). The structure of the brood chambers of these species is also dissimilar. Whereas *Myriapora* incubates their progeny in the ovicell, *Adeonella* does this in the internal brooding sac.

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## NO RULES FOR *MACOMA*? ON THE LONG-TERM TEMPORAL AND SPATIAL VARIATION OF THE BALTIC TELLINS POPULATIONS AT THE KANDALAKSHA BAY OF THE WHITE SEA

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*Macoma balthica* (Linnaeus, 1758) was extensively studied for population dynamics (Maximovich et al., 1991; Bouma, 2001; Beukema, Dekker, Naumov, 2006; Jansen, 2009) and spatial distribution (Cranford, Peer, Gordon, 1985; Ysebaert, Herman, 2002, Varfolomeeva, Naumov, 2013). However, at the White Sea a little was known about *M. balthica* population dynamics in different spatial scales so far. We examined several *M. balthica* populations to check whether the structure and patterns of dynamics are similar at the different spatial scales. Data were obtained from long-term surveys conducted by the authors under various monitoring programs in the Kandalaksha State Natural Reserve, the Saint-Petersburg State University (the Hydrobiology and Ichthyology department) and the White Sea Biological Station (Zoological Institute RAS). Those surveys were carried out within 10 locations in Kandalaksha Bay, varying in distances between them from one to 100 km. The surveys varied from 5 to 27 years in duration. Cores were sampled annually in July or first decade of August and sieved, using 0.5 mm/1 mm mesh-size sieves. All *M. balthica* specimens from 8 of 10 localities were counted and measured using micrometer eyepiece scale. General inter-annual population density dynamics from all locations were obtained and inter-annual size structure variation was reconstructed. To verify if there are linear trends and synchrony of dynamics of traced populations we used Mantel test (Zar, 2010). We used partial rate correlation function (PCRF) (see Berryman, Turchin, 2001 for details) to determine density dependent processes regulating dynamics in traced populations.

All locations show different patterns of dynamics except one common peak of density in the 1998—1999. Linear trends were revealed in dynamics in 4 of 10 traced populations. Significant signal of second order negative feedback was obtained from PCRF analysis in one *M. balthica* population only. This population is associated with dense population of predatory snail that has been found previously (Aristov, Granovich, 2011). In some cases hardly explained negative feedbacks with longer lags (6–9 years) were revealed. No correlations between patterns of dynamics in traced populations and geographical distances between locations were obtained.

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## NOVEL TOXICITY ASSAY FOR BRACKISH WATERS USING TWO CILIATE SPECIES OF *PARAMECIUM* SP.

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Brackish waters (with a salinity lower than seawater and higher than fresh water) represent a significant part of the natural waters like estuaries, lagoons, brackish seas and lakes, mangrove swamps. Estuaries and other brackish water bodies are of high importance serving as navigation waterways, fisheries, etc. The usage of brackish waters is causing their pollution, affecting thus negatively biota living in these ecosystems. Though several studies describing the combined influence of salinity and pollutant toxicity are available, most of them cover only a narrow part of the salinity range, which exist in the estuaries and other brackish waters. The aim of the present research was to assess the combined influence of salinity and toxicity of several heavy metal salts using two species of euryhaline ciliates (*Paramecium dubosqui* and *Paramecium nephridiatum*) that were previously shown to withstand wide range of salinity (from freshwater to 37‰). Additionally, the ciliates are easy to handle and fast reproducing organisms, representing an important part of food webs. To test the toxic effect of three metals (Cr as $K_2Cr_2O_7$, Cu as $CuCl_2 \times 2.5\ H_2O$, Hg as $HgCl_2$) to two ciliate species (acclimated to salinities 0.5 and 5‰), a simple 72 h exposure method based on the use of 48 well plates is proposed. The results of the tests showed that the metal toxicity to both species of ciliates was rising in line Cr<Cu<Hg with EC50 values at lower salinities being 39.6, 5.2, 0.30 mg/l for *P. dubosqui* and for *P. nephridiatum* 24.3, 5.8, 0.34 mg/l, respectively. Generally, EC50 values did not differ between the two tested salinities. The only exception was EC50 for Cr being about 2-times higher at P. *dubosqui* (61.3 mg/l. The stimulatory effects on the growth of ciliates were observed at lower concentrations of $K_2Cr_2O_7$. The study shows that assays with ciliates can serve as promising tools in the research of toxic chemical effects in highly variable environments such as estuaries.

## DISTRIBUTION OF JUVENILES OF THREE SPINE STICKLEBACK *GASTEROSTEUS ACULEATUS* L. IN NATURAL AND EXPERIMENTAL CONDITIONS

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Marine ecosystems are subjected to short- and long-term changes which mechanisms are poorly known. For example, during the 1930s considerable part of the seagrass *Zostera marina* population has disappeared in the Atlantics and the Baltic Sea. In the 1960s seagrass has disappeared in the White Sea as well. After disappearing of the seagrass, three-spined stickleback *Gasterosteus aculeatus* population significantly reduced in the White Sea. Most of scientists suggest that the decline of stickleback population was caused by the decline of the seagrass because fish are dependent on the seagrass during reproduction, i.e., males built nests in seagrass beds and juveniles grow there first weeks of their life. Our recent study in Kandalaksha Bay of the White Sea has shown the high density of the stickleback spawners during the breading season both in the seagrass beds and in brown macroalgae (*Fucus* spp. and *Ascophylium nodosum*), and in small littoral pools with green algae. At the same time, density of spawners in sand littoral zone and near small islands was notably lower. To understand why stickleback prefer to associate with aquatic vegetation, we have studied the juveniles distribution in different habitats of the Kandalaksha bay (seagrass beds, brown algae, littoral pool and sandy littoral). Through the experiments we have tried to understand mechanisms of juvenile's choice in special habitats and if the choice is influenced by their distribution in nature. Field samples were collected during August 2008–2013 in the Kandalaksha Bay with a small beach seine, 7.5 m of length, 150 $m^2$ of catch area. Juveniles were sampled at 9 stations with different types of substrate. The experiment was carried out at the marine biological station of St. Petersburg State University (Keret Archipelago, Kandalaksha Bay) in August 2008–2009 in a plastic pool 50×70×450 cm. The juveniles were offered the following types of substrates: brown macroalgae (dense), brown macroalgae (scarce), seagrass and control (no substrate). The substrates were placed in metallic cuvets 27×35 cm. Density of juveniles in pool corresponded to the natural density of 160 ind./$m^2$, their length varied from 8,5 to 18 mm. To calculate number of juveniles associated with particular substrate, we put cuvets in nets, which were put down during the experiment and did not prevent juveniles to choose substrates. At the end of experiment the nets were elevated to prevent the juveniles to go out. Then fish were pictured and then counted and measured using free software Image Tool. Each experiment continued for about 12 hours and had two replications. Field observations showed that the juvenile sticklebacks occurred mainly in the seagrass *Zostera marina* beds and in littoral pool with green algae, in fucoids their density was significantly lower. We didn't find any juveniles in sand littoral zone. In the experiments sticklebacks also preferred seagrass to fucoids, even if density of the latter was higher. These findings suggest that seagrass plays a significant role in the life of juvenile stickleback and, consequently, changes of seagrass density can be an important factor driving stickleback abundance in the White Sea.

## LIFE HISTORY OF *CALLOPORA CRATICULA* (CHEILOSTOMATA, GYMNOLAENATA) IN CHUPA INLET (KANDALAKSHA BAY, WHITE SEA)

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Life history of the cheilostome bryozoan *Callopora craticula* has been investigated for the first time. Reproduction most likely starts in May, and continues until autumn. During summer season, the population is represented by three generations:

1) mature overwintered colonies,

2) their progeny (daughter generation), and

3) grandaughter generation – descendants of the second generation. Settlement of the daughter generation occurs at the first half of July, whereas settlement of the granddaughters occurs in the middle of August. Maximum lifespan of *Callopora craticula* colonies is about 1 year 4 months.

In respect to the sexual and polypide dynamics, colonies of different generations show different patterns. Every colony consists of the sterile, female and hermaphrodite autozooids. Sterile zooids form the central (and the oldest) part of the colony whereas female zooids are placed at its periphery. In the overwintered colonies the number of fertile (female and hermaphrodite) zooids and number of zooids with functioning polypides decreases from June to August. The number of zooids with degenerated polypides increases in the same period. Towards autumn overwintered colonies die off. In the colonies of the daughter and grandaughter generations the number of fertile zooids after some increase in the beginning of their life, then decreases (from July to August), whereas the number of zooids with functioning polypides increases during this period. The number of zooids with degenerated polypides decreases during July, then number of such zooids increases a little from July to August. After winter 'dormancy' period these colonies will become a sexually mature generation next spring. Thus, every survived colony reproduces twice during its life.

## CURRENT STATUS AND LONG-TERM CHANGES OF *ZOSTERA MARINA* L. IN CASE OF THE BABIE MORE BAY (WHITE SEA)

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*Zostera marina* L., (eelgrass, sea grass) – is the flowering plant, marine hydrophyte with horizontal rhizome and ascending vegetative and generative shoots (Vekhov, 1992). Until the mid-twentieth century this species formed a large beds along the coast of Kandalaksha Gulf and Onega Bay from intertidal zone to a depth of 4–6 m (Vekhov, 1992; Brotskaya et al., 1963; Gemp, 1962; Gurvich, 1934; Meyer, 1933). In 1930's there was a mass extinction of eelgrass along the eastern and western shores of the Atlantic Ocean (e.g., DenHartog, 1994; Short et al., 1987). However no significant changes of White Sea eelgrass populations were detected until 1960's when mass mortality occurred. Only in 1980's VN Vekhov noticed that the lower boundary of the eelgrass dipped to –2 m (Vekhov, 1992). Since then *Zostera marina* population of the Kandalakshsky Gulf generally recovered, but eelgrass biomass still doesn't reach former extinction values (White Sea…, 1995). Some studies reports on final recovery of eelgrass beds (Bukin et al., 2010; Berger, 2011). Existing data doesn't confirm that trend clearly, mostly because it doesn't rest on long-term observations. The aim of our study is to describe the current state and long-term changes of eelgrass population in Babie More bay. For this bay there is probably the longest series of eelgrass observations along the White Sea coast: 1930's, 1950's, 1980's, 1997–99, 2011 (this study). According to our observations *Zostera marina* in the bay inhabits only subtidal zone at depths from –0.2 m to 2.0 m. Major beds are encountered at depths of 0.2 – 0.5 m only. In a few places we came across individual plants at depths greater than 0.5 m. Also we found typical eelgrass habitats absolutely bare. In 1932, Babie More bay was visited by GS Gurvich to investigate benthic communities. Researchers have noted extensive eelgrass bed filling all space with depths less than 4–6 m. (Gurvich, 1934). That was never seen again. In late 1950's the beds went no deeper than –2 m. Nowadays the area occupied by eelgrass in Belaia guba Bay (one of the largest shallow bay in Babie More bay) make up less than 0,1 % covered formerly. We also noticed almost complete absence of eelgrass in the shallow waters along other coasts that noticed to be fully covered with it in 1930's. Also we estimated changes of individual *Zostera* beds in 9 bays during 12–14 years. One bay among them became free of eelgrass since 1997 (Guba Losinaia). Formerly in this bay area occupied by *Zostera marina* with various densities was 0.5 ha. Apparently, eelgrass here died completely. Remarkable decrease of eelgrass density was found in other bay (Ujnaia Sokolia Guba). Only once we found an increase of the eelgrass density in Guba Voronia bay. Individual plants and sparse patches were found here in 1997. We discovered two semi close spots along the northern and southern shores of the bay and some individual plants between them. Estimated area of beds in Belaia Guba bay in 2011 was 11 ha, and in 1997 – 6 ha. That is not significant increase comparing to state of the 1930's–1950's. Moreover, when we visited the Babie More bay in July 2012, we found that *Zostera marina* disappeared in many areas of it. Numerous blackened roots of eelgrass were covered with filamentous algae. Only several shoots survived substituting dense eelgrass bed. At the same time state of *Zostera marina* population in adjacent Osinovaia Guba Bay didn't change. It seems that eelgrass community should be more stable in such sheltered and desalinated bay. However, AE Panarin reported that in the 1980s in this bay there were only two moderate patches of eelgrass about 25 m2. At the northern coast of Babie More bay, we did not notice any significant change. As can be seen from above current state of eelgrass population is significantly different from described in pre mass extinction period and little has changed during 12 years. There is no reason to account the modern dynamics of eelgrass populations as recovery. In some habitats eelgrass disappeared, in other on the contrary it increases its density and area of the beds. But in general, the population status remains substantially unchanged. Eelgrass in the Babie More bay occupies mostly shallow habitats, which are protected by configuration of the coast and islands. But even here, the meadows are localized in the innermost part of the bays. Closed and desalinated bays become refugia during mass instinctions. Eelgrass population here remains stable for a longer time then along open coast.

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## THE HEAVY METALS INFLUENCE ON THE BIOLUMINESCENCE CHARACTERISTICS VARIABILITY OF THE *MNEMIOPSIS LEIDYI* A.AGASSIZ, 1865

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Eutrophication of the shelf areas and effect of marine pollution by toxic substances causes the degradation of coastal ecosystems and are the main environmental problems for the Black Sea. The impact of heavy metals (HM) on the bioluminescence characteristics variability of alien species ctenophore *Mnemiopsis leidyi* A. Agassiz, 1865 was the objective of our study. This is the first study of the HM influence on the bioluminescence of this ctenophore. Experiments were conducted in the Department of Biophysical Ecology of IBSS NASU at the coastal area of Sevastopol (Crimea, Ukraine) in July–August 2010–2011. Ctenophores with body length of 35 – 40 mm were selected for experiments. Characteristics of the ctenophores light emission were studied using laboratory complex "Swet" under mechanical and chemical stimulations. Salts of heavy metals ($Cu_2So_4$, $ZnCl_2$, $PbCl_2$ и $HgCl_2$) in concentrations of 0.1 maximum allowable concentration (MAC), MAC and 10 MAC were used in experiments. Freshly caught specimens, contained in pure sea water, were used for a control experiment. The exposure time intervals were 1, 3 and 24 h at a T= 21 ± 2 °C. The results showed significant variability of ctenophores bioluminescence characteristics, which were caused by metal concentration and duration of exposure. The amplitude of ctenophores bioluminescence first increased and then decreased, when exposed to copper and with increasing exposure time in all experimental groups. The lowest values of the luminescence amplitude were registered at 10 MAC of copper when the intensity of individual luminescence decreased by almost 10 times with increasing exposure time from 1 to 24 h. Studies showed a considerably higher copper toxicity compared with the zinc. In the first hours of exposure (0.1 MAC zinc concentration) the bioluminescence intensity (BLI) of ctenophores was 2 – 3 times higher than recorded for control experiment. In mechanical stimulation it reached $1383.06 \pm 69.15 \cdot 10^8$ quantum·$s^{-1}$·$cm^{-2}$; and in the chemical stimulation BLI=$1127.79 \pm 56.38 \cdot 10^8$ quantum·$s^{-1}$·$cm^{-2}$. Increasing zinc concentration to 0.5 mg/l resulted in low levels of BLI of ctenophores 2 times compared with control ($p < 0.05$). Mercury and lead were considered to be the most dangerous of the investigated HM. *M. leidyi* is resistant even to high concentrations of mercury, while maintains the ability to bioluminescence after 24 hours of exposure. At high concentrations of mercury in the early hours of exposure locomotor activity of ctenophores was disturbed. After 3 h ctenophores hardly rose to the surface and after 24 h they sink to the bottom, losing to 80% of wet weight. The duration of ctenophores bioluminescence significantly varies according to the variation of HM concentration and if compared with duration of exposure. More prolonged signals (3.68 s in the chemical and 3.17 s in mechanical stimulation) were registered in the ctenophore group kept at 0.1 MAC of zinc. In all other experimental groups, bioluminescence duration significantly lowers the control, and it tends to reduce when the exposure time increases. For specimens kept at 10 MAC of mercury (in mechanical stimulation 1.46 ± 0.06 s and in chemical stimulation 1.57 ± 0.07 s) less prolonged signals were observed, especially at a daily exposure. This parameter doesn't exceed 50% of control organisms. Bioluminescence amplitude as well as duration of *M. leidyi* luminescence were minimal at all specified exposure concentrations of lead ions. In the first hours of exposure ctenophores reacted by low bioluminescence intensity at a concentration of lead 0.1 MAC. This parameter was 6 – 7 times lower than recorded for control organisms. Minimum bioluminescence was recorded for specimens, kept at a concentration of lead of 10 MAC. In the first hours of exposure light emission was 34 times lower than the bioluminescence of control specimens. At a daily exposure minimum values of BLI were recorded: with mechanical stimulation BLI=1.54 ± 0.06×10$^8$ quantum·s$^{-1}$·cm$^{-2}$, and BLI=1.66±0.07×10$^8$ quantum·s$^{-1}$·cm$^{-2}$ with chemical stimulation. Thus, it is shown that high values of HM lead to functional disturbances of hydrobionts. Heavy metals can be ranked in the following order: Zn <Cu <Hg <Pb according to the intensity of toxic effects on the ctenophore bioluminescence. So, bioluminescence parameters of ctenophores may be used as express indicator of heavy metals effect and express index of regional marine pollution.

## FEED PHYTOPLANKTON DYNAMICS AND GROWTH OF CULTIVATED OYSTERS *CRASSOSTREA GIGAS* IN THE BLACK SEA

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Effective cultivation of marine bivalve mollusks is possibly under optimal hydrological and hydrochemical conditions of the environment, under low anthropogenous influence and sufficient food supply. The combined effect of external factors on abundance and biomass of microalgae results in changes of growth of cultivated shellfish – the Pacific oysters *Crassostrea gigas*. Dynamics of abundance and biomass of phytoplankton, including feed species of microalgae, stomach fullness of cultivated mollusks and growth of the oysters *C. gigas* investigated on the shellfish farm located in coastal zone of the Crimean South Coast. The results showed that the abundance of phytoplankton in the marine farm ranged 24 – 508 million cells/m$^3$, biomass – 20 – 1070 mg/m$^3$. The analysis of food bolus of oysters showed that more than 80% of the cells were dinoflagellates with cell size up to 70 microns: *Prorocentrum micans*, *Exuviella cordata*, *Exuviella compressa*, *Scripsiella trochoidea*. And although the abundance of feed species in the phytoplankton does not exceed 15%, oysters accumulate in their stomachs sufficient. In the spring and summer months of stomach fullness was maximal up to 500 cells of microalgae per specimen. Along with phytoplankton cells, small zooplankton organisms (up to 200 microns), the larvae of bivalves, pine pollen were found in the stomachs of *C. gigas*.

The linear sizes oysters gradually increased throughout the year. As a result, shell growth was by 6 times, reaching an average of 5,06 ± 1,25 cm. Weight of mollusks began to grow rapidly only during the warmer months. Since May, the intensity of body weight increased in 80 times and reached 12,33 ± 0,1 g. Our data showed that the growth of one-year oysters *C. gigas* was maximal in July (up to 0,30 mm/day and 0,163 g/day) and is closely dependent on the dynamics of phytoplankton biomass ($r$ = 0,71 and 0,74).

Comparing the abundance of dinoflagellates in seawater and shellfish growth, a clear linear relationship was obtained, which is described by the following equations:

$\Delta H_{daily} = 0{,}025\ C_{din.} - 0{,}1107$, with $r$=0,88;

$\Delta W_{daily} = 0{,}012\ C_{din} - 0{,}044$, with $r$=0,91,

where $\Delta H_{daily}$ – a daily gain of length of shell, mm/days; $\Delta W_{daily}$ – a daily weight gain of biomass of a mollusk, g/days; $C_{din}$ – concentration the dinoflagellates microalgae, million cells/l The resulting equations can be used to predict the harvests of marine farms in the coastal waters of the Southern Coast of Crimea. Abundance and biomass of microalgae dinoflagellates can be offered as test indicators to assess of availability of feed for cultivated shellfish.

## MAXIMUM AGE OF COASTAL COD *GADUS MORHUA MARISALBI* IN THE WHITE SEA

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Age estimation is one of the most important elements in the studies of fish population dynamics, growth, recruitment and mortality under fluctuating environments and anthropogenic disturbances. The cod is common and abundant fishes in the White Sea coastal zone, which plays an important role in food webs and ecosystems functioning. Age determinations in White Sea cod were mainly based on examination of hard structures such as otoliths. However, the published data on maximum age still require additional documentation because the difficulties in interpretation of growth zones and respectively ageing otoliths of big specimens have been noted in some publications. We applied the image analysis of otolith thin-sections in age estimations in cod to get accurate data on maximum longevity of this species in the White Sea. Research surveys in the Chupa Inlet and adjacent waters of the Kandalaksha Bay were conducted in June–August 2007–2013 years (RV *Belomor*). Five the biggest specimens of 3560 fish caught in total were selected for age determination. The sectioned otolith technique was used to age selected fish. Age of these biggest individuals of cod from the Chupa Inlet (*TL* 60.2–77.0 cm; *TW* 2.4–6.1 kg) ranged between 7 and 12 years. Translucent and opaque growth zones on slices of otoliths from the fish of different ages were well defined. Multiple translucent banding (split rings) within an annual structure can occur within the same otolith. However these false bands are often incomplete, thinner or diffuse and can be distinguished from the true annuli. According to our data, maximal longevity of cod from the White Sea exceeds 12 years which is larger than previously published data. The White Sea cod demonstrates similar longevity to the conspecifics from the Baltic, North seas and from the Norwegian fjords, while it has a shorter life cycle than cod from North Atlantic (Northeast Arctic, Greenland, Iceland, Newfoundland and Labrador stocks).

# *Predator – prey, parasite – host, and other inter- or intraspecific interactions*

## WHAT TO EAT INSTEAD OF CLAMS: THE MUDSNAIL *HYDROBIA ULVAE* AS A SECOND-BEST PREY FOR YOUNG MOONSNAIL *AMAUROPSIS ISLANDICA* AT THE WHITE SEA SANDFLATS

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Iceland moonsnail *Amauropsis islandica* (Gmelin, 1791) (Naticidae: Caenogastropoda) is one of the four naticid species in the White Sea and one of three among them which inhabit intertidal zone. In these habitats they prey primarily upon 3 common species of clams: *Macoma balthica* (L., 1758), *Mya arenaria* (L., 1758) and *Mytilus edulis* L., 1758, and occasionally on gastropods *Littorina littorea* (L., 1758) and conspecifics. The mudsnail *Hydrobia ulvae* (Pennant, 1777) co-dominates in the same habitats but is considered to avoid *Amauropsis* predation due to its small size (max. shell height of the White Sea specimens is 6,2 mm. However, *Hydrobia* snails can serve as a prey for the young specimens of *Amauropsis*, which hatch from the egg-capsule of 1 *mm* size and can bore small mollusks like other naticids. Newly hatched *Amauropsis* can also prey on the young *Macoma* clams. We conducted a field experiment to check for possible predation of young *Amauropsis* upon *Hydrobia* and for its preference (if any) between *Macoma* and *Hydrobia*. 28 0,4 $dm^3$ cages were placed near the chart datum at the inner part of Youzhnaya Bay (Ryashkov Island, Kandalaksha Nature Reserve) ($\varphi$=67°00.451′ N; $\lambda$=32°34.273′ E). We exposed juvenile *Amauropsis* with *Hydrobia* as a suggested prey, *Amauropsis* with *Macoma* together with *Hydrobia*, and *Hydrobia* separately (Control) for 5 and 10 days. After certain exposure all animals and their hard remains were retrieved from the cages, counted and measured. Feeding rates of *Amauropsis* were estimated as number of preys' shells bearing beveled boreholes specific to naticids' attacks. The feeding rate of *Amauropsis* juveniles while preying upon *Hydrobia* was significantly higher in the cages with *Hydrobia* (0,35±0,04) than in the cages with *Hydrobia* combined with *Macoma* (0,21±0,02). In the latter cages consumption of *Macoma* by *Amauropsis* juveniles was significantly more intensive (0,37±0,09) than that of *Hydrobia* (0,16±0,01) for 10-day exposure. Hence we postulated that *Macoma* is preferable prey species for *Amauropsis* juveniles. These predators feed upon the largest of available prey regardless of prey species; its preferable borehole sites on *Hydrobia* shells on the last whorl in front of aperture. These results shed light on the feeding of young naticid snails at the White Sea sandflats and assign the role of *Hydrobia ulvae* as supporting prey for them at locations, where the density of *Macoma balthica* of a proper size is low.

## SAITHE (POLLACHIUS VIRENS) AND HAKE (MERLUCCIUS MERLUCCIUS) SPATIAL INTERACTIONS IN THE NORTH SEA

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We investigated the ecology and spatial distribution of saithe (*Pollachius virens*) and hake (*Merluccius merluccius*) in a relevant region for fishery economy: the North Sea. While saithe is an important commercial species with spawning stock biomass declining in recent years, hake occurrence have been increasing in the area. In order to understand if these two species are spatially correlated, their potential habitat was studied during winter using binomial generalized linear models (GLMs) based on the 1st quarter data of the International Bottom Trawl Survey from 1991 to 2012. Species occurrence was modeled as a function of different external factors at the scale of the statistical rectangle. Explanatory variables were grouped by category (abiotic, biotic and spatial factors). Biotic explanatory variables included several fish species with a supposed trophic link: saithe, hake, cod (*Gadus morhua*), Norway pout (*Trispoterus esmarkii*) herring (*Clupeus harengus*) and blue whiting (*Micromesistius poutassou*). Abiotic factors included depth, temperature and sediment type. The results were used to map potential habitat for both species and study, for the first time in the North Sea, their spatial overlap. This has been performed by comparing an early (1991–1996) and a late period (2007–2012). An increase in the probability of presence for both saithe and hake has been noticed. Although saithe coverage has remained spatially consistent over the last 20 years, hake distribution has expanded toward south. Whereas the overlap between the two species slightly expanded, the probability of presence of both species together has greatly increased.

## BIODIVERSITY OF SYMBIOTIC GASTROPODS FROM ECHINODERMS OF THE BAY OF NHATRANG (SOUTH VIETNAM)

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The family Eulimidae is characterized by specialization for symbiotic relationships with echinoderms. There are about 1500 species of such molluscs which inhabit starfishes, crinoids, sea urchins, holothurians and brittle stars from tropical waters to the temperate zone.

Eulimids from starfishes can be found on the oral side of the host, where they are better protected from predators (for example, *Thyca* spp., *Stilifer* spp.). Some species of symbionts penetrate the body surface of the host and can make galls. Crinoid-associated eulimids are able to inhabit different parts of the host body (arms, cirri, calyx), penetrating its covers between ossicles. (*Annulobalcis* spp., *Goodingia varicosa, Curveulima* spp.). Symbiotic gastropods from sea urchins move across the host body surface (*Pulicicochlea* spp.), attach to the oral side of the host (*Echineulima* spp., *Mucronalia* sp., *Pelseenaria* sp.) or form galls on the spines (*Megadenus interspinea, Monogamus parasaleniae, Sabinella troglodytes, Trochostilifer mortenseni*). Eulimids associated with holothurians are found on the dorsal side of the hosts, and are very numerous in their coelomic cavity, as endoparasites (*Enteroxenos* spp., *Entocolax* spp., *Thyonicola* spp., *Gasterosiphon deimatis, Megadenus* spp.). Symbionts from brittle stars mainly inhabit the oral side of the body and arms (*Fuscapex ophiocanthicola, Ophieulima armigeri, Ophieulima fuscoapicata, Ophieulima minima, Ophiarachnicola biformis*). The aim of this study is a description of eulimids diversity from South China Sea.

There were studied more than 3000 specimens from different classes of echinoderms collected in the Bay of Nhatrang (South China Sea) and more than 1500 eulimids were analyzed. Material was collected at depths from 0 to 20 m using SCUBA diving equipment. In some cases, the localization of symbionts on their hosts was observed under water.

As a result 21 species of gastropods from the family Eulimidae were found in the Bay of Nhatrang during several years of echinoderms investigations. Formerly 7 eulimid species were recorded for South Vietnamese waters and only for four of them hosts were recorded. Our results more than doubled the number of eulimids which was previously noted in literature. In our investigations all symbiotic gastropods species were found with their hosts and the most preferred localization of some species was detected.

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## MORPHOLOGY OF GAMETOCYST, OOCYST AND SPOROZOITES OF EXTRAORDINARY COELOMIC GREGARINE *UROSPORA TRAVISIAE* FROM MARINE POLYCHAETE

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Apicomplexans represent a very successful group of unicellular parasites that consists entirely of parasitic species infecting a wide range of vertebrates (including important pathogens of domestic animals and human) and invertebrates. Most of them possess a complicated life cycle, including three different types of reproduction: sporogony, merogony and gametogony. The life cycle of eugregarines, in general, is characterized by a lack of merogony (asexual reproduction inside the hosts), but a presence of syzygy (pregamic paired association of gamonts) and gametocyst stage (syzygy enveloped by a thick protective wall). The internal spaces of gregarine gametocyst represent a space where gametogony (sexual reproduction), fusion of gametes and sporogony (formation of invasive stages) usually take place. The crucial step in infection spreading is formation of sporozoites within a protective envelop (oocyst) during the sporogony. Despite the fact that the way of gametocyst excystation and oocyst morphology are considered as key features in gregarine taxonomy, several detailed studies on terrestrial gregarine species and only few on marine ones dealing with their architecture exist so far. Here we present our investigations on fine structure of gametocysts and oocysts with sporozoites found in marine polychaete *Travisia forbesii* Johnston, 1893 (Polychaeta, Scalibregmatidae). In the host body cavity up to three brown bodies were found. These structures comprised several white spherical objects, which were identified as gametocysts of *Urospora travisiae* Dogiel, 1910. Gametocysts are surrounded with several closely adjacent layers of flattened host coelomocytes, forming a kind of capsule around them (or other foreign objects which also can be found in brown bodies). The thick envelope of gametocyst (up to 6 μm) consists of numerous (10 - 13), closely adjacent membranous layers and a thick hyaline layer with a lot of short circumferential fibrils. Under this envelope, number of oocysts can be seen. The heteropolar spindle-shaped oocyst possesses a transparent conical collar situated at one end, while the other end is elongated in a thin curved tail. Under the scanning electron microscope (SEM), the oocyst surface appears smooth without any spines or folds; only in some cases the collar and the tail at the poles can be observed. In contrast to SEM, transmission electron microscopy reveals the presence of hair-like coating at the oocyst surface. Occasionally, the oocyst wall ruptures during preparation of samples for SEM and up to 8 longitudinally oriented sporozoites can be seen interdigitating in the middle part of oocyst. The ultrathin cross-sections confirm the presence of 4 sporozoites at the both poles, with their apical ends oriented towards the oocyst's poles. Sporozoites appear as banana-shaped and covered with a typical, for apicomplexans, three-layered pellicle consisting of plasma membrane and two membranes of inner membrane complex. The pellicle is underlined by 20 longitudinal subpellicular microtubules, situated at the equal distance at the parasite's periphery. These microtubules pass from the anterior end of the cell towards the posterior one. Sporozoites possess a large nucleus that often occupies their entire transversal section in the cell middle region (or slightly posteriorly to the middle). The peripheral electron-dense heterochromatin of the nucleus is typical for sporozoites of Apicomplexa. Several rhoptries and numerous micronemes are localized in anterior part of the cell. Residual body, situated in between the sporozoites, usually consists of several transparent and dark inclusions. It should be also mentioned that formation of sporozoites in different oocysts within one gametocyst is asynchronous. Our light microscopic observations agree with original description of *U. travisiae* oocysts published by V. A. Dogiel (Dogiel, 1910), however, this study provides completely new ultrastructural data on gametocyst, oocyst and sporozoite of marine eugregarine *U. travisiae* as a model organism for comparison with terrestrial species.

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## INVESTIGATION INTO SPECIFICITY AND STABILITY OF THE SYMBIOTIC ASSOCIATION BETWEEN THE MARINE SPONGE *HALISARCA DUJARDINI* AND BACTERIA

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Sponges play a substantial part in the marine ecosystems in that they pump large amounts of water cleaning it up from organic particles and microbes, which they digest as food source. Along with this, all sponges harbor symbiotic microorganisms.

Great amount of current data on sponge-microbe symbioses originate from the studies of tropical and subtropical species, whereas far less is known about symbiotic associations of the sponges from temperate habitats.

The distribution of the sponge *Halisarca dujardini* (Demospongiae, Halisarcida) is known to be limited to the temperate waters of the North Atlantic and the North Pacific, where it can be found along the coasts from the English Channel to the White Sea to the Barents Sea and in the coastal waters of the Bering Sea, the Avacha Bay and the Japan Sea (Ereskovsky et al. 2011).

*H. dujardini* from different seas host bacterial symbionts of one and the same morphotype which has been shown using transmission electron microscopy, as has been shown the vertical transmission of symbionts in *H. dujardini* from the White Sea – both facts pointing at the specificity of the association (Ereskovsky et al. 2011, 2005).

On that ground we have set up a more thorough investigation into the bacterial symbiosis of *H. dujardini*, our initial task being to compare 16S rRNA sequences from the White Sea sponge specimens.

The alignment of 16S rRNA sequence fragments from four sponge individuals revealed their almost 100% identity. Among 16S rRNA sequence fragments stored in the GenBank databases there were no samples with the homology level exceeding 93%, resulting in a separate clade formed by the *H. dujardini* symbiont on the phylogenetic tree within Alphaproteobacteria.

Of the ten sequences showing the greatest homology with that of *H. dujardini* symbionts three were recovered from the marine sponges *Halichondria oshoro* and *H. okadai* living along the coasts of Alaska and Japan, respectively. The origin of the six remaining sequences is the region of East and Southeast Asia.

Our next step being to determine the 16S rRNA sequences from *H. dujardini* of the other seas and to compare them with those from the White Sea, we would like to test our current hypothesis that the symbiosis in question could have originated in the Pacific and persisted during the subsequent distribution of *H. dujardini.*

## COMPETITIVE INTERACTION BETWEEN *FUCUS SERRATUS* AND *PALMARIA PALMATA*

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Competitive relationships between algae are a critical determinant of the abundance of species, their distribution and biomass of algae communities along with other natural and anthropogenic factors (Paine, 1990). Interspecific interactions can define structured community, the number of species; the contribution of each species in the production of all phytocenosis.In the intertidal zone of the Barents Sea on the lower intertidal horizon can often find association of algae, where the dominant species are *Fucus serratus* L. and *Palmaria palmata* L. (Kuntze). Both species are harvested and have great economic importance. While palmaria is epibionts of fucus, but data on interference between these species are not present. Today we know a number of mechanisms, both positive and negative influence on each other algae (Nabivaylo, Titlyanov, 2006), but all of them are species-specific and general trends are observed weakly. In case the ratio basifit – epiphytic usually manifested competition for resources (the light absorbed by the substance) and the space (Edelsteinetal, 1976; Rytheretal, 1981). Epiphytes thallus inhibit growth of basiphyte by increasing the total mass that is bazifita detachment from the substrate; reduce the overall metabolism using allelopathic compounds, or cases of positive association has some algae on each other (Harlin, 1987; Svirskietal, 1993; Friedlanderetal, 1996). Purpose – to identify morphological and physiological reactions *F.* serratus and *P. palmata* in co-culture.

The study was conducted in August- September 2013. For the work were selected 40 young plants of *F. serratus* and 50 *P. palmate* from the intertidal zone of Murman coast (Barents Sea). Cultivated plants of different species together (experiment), as well as 2 more vessels used the same amount of control. For the experiment used a transparent 3-liter capacity, cultivation of algae conducted 4 weeks termostate room at 8 degrees Celsius, with constant stirring water with a salinity of 30 ppm with water change daily round. At the end of each week at Palmar measured mass and weight except in fucoids also measured the length. At the end of the experiment was calculated absolute growth rate for length and weight, as well as the content of chlorophyll "a" (... plastid pigments, 1964; Chakchir, Alekseeva, 2002). The results further processed using descriptive statistics.

The study found that the rate of growth in seaweeds in the experiment did not differ from that in controls. Probably, the presence of epiphytes does not affect the growth processes of fucus. Intricate layered fronds high speed mineral nutrition and psevdoparenhimnoe structure allows them to assimilate organic and use it on the growth processes, even in the complete absence of visible light (Matishov, Makarov, 2004). Secreted substance *P. palmata* apparently do not affect the general physiological activity of *F. serratus*. Thus, fucus can serve as a substrate for epiphytes, without experiencing adverse effects. This is confirmed by data on chlorophyll content at the end of the experiment. The content of pigments in plants cultivated with the control Palmar same.At Palmar manifested other laws, when cultivated in a place with Bladder growth rates in Palmar significantly higher than in controls. In control of the P. palmata throughout the experiment reduced weight, increased the number of algae secrete mucus. By the end of 4 weeks of the experiment began algae green color, apparently, was the destruction of additional masking fikobilinovyh pigments chlorophyll. Palmaria cultivated with fucus on the second week of the experiment fully acclimated to continue her weight gain was recorded. In addition to the end of the experiment, the chlorophyll content of the control samples was 4 times lower than that of the algae in the experiment. Thus, under the conditions of this experiment *P. palmata*, apparently requires the presence *F. serratus*. In this fucus show no visible reaction to the presence of Palmaria. However, the facts are known as the increase of the growth rate in the presence of fucus algae red algae, and vice versa dense thickets of red algae inhibit the growth of seedlings of *F. serratus* (Brawley, Johnson, 1991). Probably, in this case, *P. palmata* accumulates substances secreted by fucus. Previously mentioned species-specific metabolites, which can not only act negatively to close the growing algae, but also positively (Ferreretal., 1997).

Revealed that in co- cultivation of *P. palmata* has no effect on morphological and physiological parameters of *F. serratus*, but must be present for Palmar basifita.Thus, the experimental results show that among the brown alga *F. serratus* and red *P. palmata* in natural conditions is likely to occur unilaterally advantageous positive interaction – commensalism, in particular kvartiranstvo rather than mutualism as previously assumed.

# REVEALING LIPARID FISH EGG CLUTCH INSIDE THE GOLDEN KING CRAB *LITHODES AEQUISPINUS* BENEDICT, 1895 (DECAPODA, ANOMURA, LITHODIDAE): COMMENSALISM OR PARASITISM?

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The golden king crab, *Lithodes aequispinus,* is a most common representative of decapods, which are widely spread in the northern Pacific from the Pacific sea-shore of the central Japan to the southern part of the British Columbia, including the continental slope of the Okhotsk Sea and the Bering Sea. The main commercial stocks of the golden king crab are located in the northern part of the Okhotsk Sea and their fishing in Russia has been conducted since 1968.

The major gatherings of the golden king crab in the northern Okhotsk Sea are mainly concentrated at the depths of 250–650 m. To a lesser degree crabs are able to penetrate along the continental slope down to 850 m and then go up to 150 m. Chiefly, it is observed in the regions with a narrow shelf and steep drop-offs (western Kamchatka, eastern Sakhalin, Kashevarov Bank). Crabs are distributed as a wide strip and hardly registered beyond the mentioned above isobaths in the areas with gentle sloping.

Liparid fishes are regularly observed in the pot catches among the golden king crab. *Careproctus rastrinus* and *C. marginatus* were registered in the pots more often. Biology of these snailfish remains poorly known. However, they are known to have a special instrument which allow to provide better conditions for eggs development – an extended ovipositor with the aid of which fish deposit eggs into the branchial chambers of lithodid crabs. It is likely that snailfish females reach the crabs from behind and using a rather big space between the back edge of the carapace and abdomen they deposit eggs under the crab's carapace. The eggs deposited into the branchial chambers of the crab are placed in the most favorable conditions for development. They are protected from the predaceous organisms and at the same time they are constantly supplied with oxygen by means of gill movements. Such egg clutches are described in literature for some lithodid species, including golden king crab, but for other habitats. Same relationships between snailfish and crab species inhabiting the northern Sea of Okhotsk are not described in literature. At present there is no definite answer whether such a relationship is parasitism or a type of commensalism (cohabitation).

Comprehensive investigations of the golden king crab ecology were conducted within 2010–2013 years period. More than 15 thousand crab samples were examined. The presence of snailfish eggs were checked up at every crab individual almost on the whole of continental slope area drawn into research survey from 144°00´ to 154°20´E at the depth of 250–750 m. Maximum portion of crabs with *Careproctus* egg clutches inside was 27.7% and 1.3% in average on the whole research area. Crabs with snailfish clutches were observed mainly on the outer edge of the continental shelf, areas of seston-feeders domination where crabs formed feeding clusters.

Liparid clutch were ball-shaped with the diameter of 4–7 cm, containing 4–5 mm eggs at different stages of development. The number of eggs in the clutches (N=44) varied from 149 to 759 making up in average 473±26 eggs. Clutches were registered mainly in male crabs (75%). The carapace width of crab with eggs inside differed from 82 to 183 mm. Maximum number of clutches at one crab did not exceed three. The number of egg clutches depended on the size of a crab. Three clutches were observed in the individual with the carapace width of 150 mm. The more the size of a crab increased the bigger amount of snailfish eggs it had. In most cases clutches located at the left side of crab carapace (64%).

Determination of species affiliation of the eggs is difficult. However, the conducted analysis showed that clutches inside the crab probably belong to *C. rastrinus* according to egg size and gonads maturity stage of this species during the research period. Tissue of some common snailfish representatives (*C. colletti, C. rastrinus, C. roseofuscus, C. macrodiscus, C. marginatus*) occurring on the shelf and continental slope of the North-Okhotomorsk area and samples of eggs deposited in the gill chambers of the golden king crab were gathered for genetic research (in 2013) for more accurate determination of the species affiliation of eggs. As long as the golden king crab inhabits a wide range of depths it is probable that at different depths the liparid species and genera composition depositing their eggs may change.

On the one hand such symbiotic relationships between the golden king crab and snailfish may be called commensalism in the form of cohabitation as it doesn't lead to lethal or serious damage of the crab health. However we observed tissue necrosis at gill filaments under one of the egg clutches. Besides snailfish clutches on the crab gills may adversely affect on the crab oxygen supply. Consequently, basing on the received data concerning the influence of the *Careproctus* species on the golden king crab we may consider these relationships as clutch parasitism.

## SHORT-TERM DYNAMICS OF PERIPHYTIC DIATOM COMMUNITIES ON THE COLONIAL HYDROID *OBELIA LONGISSIMA* (PALLAS 1776)

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Summer is the season of active growth of diatoms on the stems of colonial hydroids inhabiting the White Sea, especially littoral species in the family *Campanulariidae*, which are characterized by large elaborately branched stems covered with hydranths enclosed by hydrothecae. Hydroids feed on zooplankton: food is captured when prey comes into contact with the tentacles of hydranths. This feeding strategy is more efficient in streaming water. As the flow of water around the stems slows down, the number of prey captured per unit of time declines as well.

Diatomic fouling (microepiphyton) undermines the efficiency of feeding in hydroids. As the density of periphytic communities increase, the velocity of water in the area of direct contact with hydroids declines, obstructing the contact of prey with hydranth tentacles.

The process of microepiphytic biofouling overlaps with the hydranths' own development cycles: in the case of *Obelia longissima* the life span of hydranths is short (usually 7–10 days), after which they are resorbed and their hydrothecae fall off, and new hydranths are formed in their place, with hydrothecae not yet colonized by periphyton.

The purpose of the study was to describe the diatomic colonization of the perisarc of large stems of *O. longissima*, taking into account the dynamics of their spatial distribution and possible impact on the life of the hydroid.

At the end of August — beginning of September, the period of hydroids' active growth, two actively branching colonies, 20 cm long each, were selected for observation. Throughout the experiment the colonies were kept in the natural environment, i.e. growing on the lateral surface of a floating platform, submerged to a depth of 0.015 m. Every 24 hours for 10 days in a row the colonies were removed from water and one internode on each of the selected branches was observed, including the hydrotheca, pedicel and segment of the stalk; the distribution of periphytic diatoms was mapped, and division, attachment (immigration) and loss (elimination) of cells were quantified.

To describe the general pattern of periphyton distribution on peripheral branches of a colony of *O. longissima*, it was decided to perform simultaneous count of fouling cells on hydrothecae and internodes of 61 branches with varying numbers of hydranths (between 4 and 10). Comparison of the intensity of fouling on the top ten hydrothecae of a stem demonstrated that fouling processes are most active at 3–5 hydrothecae proximal from the tip of the branch, and less pronounced those closer to the base of the branch. Accumulation of diatoms is more rapid on the perisarc of hydrotheca than on the pedicels and stalk. It is caused by increased water circulation activated by moving tentacles. It was also established that the species composition of periphytic communities is dominated by *Synedra* and *Licmophora*.

Settling begins on the third day after the stem internode and the hydrotheca that crowns it are fully formed. Maximum rate of microepiphytic biomass increase is observed on the 6–7th day on internodes and on the 5–6th day on hydrothecae, and is mainly due to cell division and to a lesser extent to immigration. Peak biomass is observed on the 7th day after organ formation on stems, and on the 6th day on hydrothecae.

This is followed by bulk elimination of diatom cells on the 7th day on hydrothecae and on the 8th day on internodes. Resorption of hydranths is observed around the same time. The regeneration cycle of hydrothecae does not affect their pedicels and the perisarc of internodes. Population decline on the internodes is due to sloughing off of larger colonies (>4 cells) of *Synedra* and *Licmophora*, which are characterized by higher drag — only one cell is left of each colony. Epiphytes growing on hydrothecae are eliminated by virtue of hydrothecae themselves being lost.

Less abundant secondary fouling is observed on the 9th day on internodes and on the 10th day on hydrothecae (on newly formed 'cups'); it is associated with the division of residual cells on the internodes (to a lesser extent — by immigration), the availability of space on newly formed hydrothecae, and the proliferation of newly settled cells.

It can be concluded that biofouling of *O. longissima* occurs along the margins of the colony, affecting the distal parts of peripheral branches.

# INDIRECT EFFECTS OF THE INVASIVE PACIFIC OYSTER REGULATE THE POPULATION STRUCTURE OF BLUE MUSSELS

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Species invasion is of increasing concern as non-native species often have negative impact on ecosystems, which they were introduced to. Invaders negatively affect the abundance of native species due to direct interactions like predation and competition. Additionally, invaders may benefit native biota by imposing indirect effects on resident species interactions. Habitat modifying species can serve as initiators of nontrophic indirect interactions that, like trophic pathways, can involve both density-mediated indirect interactions (DMIIs) and trait-mediated indirect interactions (TMIIs). Most studies dealing with TMIIs often implicitly assumed that all individuals within a population display trait changes with the same order of magnitude. TMIIs within size-structured populations may vary strongly with the size of individuals. Here, we experimentally demonstrate that an invasive habitat modifying species of European coastal waters alters the population structure of native blue mussels (*Mytilus edulis*) by modifying the size specific predator-prey interaction between the mussels and the shore crab (*Carcinus maenas*). In laboratory split-plot experiments, the presence of Pacific oysters (*Crassostrea gigas*) mitigated the mortality of unconditioned mussels as well as mussels that were acclimatized in presence of predatory cues, while being endangered to predation by crabs of two different size classes. The reduction in mortality was size-dependent of both the predators and the prey. Oyster presence most notably reduced mussel mortality in presence of small crabs, while the mortality rate in presence of big crabs was much less affected by the introduction of oysters. Mussels that mostly did profit by the presence of oysters were the ones of the recruitment stages, smaller than 20 mm in shell length. Our results suggest that oysters cause a strong shift in the population structure of *M. edulis*, reducing particularly the mortality of smaller sized mussels.

# BORED TO DEATH: EFFECT OF THE PREDATORY WHELK *BOREOTROPHON CLATHRATUS* ON THE BARNACLE *BALANUS CRENATUS* IN THE WHITE SEA SHALLOW SUBTIDAL

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Facilitation can amplify the effect of predation on community structure: a predator affecting a foundation species would indirectly alter the dependent assemblage. The acorn barnacle *Balanus crenatus* is a principal foundation species in the White Sea shallow subtidal. The clusters one develops on shells and gravel regularly contain empty barnacle shells (hereafter "dead barnacles") remaining after their death. According to our field observations near Solovetsky islands (the White Sea), 8% of dead barnacles had through perforations of unknown origin. Incomplete perforations (likely the traces of failed attacks) were also frequent on both live and dead barnacles. The only locally common species potentially capable of boring holes in prey shells was a whelk *Boreotrophon clathratus* of completely unidentified feeding habits. In a field experiment we manipulated the density of the whelks to assess their effect on barnacles. We exposed the cages with initially live barnacle clusters at the 12 m depth for a year. Treatments included full cage whelk enclosures and exclosures, partial cages and open cages. Each cage contained about 50 adult *B. crenatus* in 2–3 clusters with the addition of 8 adult *B. clathratus* in predator enclosures. Presence of the whelks severely increased the mortality of barnacles (excluding recruits), which was 2% in full cages (exclosures), 4% in open cages, 6% in partial cages and 37% in predator enclosures. The proportion of perforated shells in dead barnacles was 0%, 42%, 67% and 91% correspondingly. Since empty barnacle shells attract markedly different sessile and motile macrobenthic fauna than live barnacles, predation by *B. clathratus* would show up in changing the whole dependent assemblage of this foundation species.

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# *Marine communities and food webs*

## GLOBAL CHANGE, ZOOPLANKTON SHIFTS, AND C, N AND P CYCLES IN THE SOUTHERN OCEAN

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The transfer of matter and energy from autotrophs to upper consumers in the Southern Ocean is essentially controlled by two groups of zooplankton, krill and salps. While krill (mainly *Euphausia superba*) is almost the unique food source for Antarctic fish, birds and mammals, salps (*Salpa thompsoni*) are of very indifferent nutritious value. Salps play a role at least as important as krill in the carbon cycle, filtering and packing biogenic carbon into larger and heavier faecal pellets than krill, accelerating the vertical flux of matter towards the long-lived and even sequestered carbon pools. Both groups show huge temporal and spatial fluctuations, with the alternation of krill-dominated and salp-dominated years. At the same time, the continuous decreasing trend of krill populations along the last forty years has lead to predict a shift in Antarctic ecosystems, with the global substitution of krill by salps. The drivers of the change are not clear, but warmer temperatures, the extension of sea ice, and the decimation of whales appear as the most probable sources. Another consequence of the high warming rates in some Antarctic areas would be the reduction of the individual biomass spectrum. Under these conditions, not only the populations depending of krill as food source will be severely threated, but the removal rates and fate of biogenic carbon, and the regeneration rates of nutrients by zooplankton excretion would change. In order to ascertaining the possible consequences for the cycling of biogenic carbon and the stoichiometry of regenerated nutrients of the predicted zooplankton shifts in the Southern Ocean we estimated the metabolic carbon requirements and inorganic N and P excretion rates of three major zooplankton groups in the Southern Ocean in the vicinity of the Antarctic Peninsula in February 2009. The carbon respiratory demands and $NH_4$-N and $PO_4$-P excretion rates of < 5 mm size copepods, krill (adult *E. superba* and *E. crystalloropias* and furcilia spp) and salps (blastozoids of *Salpa thompsoni*) were estimated by incubation experiments. The carbon-specific metabolic rates and N:P metabolic quotients of salps were higher than those of krill (*Furcilia* spp. and adults) and copepods. There was also a negative relation between average individual zooplankton biomass and their metabolic rates, each metabolic process showing a particular response that leaded to different metabolic N:P ratios as a function of individual biomass. The predicted zooplankton shifts in the Southern Ocean would therefore encompass not only the substitution of a pivotal group of Antarctic food webs (krill) by one of low nutritive value (salps). In a zooplankton community dominated by salps and of reduced individual size (biomass) there will be an increase of the zooplankton metabolic carbon demand and therefore of the proportion of primary production that should be allocated to compensate for zooplankton respiratory C-losses. At the same time, the production by salps of larger, faster sinking faecal pellets will increase the sequestration rate of biogenic carbon. Regarding the changes in excretion rates and N:P stoichiometry of the metabolic products by zooplankton, the characteristics of the dissolved nutrient pool could be modified, accelerating the changes on the functional and structural properties of primary producers (i.e., from diatoms to haptophytes) that would accelerate the change for the whole Antarctic ecosystem.

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## TRANSPORT OF THE ELEMENTS THROUGH THE FOOD CHAINS IN THE WHITE SEA ECOSYSTEM: AN EXPERIMENTAL APPROACH

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Organic matter plays a significant role in trace metal's migration through the ecosystems (Monin, Lisitsyn, 1983). Biogenic migration mechanisms are based on the uptake of phytoplankton (diatoms, dinoflagellates, etc.) of dissolved trace metals from aqueous phase and their accumulation in the cells, thus transferring the dissolved substance into particular matter. Feeding on the phytoplankton and other suspended particles, zooplanktons actively ingest them and then transfer into the fecal pellets, which, in turn, deposit on the marine bottom at the high accumulation rates (Lisitsyn, 2003). The organism ability to accumulate elements is widely used for biomonitoring (Saenko, 1992; Szefer, 2002). Nevertheless, the data on the transfer of trace metals through the food chains in the marine ecosystems, including the White Sea, are lacking.

The experiments were carried out at the laboratory of the White Sea Biological Station of Zoological Institute of the RAS in June 2013 (Cape Kartesh). The research was conducted in conditions close to natural (without adding the artificial salts). We have used "conditionally polluted" food (sampling site was nearby the source of anthropogenic pollution) and "conditionally unpolluted" customers (sampling point is natural ecosystems).

The seston sampled close by Chupa settlenet ("polluted" area) was characterized by the elevated concentrations of all the studied elements comparing to the "unpolluted" seston (Cape Kartesh). The concentrations of the elements refer to the line Pb<As<Ni<Co< Cr<Cu<Fe<Mn<Cd<Zn. Similar pattern was observed for the zooplankton, when the concentrations of the trace metals were higher in the animals collected in the "polluted" area. The concentrations of the elements in the zooplankton refer to the line Ni>Cr>As>Co>Mn>Fe>Pb>Cu>Zn>Cd.

In the experiments, the zooplankton accumulated the pollutants actively during the exposure period (24—48 h), particularly Ni, Cr, As, and Co, which referred well to the concentrations of these elements in the seston. However, Pb was not accumulated so actively. The accumulation rates of the elements were: Fe – 65.25; Ni – 4.88; Zn – 2.51; Mn – 2.03; Cu – 1.32; Pb – 1.21; As – 0.54; Cr – 0.07; Co – 0.05; Cd – 0.01 μg/g DW $h^{-1}$.

The zooplankton sampled close by Chupa settlement, was characterized by the elevated concentrations of Fe, Mn, Cr, Co, Ni comparing to the zooplankton sampled nearby Cape Kartesh. Generally, the zooplankton accumulated only the insignificant part of the total bulk of the element income to their organisms with the food. The most of the ingested elements leave the zooplankton in the pellets. We did find significant differences in accumulating the elements in the pellets originated from the "unpolluted" zooplankton feeding on "polluted" seston to the pellets (1) that were obtained from the "unpolluted" zooplankton feeding on "unpolluted" food (2), particularly, Fe, Co, Ni, Pb, and Mn were of the highest concentration in the treatment (1), the concentrations of Cu and Cd were similar, but Cr, Zn, and As accumulated mostly in the pellets originated from treatment (2). The rates of non-assimilated trace metals were 71.88% (Zn); 23.17% (Mn); 93.96% (Cu); 59.28 (Pb); 98.97% (Cr); 76.96% (Co); 31.78 (As); and 61.42% (Cd).

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## THE ROLE OF THE INVASIVE BIVALVE *ANADARA KAGOSHIMENSIS* IN CONTEMPORARY STATE OF THE NORTHEASTERN BLACK SEA COASTAL BIOCENOSIS

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Bivalves play significant role in the Black Sea coastal biocenosis, on soft substrata they form 12 communities from 16 described (Kiseleva, 1981). Thus, any change in the species composition and structure of bivalve's assemblages will have a visible impact on the benthic community in general. During the last quarter of the XX century benthic community structure was heavily impacted by the carnivorous gastropod species *Rapana venosa* in addition to the invasive ctenophore *Mnemiopsis leidyi* (Shiganova et al., 2008). *Mnemiopsis* predation on bivalve larvae restricted the settlement of young bivalves, whereas adult bivalves were consumed by the predatory gastropod species *Rapana*. As a result, during the 1990-s a serious degradation of macrozoobenthic communities was observed. One of the dominant species became the invasive Indo-Pacific clam *Anadara kagoshimensis*, which competed for food (filter-feeder) and space with native species. (Chikina and Kucheruk, 2005). This study, made on the base of prolonged data collection (2001–2005, 2007 and 2012), is focused on the long-term variability of *A. kagoshimensis* assemblages and its role in contemporary structure and dynamics of coastal bottom communities. Sampling was carried out in the northeastern part of the Black Sea. During every survey it was made 5 stations at depth range from 10 to 35 m, at each station five grabs "Ocean" with sampling area 0,1 $m^2$ were taken. The data were analyzed using univariate and multivariate statistics (the PRIMER software package). Abundance comparison analyses were used in order to assess the recruitment and fluctuations in the quantity of bivalves during the investigated periods. The results of analyses showed that total number of species in the investigated area fluctuated without a clear trend, though diversity (Shannon-Wiener's *H*), and evenness (Pielou's *J*) increased with time. While some taxa exhibited small to moderate changes (e.g. the polychaetes, crustaceans) bivalves varied greatly. In addition to temporal changes in density, several of the dominant bivalve species also exhibited shifts in distribution. During all aforementioned periods two separate groups were clearly distinguished according to the depth: 10–15 m and 20–30 m. And while in the depth range 10–15 m we observed the slow recovery of the community structure after the mass recruitment of *C. gallina* (registered in 2001), deeper, *Anadara kagoshimensis* was dominating during 2001-2004, and former dominants – *Chamelea gallina* and *Pitar rudis* were pushed aside to the borders of the community (less than 20 m for *Chamelea* and deeper than 30 m for *Pitar*). But the data obtained in 2005, 2007 and 2012 showed that the density of *A.kagoshimensis* fell down significantly, whereas *C. gallina* and *P. rudis* share was increasing during this time period. The mean size of *A.kagoshimensis* at 20–30 m also decreased 10-fold after 2004. *C. gallina* size and population density did not change significantly from 2004, *P. rudis* size was lower in 2005-2007, but in 2012 was equal to 2004 values, and from 2004 to 2012 its density increased 10-times. The parallel 4–6-fold decrease of *Rapana venosa* density and biomass was observed in 2005, 2007 and 2012. We suppose, that one of the mechanisms influencing competition among bivalve species and altering local community structure is *R. venosa* clear feeding preference for the invasive *A. kagoshimensis,* as it was shown previously in a caging experiment in natural environment in the Northern Adriatic Sea (Savini, Occhipinti-Ambrogi, 2006). Thus, in the northeastern part of the Black Sea selective predation plays an important role in regulating the population of the bivalves, weakening the competitive pressure of the alien *A. kagoshimensis* on other bivalve and supporting the re-colonization of the habitat by native species.

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## SIMULATING EFFECTS OF SPATIAL BASED MANAGEMENT OF TRAWLING FISHERIES USING THE NEW MODEL SMART: THE CASE OF DEEP WATER ROSE SHRIMP AND HAKE IN THE STRAIT OF SICILY

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The Strait of Sicily is one of the main productive areas for demersal fisheries in the Mediterranean, being deep-water shrimps (DPS) the main target species. DPS, together with other species among which the Hake (HKE) is the most important by-catched species in weight, is fished exclusively by bottom otter trawl. According to the available stock assessments presented at the General Fisheries Commission for the Mediterranean (GFCM), both species are in overfishing, due to both high fishing mortalities and poor exploitation pattern, being the HKE in a worst state. Considering the fine mesh size used in shrimp fisheries, the protection of stable nurseries was repeatedly proposed as an effective measure to improve the status of exploited stocks in the Mediterranean. The knowledge of areas where the recruits are stably more concentrated during the years, together with the availability of a new predictive model (called SMART), which combines information from scientific surveys, commercial catch and fleet behaviour, allowed us to assess the effectiveness of nurseries protection on stock status of DPS and HKE under different management scenarios. Taking into account the stock assessment advice of GFCM on the DPS stock in the Strait of Sicily, the tradeoff between yield and gains of fishery and biomass at sea of stock was investigated. Aiming to improve the exploitation pattern of the investigated species optimal strategies for selective reduction of fishing effort on spatial bases were investigated. The combination of the reduction of fishing effort with nurseries closures was the best approach to move the stocks toward more sustainable state.

## TROPHIC-FUNCTIONAL ANALYSIS OF POLYCHAETA SYNTAXON IN THE AREA OF MARINE TERMINAL FOR RE-GASIFYING LIQUEFIED NATURAL GAS (LNG) IN THE NORTH ADRIATIC SEA

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The first offshore LNG Terminal in Italy and the first in the world Gravity Based Structure (GBS) for unloading, storing and regasifying liquid gas was realised in the North Adriatic Sea. The Institute for Environmental Protection and Research (ISPRA, formerly ICRAM) elaborated and carried out a multidisciplinary monitoring plan according with the environmental prescriptions, given by the Italian Ministry of the Environment at verifying possible impacts on marine environment associated to the project. ISPRA carried out monitoring activities both before the installation of the structure and during construction and production phases. Five campaigns were carried out: one before the laying of the terminal (June 2006), one during the laying of it (October 2008) and three afterwards (September 2010, July 2011, July 2012). Trophic-functional analysis together with univariate and multivariate processing of soft-bottom Polychaeta assemblages were performed to evaluate possible effects due to the installation and activities of

LNG Terminal. Multivariate analysis showed slight similarities between campaigns of July 2011 and July 2012. Polychaeta assemblages showed slight changes during campaigns carried out after the installation, as a large number of deposit feeders and burrow feeders increased, compared to previous campaigns. Trophic analyses of Polychaeta syntaxon, particularly suitable to categorization analysis, allow us assuming real impact didn't occur on this macrozoobenthic component due to the LNG Terminal.

## MACROZOOBENTHOS OF BABIE MORE INLET (THE WHITE SEA)

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Babie More Inlet is unique large shallow water lagoon separating from Kandalaksha Bay of the White Sea. The lagoon is about of seven kilometers across and it has the area is of 40 square kilometers. The lagoon is protected as a part of the Kandalaksha State Natural Reserve.

The inlet has two shallow sills at the entrances and several depressions in the inner part. The northern sill is less than one meter depth while the southern one is about 7 meters in the channel. The water exchange with the open part of the White Sea is restricted by these sills. Due to rapid postglacial crust elevation the depths of these sills tend to reduce with the time followed by correspondent reduction of water exchange. Several depressions in the central basin of inlet approach the depth of 23 m in the south part and over 38 in the north, separated by shallows of 5 – 10 m. Low water exchange with open sea and complicate bottom relief caused significant water stratification in the hollows of the inlet in summer. Prominent thermo- and halocline divides the water column by two layers at the depth of ca. 10–15 m. The upper layer is variable by thermal and salinity conditions. In mid-summer it has a temperature over +16°C and salinity of 22–24 psu, the deep layer contain cool and saline water (temperature is below zero and salinity about 27 psu).

This hydrological conditions and remaining the cold «winter» water in the hollows account for presence of the Arctic fauna on relatively low depths. Despite widespread presence of this type of reservoirs in the White Sea, not all of them are fairly well understood in the hydrological and ecological aspects. The aim of this work was to study the current state of macrozoobenthic communities of Babie More Inlet and compare the data with earlier researches (Gurvich, 1934, Brotskaya et al., 1963).

The present study is based on material collected on 22 benthic stations (with two replicates each) in July 2013. Samples were taken with Day grab (sampling area 0.1 m$^2$) at the depths ranged from 5 to 31 m. Samples were processed and analyzed partly by students of the Biological faculty of M. V. Lomonosov Moscow State University during the summer practices and by zoologists of the White Sea Biological Station of Zoological Institute. Sampling grid was planned on the basis of bathymetric and sonar studies and in relation to sediment composition evaluated by sedimentological sampling.

Totally 92 macrobenthic species were found in samples. Mean local diversity is 10–15 species per station and decrease with the depth. According to species composition and dominance structure two types of communities are present in benthos at these depths. In the shallow water zone at the depths 5–13 m the community is dominated by *Alitta virens* – large predatory polychaete. Mean biomass is 56.84 g/m$^2$. Among 45 species living there most (ca 85%) belongs to boreal by origin. Deep water complex occurs at depths 11–31 m, the dominant species there are *Portlandia arctica* and *Minuspio cirrifera*. Mean biomass is 16.6 g/m$^2$. Totally 44 species were found there with strong prevalence of arctic species (46%). Outlined communities are well separated with high level of similarity within the stations of each type and low similarity levels between them.

Comparison with previous studies evaluates the remarkable stability in hydrological structure of the inlet and significant changes in communities' composition and structure during last 80 years (Gurvich, 1934, Brotskaya et al., 1963). This work provides insight into the current state of the Babie More macrozoobentos communities and their temporal dynamics. Inlets of this type are unique, and the conditions hindered water exchange makes it extremely vulnerable. Such semi-isolated inlets are of theoretical interest as a model for the study of the evolution of shallow water benthic communities due to geological and hydrological changes.

## COMMUNITY COMPOSITION IN REDOX ZONE OF SALT LAKES SEPARATING FROM THE WHITE SEA

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Because of postglacial isostatic uplift with an average speed of 32 cm per century, many of the White Sea bays are separated gradually from the sea. At the intermediate stages, usually the meromixis is observed. At the boundary of aerobic and anaerobic layers there is of 10-50 cm thick redox zone colored in green or red with sharp physical and chemical gradients. The green layer caused by development of green phototrophic sulfur bacteria was found in three reservoirs that are further advanced in isolation from the sea. The red layer due to blooming of cryptophyte algae *Rhodomonas* sp. was found in three water bodies with regularly seawater inflow.

Large amount of unicellular and multicellular heterotrophic organisms often develop in the redox zone. To identify the organisms we used a molecular genetic approach. Total DNA was extracted, 18S rRNA gene amplified, PCR fragments were purified, extracted using the MinElute Gel Extraction Kit (QIAGEN) and cloned into the vector pTZ57R/T.

Two infusorian species were identified, one heterotrophic protozoan from Cercozoa group, and one cryptophyte algae species. First ciliate species found in the lagoon at Green Cape shows 99% similarity by 18S rRNA gene with *Euplotes elegans* (GenBank No DQ309868) from Mariager Fjord (Schwarz et. al., 2007) and from the fjord Framvaren EF527105; 18S rRNA sequence of another ciliate species from the lagoon on the Zeleny Cape and lake Trekhtzvetnoe has 99% similarity with uncultivated marine eukaryote (EF527105 and DQ103855), and 98% similarity with *Prorodon teres* (X71140.1). Partial sequence of 18S rRNA gene of the heterotrophic protozoan from group Cercozoa found in the Lake Elovoe has high sequence similarity with an uncultivated Cercozoa (FN263034, JQ226494.1) from oxygen-deficient zone in northeast Pacific and JN090864.1 from freshwater lake Karl in Greece (Oikonomou et. al., 2012). The nucleotide sequence of *Rhodomonas* sp. from the lake Kislo-Sladkoe and lagoon at Zeleny Cape has 99% similarity with the strain *Rhodomonas* sp. RCC2020 (JN934672) isolated from the deep chlorophyll maximum in Beaufort Sea at the depth of 40 m.

Bloom of unicellular algae *Euglena* sp. was discovered in the chemocline of Lake Trekhtzvetnoe in February 2014, and massive development of heterotrophic dinoflagellates *Oxyrrhis marina* was revealed in the lagoon at Green Cape at September 2012.

The resulting list of species allows outlining some features of community. At the basis there are different mixotrophic organisms (*Rhodomonas*, *Euglena*) capable of photosynthesis as well as of organic matter nutrition. It is important for adaptation to environment with hydrogen sulfide and big amount of bacterial mass as a potential food source. Three other detected organisms are predators able to comsume large cells of algae as well as to phagocytize bacteria. Ciliates *E. elegans* are resistant to oxygen deficiency. The enzyme system of *O. marina* allows it to live in the absence of oxygen (Altenbach et al., 2012).

## MICROBIAL COMMUNITY STRUCTURE OF TWO ANCHIALINE CAVES ON MLJET ISLAND (ADRIATIC SEA)

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The microbial abundances, including bacteria, viruses, and heterotrophic nanoflagellates, was determined for two anchialine caves located on the Island of Mljet (Adriatic Sea): Bjejajka Cave and Lenga Pit. Both caves are situated approximately 100 m from the coast with extensive subterranean connections to the sea, resulting in noticeable marine and terrestrial, influences. Because of the shallow settings of the studied caves, they represent habitats with a minimal light or complete darkness where photosynthesis is minimal or not possible. Thus, during the surveys there was no evidence of cyanobacterial cells in either caves, but the presence of bacteria, viruses and heterotrophic nanoflagellates (HNF) was established. Further, bacterial abundance was higher in caves in comparison to surrounding open seawater. In the surrounding seawater the predominance of the LNA group over HNA is determined, which also indicates the differences in relation to the studied caves. In fact, the dominance of HNA group of bacteria in caves together with higher total bacterial abundance indicates that the caves are of higher trophic level than the surrounding seawater. With regard to bacterial diversity, both caves had a unique makeup of bacterial populations and low diversity, with the chemolithoautotrophic *Epsilonproteobacteria* representing the most abundant taxonomic group. To examine the mechanisms regulating bacterial abundance in these habitats, we observed the relationship between bacteria and heterotrophic nanoflagellates (HNF) and between bacteria and viruses. The importance of predation in controlling bacteria (top down control) and, consequently, the domination of bottom up control of HNF were observed in both caves.

## SUSPENSION AND DEPOSIT-FEEDING SEA CUCUMBERS AS EXTRACTIVE SPECIES IN CANADIAN OPEN WATER INTEGRATED MULTI-TROPHIC AQUACULTURE (IMTA) SETTINGS

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Integrated multi-trophic aquaculture (IMTA) is a technique whereby both inorganic extractive species (*e.g.* seaweeds) and organic extractive species (*e.g.* bivalves) are grown in close proximity to traditional fed finfish culture to utilize some of the waste products (soluble inorganics, excess feed and faeces) and reduce environmental impacts. There are many challenges associated with selecting the most appropriate extractive species given the differences in oceanographic conditions, culture techniques and limited knowledge available on the ecology of the species being considered. The orange footed sea cucumber (*Cucumaria frondosa*), a suspension feeding species on the east coast, and the California sea cucumber (*Parastichopus californicus*), a deposit feeding species on the west coast are being evaluated as potential organic extractive species in their respective IMTA settings in Canada. It is their different feeding ecologies and behaviours that present unique challenges and opportunities in assessing their value as a mitigative species. This includes developing new techniques and designing equipment for both species to measure their feeding and defecation characteristics in the laboratory and the field. When exposed to the assemblage of natural particles in the environment ranging in organic composition from 30 to50% *C. frondosa* is capable of absorbing the material with an average efficiency of 70± 3 %. When *C. frondosa* is exposed to particles of higher organic content (>60%) such as salmon food and faeces their absorption efficiency (AE) can be elevated above 80%. When exposed to natural sediment with a relatively low organic content (1.6%), *P. californicus* exhibits a relatively low AE of approximately 24%. This value nearly doubles to ~45% when it is fed an organically-rich (86.8% organic content) diet of sablefish faeces. As with other Holothuroid species, both *C. frondosa* and *P. californicus* show elevated AEs with increasing organic content of the feed. Field trials with *P. californicus* have shown that the species can reduce total organic carbon and total nitrogen levels underneath a commercial sablefish farm by an average of 60.3% and 62.3%, respectively, showing its usefulness in reducing organic levels underneath fed finfish in an IMTA setting. Both and *C. frondosa* and *P. californicus* have a great deal of potential as organic - extractive species in the local IMTA setting based on the efficiency of absorption of waste particles and the reduction in organic content levels in field trials with finfish. Ongoing studies with the former species are identifying the quantity of material being removed from the water column and deposited on the bottom.

## ZOOPLANKTON COMMUNITIES OF THE SCOOP-TYPE INLETS OF THE WHITE SEA IN REGARD TO THEIR HYDROLOGICAL STRUCTURE

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Zooplankton communities of the White Sea are characterized by the combination of the species of different biogeographical origin (Atlantic and Arctic). The seasonal dynamics of the vertical distribution of the certain species depend highly on the temperature preferences of the species, food availability, and, as a result, their life cycle strategies. The vertical structure of the zooplankton communities is well studied for the open and neritic areas of the White Sea for a long time period; however, small scopp-type inlets did not receive much attention so far. We have studied the seasonal dynamics of the vertical distribution of the zooplankton species in regard to the environment in Nikolskaya Inlet in 1999 (ice-free period) using "classical" methods of hydrology and have performed a targeted study of the correspondence of the zooplankton in regard to fine *T, S*-structure of the water column in Babye More Inlet in July of 2013, when a new sampling approach was applied to collect the zooplankton. Both studies evidence on a specific hydrological regime in the scoop-type inlets resembling the model of the "deep sea" (Kandalaksha Bay and Basin) during the summer period. We argue that relatively shallow (less than 60 m), but isolated scoop-type inlets may serve as the secondary pools maintaining the vertical structure of the zooplankton community through the year as it is observed for the deep areas of the White Sea (200–340 m).

## SYNECOLOGICAL ASPECTS OF *ONCAEA VENUSTA* AND *ONCAEA MEDIA* (CRUSTACEA: COPEPODA) IN THE COLOMBIAN PACIFIC OCEAN

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Although the small planktonic copepods (< 1 mm) are the most abundant metazoans on Earth, and their essential position in marine food webs is recognized, this community has been poorly studied in Colombia. Seeing that *O. venusta* and *O. media* were predominant within the copepod community (60 species) in June-July and August-September 2001 in the Colombian Pacific Ocean, their distribution and abundance were evaluated. Zooplankton samples were collected at the surface with a conic net (50 cm opening, 303 µm mesh) and the copepods extracted from subsamples of 10 ml. In general terms, both species were widely distributed and showed the highest average abundances in neritic waters in the first period and in oceanic waters in the second one. Salinity and temperature had some influence on their horizontal distribution, and light on vertical migration, since higher abundances were registered by night, full moon and last quarter. Phytoplankton seemed not to be very significant for *O. venusta* and *O. media*, but in further analysis it is necessary consider their feeding ecology, their role as prey for predators at higher trophic levels, and aspects of reproductive biology which allow sufficient reproductive success to counter predation losses. Variations between the two periods were due possibly to these factors and changes of hydrographic conditions. During this study, a weak La Niña event occurred in Ecuador and *O. venusta* was the predominant species mainly near the Galapagos Islands.

## SEASONAL CHANGES IN MEIOBENTHOS COMMUNITIES: COMPARISON OF TROPICAL AND ARCTIC TIDAL FLATS

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Seasonal changes of quantities of all meiobenthos groups are well known for temperate and polar regions. However, seasonality in abundances is typical for tropical intertidal also. Seasonal studies were undertaken on the White Sea intertidal zone and in mangrove intertidal in Red River delta (Vietnam). Prominent seasonal variations were found in every meiofaunal taxa in both regions. Samples in Red river delta were taken in three localities on muddy intertidal with *Kandelia candel* (L.) vegetation. One sample series were collected inside mangrove bush, the second on the border of mangroves and the third on the open tide flat. On the White Sea two transects across intertidal zone were collected seasonally on high energy beach composed by coarse to medium sand and in the sheltered muddy intertidal. In all sites and seasons nematodes are the most abundant group followed by harpacticoid copepods. Other meiobenthic groups including annelids, tardigrades, ostracods, gastrotrihs etc were much less abundant. Significant seasonal changes occur in every taxon in all sites of both regions. On the White Sea intertidal minimal values occur in mid-winter (January) and metazoan abundance increases already in early spring (April) despite of ice coverage on the intertidal. On the Red River stations maximal metazoan abundance was record in spring (April), lowest values registered in January in mangrove sites and in November on the open flat. Seasonal trends of nematodes and harpacticoid copepods were different. Maximal nematodes density appears in Spring and Summer while harpacticoids were more numerous in Winter time (at least at two stations form three). By magnitude temporal variability on the White Sea stations approaches two orders for nematodes and one for harpacticoids. In Red river sites nematodes max to min ratio was up to six, for harpacticoids it approaches two orders of magnitude. Meta-analysis of literature data exhibits high seasonal variability both in tropical and polar tidal zones. Seasonal changes occur in most of investigated areas at all latitudinal zones. Factors which are responsible for seasonal changes in meiobenthic associations are discussed.

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## TWENTY-SEVEN-YEARS-LONG DYNAMICS OF BIOMASS IN FOURTEEN BENTHIC SPECIES FROM TWO SITES AT THE WHITE SEA INTERTIDAL

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Intertidal communities from two small muddy-sandy White Sea bights located in a distance of 2 km from each other were monitored during 27 years (1987–2014). Four surveys were carried out annually every hydrological season at four sampling stations in each bight, three samples of 0.015 $m^2$ at each station.

For 14 species of about 100 found, material obtained was sufficient for further analysis: *Tubificoides benedeni* (Udekem, 1855), *Capitella capitata* (Fabricius, 1780), *Phyllodoce maculata* (Linnaeus, 1767), *Pygospio elegans* Claparède, 1863, juveniles of *Arenicola marina* (Linnaeus, 1758), *Scoloplos armiger* (O. F. Müller, 1776), *Jaera albifrons* Leach, 1814, *Chironomus salinarius* Kieffer, 1915, *Halocladius vitripennis* (Meigen, 1818), *Hydrobia ulvae* (Pennant, 1777), *Littorina saxatilis* (Olivi, 1792), *Macoma balthica* (Linnaeus, 1758), *Cladophora sericea* (Hudson) Kützing, 1843 and *Zostera marina* Linnaeus, 1753.

Trends in dynamics of biomass were extracted by eigenvector filtering (SSA). Seven different patterns of seasonal dynamics were discovered. In most cases, minimum biomass was encountered in spring, while maximum one in autumn.

Long-term trends of biomass in most individual species from both bights were different. Since oscillations of main abiotic factors in neighbouring bights are similar, biotic interactions in local communities should be used for explanation of this phenomenon.

In the first bight, main trends of biomass in deposit feeders *Tubificoides benedeni*, *Jaera albifrons* and *Macoma balthica* followed main trend of dynamics of *Cladophora sericea* with a lag of 2–4 years. It can be interpreted as trophic interactions since this annual alga is an important source of detritus at the White Sea intertidal.

More complicated processes were observed in the second bight. In the beginning of 2000-s, main trends of biomass in *Zostera marina*, *Chironomus salinarius*, *Halocladius vitripennis* and *Phyllodoce maculata* increased at least twice for a relatively short period. Biomass of *Cladophora sericea*, *Tubificoides benedeni* and *Jaera albifrons* increased as well almost simultaneously, but it is still high up to now. It is probably enough that increasing of seaweeds prevented washing out of *Cladophora sericea* thalli from the bight causing upgrowth of deposit feeder's biomass.

## MACROZOOBENTHIC ASSEMBLAGES ASSOCIATED WITH *SACCHARINA LATISSIMA*: THE INFLUENCE OF HYDRODYNAMICS

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Kelp forests are common in a shallow subtidal and occur in the wide range of hydrodynamic conditions. In the White Sea *Saccharina latissima* quite often forms monodominant assemblages, and in the two of them located at straits with low and high current velocity we studied the structure of macrozoobenthic assemblage confined within haptera of *S. latissima* (hereafter "CH") as well as that one formed within surrounding sediments (hereafter "CS"). We aimed

i) to test how large are flow-driven variations in the community structure of CH,

ii) to estimate heterogeneity in the structure of CS according to the distance gradient from haptera, and

iii) to assess whether interannual changes in community structure of CH and CS are significant.

The material was collected by SCUBA diving in August in 2009–2011 and in June – August in 2012 in the Kandalaksha Bay (White Sea) at two sites. Both of them had the same depth (4–5 m) and salinity (midsummer bottom-water salinity was 23ppt) but different current velocity: up to 0.5–0.7 m/sec (hereinafter «Site 1») and less then 0.05–0.15 m/sec (hereinafter «Site 2»). Each set of samples was arranged in a small transect including individual of *S. latissima* (with a stone) and three sediment samples (S=1/182 sq. m) disposed in a row along main current direction, first one near the stone and others at 10 cm distance from each other. One additional sediment sample (S=1/182 sq. m) near each transect was collected to estimate particle size distribution and organic matter content. We used principal component analysis to reveal patterns of spatial distribution of macrozoobenthos and in 2009 the influence of two factors was recognized, first one explained 17.4% of variance and the second one – 8.1%. Haptera samples from both sites were grouped together while sediment samples from Site 1 and 2 formed independent groups. High positive correlation was revealed between Factor 1 loadings and current velocity (Pearson, 0.81, $p<0.01$). We interpreted Factor 1 as "flow rate or sediment grain size" and Factor 2 as "biotope (dwelling in sediment or confined within haptera)". CH at both sites demonstrated higher species richness and were more similar in species composition (Jaccard index, 0.8) than CH and CS from each site (Jaccard index, 0.5 and 0.4 for Site 1 and 2 respectively). We failed to found any tendency in spatial distribution of macrozoobenthos within transects according to the distance gradient from haptera despite that samples within transect revealed varying loadings for both factors. We suggested that such differences might be explained by small-scale heterogeneity in sediment grain-size distribution. In subsequent years (2010–2012) we found drastically decreasing of species richness, density and biomass in CS at both sites while CH demonstrated no significant differences in abundance indexes at both sites during all 4 years. We failed to find any pattern in spatial distribution of macrozoobenthos in 2010–2012. We also observed significant interannual changes in the trophic structure in CS at both sites during all 4 years. Trophic structure of CH also varied but changes were minor and thus we could suggest that CH stability is defined by physical characters of the habitat itself: haptera attached to stone (stones) gives an advantage to sessile organisms since it is raised above the sediment level; it serves as a shelter possessing small cavities which also contributes in detritus accumulation – all these factors attract animals exploiting different feeding strategies. Analyzing possible reasons of registered instability in the macrozoobenthic community structure amongst abiotic characters we could point the increasing of water temperature: +8$^{O}$ C 2009 and +11$^{O}$ C in 2010–2012 (bottom layer; middle August), and decreasing of organic matter content in the sediments at Site 2 (but reliable differences were pointed only between 2009 and 2010 (Student test 8.33, $p<<0.01$). One might suppose that interannual changes in density and abundance of different species might be also caused by biotic interactions but we still have not enough data about integrative mechanisms in such assemblages. Basing on these data we can conclude that

i) species composition, community structure and abundance indexes of CH are similar and do not depend on current velocity;

ii) CH and CS are quite different at any flow rate;

iii) unfortunately, significant interannual changes in community structure and abundance of CS make it impossible to prove that there are differences depending on current velocity.

## MARINE BENTHIC MACROPHYTES (MACROALGAE AND MARINE ANGIOSPERMS) AS BIOINDICATORS OF THE ECOLOGICAL STATUS IN THE MARMARA SEA (TURKEY)

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Assessing the ecological status of coastal waters, seaweeds (macroalgae) and seagrasses (marine angiosperms) are one of the biological quality elements. Proposed by the European Water Framework Directive (WFD), macrovegetation monitoring is an important tool in evaluating and predicting the anthropogenic stress on the marine environment.

In regards to WFD, a study to assess the ecological status according to macrophytes in the Marmara Sea was performed.

The study was completed in 2013 August and October, by sample collection from 30 stations. Samples were collected from 0 to 3 m by free diving. Quadrat (20×20 cm) and photoquadrat methods were used for macroalgae and seagrass sampling. The biodiversity and coverage percentages of Macrophytes dispersed in the study area were determined according to the stations. The findings were evaluated according to the Ecological Evaluation Index (EEI) standards as proposed by the European Water Framework Directive (WFD, 2000/60/EC). As a result, 2 sampling sites for macroalgae of the Marmara Sea coast were classified as High, 5 as Good, 10 as moderate, 9 as low and 4 as poor ecological status. However, when the general status is considered, the status can be classified as good-moderate-low.

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## LONG-TERM DYNAMICS IN FOUR BLUE MUSSEL SUBLITORAL COMMUNITIES (KANDALAKSHA BAY, WHITE SEA)

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Monitoring of four *Mytilus edulis* Linnaeus, 1758 sublitoral communities from Kandalaksha Bay was carried out by the White Sea Biological Station of Zoological Institute RAS since 1981 until 1993. Mussel communities were studied in the Padan Bight, Umba River estuary and at southern and northern shores of the Knyazhaya Bight. All material was sampled using 0.05 m$^2$ corer. All sea-bottom organisms were weighed with an accuracy of 0.001g. Besides, *Mytilus edulis* and *Balanus crenatus* Bruguière, 1789 specimens were measured with an accuracy of 0.1 mm. In total, 272 benthic cores were sampled.

All quantitative data were recalculated to 1 m$^2$ and stored in the DataBase "White Sea Benthos" developed by A. D. Naumov. Different methods of linear statistics and multidimensional analysis were applied to describe the dynamics of communities.

The Padan Bight is a narrow sea gulf. Mussel settlement was located on a rocky ground varying in depth between 0.5 and 2 m.

In the Umba River estuary, mussel community occupied depth of 4 to 5 m on the edge of a rocky trough of 15 m depth.

In the Knyazhaya Bight, two mussel assemblages were studied. One of them was situated on the northern side of the bight on the silty sediment, while another one on the southern side on the rocky ground. Both of them were located at same depth of 2 to 5 meters.

Totally about 130 benthic species were recorded through the all period of investigations. Biomass of dominating species *Mytilus edulis* amounted up to 60 kg/m$^2$, while its average value was equal to 12 kg/m$^2$. Communities in the Knyazhaya Bight were characterized by presence of pronounced subdominant species *Balanus crenatus* having biomass amounting up to 3 kg/m$^2$. Relatively high biomass values of *Alitta virens* (M. Sars, 1835) were recorded in the Padan and Knyazhaya Bights. It was correlated with that of *Mytilus edulis*. *Alitta virens* seems to be a deposit feeder in these communities.

Eigenvector filtering method (SSA) was used to describe the multiyear dynamics of most abundant species. Some of them demonstrated pronounced quasi-cyclic dynamics, whereas most species just followed relatively stable trends with rather stochastic fluctuations during observation period. The quasi-cyclic dynamics was rather attributed to community in the Padan Bight. Generally, this community appeared to be more stable due to the more regular dynamics of its species, which demonstrated sufficiently pronounced quasi-cycles and relatively stable trends. On the contrary, communities in the Umba and Knyazhaya Bights looked more stochastic.

## BENTHIC ASSEMBLAGES IN A LOW PH ENVIRONMENT: A FUNCTIONAL ANALYSIS ON AMPHIPODS FROM POSIDONIA OCEANICA MEADOWS

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Ocean acidification is possibly one of the most serious threats facing marine life. It is likely to cause a decrease in biodiversity which may lead to shifts in ecosystem structure. In benthic systems, crustacean amphipods, due to their structural and functional role, have become important in assessing biodiversity, and have long been known as sensitive environmental indicators. The present study was framed within a wider research programme, aimed at investigating the effect of low pH values on benthic assemblages. It was conducted at the Castello Aragonese, an area off the Island of Ischia (Gulf of Naples, Italy), characterized by a natural pH gradient due to volcanic $CO_2$ vents. In this 'natural laboratory', amphipods were collected from *Posidonia oceanica* meadows at approx. 3 m depth, by means of an air-lift sampler (40×40 cm). Two stations (control: pH 8.1 and acidified: pH 7.8) at each side of the Castello (South and North) were sampled in March, July and November 2011, for a total of 48 samples. Overall, 18,880 individuals, belonging to 67 species, 47 genera and 25 families, were identified. The functional analysis was performed assigning each amphipod species to feeding guilds and ethological categories. As a main trend, the trophic diversity is maintained in presence of volcanic $CO_2$ vents. Deposit feeders (e.g. *Metaphoxus* *simplex*) and deposit-suspension feeders (e.g. *Ampelisca serraticaudata*) increased in acidified stations in comparison to herbivorous forms (e.g. *Apherusa* cf. *chiereghinii*), even in November when these are dominant. The nMDS ordination coupled with cluster analysis showed a disjunction between control and acidified stations. Furthermore, even if a common feature in *Posidonia oceanica* is the dominance of epifaunal forms, mainly free-living and to a lesser extent domicolous, it is worth to note that in acidified stations infaunal amphipods, both free-burrowing and tube-building, increased in comparison to epifaunal forms. Differences in trophic and ethological structures were primarily due to changes in plant features, an indirect effect of low pH values. In fact, the lower leaf height (low plant growth rate and high grazing pressure by fishes) and plant epiphyte cover may determine the increase of taxa mainly related to the under-canopy layer, infaunal deposit and deposit-suspension feeders, and the decrease of species which live in the leaf stratum herbivorous epifaunal free-living. The functional approach gave new insights and the results showed to be consistent to those previously achieved by the structural analysis which mainly pointed out that amphipod assemblages living in *Posidonia oceanica* meadows are not affected by the volcanic $CO_2$ vents present at the Castello, and appear to be tolerant, well adapted or even favour low pH. But, the differences found suggest a possible ecological shift not only in assemblage structure but also function under future acidification scenarios, with changes in the plant and the vagile mesofauna interactions, and therefore in *Posidonia oceanica* food webs.

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## STRUCTURE OF MICROBIAL COMMUNITY IN ESTUARY AREAS ALONG THE EASTERN ADRIATIC COAST

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The structure of the microbial food web was studied in six estuary areas along the eastern Adriatic coast during March, July and October 2012. Heterotrophic bacteria and autotrophic picoplankton (APP), particularly picoeukaryotes and *Synechococcus*, reached marked abundance and biomass, and thus play an important role in the microbial food web. Similarity analysis, based on abundances of all studied picoplankton and nanoplankton groups, showed clear separation of the two northernmost estuaries in March and October, and the southernmost estuary in July. However, the studied estuaries showed many more similarities than differences. High nitrogen/phosphorus ratio was a common feature for all of them, suggesting phosphorus-limited environments. Some characteristics of the microbial food web could be associated with oligotrophic environments (heterotrophic/autotrophic ratio > 1, high contribution of low nucleic acid (LNA) bacteria), and others with more eutrophic environments (domination of picoeukaryote biomass within the APP community, as well as domination of *Synechococcus* over *Prochlorococcus* biomass). On the other hand, relationships within the picoplankton community, as well as domination of bottom-up vs. top-down control of bacteria, varied on a spatial and temporal scale. Stable viruses (virus-like particles) abundance was found in all estuaries, and they showed strong correlation with bacteria, and occasionally with all APP groups (picoeukaryotes, *Synechococcus* and *Prochlorococcus*). LNA bacteria were abundant in all estuaries and these bacteria could be described as a form of adaptation to environmental conditions rather than metabolically inactive bacteria. This paper highlights the potential importance of the picoplankton community not only in the open Adriatic Sea, but also in coastal/estuarine environments.

## BIOGEOGRAPHIC AND DISTRIBUTION TRENDS OF CHEILOSTOME BRYOZOAN ASSAMBLAGES IN ONE DEEP WATER SEAMOUNT: THE GALICIA BANK (NE ATLANTIC)

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The Galicia Bank is an extensive plateau situated to the northwest of the Iberian Peninsula, c. 200 km off the western Galician coast at about 42°67’N latitude and 11°74’W longitude. This structure has a minimum depth of about 600 m. The bank is characterized by complex geomorphological and sedimentary structures, and is influenced by contrasting water masses of both northern and southern origins, especially by the Mediterranean outflow water (MOW) that influences the sampled depths. Knowledge of the Galicia Bank fauna is extremely scarce. Recently, different taxonomic groups were started to be studied, and several papers on Cnidaria, Mollusca, Crustacea and Pisces have been published. However, bryozoans were not among them, and no previous data existed. A total of 5020 colonies of Cheilostomata were studied during this work, from 27 localities distributed between 675 m and 1697 m, and collected during the campaign INDEMARES (2011), Victor Hansen (1997) and Seamount 1 (1987). A total of 24 species was identified, twelve of them are new to science, implied a high percentage of possible endemic species. The already known species are "common" in deep waters from nearby areas of the continental slope, except for *Alderina canariensis*, which has been described only from the Canary Islands. Different statistical analyses were carried out to detected differences between, or clusters of, the various localities (MDS, cluster analysis, ANOSIM, SIMPER), and calculations of diversity indices were additionally performed (Margalef, Shannon, Simpson). These analyses show the existence of two groups or communities with a high statistical support ($P<0.001$, $R$: 0.83 for the presence/absence matrix; $P<0.001$, $R$: 0.902 for the abundance matrix). One of these groups is situated on the top of the bank, at localities between 765 m and 880 m depth, where the substratum is formed by coral patches and small rocks that are separated by long stretches of sand. In concordance with recent studies on the geographic distribution of various other taxa, this group inhabits an area that is little influenced by the MOW. The second group was detected between 938 m and 1697 m depth in localities with abundant tridimensional habitats formed by coral skeletons and rocks, and with a greater influence by the MOW. Nevertheless, both areas seem to have similar diversity values.

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## MACROZOOBENTHIC ASSEMBLAGES AROUND A MARINE TERMINAL FOR RE-GASIFYING LIQUEFIED NATURAL GAS (LNG) IN THE NORTH ADRIATIC SEA (ITALY)

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In 1998 the project of a marine terminal for re-gasifying Liquefied Natural Gas (LNG) in the North Adriatic Sea was authorized, in order to make Italy less dependent on individual countries as regarding the demand for natural gas. This is the first offshore LNG terminal in Italy and the first in the world Gravity Based Structure (GBS), for unloading, storing and re-gasifying. The Institute for Environmental Protection and Research (ISPRA, formerly ICRAM) elaborated and carried out a multidisciplinary monitoring plan according with the environmental prescriptions, given by the Italian Ministry of the Environment at verifying possible impacts on marine environment associated to the project. ISPRA carried out monitoring activities before the installation of the structure and during the construction and production phases. Then, together with other parameters, the soft-bottom macrozoobenthic assemblages structure around the LNG Terminal has been studied during throughout the period from 2006 until 2012 (June 2006, October 2008, September 2010, July 2011, July 2012). Univariate and multivariate analyses were performed, by comparing the structure of the benthic communities before and after the installation of the terminal, and then during its operation. Sediment grain-size characteristics were analyzed. In general well-structured assemblages were observed: all principal taxa were normally represented both quantitatively and qualitatively. Results let us assume not real impact happened on macrofauna assemblages, and in case it occurred, it was temporary. Multidisciplinary environmental monitoring plan performed during the operations becomes an essential tool to verify the actual effects on all marine habitats, allowing to intervene quickly and to minimize any possible negative effects. In particular, our monitoring plan has allowed us to monitor impact degree on surrounding environment, permitting to gain a high amount of data, which will let us to optimize field and laboratory work and could provide a reference for this type of studies in the future.

## MICROBIAL COMMUNITY ASSOCIATED WITH *ACARTIA ITALICA* IN ANOXIC AND SULFIDE MARINE CONDITIONS

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Meromictic lakes might represent current analogs to the ancient oceanic state. Understanding the geochemistry and the microbial community composition might be essential for recognizing important pathways of organic matter production and transformation under sulfidic conditions. The aim of this study was to analyze the bacterial community structure associated with copepods and compared with community structure profiles of free-living bacteria in the stratified meromictic water column. Our study was conducted in a salty lake Rogoznica, situated on the eastern coast of the Adriatic Sea. The lake is permanently stratified and the biogeochemical/redox cycling of sulphur has a profound influence on the distribution of microorganisms. The zooplankton community was characterized by monocultures of copepod *Acartia italic* and forty-four clones were obtained from the clone library of copepod associated bacteria. The largest group of copepod associated clones belonged to *Cyanobacteria* (50%), with representatives of Subsection I and Subsection III. Within Subsection III group, clones were affiliated with *Trichodesmium* (80%) and with *Bacteriodetes* (20%), with most representatives of *Flavobactriaceae* (91%). The vertical profile of the free-living bacterial community structure in the lake showed a pronounced change in bacterial community structure on transition from the well oxygenated upper layers to the hypoxic and anoxic bottom layers of the water column. The bacterial community structure above chemocline was dominated by *Bacteriodetes* (44%), represented mostly by *Sphingobacteria* (31%), *Flavobacteria* and some uncultured *Bacterioidia*. A smaller percentage of clones belonged to *Alphaprotoebacteria* (21%), of which more than half belonged to the SAR 11 clade, *Gammaproteobacteria* (7%), *Cyanobacteria* (Subsection I) (10%), *Actinobacteria* (7%) and *Opitutae* (10%) class of *Verrucomicrobia*. Below the chemocline the bacterial community was dominated by *Chlorobiaceae* (86%), with representatives *Chlorobium* and *Prosthecochloris*, and a small percentage of *Cyanobacteria* (7%) and of *Deltaproteobacteria* (7%). In the bottom layer of the lake, the bacterial community was again more diverse and affiliated with *Chlorobiaceae* (33%) and *Deltaproteobacteria* were more abundant (20%). In addition to higher relative abundance, the diversity within *Deltaproteobacteria* was higher, with representatives of *Bacteriovoraceae*, *Desulfarculaceae* and *Desulfobacteraceae*. Equal percentages (7%) of clones were affiliated with *Rhodospirillaceae* (*Alphaproteobacteria*), *Cyanobacteria*, with two candidate divisions, OD-1 and BD1-5, with *Spirochaetes*, which were present only in this assemblage and with *Chitinophagaceae* (*Sphingoproteobacteria*).

## PECULIARITIES OF THE DISTRIBUTION OF PHYTOPLANKTON IN FRANZ JOSEF LAND DURING THE SUMMER PERIOD OF 2013

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Recently, much attention is paid for the studying the marine ecosystems of the Polar Regions, which is preconditioned by their vulnerability to the climatic shifts and anthropogenic load (Matishov, 2011). The studies of the plankton communities are of the primary importance since they react to the environmental changes the most (Makarevich, Druzhkova, 2010).

The sampling was performed during the complex expedition "Pristine Seas" organized by National Geographic Society (USA) and National Park "Russian Arctic" (Russia). The sampling depths were assessed in accordance to CTD profiles in real-time approach. The phytoplankton was sampled by Niskin bottles, fixed and counted using the standard methods. The biomass was calculated by the approach of the geometrical similarity (Microalgae…, 2008).

Dinoflagellates had the highest biodiversity (more than 50% from the total species number), and *Protoperidinium* genus was the most diverse by the species number (*P. breve, P. brevipes, P. cerasus, P. depressum, P. islandicum, P. granii, P. ovatum, P. pellucidum,* and *P. pyriforme*). *Chaetoceros* genus was the most diverse within the Diatomea (*C. atlanticus, C. borealis, C. decipiens,* and *C. socialis*). The representatives of Chrysophyceae, Eutreptiaceae, Prasinophyceae, Raphidophyceae, and some unidentified flagellates have been registered also. In the neritic areas, the ratio of Dinoflagellates was minimal, at the deep stations (main straights), the opposite pattern was observed.

The population density of the phytoplankton was relatively low during the study period (thousands to several hundreds of thousands cells per liter). The neritic stations were characterized mostly by low population density comparing to the open areas (deep stations). The maximal impact to the population density belonged to the microalgae of Chrysophyceae family (*Dinobryon balticum* and *Phaeocystis* sp.) and to some unidentified flagellates.

The total biomass ranged from dozens to hundreds of mg per liter. The minimal biomass was registered for the neritic stations. *Protoperidinium* species (*P. brevipes, P. islandicum, P. granii,* and *P. ovatum*) had the highest impact to the total biomass. The pycnocline was characterized by the highest biodiversity, population density and biomass of the microalgae comparing to the sub-surface and twilight water depths.

The authors are grateful to National Geographic Society (USA) and National Park "Russian Arctic" (Russia) for the support.

## USING ECOLOGICAL GROUPINGS TO ASSESS THE IMPACT OF HUMAN ACTIVITIES

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Human activities in the marine environment are increasing, not only in terms of the spatial range, distribution and intensity, but also in terms of the breadth of activities undertaken.

This presentation describes JNCC's approach to assess the sensitivity of marine features (habitats and species) to damage from pressures exerted by human activities. The conceptual framework considers sensitivity to be a combination of a features resistance (or tolerance) and resilience (or recoverability) to a set of defined pressures. Pressures are not activity specific and a single pressure can result from several different activities.

Historically, sensitivity assessments have been carried out on individual species or, in the case of biotopes, on key species that are present within a community. The method has since been applied at various scales: species, habitat, and broadscale habitat. Using this approach, direct evidence of sensitivity of species or similar species to environmental factors is required, but in offshore waters, and particularly for deep sea species, this information is often not available. JNCC have developed an approach which uses ecological groups, comprised of collections of species with similar biological traits, in order to conduct sensitivity assessments e.g. soft bodied or flexible epifauna. The approach assumes that components of a group will have comparable resistance and resilience to pressure because of the similarity in biological traits.

A benefit of the ecological groupings approach is that it allows species with robust evidence underpinning sensitivity assessments to act as surrogates or proxies for species in the same ecological group for which such direct evidence is not available.

This work will help support JNCC in leading the UK Marine Biodiversity Monitoring R&D Programme to satisfy requirements of the Marine Strategy Framework Directive.

## IMPACT OF SEA-CAGE FISH FARMS: SHORT-TERM RECOVERY OF BENTHIC COMMUNITIES

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The fallowing practice, where fish production is temporally paused, is commonly used as a management tool for reducing benthic impacts induced by sea-cage fish farming. In order to prevent adverse effects of fish farming to the marine environment, an understanding of recovery processes occurring during the fallowing is essential. Present study aimed to assess the short-term recovery dynamics of macrofauna communities in response to different fallowing timing at two Atlantic salmon (*Salmo salar*) farms that have been fallowed for 2 and 6 months. Macrofauna and sediment characteristics were sampled in spring, summer and autumn 2012 at the Norwegian coast. Samples were taken at two stations near the fish farms and at two reference stations located 500 and 1000 m away from the fish farms. The results showed no differences in the sediment characteristics (such as TOC, pH, Eh) among the stations. In contrast, macrofauna analysis indicated highly disturbed environment at the cage stations during production cycle and a short period after fish harvesting with high abundances of opportunistic Capitellidae, low diversity measures and significantly different community structure compared to the reference stations. Improvement of macrofauna characteristics was observed at both cage stations during the fallowing time. However, different successional stages were found as a result of difference in the fallowing timing. At the cage station with fallowing time of 2 months, macrofauna community showed a very early stage of succession, with a significant decline of Capitellidae only. At the cage station with fallowing time of 6 months macrofauna community showed a general increase in diversity and changes in taxa composition, resulting in a higher similarity of community structure with the reference stations. The observed changes in the macrofauna community indicated a specific short-term response to the fallowing periods, but the communities still showed clear indications of disturbance after the fallowing time of up to 6 month.

# Miscellaneous

## FAUNISTIC COMPARISON AND BIOGEOGRAPHICAL DIVISION OF THE POLAR OCEAN EURASIAN SEAS AND CENTRAL BASIN, BASED ON DISTRIBUTION OF HYDROZOANS (CNIDARIA; HYDROZOA)

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Hydroids and hydromedusae (class Hydrozoa; subclass Leptolida) of Russian Arctic seas (often referred to as the “northern seas”) have been investigated for many years, and the fauna has been extensively revised faunistically, taxonomically, and biogeographically. Six seas exist in the Eurasian Arctic Ocean, all of them completely or partly related to Russia. The Central Polar Basin is regarded as a self-dependent region of the Arctic Ocean. The hydrozoan fauna of this enormous area includes 167 species (besides Leptolida about six more species being Siphonophora, but not estimated here). The richest fauna, comprising 133 species, occurs in the Barents Sea. The hydrozoan fauna of the White Sea, directly connected to the Barents Sea, is a 100% subset of that found in the Barents Sea. In the seas farther east, hydrozoan species composition is remarkably reduced, although it is similar in each of them. Numbers of hydrozoan species known from the White Sea, Kara Sea, Laptev Sea, East Siberian Sea, Chukchi Sea and Central Polar Basin are, respectively, 85, 72, 78, 70, 67 and 50. Measures of similarity among all these local faunistic lists is high, but the measure of inclusion into the richest fauna of the Barents Sea is extremely high: similarity values vary from 0.84 (min.- Central Polar Basin) – 0.87 – 0.90 – 0.93 – 0.97 – 1.00 (max. - the White Sea). Biogeographically, this fauna consists of several groups, as follows: strictly arctic species (Arctic endemics), boreal-arctic and subtropic-boreal-arctic species, cosmopolitan species, some (not all) bipolar species and boreal species extending into some Arctic seas (usually at the margins or in environments having warmer streams). The number of strictly arctic hydrozoan species in the entire region is not at all large, comprising just 17 species (12%). Arctic circumpolar (8 spp.), arctic eurasian (8) and arctic amerasian (1) species can be distinguished. Percentage and composition of arctic species is rather similar in all seas, but somewhat lower in the marginal seas: especially in the White Sea (due to the notable role of Atlantic boreal species) and in the Chukchi Sea (due to Pacific boreal species). The Arctic Ocean is populated mostly by boreal-arctic hydrozoans, which comprise more than one-half of the species everywhere. Species composition of Hydrozoa throughout Russian Eurasia is very monotonous. The exception occurs in marginal parts – the west part of the Barents Sea and the south-east part of the Chukchi Sea, where a closeness of many species distribution areas contours (named as “synperates”) were registered. Along the synperates both in the middle of the Barents Sea (remarkably) and in the Chukchi Sea (somewhat less remarkably), substantial changes of biogeographical fauna types have been observed. These changes designate the borders between biogeographical divisions of high hierarchical level, of boreal and arctic types. A North Atlantic faunistic complex absolutely predominates in waters of the Arctic Ocean. It consists of a boreal species group and a boreal-arctic group, common to North Atlantic waters. Almost all boreal species of Hydrozoa disappear in the eastern part of the Barents Sea. In the western part of the Barents Sea, seven species of the warm-water superfamily Plumularoidea are known, but all are absent from the middle of the Barents Sea eastward. To the east, all areas of the Russian and Canadian Arctic regions, and the Central Polar Basin, are a "Plumularioidea-free” area. Absence of that superfamily may be used as an indicator of Arctic waters, and the group constitutes a borderline marker between biogeographical divisions of boreal and Arctic types. One very large and complicated group of hydrozoan species is arctic ubiquitists. It is both a mixed and the largest group (totaling 64 species), and is composed of commonplace arctic species (6 species), boreal-arctic and mostly cyrcumpolar species (53 species) and five multizonal and almost cosmopolitan species. The same arctic ubiquitists, a majority of them boreal-arctic species, comprise the main element of hydrozoans in all Arctic seas. This faunistic main element is responsible for the high similarity and faunal uniformity from one sea to the next across many thousands of kilometers along the northern Eurasian coast. From a biogeographical analysis of faunistic data and species distributions of Hydrozoa, all temperate and cold waters of the Eurasian seas and the Central Polar Basin were referred to a single Arctatlantic biogeographical realm. Biogeographical subdivisions within this realm have rather low hierarchical rank, the result of low endemism, high faunal similarity across the northern seas, and the predominance of North Atlantic fauna in the Russian northern seas as far as the easternmost Chukchi Sea. That rather uniform assemblage of hydrozoan species ranges across the enormous expanse of the Eurasian Arctic.

## GENETIC DIVERSITY OF BEAKED REDFISH (*SEBASTES MENTELLA*) POPULATIONS IN THE NORTH ATLANTIC AND THE ARCTIC OCEAN

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Global climate changes have currently made possible variability of genetic diversity among marine populations a subject of active research (review: Pauls et al., 2013). In this context, it is particularly important to study the genetic diversity of species with a longitudinally extended distribution range, as this will facilitate the projections of future gene pool changes in northern populations under steady climate warming. The focus of this study is on the diversity of the mtDNA D-loop in beaked redfish sampled in some areas of the North Atlantic and the Arctic Ocean. The research revealed a considerable difference in the number of observed haplotypes. In the analysed sequence of the southern populations, we identified 31 haplotypes, while in the northern populations 12 haplotypes were revealed. A similar latitudinal decline was also observed for allozyme diversity. One of the reasons behind the reduced genetic diversity of beaked redfish in the Arctic Ocean may consist in the post-glacial colonization of this marine area from only one refugium, while the northern Atlantic Ocean was colonized from two or more refugia, as ca. 21 thousand years ago, during the Last Glacial Maximum, fish distribution in the Atlantic was notably shifted to the south in comparison with modern age (Kettle et al., 2011). It should be noted that there is evidence suggesting that some fish species in post-glacial age migrated to the Barents Sea from the Pacific (Artamonova, Kucheryavyy, 2010; Laakkonen et al., 2013), but redfish species did not use that dispersion route. Another reason to explain high genetic diversity in redfish samples collected in the North Atlantic may consist in the intense interspecific hybridization between *S. mentella* and other redfish species, *S. viviparus*, *S. marinus* and *S. fasciatus*, in the southern parts of the distribution range (Artamonova et al., 2013, and references given in this paper). It is interesting that the above species, with the exception of *S. fasciatus*, also inhabit the Arctic Ocean, however, no interspecies hybrids were observed there.

The study was granted a support from the Russian Foundation for Basic Research (grant no. 14-04-00213) and the programme “Russian Biological Resources: Dynamics in the Context of Global Climate and Anthropogenic Impacts”.

## TWO CASES OF CRYPTIC SPECIES IN POLYCLADIDA (RHABDITHOPHORA: PLATYHELMINTHES)

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Plathelminthes of the order Polycladida live in all marine environments from coral reefs and rocky shores to soft bottoms in all oceans (Newman & Cannon, 2003; Quiroga et al. 2004a). The main characteristic of the group is their simple and flat body with a much ramified intestine. In the world, the biodiversity of Polycladida is relatively poorly known when compared to other marine invertebrates groups. There are around 900 valid Polycladida species, the characters used in the taxonomy of the group are related to the reproductive anatomy, arrangement of eyespots, type and form of pseudotentacles and pharynx (Hyman, 1951; Faubel, 1984; Bolaños et al. 2007; Brusa et al., 2009; Bahia et al. 2012). The coloration pattern can also be used in telling species apart (Newman & Cannon, 1995; Litvaitis & Newman, 2001). The morphological simplicity of these animals and the taxonomy based on very few morphological characters cause taxonomic and systematic problems, and can camuflate cryptic species, as it was previously reported in other marine invertebrate groups (Knowlton, 1993; Klautau et al. 1999; Held & Wägele, 2005). It is important to note that to solve such problems has the power to change regional estimatives of diversity, essential to species and habitats conservation purposess, and can modify general faunal and biogeographical patterns.

An interesting case of posible species complex is the Polycladida species *Thysanozoon brocchii* Risso, 1818. This species is supposed to have a wide geographical distribution, with records from Gulf of Naples, Italy (Risso, 1818) (type locality), Brazil (Marcus, 1949; Marcus & Marcus, 1968), Argentina (Brusa et al. 2009), and possibly Japan (Yeki & Kaburaki, 1918) and west and south of Africa (Laidlaw, 1902). In the specimens herein studied were observed differences in dorsal papillae form and coloration pattern, hwever these were not reflected in the results found. The maximum-likelihood analysis of 28S marker of specimens of *Thysanozoon brocchii* complex from different localities of the brazilian coast and Mediterranean Sea point to the presence of only one species through all this range. One animal of the genus *Thysanozoon* found at Northeastern Brazil were considered different morfologically and also molecularly.

The maximum likelihood analysis with sequences of 28S marker of the *Pseudoceros bicolor* complex confirmed the results of Litvaitis *et al.* 2010. The clade *Pseudoceros rawlinsonae* and the clade *Pseudoceros bicolor* were clearly separated (99 and 98% similarity, respectively). A new morphotype found in Northeastern Brazil similar with the complex, but without the characteristic marginal band, was grouped with P. bicolor clade and can represent a new species. But to make final affirmations on both cases there are necessary more comparisons between diagnostic molecular characters (fixed differences between sequences) and posterior analysis (ex.: ABGD, GMYC) and the inclusion of other markers which is the next step of this work.

## GOING FURTHER SOUTH, AN INTEGRATIVE APPROACH TO THE NUDIBRANCH FAMILY TRITONIIDAE (GASTROPODA: HETEROBRANCHIA)

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Nudibranchia are conspicuous, highly diverse, worldwide distributed shell-less marine mollusks. The nudibranch fauna in Antarctic and sub-Antarctic waters may be especially rich, yet species tend to be morphologically variable or, alternatively, complexes of cryptic species may exist. Southern Ocean tritoniids are macroscopic and commonly sampled, but their taxonomy has not yet been well-established. Incomplete morphoanatomical descriptions, unknown ranges of variation, apparently wide distributional ranges of currently valid species, and the lack of molecular data contribute to taxonomic uncertainty. In the Pleistocene, organisms from Magellanic and Antarctic waters have been subjected to several glaciation cycles. In the Magellanic region, the effects of alternating periods of population decrease, fragmentation or extinction, and subsequent expansion of surviving lineages has hardly been explored yet. In Antarctica, this complex history supposedly induced the so-called biodiversity pump, which has lead to multiple phenotypically similar but ecologically and genetically specialized species, e.g. in the direct developing dorid nudibranch "*Doris kerguelenensis*" complex. We do not know much about the exact position and role of refuges and ways of dispersal of hardly mobile direct developers, and there is no molecular data available on southern nudibranchs having a planktonic larval stage. In this work, we explore the species level taxonomy, phylogenetic relationships and geographic distributions of the nudibranch family Tritoniidae, including members with planktonic larvae. Since 1991, we collected hundreds of tritoniid specimens from southern South America, subantarctic islands and Antarctica. During numerous expeditions with e.g. 'RV Polarstern', specimens were observed, documented alive, and fixed for multiple purposes. Specimens were dissected, described anatomically, and compared with type material. Tissue samples were analyzed under scanning electron microscope or embedded for histological study. DNA from muscle and mantle tissue was extracted and sequenced for mitochondrial and nuclear markers. Preliminary results from our combined approach (i.e. traditional morphological knowledge and molecular data) validate current concepts on a few species such as *Tritonia odhneri.* Integrative results suggest that *Tritonia challengeriana* and *T. antarctica* form a not yet fully resolved species complex across the Polar Front, similar to what was found in the direct developing *D. kerguelenensis.* The monotypic *Tritoniella* is recovered as a clade in multi-locus analyses, but showing considerable morphological variation. More sensitive genetic markers may be necessary to resolve such highly complex, potentially quite recent diversifications.

## *MALDANE ARCTICA* DETINOVA, 1985 (MALDANIDAE MALMGREN, 1867): A NEW SPECIES FOR THE WHITE SEA

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In the seas of the Arctic Ocean, genus *Maldane* Grube, 1860 (Maldanidae Malmgren, 1867) is presented by two species (Jirkov, 2001, 2013): *Maldane sarsi* Malmgren, 1865 – shelf Arctic-Atlantic-Pacific species widespread on the shelf of the Arctic Ocean at depths of 6 – 1745 m and *M. arctica* Detinova, 1985 – eurybathic panarctic species widespread in the Barents Sea at depths of 300 m or more. Both species are morphologically similar and have similar ecological features (Ushakov, 1955, Jirkov, 2001, 2013).

Up to now, only species *M. sarsi* which often forms large settlements on soft sediments almost throughout of the entire water-body except the Gorlo Strait has been registered in the White Sea. Its absence in the last area can be explained by rigorous hydrodynamic regime and peculiarities of distribution of bottom sediments there (Deriugin, 1928, Lukanin et al, 1995, Babkov, 1998, Denisenko et al, 2006, Solyanko et al, 2012).

Morphologically these two species are different – *Maldane sarsi* is missing chaetae on the first and the second segment and has a glandular crest on the dorsal side of the fifth segment. In addition, anal disc of *M. sarsi* is divided into two equal parts by side incisions, while in *M. arctica* it is divided into a smaller one, ventral, and a large one, dorsal.

Polychaetes of genus *Maldane* lacking glandular crest were found while processing of samples from the Onega Bay (the White Sea) collected in 2010 by a group of researchers headed by V.A. Spiridonov, Institute of Oceanology RAS (the station coordinates 65°09,730′ N, 35°02,999′ E; 58 m depth, bottom temperature 3,8°C; van Veen grab 0.1 m², samples washed through a sieve mesh size 1 mm, 4% formaldehyde fixation). At the other stations of this survey, specimens of this genus, if found, possessed the mentioned crest.

Thus, a new for the White Sea species *Maldane arctica* Detinova, 1985 has been found at the mentioned station.

## FAUNA ASSOCIATED WITH *TOXOPNEUSTES PILEOLUS* AND *TRIPNEUSTES GRATILLA* FROM THE BAY OF NHATRANG, VIETNAM

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Tropical regular sea urchins serve as microhabitats for diverse symbiotic fauna underestimated during biodiversity surveys, but playing an important role in trophic food webs. It is better known for Diadematidae sea urchins, and fragmentary for the other taxonomic groups including Toxopneustidae. The aim of this report was studies of symbiotic fauna associated with sea urchins *Toxopneustes pileolus* and *Tripneustes gratilla*. These sea urchins have a numerous toxic globiferous pedicellarias. *Toxopneustes pileolus* is covered by large pedicellarias (3–4 mm in diameter), while *Tripneustes gratilla* is covered by small ones (0.3–0.4 mm). Toxin of *Toxopneustes pileolus* is more dangerous. Taking into account toxicity of these species we suggested that symbiotic faunas associated with them differ from that of other regular sea urchins. The study was conducted in April–May 2012–2013 in the Bay of Nhatrang, South-China Sea, Vietnam. Seventy-nine specimens of *Toxopneustes pileolus* and thirty-one of *Tripneustes gratilla* were collected by hand using SCUBA equipment from the depths 10–27 m. Each individual sea urchin was placed in zip-lock plastic bag to avoid loss of symbionts. In the laboratory, echinoids were carefully checked for symbionts by eye and then washed with an isotonic solution of magnesium chloride. All removed symbionts were fixed in 70% alcohol for further identification and counting. Six species of macrosymbionts were found in associations with each sea urchin species, while species composition of faunas was different. *Tripneustes gratilla* harbored shrimps *Gnathophiloides minery* (Caridea, Gnathophyllidae) and *Arete dorsalis* (Caridea, Alpheidae), gastropods *Vitreobalcis* sp. and *Vitreolina* sp. (Eulimidae), brittle-stars *Ophiosphaera* sp. (Ophiuroidea, Amphiuridae), and unidentified Leucothoidae amphipod. Crustaceans and gastropods were found among echinoid spines, brittle stars were located near the host mouth. *Toxopneustes pileolus* harbored shrimps *G. minery* (Caridea, Gnathophyllidae), polychaetes *Hololepidella* sp. and *Astralougeneria* sp. (Polychaeta, Polynoidae), gastropods *Vitreolina* sp. (Eulimidae), unidentified Leucothoidae amphipods, and poeciloistomatoid copepods. All symbionts were found among echinoid spines. The most abundant symbionts of *T. gratilla* were *Ophiodaphne formata* and *Vitreobalcis* sp. (the prevalence were 32.3% and 25.8% respectively) never found on *T. pileolus*, while in *T. pileolus* the most abundant symbionts were *Hololepidella* sp. and poeciloistomatoid copepods (the prevalence were 72.2% and 25.3% respectively) never found on *T. gratilla*. Three species of symbionts, *Vitreobalcis* sp., *G. minery* and leucothoid amphipods were common for both echinoids. The comparison of faunal composition associated with these two sea urchins with other studied sea urchin symbiotic faunas demonstrated low specificity of *T. gratilla* symbiotic assemblage and high specificity of *T. gratilla* assemblage. We consider this difference as a result of high toxicity and peculiar shape of *T. pileolus* pedicellarias forming microhabitat for symbionts between canopy of pedicellaria and echinoid test favorable for establishment of highly specific symbiotic assemblage.

## HYDROTHERMALLY ACTIVE ENVIRONMENT – SEAWATER AND COMMUNITIES

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Active shallow water hydrothermal activity is present at the Azorean shores. Organisms associated to hydrothermal activity are chronically exposed to extreme environments characterized by “natural thermal pollution”, high metal concentrations as well as acidic seawater due to the natural CO2 flux released from volcanic activity. In the present study, aimed at evaluating the influence of shallow water hydrothermal vents on communities living in such habitats, fluids and communities were compared between a shallow water hydrothermally active site and three sites not exposed to hydrothermal activity. At the four sites, algae and macroinvertebrates diversity and abundance, and seawater parameters were evaluated. Gas analysis was performed. Coralline algal species and echinoderms presented lower percentage cover at the hydrothermally active site, contrarily to green algae and Hydrozoa which were more abundant at that location, suggesting that organisms with calcareous structures might be affected by ocean acidification.

## DEVELOPMENT OF NEW SPECIES OF AGAMOCOCCIDIAN *RHYTIDOCYSTIS* SP. FROM *TRAVISIA FORBESII*

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Agamococcidia represent a small and poorly investigated group belonging to the phylum Apicomplexa, inhabiting the intestine of marine polychaetes (fam. Rhytidocystidae) and gastoderm of Hexacorallia (fam. Gemmocystidae). Based on light microscopic observations, they show an unusual life cycle lacking the gametogony and merogony. It was shown in *Gemmocystis cylindrus* Upton and Peters, 1986 that sporozoites form a paired association, similar to syzygy of gregarines, fuse and then secrete an envelope around them. During sporogony, four sporozoites develop within this envelope. In *Rhytidocystis henneguyi* de Beauchamp, 1912 from *Ophelia neglecta* it was shown that it develops in the intestinal, connective, chloragogenic tissue or in blood sinus. Mature trophozoites form several sporoblasts (mechanism unknown), which secrete an envelope around themselves and undergo sporogony. This study focuses on light and electron microscopic (EM) investigation of intestinal parasite from White Sea polychaete *Travisia forbesii* Johnston, 1893 (Polychaeta, Scalibregmatidae). In host intestine, several developmental stages of agamococcidian *Rhythidocystis* sp. with intracellular localization were observed. The distribution of this parasite was uniform along the middle third of intestine. Some developmental stages appeared as white dots of various shape and size. After being picked out mechanically from the host tissue, they transformed into oval or round, immotile cells. Under transmission electron microscope, we observed putative sporozoites, several stages of growing trophozoites, paired associations and presumably zygotes or early oocysts. Putative sporozoites were of oval shape and localized in the cytoplasm of the entherocytes. No parasitophorous vacuole was observed. They were covered by a trimembrane pellicle (plasmalemma + inner membrane complex); their cytoplasm was packed with several mitochondria, large vacuole and a network of rough endoplasmic reticulum. As no organelles of apical complex were seen, we assume that this stage could be very young trophozoites, which already lost their apical organelles and start to mature. Several stages of maturing trophozoites were found in ultra-thin sections. First one stage was oval-shaped and possessed cytoplasm filled with lipid droplets, protein inclusions, amylopectin granules and round to oval nucleus with a dense nucleolus. Numerous giant mitochondria with tubular cristae could be observed at the cell periphery closely adjacent to the pellicle. Second oval to round stage exhibited, in comparison with the previous stage, darker cytoplasm filled with the same set of inclusions and more condense mitochondria localized at the cell periphery. The last one stage of maturing trophozoites was at least two times larger than previous stages. Its pellicle formed numerous invaginations, similar to those observed in artificially released gamonts. These structures resembled short folds; there were several interconnected groups of 4-5 folds arranged in rosette-like pattern. Numerous micropore openings were located between the individual folds as well as on their tops. Micropores formed straight or curved lines, crossing each other. The micropores, with a structure typical for Apicomplexa, could be found in all maturation stages of trophozoites. The cytoplasm was packed with numerous reserve granules, Golgi bodies, hypertrophied mitochondria, endoplasmic reticulum and central lobed nucleus. Some of these forms possessed rhizoid-like appendages. During maturation, probably in its first half, the parasites induced formation of a syncytium from several surrounding host cells. Apical part of this syncytium showed usual morphology, but its basal part lacked all organelles and inclusions. Occasionally, two and more profiles of mature gamonts could be found in one syncytium. Evidently paired associations, confirmed by a presence of two lobed nuclei, were also observed. Their contact was straight or interlobed and the space between adjacent partners contained fibrillar material interconnecting their membranes. Structures considered to be zygotes possessed much more condensed cytoplasm with amylopectin granules and strongly electrondense vacuoles. Their relatively small nucleus with a round dense nucleolus was surrounded by an endoplasmic reticulum. We assume that sporozoite penetrates into the epithelial cell, and later during trophozoite development it moves to the base of intestinal epithelium cell and induces the formation of syncytium around itself. After, there could be at least two ways of further development: i) mature trophozoites bud sporoblasts (we never observed this process), which form an envelope and proceed into the sporogony; ii) two mature trophozoites form an association, fuse and then undergo sporogonic divisions, as observed in *G. cylindrus*, or bud sporoblasts. Alternatively, two (or more) sporozoites penetrate one host cell, form an association of two partners (neogamy, known for some gregarines), mature and subsequently fuse. This zygote could either bud the sporoblasts that form sporozoites, or directly progress into the sporogonic stage to form infective zoites.

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## SEQUENCE ANALYSIS OF NEW *STYELA RUSTICA* PROTEIN

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Ascidians belong to the subphylum Tunicata, which is one of the most ancient groups of chordates. A characteristic feature of these animals is their integument – tunica. Tunica is composed of polysaccharides and proteins sclerotized by quinon tanning. Sclerotization process is executed by means of phenoloxidase (PO) system (Chaga, Solovey, 1986), which is also involved in animal defense (Smith, 1996) and allorecognition (Akita, Hoshi, 1995). Components of phenoloxidase system, such as phenoloxidase, polyphenolic compounds, cationic proteins, are localized in morular blood cells (Smith, 1970). Two major proteins p48 and p26 kDa expressed in morular cells of *Styela rustica* were shown to participate in tunic repair. They are supposed to be the part of phenoloxidase system (Podgornaya, Shaposhnikova, 1998).

Specific antibodies raised against p48 and p28 also stain granules inside test cells, surrounding oocytes of *S. rustica*. Ascidians' oocytes are surrounded by both test and morular cells. Latter participate in adult tunic formation. Whereas, test cells are present only during embryogenesis. Some authors believe that they are involved in formation of larval tunic. Thus we can assume that two major proteins of *Stiela rustica*'s morular cells, p26 and p48, play an important role at the larval and adult stages of ascidians. However their primary structure and function remain unclear.

We held MS-MS analysis, which allowed us to determine the amino acid sequences of several short peptides – tryptic digestion products of two proteins. One of these peptides, prepared from p26 protein, had a high probability of precise amino acid sequence. Sequence of this peptide was used to design degenerate primers. Then we synthesized cDNA on the basis of poly(A)RNA from ascidian blood cells and used it as a matrix in RACE-PCR with degenerate primers. The product of RACE-PCR was cloned and sequenced. In this way we obtained a sequence which contained open reading frame 567 nucleotides long. Comparison of this sequence with known sequences using online databases showed that our sequence is unique/new and was not described previously. Open reading frame of 567 nucleotides must correspond to the part of p26 gene. In the near future we want to get full-length gene coding for p26 kDa protein.

## THE ADRIATIC ICHTHYOFAUNA: UPDATES (2010–2013)

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In the period of 2010–2013, eight new fish species have been added to the Check list of Adriatic fishes (first records – *Lobotes surinamensis*, *Siganus luridus*, *Paranthias furcifer*, *Holacanthus ciliaris*, *Elates ransonnetti*, *Enchelycore anatina*, *Caranx rhonchus* and *Lagocephalus sceleratus*). Second records were observed for *L. surinamensis*, *E. anatina*, *Caranx crysos* and *L. sceleartus* indicating that those species are establishing their populations in its new region. New additional record or rare species *Tylosurus acus* *imperialis* was observed in 2011, while of very rare species *Ruvettus pretiosus* in 2013. Of 14 *Lessepsian migrants* that were recorded in the Adriatic, it seems that *Fistularia commersonii*, and *Siganus luridus* are successful invaders.

During the last few decades, various factors including climate change, anthropogenic activity and lessepsian migration have altered composition of Adriatic ichthyofauna. Furthermore, extensive investigations carried out in the Adriatic Sea in the last few decades allowed us to recognize species previously unknown from this area. These changes are reflected in the number of species quoted in the checklist of Adriatic fishes, from 407 in 1996 to 449 in 2011. Today, this number is 453 to the best of our knowledge. Beside first time occurences of newly arrived or newly discovered species, a trend of northward spreading and expansion of previously rare species has also been observed.

Among mentioned species, shortly after their first records, second records of *L. surinamensis*, *S. luridus*, *E. anatina* and *L. sceleratus* followed. Additionally, findings of juveniles of *Fistularia commersonii* and *Siganus luridus* and immature specimens of *Caranx crysos* in the southern Adriatic might indicate establishment of populations of these species. Of all lessepsian migrants encountered in the Adriatic to this date (14) it seems that only *F. commersonii* and *S. luridus* can be considered as successful immigrants although evidence of established populations of these species is still sparse. Furthermore, it is unclear, whether *E. anatina* is a previously established, but overlooked inhabitant of the Adriatic Sea or only a recent immigrant. Two records of *L. sceleratus* from two distinct areas of the eastern Adriatic may indicate an early phase of colonization especially if we take into account a rather fast spreading of this species in the Mediterranean Sea. Among species which are considered rare or very rare in the Adriatic Sea, new occurences of *Tylosurus acus* imperialis and *Ruvettus pretiosus* were recorded.

## DECREASING CALCIUM CARBONATE SATURATION STATES IN THE ICELAND SEA AND THE DEPTH DISTRIBUTION OF MAJOR CALCIFYING BENTHIC TAXA

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The saturation state for calcium carbonate (aragonite, calcite or various high magnesium calcites) is an important environmental parameter for marine calcifying organisms. Due to rising concentrations of atmospheric $CO_2$, as a result of anthropogenic activities, the oceans are becoming more acidic and the calcium carbonate saturation states are decreasing. At high latitudes, aragonite is already nearing undersaturation in surface waters and becomes undersaturated at relatively shallow depths (due to the negative effect of pressure and low temperatures). Unprotected aragonitic shells start to dissolve if bathed in seawater that is undersaturated with respect to aragonite ($\Omega_{aragonite} < 1$). The aragonite saturation horizon (ASH, the depth at which seawater is saturated, $\Omega_{aragonite} = 1$) is currently at approx. 1700 m depth in the Iceland Sea and is shoaling at a rate of 4 meters per year (Olafsson et al. 2009). Based on the Iceland Sea topography, 800 km$^2$ of benthic habitat is added to undersaturated areas every year. Isoclines for $\Omega_{aragonite}$ = 1.1, 1.2, and 1.3 are shallower and shoaling at a more rapid rate than the ASH.

We reveal the shoaling rates of various $\Omega_{aragonite}$ and $\Omega_{calcite}$ isoclines in the Iceland Sea. These changes are then put into context with the depth distribution of major benthic calcifying taxa in the Iceland Sea, based on a benthic sampling program (BIOICE). The BIOICE project was conducted around Iceland over the years 1994 to 2004, with ~1200 samples collected from a depth range of 20–3000 meters.

## *HIATELLA ARCTICA* AND *H. GALLICANA*: ARE THEY DISTINCT SPECIES?

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Mollusks of genus *Hiatella* are subtidal bivalves which occur in the seas of Northern hemisphere. Adult specimens of *Hiatella* are not well identified by the conchological criteria; morphological differences can be found on juvenile stages only. Taxonomy and species diversity of the genus *Hiatella* are complicated and were revised repeatedly (Jeffreys, 1869; Winckworth, 1932; Hunter, 1949; Simone et al., 2008 etc.). The most common species are *H. arctica, H. gallicana* and *H. pholadis*. In the White Sea, two species of the genus were found: *Hiatella actica* (Deryugin, 1928) and the second one, which was determined as *H. pholadis* (Naumov, 2006) or *H. gallicana* (Lezin, Flyachinskaya, Khalaman, 2010).

Adult mollusks from the White Sea are morphologically indistinguishable. Young specimens of *H. arctica* have well-marked spines and ridges at the posterior region of the shell. *H. gallicana* juveniles have smooth shells without spines. Spawning and settlement of these two species occur at different times:

*H. arctica* reproduces in summer, while *H. gallicana* – in early autumn. Despite that, 28s RNA analysis did not confirm differences between these two species (Lezin, Flyachinskaya, Khalaman, 2010). Furthermore, the intermediate forms of *Hiatella* (with features of both species simultaneously) were recorded.

Ecological preferences of *H. arctica* and *H. gallicana* generally do not differ; both species can be found in mixed populations. Basing on the two species cohabitation the role of temperature in the formation of the morphological differences has been suggested.

To test this hypothesis the following experiments were performed. Pre-metamorphic *Hiatella* larvae were reared in the laboratory at different temperature conditions (+5, +8 and +12°C). The experiments continued until the animals reached shell size 700 µm and formed elements of shell sculpture. At 12°C, mollusks formed shells with well-developed spines and ridges. Shells of mollusks reared at 5°C were smooth and did not bear spines. At intermediate temperature 8°C shells were smooth with knobs at the same position as spines.

Experiments were performed with larvae collected in summer and in autumn. Results obtained in different seasons were identical.

Our results show that the main taxonomic character of the species (shell sculpture) is not valid. Presence or absence of spines and ridges represent phenotypic variability in relation to temperature conditions. These data confirm the earlier doubts about the validity of the species status of *H. arctica*, *H. gallicana*, *H. rugosa* and *H. pholadis* (Jeffreys, 1869, Gorbunov, 1952, Keen, 1971, Beu, 1971, etc.) and demonstrate the need for another revision of the genus *Hiatella*.

## NEW GREGARINE SPECIES PARASITIZING THE LITTORAL AMPHIPOD *GAMMARUS DUEBENI* (*DUEBENI*)

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*Gammarus duebeni* (*duebeni*) is a widespread boreal Atlantic amphipod. This species is common for northern Arctic seas. Particularly *G. duebeni* (*duebeni*) occurs in the White Sea. As a rule, *Gammarus duebeni* (*duebeni*) inhabits the littoral zone preferring brackish water regions. Despite the wide distribution of these amphipods current knowledge about their parasites is meagre. A few species of parasites were described from this host: gregarines *Cephaloidophora maculata* (Codreanu-Bălcescu, 1996), *Cephaloidophora elongata* (Tuzet, Ormieres, 1962) and several microsporidian spesies (Bulnheim, 1973; Dunn, 1993; Terry, 1998). Here, I present preliminarily results of the investigation of parasites from the amphipoda *G. duebeni* (*duebeni*) sampled at the littoral zone near the Marine Biological station of St. Petersburg state university in July-August, 2013. Three new gregarine species were found in 185 individuals of *G. duebeni* (*duebeni*). These gregarines inhabited the host intestines.

1. A septate gregarine *Heliospora* sp. The infection rate was 4,3%, while the intensity varied from 8 to 73 cells per host. Mature trophozoits (gamonts) were of septate, thin, elongated shape with a broadly oblong protomerite (6,5±0,6 µm in length, 7,14±0,53 µm in width, *N*=27) and an elongated deutomerite (152,74±1,3 µm in length, 9,19±0,82 µm in wide, *N*=27) having a spherical nucleus (9,9±0,72 µm in diameter, *N* = 26) in its central part. Young trophozoits were attached to the host cell by a simple knob-like epimerite embedded into a depression of the of the host intestinal epithelium cell. After its detaching from the host epithelium, gregarines formed early caudo-frontal associations. Detached trophozoits demonstrated gliding motility typical of septate gregarines. No gametocyst stage was found.

2. A septate eugregarine *Cephaloidophora* sp. The rate of infection was 13,5%, the infestation varied from 2 to 300 individuals per host. Mature trophozoits had short body with a bell-shaped epimerite (9,97±0,02 µm in length, 13,35±0,03 µm in width, *N*=32) and a broadly obpanduriform deutomerite (28,95±0,05 µm in length, 16,02±0,05 µm in width, *N*=32) with a spherical nucleus (7,26±0,01 µm in diameter, N = 32) located near the septum or in the deutomerite center. Also, mature trophozoits (including free individuals) possessed a lenticular epimerite on the front end of the protomerite. Young trophozoits developed inside host epithelial cells, intracellularly, within a parasitophorous vacuole. They formed early caudo-frontal associations. Free parasite cells demonstrated gliding motility typical for septate gregarines. Gametocyst stages were not found.

3. Aseptate gregarine of uncertain taxonomic position. The rate of infection was 30,8%, the intensity varied from 1 to 93 individuals per host. Mature trophozoits had flattened, elongated body (length 168,3±0,44 µm, width 15,6±0,03 µm, N=33) with an oval nucleus (length 15,31±0,05 µm, wide 11,95±0,02 µm, *N*=33) in the central part of the parasite body. Interestingly, the parasite cell became narrow in this site. Young trophozoits developed extracellularly; they attached to the host cell by the front end expanded as s suck. Observed detached trophozoits were always single. No gametocysts were found. Usually mature

trophozoits demonstrated gliding motility; however, young attached individuals were capable of bending and twisting of the entire cell. The last type of motility was not described for eugregarines parasitizing in arthropods. Probably, this type of movement is depends on the construction of the epicyte of these parasites. Epiphytic folds were low, club-shaped in their apex. Longitudinal folds were slightly twisted spiral with regards to the cell axis. Systematic positions of septate gregarines parasitizing in Gammarus duebeni (duebeni) are well defined on the base of the parasite morphology and its specialization to the host. However, the systematic position of the aseptate gregarine remains uncertain. Undoubtedly, this gregarine belongs to the group Aseptatorina within the class Eugregarinorida. In the course of further research, we hope to get more ultrastructural and molecular data witch are necessary for detailed description of this species.

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## MOLECULAR DIVERSITY OF *CERASTODERMA EDULE* AT THE RANGE EDGE IN THE BARENTS SEA

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The northern part of marine boreal species' range is expected to show strong evidences of postglacial demographic changes in population history – expansions, contractions etc. Here, we focus on the range edge populations of the common cockle, *Cerastoderma edule*, a widespread Atlantic bivalve, to infer the possible postglacial population/demographic events in northern part of the range of this species.

Samples were collected from eight locations from the Barents Sea, as well as from 5 locations across the Norwegian, the North, the Irish Seas and the Bay of Biscay. We isolated 587 bp cytochrome c oxidase-1 (COI) mitochondrial DNA sequences, which were amplified with specifically designed primers. Additional mtDNA sequence data were mined from GenBank. All Barents Sea localities exhibit presence of the same dominant haplotype. It is also present in northern Norwegian Sea site – Bodø, but does not occur in Bergen (southern Norwegian Sea), where haplotype composition is similar to the North Sea sites. In general, the Norwegian Sea localities are characterized by more private-to-site haplotypes, while two easternmost localities in the Barents Sea lack diversity, comprising only one haplotype.

Population genetic structures were characterized by calculating Φst with analysis of molecular variance. Whole dataset showed Φst values significantly different from zero, reflecting existence of composite genetic structure. Thus, we calculated pairwise values of Φst among individual samples to divide them into geographically proximate groups where adjacent samples would not demonstrate any internal subdivision. As a result, the only possible group in the Barents Sea comprises four out of five locations at the East Murman ("EM"), excluding Shelpino site which consisted of "western" haplotypes. Upon this, we suggest that cryptic population structure exists at the range edge. This patchy pattern of spatial population arrangement is generally consistent with the assumption of irregular long-distance dispersal from Norwegian populations. We applied two methods, mtDNA mismatch analysis and bayesian skyline plots (BSPs), to estimate the magnitude and timing of past changes in population size. As expected, both analyses marked signatures of demographic expansions for "EM" and other Barents and Norwegian Sea sites. Moreover, according to BSPs expansion events in the "EM" group are approximately twice more recent than in Norwegian Sea sites. Interestingly, the time to most recent common ancestor in "EM" is comparable to such in subpopulation of southern part of the *C. edule* range, and both are shorter than time to MRCA in the North Sea populations.

Our results indicate that *Cerastoderma edule* populations present in the northern part of the range – in the Barents and the Norwegian Seas – were founded in different postglacial periods, and range edge populations shows regional heterogeneity. This cryptic population structure can be interpreted as a result of mixing settling larvae from differentiated "upstream" source populations. This scenario also explains how local populations with atypical haplotype diversity can appear. In Shelpino, such population was more similar to Norwegian sites than to neighboring Murman ones, and became extinct probably due to absence of new individuals arising either from immigration or local breeding.

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## INVASION GENETICS OF THE INTRODUCED ATLANTIC ROCK CRAB (*CANCER IRRORATUS*) IN ICELANDIC WATERS

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The Atlantic rock crab (*Cancer irroratus*) was first recorded in Iceland in 2006 and has since then rapidly spread throughout the country‘s southwestern and western coastal waters. The transport of larvae in ballast water is regarded as the most probable means by which introduction into Iceland occurred. As this species is commercially valuable, it may be possible to establish a viable industry harvesting rock crabs in Iceland, however to do this more information on species wide genetic diversity and demography is required. In this study genetic variation at seven microsatellite markers was analysed in samples from Iceland and five sites in North America, capturing most of the known range of this species. Our result divided samples from the native range into two groups, divided by a previously proposed barrier to gene flow, compatible with local hydrographic factors restricting larval-mediated gene flow. The Icelandic population was markedly differentiated from all other samples, but exhibited comparable levels of genetic diversity with no evidence of small population effects or genetic bottlenecks. No single population could be identified as a source for the Icelandic population. Genetic data indicate that the number of founders of the Icelandic population was sufficient to retain genetic variation. As the Icelandic population shows evidence of self-recruitment and population expansion, it may represent a potential harvestable resource in Iceland.

## CONVERSATION WITH A BIOLUMINESCENT PLANKTONIC WORM (POLYCHAETA: TOMOPTERIDAE)

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The main function of bioluminescence is to communicate. Showy or inconspicuous, attractive or deterrent, light signals are exchanged in the ocean between individuals, males and females, prey and predators. Despite a remarkable diversification of the visual adaptations, especially in the deep-sea, some bioluminescent emissions escape the eyes of most marine organisms. In this context, the yellow light flashes emitted by *Tomopteris helgolandica* (Polychaeta, Annelida) could be intraspecific private communication signals. Such a function has been previously suggested in the stomiid fishes which both produce and see red light emissions. But, is *T. helgolandica* able to perceive its own light? Basically, we know that 3-days larvae develop a pair of pigmented ocelli consisting of seven large rhabdomeric sensory cells topped by a lens. These early stages are positively phototactic but behavioral observations of adult specimens of the yellow-emitter *T. septentrionalis* have revealed photophobic responses to blue light flashes simulating dinoflagellate bioluminescence. Through a similar approach, we have tested the behavioral effect of simulated bioluminescent signals on our model species. Isolated specimen were placed under infra-red lighting in a round aquarium and filmed by a coupled CCD video recording system. One camera was sensitive to the IR so we can track the animal moving. Simultaneously, an intensified camera only recorded the bioluminescent events. Manually controlled light signals were applied through a fake worm – provided with optic fibers reproducing the distribution pattern of *T. helgolandica*‘s photogenic organs – immersed in the seawater. We tested 0,2 $s^{-1}$ flashes and continuous signals as well as five different light colors (blue, green, yellow, orange and red). The 50h of video collected were analyzed using the video tracking software Ethovision XT (Noldus Information Technology). Spontaneous light emissions have been observed during physical contacts with the fake worm and during stressfull situations like emersion but they did not seem to appear in response to the simulated light signals. They did not demonstrate specific interest in the yellow light emission but seemed attracted by the continuous blue light signals. These results lead us to reassess the virtually admitted hypothesis of intraspecific communication. We are now currently testing the hypothesis that *T. helgolandica* might, on the one side, use light signals against its predators as suggested by its responses to mechanical stimuli, and on the other side, take advantage of the bioluminescence of its own preys.

## INVASION OF THE ATLANTIC ROCK CRAB (*CANCER IRRORATUS*) IN ICELANDIC WATERS

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With the increase in global oceanic trade the establishment of non-indigenous marine organisms has become a major environmental and economic problem worldwide. Most marine invasions have resulted from commercial shipping, with ballast water and ship hulls as the main propagule pressure. In the year 2006 the Atlantic rock crab (*Cancer irroratus*) was reported for the first time in Icelandic waters, Eastern North Atlantic. This is the first record of this relatively large crab species outside its natural range off the east coast of North America. The crab was most likely transferred to Iceland as larvae in ballast water and has since successfully established a reproducing population in its new habitat. In order to study the colonization of the rock crab in Icelandic waters, we sampled adults by using baited traps and larvae by means of plankton net and studied the size structure and distribution of the species in the area where it was first found. Two native crab species, the European green crab (*Carcinus maenas*) and the spider crab (*Hyas araneus*), which inhabit the same areas, were studied in parallel for comparison. The former species is currently influencing the Atlantic rock crab in its natural habitat. In addition, we searched for rock crab larvae at selected sites in western and northern Iceland. Currently the species is distributed along the western coast of Iceland. Adult specimens are now common in Faxaflói Bay, Southwest Iceland, but with sporadic occurrences in western and northwestern Icelandic waters. The green crab and the spider crab are the only native brachyuran decapod species commonly found in its new habitat, but despite its recent colonization the rock crab was the most abundant brachyuran in the areas studied in Southwest Iceland. Egg bearing rock crab and green crab females were found from June to October, while egg bearing spider crab females were seen from July to December. Both rock crab and green crab larvae were abundant in mid-summer but rare in both spring and autumn, which is opposite of what was observed for the spider crab. The size and abundance of adult crabs, their reproductive conditions, and occurrence of all larval stages, indicate that the Atlantic rock crab has successfully colonized Iceland.

## ON THE SPECIES OF *NANNOCALANUS SEWELLI* AND *N. MINOR* (COPEPODA, CALANOIDA) FROM THE INDIAN AND PACIFIC OCEANS

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Until recently it was believed that the genus *Nannocalanus* Sars, 1925 – monotypic, and all its representatives from different areas of the World Ocean diagnosed as *N. minor* (Claus, 1863). However, even R.B.S. Sewell (1929) in the northern parts of the Indian Ocean noted the presence of two forms of this species: *N. minor* f. *minor* and *N. minor* f. *major*. Rather recently in zooplankton samples from South-East part of the Pacific Ocean (SEP) was discovered and described a second spesies of this genus, *N. elegans* Andronov, 2001. Author of this species noted that there are the females and males *N. minor* in these samples. More recent research (Kazus, 2009) showed that the representatives of the genus *Nannocalanus* of the northern part of the Indian Ocean are two distinct species, *N. major* Sewell and *N. sewelli* Kazus, whose females are distinctly different, mainly the structural features of the genital segment. A little later it became clear that according this feature the females *N. sewelli* virtually indistinguishable from the females of *N. minor* (SEP), but differ greatly from the females *N. minor* from waters, surrounding island Sicily – the area of description and redescription of this species [Claus, 1863; Andronov et al., 2005; Ivanova (Kazus), 2011].

The purpose of this article – to attract additional morphological characteristics and location the cover pores on the body females *Nannocalanus* to determine the species *N. sewelli* (Indian Ocean) and *N. minor* (SEP).

For this research were used representatives of these species taken from the same samples of zooplankton from which was obtained material for description *N. minor* from SEP and *N. sewelli* (Andronov, 2001; Kazus, 2009). Staining of the integument of crustacea performed by Naumova and Alekseev (2005). The cover pores' peculiarity of location was investigated only in the females of the species which are discussed. The main morphological characteristics the females of these species are:

*N. minor* from SEP: 1.56–2,00 mm body length, average – 1.75 mm ($n$ = 20). On the inner edge of coxa fifth pair of swimming legs (P5) locate 14–25 teeth, average – 18.21 ($n$ = 40) (Andronov, 2001). In addition was revealed that there is a longitudinal row of teeth on the XV–XXIII ancestral segments of antennule, however, in some specimen these rows of teeth begin only with XVI segment. The ratio of the width of operculum to the maximum width of the genital segment – 0.54–0.66 (*n* = 14). The ratio of the width of operculum in the zone of its bend to the length of operculum – 0.96–1.16 (*n* = 14).

*N. sewelli* from the Indian Ocean: body length – 1.6–1.9 mm, average 1.7±0.06 mm (*n* = 113). There is a longitudinal row of teeth on the XV–XIII ancestral segments of antennule. Quantity of teeth on the inner edge of coxa P5 – 10–16, average – 13±1.4 (*n* = 58). The ratio of the width of operculum to the maximum width of the genital segment – 0.60–0.68 (*n* = 16). The ratio of the width of operculum in the zone of its bend to the length of operculum – 1–1.2 (*n* = 16) (Kazus, 2009).

As you can see, the main differences between the females *N. minor* and *N. sewelli*, discovered earlier, are only in the quantity of teeth on the inner edge of coxa P5 (14–25 and 10–16 accordingly).

Comparing the character of location cover pores on the thoracic segments and abdomen segments of the females *N. minor* (*n* =32) and *N. sewelli* (*n* =51) revealed, that these characteristics are coincided completely. In the distal part of the genital segment of the abdomen (left view), both the pores locate on the same level relatively of the distal edge of the segment. You can see dorsally only the one of these pores, located at the base of chitin fold, approximately 1/3 of the length of this segment from the distal edge. In the second segment of the abdomen (left view), the pores in its middle part are at different levels relatively of its distal edge. On the dorsal side in the middle part of the second, third and fourth segments there is only one pair of pores.

Thus, the similarity in the location of the cover pores on the genital segment of females together with of other morphological characters lead to the conclusion, that the females *Nannocalanus* from SEP were indentified as *N. minor*, and the females *N. sewelli* from the northern parts of the Indian Ocean belong to the same species with priority name *Nannocalanus sewelli* Kazus, 2009.

## *AURELIA AURITA*: COSMOPOLITIC ANIMAL OR NOTHING BUT A COMPLEX OF SPECIES? MOLECULAR AND MORPHOLOGICAL ASSAY

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*Aurelia aurita* is known as a cosmopolitic species of Scyphozoa jellyfishes, widespread in marine coastal waters from north to south. It has a complex life cycle, realized by sedentary polyp and free swimming medusa. Despite medusa`s high dispersion possibility, some populations of *A. aurita* are isolated by various geographical barriers and thus live in very different environmental conditions, for example, water temperature, salinity or other factors. Together with the absence of valuable descriptions and well-defined characters it allows to suggest existence of a cryptic species complex within *A.aurita*. Recent studies have revealed some differences between several populations, but no comprehensive analyses was done.

In our work individuals of two laboratory strains of *A. aurita* were studied: “White Sea” (White Sea, Arctic Ocean) and “Roscoff” (from Roscoff marine aquarium, France). We focused on three different life cycle stages (polyp, strobila and ephyra) obtained from laboratory cultures. Both strains were cultured at the same conditions. To perform the comprehensive assay we examined both morphological and molecular features. For genetic analyses whole transcriptomes and certain gene sequences from strobila and ephyra stages were used.

Morphological analysis has revealed significant differences between two strains at each stage. Polyps could be well distinguished by body proportions and budding features. “White sea” strain polyps are wider than “Roscoff” ($F_{1,75}$ =64,016, p>0,1) but possess smaller tentacles ($F_{1,73}$=21,25, p>0,1). Individual “Roscoff” polyps are localised relatively far from each other while “White sea” strain polyps form compact colonies.

Strobiles differ in size, color, development rate and number of ephyres. “White sea” strain strobiles are visually bigger and usually possess 8-10 ephyres. “Roscoff” strain strobiles while been smaller possess 16–22 ephyres. Ephyres have differences in color and body proportions. Lappets in “Roscoff” strain are significantly longer than in “White sea ($F_{1,28}$=144,7 p<0,1).

The variation in single sequence is between 4 to 10 percent for conservative genes like EF1α, EGF and tubulines. For cnidarian specific gene mesoglein the level of differences is 12,3%. Three minicollagen sequences have 63,8 % differences.

Comparison of two transcriptomes shows significant level of differences, which was also confirmed by morphological studies. In average, difference level vary between 9 and 12 percent. About a quarter of contigs have difference level higher than 13%. Another quarter of contigs possess less than 8% differences up to full congruence.

Taking this into account, we can conclude that that "Roscoff" and "White sea" strains might be considered as two separate species. Thus, *Aurelia aurita* could be represented by a complex of geographically isolated different species. The revision of the group is highly needed to confirm this hypothesis.

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## KARYOLOGICAL AND MOLECULAR PHYLOGENETIC ANALYSIS OF THREE POPULATIONS OF *AURELIA AURITA* (WHITE, BLACK AND JAPANESE SEAS)

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Today it is believed that the genus Aurelia comprises three species: *A. limbata*, *A. labiata* and *A. aurita*. Perhaps due to its ubiquity, A. aurita has become a popular research organism for studies as diverse as protein chemistry, development, ecology, ethology, and hydrodynamics (Arai, 1997). *A. aurita* also is economically important because worldwide it preys on or competes with larvae of commercial fisheries and because swarms of medusae may impede trawling or block power-plant intakes (Möller, 1980). The systematics of *A. aurita* therefore is of considerable scientific, economic, and general interest.

Aurelia has a typical bipartite scyphozoan life history in which benthic scyphopolyps asexually strobilate ephyrae that grow into sexual medusae, the females of which brood larvae that settle into the shallow coastal benthos within a few days of being released. Of these life stages, the medusa probably is the principal dispersal phase because only the medusa is both long-lived (several months to more than one year; (Hamner and Jenssen, 1974)) and planktonic (Arai, 1997). The potential of medusae for distant dispersal is consistent with the current classification of *A. aurita* as a circumglobal, almost cosmopolitan, species (Kramp, 1968; Russell, 1970). However, *A. aurita* medusae in Saanich Inlet, British Columbia, and perhaps elsewhere, migrate directionally (Hamner et al., 1994), maintaining breeding aggregations within isolated inlets and probably limiting gene flow among populations. Consistent with limited gene flow, allozyme differences have been found between populations of *A. aurita* in the eastern and western Atlantic Ocean, the Gulf of Mexico, and the eastern and western Pacific Ocean (Greenberg et al., 1996; Zubkoff and Linn, 1975).

In this work we compare three populations of *Aurelia aurita* ("cosmopolitan species"): from the White, Black and Japanese Seas. We sequenced 18S and 28S RNA genes. We have constructed phylogenetic trees of objects from these three populations based on rRNA genes sequences.

We received karyotypes of *Aurelia* species from these populations and they differ greatly between themselves: *Aurelia* karyotype from the Japanese Sea has three pairs of submetacentric and 14 pairs of acrocentric chromosomes ($2n = 34$), while the karyotypes of *Aurelia* from the White and Black Seas are the same (8 pairs of submetacentric and 11 pairs of acrocentric chromosomes ($2n = 38$).

## THE LIPIDS AND FATTY ACIDS OF THE HADAL AMPHIPODS *HIRONDELLEA DUBIA* AND *SCOPELOCHEIRUS SCHELLENBERGI*

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The hadal zone, deeper than 6 km depth, is only found within the deepest ocean trenches. Amphipods are a significant component of the fauna at such depths and thus are vital for the circulation and dispersal of organic material. Very little is known of the ecology and physiology of hadal organisms due to the difficulty and cost in sampling. The Kermadec Trench in the south west Pacific ocean reaches 10 km depth. The two deepest and most ubiquitous species, *Hirondellea dubia* and *Scopelocheirus schellenbergi* dominate catches at hadal depths.

Lipids are vital to all organisms and are of key importance in buoyancy control and homeoviscous adaptations to the high hydrostatic pressures and low temperatures experienced by deep sea animals. The lipids and fatty acids of two hadal amphipod species were analysed. A total of 50 individuals of *H. dubia and 46 S. schellenbergi* were collected from 7014-9281 and 6097-8148 m depth respectively. The samples were analysed in order to investigate their lipid physiology, nutritional ecology, reproduction and development and buoyancy. Total lipid, lipid composition and fatty acid analysis of membrane and storage lipids are investigated to this effect.

## GAMMARIDEAN AMPHIPODA (CRUSTACEA) OF THE CHUKCHI SEA: THE SUMMARY

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Amphipod fauna and distribution is studied in the Chukchi Sea for more than 100 years. The most recent investigations in the field were made in 2010s by several expeditions organized by the RUSALCA project (www.rusalcaproject.com). A list of Amphipod taxa found by these expeditions in the years 2009–2012 is present following by the summary of the past collections. Biogeographic peculiarities of the amphipod fauna is given in the light of the overall biogeography of the Chukchi Sea. Ecological factors shaping the distribution of the most abundant species are analysed. Recent changes in species distribution are present and their possible reasons discussed.

## CALANOIDA OF THE WORLD OCEAN DWELLING IN THE VICINITY OF THE SEA BED

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The benthopelagic calanoid copepod fauna, especially, from the deep-sea habitats is still poorly known. Following to the recent development of special gear for the near-bottom sampling (Brenke, 2005), collections of hyperbenthic calanoids became more representative. Many taxa have been found in these collections and about 40% of the discovered genera appeared obligate inhabitants of the near-bottom. Processing of these samples is still in progress, while numbers of new species and genera are already described. Considering these recently obtained data, diversity of benthopelagic calanoids in the World Ocean is now estimated as being rather high. New calanoids found in the near-bottom contribute to the amazing discoveries of new crustacean species and genera, e.g., 2 new calanoid families, 9 genera and 18 species dwelling in the vicinity of the sea bed have been described just in recent 5 years (Markhaseva & Schulz, 2008, 2009, 2010; Markhaseva et al., 2008, 2013, Renz et al., 2012, 2013, etc.).

Only two calanoid superfamilies (Calanoida and Eucalanoida) have no obligatory representatives in the near-bottom environment, while the rest of calanoid superfamilies contain benthopelagic species/genera/families. Basic in the near- bottom fauna of the open-sea are representatives of Clausocalanoidea (63% of genera) and Arietelloidea (19%), and less presented are Ryocalanoidea, Spinocalanoidea and Bathypontioidea. Members of Clausocalanoidea, Spinocalanoidea and Ryocalanoidea are recorded in all of 3 biogeographical supra areas of the World Ocean (*sensu* Nesis, 1982), however, only Clausocalanoidea are really widespread in all latitudinal zones. The highest number of the near-bottom genera is registered in the tropical Atlantic (52) and Pacific (44). Benthopelagic calanoid faunas of these regions demonstrate similarity to each other, as well as, to the Antarctic and Boreal Atlantic near-bottom faunas (> 50% by Chekanovsky-Sorensen's and Bray-Curtis indexes). The connection between vertical and biogeographical distribution of the hyperbenthic calanoids in the World Ocean is revealed - genera with a wide range of vertical distribution, usually, also have a wide range of latitudinal distribution. Of 18 genera, cosmopolitan, nearly cosmopolitan, or recorded from all of 3 supra areas, only 2 genera are restricted exclusively to shelf (*Stephos*), or abyssal (*Kyphocalanus*). The remaining 16 genera have a wide range of vertical distribution and inhabit depths from abyssal plains to:

1) shelf (*Tharybis*, *Xanthocalanus*, *Bradyidius*, *Brachyclanus*, *Comantenna* and *Scolecitrichopsis*),

2) shelf break (*Neoscolecithrix*, *Bradyetes* and *Xantharus*), and

3) upper (*Rythabis* and *Byrathis*), or middle continental slope (*Ryocalanus*, *Brodskius*, *Damkaeria*, *Pseudeuchaeta* and *Pseudotharybis*).

First time recorded in the Southern Ocean are benthopelagic representatives of the superfamilies Ryocalanoidea and Arietelloidea and 7 genera (*Bradyetes, Pseudotharybis, Byrathis, Omorius*, *Neoscolecithrix, Rythabis,* and *Brodskius*), and for the Atlantic Ocean first time registered are genera *Crassantenna, Parkius* and *Omorius* (published and unpublished data).

Most of the new recently described benthopelagic calanoid genera belong to the superfamily Clausocalanoidea. Clausocalanoideans are the most evolutionary advanced among calanoids (Park, 1986, Bradford-Grieve, 2004). More probably, they are of primarily benthopelagic origin (Markhaseva & Schulz, 2006).The near-bottom clausocalanoideans demonstrate examples of plesiomorphic characters retained in benthopelagic taxa, but lost in their pelagic relatives and are characterized by the presence of a combination of both primitive and derived characters – heterobathmy (Takhtajan, 1966). Clausocalanoideans are supposed to have evolved in the benthopelagic realm, however, it is not clear in shallow or in deep near-bottom. The evolutionary trend in the ancestral near-bottom clausocalanoideans was probably linked with a splitting up and the multiplication of their adaptive zones in the vicinity of the sea bed. Clausocalanoidea is the most numerous and diverse benthopelagic calanoid superfamily, that is why its study is very interesting for the understanding of structure and functioning of the near-bottom World Ocean's communities. Hopefully, new materials from the deep near-bottom will add more information, as each new deep-sea expedition contribute new materials on the diversity of the benthopelagic calanoids and numbers of new taxa await their description

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### *SELENIDIUM* SP. (APICOMPLEXA: ARCHIGREGARINIDA) FROM THE INTESTINE OF PYGOSPIO ELEGANS (POLYCHAETA): FINE STRUCTURE AND PHYLOGENETIC POSITION

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The apicomplexans are obligate unicellular parasites including the most infamous and well-studied pathogens, e.g., *Plasmodium*, *Toxoplasma*, *Eimeria* and others which cause incalculable morbidity and mortality to humans and animals. Archigregarines are supposed to be the most plesiomorphic apicomplexans. They are exclusively parasites of marine invertebrates with extracellular localization within the host; their mature, elongated trophozoites (gamonts) still possess whole-cell motility and retain in the apical region a set of distinct organelles typical for apicomplexan infective stages (zoites). This unique set of organelles includes rhoptries, micronemes, an apical polar ring and a conoid. Thereby phylogenetic studies on archigregarines have a significant impact on inferences about the Apicomplexa evolution. The current knowledge of diversity and phylogenetic relationships of Archigregarinida is still meager. Phylogenetic studies based on 18S rDNA exposed that archigregarines formed few branches hardly grouping to one another and keeping uncertain position within Apicomplexa. Here, we report results of light (LM) and electron (EM) microscopy, and the molecular phylogeny of *Selenidium* sp. parasitizing the gut of *Pygospio elegans* (Polychaeta: Spionidae) sampled at the White Sea sand-silt littoral zone. Both attached and non-attached trophozoites were found in the host intestine. They showed very active nematode-like bending and twisting of the entire cell. Parasites detached very easily from the host intestinal epithelium during dissection. Non-attached trophozoites were aseptate, elongated and slightly flattened with the hook-like bent anterior end. The parasites were of 34–288 μm (av. 144, n=79) in length and 4–25 μm (av. 12, n=76) in width; an oval nucleus (6–22 μm [av. 17, n=40] x 5–11 μm [av. 8.4, n=26]) with a nucleolus was located in the widest part of the cell being expanded along its longitudinal axis. The syzygy was caudo-caudal; at this stage, the gamonts continued to move asynchronously. In the host, *Selenidium* sp. showed neither gametocysts nor stages of asexual multiplication (merogony). LM demonstrated the presence of 10–12 longitudinal superficial lines per flattened side of the cell and an intracellular axial streak extending from the anterior to the posterior ends. The axial streak formed an expansion around the nucleus and numerous radial threads toward the cell periphery. A similar axial system has been described for other parasites from spionids such as *S. spionis*, *S. pendula* and *S. axiferens*. Under scanning EM, the whole *Selenidium* sp. surface displayed approximately 28 broad and low folds separated by grooves corresponding to longitudinal superficial lines seen under LM. Numerous micropores were located at the bottom of grooves. Transmission EM showed that trophozoites were covered by a trimembrane pellicle (plasmalemma + inner membrane complex typical for apicomplexans) underlined by longitudinally oriented subpellicular microtubules. Microtubules were arranged in a single layer, the continuity of which was interrupted under the grooves where micropores were situated. Under the main layer, groups of additional irregularly arranged microtubules were present. Each microtubule was surrounded by an electron light sheath. The whole cytoplasm was indistinctly differentiated into two areas: an ectocyte, a narrow cortical region containing microtubules, mitochondria and multiple membrane-bound vesicles; and an endocyte containing the nucleus, majority of cellular organelles, amylopectin granules, lipid droplets and other inclusions. Observed cell organelles and inclusions were typical for archigregarines in general. The distribution of organelles and inclusions was not homogeneous, with narrow electron light spaces in cytoplasm irregularly arranged around the nucleus and along the cell axis. This heterogeneity along with different density of the cytoplasm could be the basis of the axial system observed in different archigregarines from spionids. The axial system deserves further investigations especially in the light of its putative role in cell motility, the so called 'concept of statomotor' (Fowell, 1936). Semi- and ultrathin sections of dissected pieces of trophozoite-infected intestines showed that the anterior end of *Selenidium* sp. was stretched (6–8 µm in length) and anchored between folds of the host intestinal epithelium. A direct contact between the host cell and attached parasite was not observed. Subcellular organization of the elongated anterior end was the same as that of the rest part of the parasite cell (pellicle, micropores, microtubules, mitochondria). In addition, several rhoptries and multiple groups of micronemes were present in the anterior end of *Selenidium* sp. We found no traces of the conoid and apical polar ring that might be a consequence of reduction of some apical organelles during trophozoite development. We can also suggest that the reason of this was our failure to obtain complete serial ultrathin sections. Thus, the fate of apical organelles is another subject for further investigation in this parasite. ML and Bayesian analysis of 18S rDNA data showed that *Selenidium* sp. from *Pygospio elegans* belonged to one of the archigregarine branches including four other parasites of polychaetes Sabellariidae and Spionidae: *Selenidium serpulae, S. boccardiella, S.* cf. *mesnili, S. idanthyrsae.* Unexpectedly, the analysis proved the full identity of sequences from specimens collected from different hosts and places: *Selenidium* sp. from *Pygospio elegans*, the White Sea, and *Selenidium* sp. from *Polydora glycymerica*, the Sea of Japan. This evidences that biogeographical distribution of archigregarines is probably more extensive then usually assumed, and that the traditionally used for gregarines systematic principle 'new host – new species' should be revised. To highlight the taxonomic status of the archigregarine involved in the present study, further investigations are needed including the comparison with other parasites from Spionidae polychaetes.

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## FINE STRUCTURE OF *POLYRHABDINA* SP. (APICOMPLEXA: EUGREGARINIDA), WITH EMPHASIS ON THE TAXONOMIC POSITION OF POLYRHABDINES

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Apicomplexans form a large and diverse group of unicellular parasites inhabiting invertebrates and vertebrates. Gregarines are mostly extracellular apicomplexan parasites that occur in the intestine, coelom and reproductive organs of marine, freshwater and terrestrial invertebrates. Most gregarines infecting the intestine of marine invertebrates have been described within the family Lecudinidae and the type genus *Lecudina*. The diversity of these 'marine' parasites is vast and still poorly understood. Moreover the family Lecudinidae is probably a taxonomic mixture; some species considered to be 'lecudinids' may well belong to other families of aseptate eugregarines. The genus *Polyrabdina* (=*Polyrhabdina* by Caullery & Mesnil, 1914, presently accepted) was established by Mingazzini, 1891 for *Gregarina spionis* Kolliker, 1848 from polychaetes *Malacoceros fuliginosus*. To date this genus comprises six species of parasites inhabiting marine worms of the family Spionidae; *Polyrhabdina spionis* is the type species. The identification of *Polyrhabdina* species is very difficult, as all of the original descriptions are based solely on line drawings. Furthermore, the descriptions are limited to the trophozoite stage with special attention to attachment organelles. In attached cells of *Polyrhabdina*, this globular organelle is embedded in a depression of the host intestinal epithelium cell. Some authors mentioned hook-like processes on the apical surface in addition to the circlet of tiny teeth at the base of the attachment organelle (AO). In contrast, other scientists described the AO without hooks on its surface, but with a collar at its base. There was no consensus on the definition of the AO: mucron or epimerite. Here, we present results of the fine structure study of an aseptate eugregarine *Polyrhabdina sp.*, a parasite of the spionid polychaete *Pygospio elegans*. About 50% of marine worms sampled at the silt-sand littoral zone near the White Sea biological station of St. Petersburg state university were infected with this gregarine. Both attached and non-attached parasites were found in the host intestine. The detached individuals measured about 28 – 288.4 µm (av. 123.3 µm, n=40) x 14 – 50.4 µm (av. 34.8 µm, n=40). As a rule, they were of ellipsoid shape and circular in cross section. Pear-shaped, slightly elongated or curved cells also occurred. Parasites had a large nucleus with one nucleolus. The non-attached cells demonstrated gliding motility. The cell surface of parasites was covered with numerous longitudinal epicytic folds. Some folds were straight, some ones were slightly undulated. Ultrathin cross-sections of gregarines showed that the organization of each fold was typical of that of eugregarines: a three-membrane pellicle (plasmalemma + inner membrane complex [IMC]), an electron-dense fibrillar layer (internal lamina) underlying the innermost membrane of the IMC. The internal lamina formed an additional loop between adjacent folds, but no connection at the base of each fold. In this case, the cytoplasm of each fold connects freely with the bulk of the cell cytoplasm. At the fold tip, 10–12 apical arcs could be seen between the plasmalemma and IMC as well as 10–12 apical filaments under the IMC. Typical micropores were located on side surfaces of the epicytic folds. The attached trophozoites were anchored in the intestinal epithelium by a globular AO (9 μm in diameter). The AO formed a skirt-like circular fold (2.6 μm in length) at the base. This circular fold was localized epicellularly and limited the zone of AO penetration to the host cell. The AO was very rarely observed in non-attached parasites. Trophozoites released accidentally from the intestinal epithelium during material preparation had attachment organelles with damaged surfaces. Longitudinal ultrathin sections through the attachment site of the host and parasite cells demonstrated that the AO was only covered by a plasma membrane. There was a close contact between the plasma membrane of the AO and the plasmalemma of the host epithelial cell. The skirt-like circular fold represented a thin cytoplasmic extension of the AO covered by the host membrane and parasite plasma membrane. The cytoplasm of the AO exhibited obvious zonation: a finely granular cortical zone located peripherally under the plasma membrane and filled the circular fold; a vesicular cytoplasm of the central part with occasional organelles typical for the rest of the parasite body (e.g., amylopectin granules). No septum was observed between the AO and the rest of the cell. However, at the base of the AO there was an annular membrane junction formed by the plasmalemma of the host cell and the plasma membrane with IMC of the parasite. In this region, the cytoplasm was organized as a ring enriched by some fibrillar material. From the annular membrane junction a thin fibrillar layer extended to the cell body being spread under the pellicle; then it transformed to the internal lamina of the pellicle. There is a need to add that several gregarines *Polyrhabdina* sp. were infected with microsporidia *Metchnikovella spiralis* and *M. incurvata*. Interestingly, the microsporidian stages also occupied the AO of the host. We believe that the AO of *Polyrhabdina* sp. represents an epimerite. Its structure resembles that in some septate eugregarines, but differs from the mucron in lecudinids. Additionally we compared scanning electron microphotographs of *Polyrhabdina* sp. and *P. spionis* isolated from polychaetes *Malacoceros fuliginosus*, which were sampled at the littoral zone near the Biological station of Roscoff. Gregarines of both species share the same attachment apparatus: the globular epimerite with the circular fold around its base. At the end of the attached stage, polyrhabdines separate from the host epithelium. The alternative possible ways of the separation mechanism can be considered: throwing the epimerite away from the parasite cell or retracting the epimerite inside the parasite body as a result of the contraction of the fibrils located at the epimerite base. Following Kamm (1922) and her successors we propose to exclude the genus *Polyrhabdina* from the family Lecudinidae and place it in its own family Polyrhabdinidae.

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## SEAWEEDS IN THE FJORDS REGIONS OF SOUTHERN CHILE: BIODIVERSITY INCLUDING ANTIOXIDANT COMPOUND PROFILES AS AN ADDITIONAL PARAMETER

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The fjord region of southern Chile is characterized by a high biodiversity due to the subantarctic water, equatorial subsurface water and western Pacific subsurface water it receives, together with the fact that in the interior zone, all these are mixed with freshwater from precipitation, river flow, and meltwater from Cordilleran glaciers. Several studies of the Comau fjord, for example, report this biodiversity particularly considering anemones and corals. However, the distribution of seaweed in this ecosystem has not previously been reported. Seaweeds are very rich in different compounds that may exhibit significant biological activity, including a class of phenolic antioxidant compounds, the phlorotannins, not found in other natural products. The potential applications of these bioactive compounds make it especially interesting to characterize seaweed according to its antioxidant compound profile. The aim of the work reported here was to characterize the biodiversity of seaweeds in Comau Fjord, considering not only taxonomy, but also antioxidant compound profiles. To that end, seaweed samples were collected from the submareal and intermareal areas surrounding the Huinay Scientific Field Station, at Comau Fjord, in October 2013. The samples were identified according to morphological characteristics, dried in an oven at 60°C for 2 h and the following analyses were carried out according to procedures previously described for seaweeds: total polyphenol content (extractable and hydrolysable), polyphenol profile by HPLC-DAD, antioxidant capacity by FRAP (ferric reducing antioxidant power assay) and ABTS (2,2'-azino-bis(3-ethylbenzo-thiazoline-6-sulfonic acid) assays. The six most abundant seaweeds in the area were finally selected for analysis: 2 brown (*Macrocystis* and *Scytosiphon*), 2 green (*Ulva* and *Enteromorpha*) and 2 red (*Gracilaria* and *Callophyllis*) seaweeds. *Scytosiphon* showed the highest extractable polyphenol content (1,297 mg/100 g dry weight), which was between three- and four-fold that of the other samples. The two red seaweeds showed the highest hydrolysable polyphenol content: approximately 600 mg/100 g dry weight. The HPLC-DAD profiles of hydrolysable polyphenols in *Gracilaria*, *Macrocystis* and *Ulva*) (one for each color of seaweed, selected according to their abundance and their polyphenol content) showed the presence of hydroxycinnamic acids, hydroxybenzoic acids and flavonols. *Enteromorpha* showed the highest antioxidant capacity, both in terms of reducing capacity (FRAP assay) and free radical scavenging (ABTS assay). In conclusion, we identified the 6 most abundant seaweeds in Comau Fjord including their antioxidant compound profiles and associated antioxidant capacity as additional parameters. Some of the seaweeds showed a remarkable content of bioactive compounds that should be further studied in order to find possible biomedical applications for them as well as to carry out a classification of Chilean seaweeds in terms of their bioactive compound profiles.

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## MARINE INVERTEBRATES AS THE OUT-GROUP FOR BILATERIA DIFFERENTIATION PATHWAYS

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The model organisms of biology are selected for their ability to answer questions cutting across the boundaries of traditional disciplines and incorporating molecular, organismal and zoological studies. The growing interest in out-groups to the Bilateria reflects the strategic shift. Marine invertebrates, such as Cnidaria and Protochordata (ascidia) represent good out-groups.

Up to now molecular studies of marine invertebrates have emphasized a candidate gene approach, characterizing invertebrate homologs of genes with conserved functions in the Bilateria. These studies revealed an unexpected complexity in the genomic regulatory systems and the developmental patterning mechanisms, blurring the boundary between the supposedly “simple” Cnidaria and ascidia and the “complex” Bilateria.

The comparative “gene approach” studies make obvious a similar gene pattern in the same differentiation pathways in distant species to such an extent that the very term “tissue” becomes uncertain. For instance, if *Aurelia aurita* medusa possesses striated muscles with gene expression characteristic of the myogenic pathway, could they be designated a special tissue in spite of their origin?

The “candidate gene approach” makes it possible to check whether there are any of the known vertebrate genes, but such a way leads nowhere if a special gene, absent in other animals, makes inbertebrate tissues so different from the rest of the internal medium tissues. In an attempt to find genes specific for precise invertebrate proteins we used quite a different way than the candidate gene approach.

We began with the question – what is the difference between the medusa and the polyp body plan? In molecular terms it led to the new protein mesoglein identification and its’ gene cloning. Mesoglein possession of ZP domain attracted our attention to the oocyte contact plate, which could be the first sign of the future Zona Pellucida. Mesoglein happens to be expressed only by mesogleal cells (Mc) of the adult medusa. It seems that mesoglein expression may help to distinguish the tissue identify of mesoglea as a distinct layer from ectoderm. But the overview of all our results rather confirms that Mc and, probably, the whole mesoglea originate from ectoderm.

The origin of the ascidian morula cells, which participate in the adult tunic formation is also not clear. The test cells with similar to morula cells antigens surround the ascidian oocyte and involved in the formation of the larval tunic.

We found two major proteins of *Stiela rustica* morula cells – p26 and p48 kDa. MS-MS analysis determined the probability of several amino acid sequences of the tryptic fragments of proteins, which allow to produce degenerate primers for p26. We used RACE-PCR on cDNA (prepare from poly(A)RNA ascidian blood cells), and obtained fragment of open reading frame of 567 nucleotides. This sequence is unique and not described previously. The full-length gene of the p26 will help to answer the questions about its’ differential expression.

The identification of a single gene and the demonstration of its presence in a tissue layer of interest do not provide a positive solution of its’ origin. It only shows that the candidate gene approach is insufficient to fully characterize tissues and that an unbiased approach will be necessary: complete systems should be compared and next generation sequencing techniques give such a possibility.

The results of current work will come in molecular biology terms – with precise figures, gene patterns and sequences. This type of information does not agree happily with the way of thinking in classical terms such as “tissues” or “germ layers”. There is an urgent necessity of a new biological language, one combining the classical point of view with the formal and exact computer and database-based language of modern biology.

## A NEW CHRYSOCHROMULINA SPECIES FROM THE BAY OF BISCAY

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A marine species of the genus *Chrysochromulina* is described by means of light and electron microscopy and SSU and LSU rDNA sequencing. It was brought into culture from surface samples collected on September of 2006 on the seaward part of the Nervión river estuary (Bay of Biscay, Spain) using the serial dilution technique. The cells are saddle shaped (3.3–6.6 µm), possess two equal flagella (10–17 µm), a coiling haptonema (42–75 µm) and two chloroplasts. The cover is composed of a proximal layer of oval to spherical plate scales (330–570 nm) and a distal layer of spine scales (339-616 nm). Morphologically it is similar to *C. rotalis,* but phylogenetic analyses based on SSU and LSU rDNA sequences indicate that it is a new species.

## ULTRASTRUCTURAL CHARACTERISTICS OF TEST CELLS IN ASCIDIANS WITH DIFFERENT TADPOLE DEVELOPMENT

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Ascidians (Ascidiacea, Tunicata) are very interesting for evolutionary studies as one of the key basal chordate groups. In adult ascidians both epidermal and “blood” (morula type) cells take part in forming and modifying of tunic extracellular matrix. However it is not clear enough how to form and modify larval tunic. Ascidians have a unique cell type surrounding oocyte – test cells. This cell functions and origin are under discussion. There is a hypothesis about participation of test cells in larval tunic formation. The other one hypothesize that test cells are mesenchymal cells descendants as the blood cells. We found that antibodies against morula cell protein of ascidian Styela rustica bind antigens not only in morula cells but also in test cells in several species. The aim of this study was to compare ultrastructural characteristics of test cells in ascidians with different larval development, Styela rustica and Molgula citrina, members of order Stolidobranchiata.

The test cell cytoplasm of M. citrina mature test cells is filled by the granules with diameter 2–4 mkm, and the rER cisterns. Granule material is rather dense and homogenous, it resembles dense core of morula cell complex granules. When the larval development starts granule material begins to loose. Then it is released into perivitelling space where it forms structures called “ornament” on the surface of forming larval tunic. Granule material packing in S. rustica test cells is quite different. The hyaline cytoplasm of mature test cells is filled with granules of at least two types: the granules containing loose fibrillar structure are the prevailing type ($d$=4–5 mkm), and also small, dense heterogeneous granules ($d$=2–4 mkm) are present. According to the results of histochemical analysis the granules of morula cells contain basic proteins whereas test cell granules contain a great moiety of acid carbohydrates combined with proteins in S. rustica but not in M. citrina. The latter has test cell granules with protein predomination over polysaccharides. Notwithstanding that histochemical features of test cells of these species are different the existence of common antigenic sights might point out indirectly at similar functions in tunic formation and/or modification.

M. citrina has internal fertilization, internal larval development and adultation larvae, whereas S. rustica possesses external fertilization and free-swimming larvae. Finding differences in test cell ultrastructural characteristics in M. citrina and S.rustica might be determined by the different ways in larval tunic formation in ascidians with different ways of larval development.

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# RETROTRANSPOSONS OF DIFFERENT FAMILIES PARTICIPATE IN THE TREMATODE *HIMASTHLA ELONGATA* PARTHENITAE CLONAL DIVERSITY

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Transposable elements (TE) are widely spread in all major phylogenetic groups and comprise a significant part of eukaryotic genomes. TE are divided in 2 classes: retrotransposons and DNA transposons. Transposition of DNA transposons is controlled by a “cut-and-paste” mechanism; retrotransposons move with reverse transcription through RNA-intermediate. The study of repeated sequences is very important for understanding the genome organization and evolution of living organisms. Unfortunately, the transposon nature and functions have been poorly investigated, considering their number in the genome. The study of mobile elements' function requires an appropriate object. A small marine parasitic flatworm – *Himasthla elongata* (Trematoda, Echinostomatidae) (Mehlis, 1831) is the object of our research. Parasites have a complicated lifecycle with alterations of hosts and reproduction types. It has been believed for a long time that the worms’ parthenogenetic generation, redia or daughter sporocysts, that arise from one miracidium and inhabit a mollusk, as well as larvae produced by it, cercariae, constitute a clonal population and should have the same genotype. But it is known, that cercariae have different infectivity rates and geo- and photo-orientation inside clonal populations. Thereby, the polymorphism could be expected and it increases the parasite’s genetic variability and, accordingly, the chance for successful host invasion.

We found that the S-SAP (Sequence-Specific Amplification Polymorphism) method revealed clonal variability in the genomes of *H. elongata* larvae. The method provides the result as the number of bands, variable or conserved, on the sequencing gel electrophoresis. Cloning of several bands from S-SAP electrophoresis patterns was performed. Sequence analysis allowed to find the presence of CR1-like and RTEX-like non-LTR (Long Terminal Repeat) retroelement fragments in the bands with less variation (i.e. conservative regions on electrophoresis pattern). We determined the dispersed distribution of CR1-like retroelement fragments in *H. elongata* genome by fluorescent *in situ* hybridization (FISH). The signal is scattered through the nuclei and chromosomes, which is usual for the representatives of non-LTR element class. CR1-like elements are concentrated in some regions but do not produce large clusters. Bands from the variable regions of the electrophoresis pattern contained SR2-like non-LTR retroelement and Saci-like LTR retroelement fragments. Some sequences have no stop codons or frame shifts and appear to belong to active retrotransposon copies. It has been found recently that transposon transcription is very important for early development. So, the source of clonal variability could be provided during normal worm embryogenesis. Thus, it has been shown that

1) cercariae of trematode *H. elongata* have clonal diversity,

2) the S-SAP method allows to obtain patterns of fragment distribution characteristic for individual cercariae, and

3) retrotransposons of different families are the input to the pattern of polymorphic fragments and could be the source of the clonal diversity.

# POPULATION GENETIC ANALYSIS OF ATLANTIC BONITO *SARDA SARDA* USING SEQUENCE ANALYSIS OF MTDNA D-LOOP REGION

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In this study mitochondrial DNA D-loop gene sequencing was used to investigate genetic structure of 11 Atlantic bonito *Sarda sarda* populations from the Black Sea, Marmara, Aegean, Mediterranean Seas and Adriatic Sea. Spatio-temporal sub-sampling was achieved from the same location and time for 2011 and 2012 years. The total sequence length, variable sites and parsimony informative sites were 868 bp, 12 bp and 7 bp from 222 individuals respectively. The nucleotide frequencies are 32.55% (A), 31.32% (T/U), 14.44% (C), and 21.68% (G). There were no genetic differences between the sub-samples therefore they were combined as one population. The total number of haplotypes was 19, and the highest number of haplotypes was observed in the Iskenderun Bay sample and the lowest number of haplotypes was observed in the Bulgarian sample. Low genetic diversity was observed within populations, and mean genetic diversity within populations and mean genetic divergence between populations were 0.0009 and 0.0013 respectively. *S. sarda* was divided into three genetically different populations ($P<0.001$). *S. sarda* in the Black and Marmara Sea comprise one genetic unit, and *S. sarda* in the Aegean and Mediterranean coast of Turkey constitute the genetically different second unit. The Adriatic Sea sample was also genetically different from these two units.

## PHYLOGENETIC RELATIONSHIP OF NINE SCOMBRID SPECIES INFERRED FROM MITOCHONDRIAL DNA SEQUENCES OF COI REGION

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The phylogenetic relationships among nine Scombrid species (*Thunnus alalunga*, *Thunnus thynnus*, *Euthynnus alletteratus*, *Auxis rochei*, *Katsuwonus pelamis*, *Sarda sarda*, *Scomber japonicus*, *Scomber scombrus*, *Scomberomorus commerson*) distributed along the Mediterranean Sea was examined using mitochondrial sequencing of Cytochrome Oxidase subunit I. Mean genetic diversity within and between species were found as 0.002 and 0,117 respectively. The lowest genetic distance was observed between *T. alalunga* and *T. thynnus* (0.005) while the highest was between S. japonicus and Indo-Pasific originated *S. commerson* (0.201). Intraspesific genetic diversity within *K. pelamis* and *E. alletteratus* was zero while it was highest in *S. commerson* (0.005). The three different phylogenetic approaches (NJ, MP, ME) resulted in similar tree topologies. In Neighbour joining phylogenetic tree, two main phylogenetic nodes were detected; in the first node, *S. scombrus* and *S. japonicus* grouped together. *S. commerson* was most divegentlt clustered in the first branch of the second main node, and sisterly branched to *S. sarda*. *A. rochei*, *E. alletteratu*s, *K. pelamis*, *T. thynnus* and *T. alalunga* were grouped together in third branch in which *T. thynnus* and *T. alalunga* showed very close relationship.

## ULVALES OF THE GERMAN BALTIC SEA COAST: MORPHOLOGICAL PLASTICITY, RANGE EXPANSIONS AND CRYPTIC SPECIES

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Green algae of the order Ulvales often exhibit extreme morphological plasticity, which impedes their identification without DNA sequencing. We here present a study of macroscopic Ulvales that was primarily based upon barcoding of the tufA marker gene and aimed at adapting species lists and taxonomic keys for the German Baltic Sea coast to the existing species inventory in this area. Extreme morphological plasticity – ranging from tubular to sheet-like thalli that consisted of one or two cell layers – was detected for the two most abundant species in the area, *Ulva linza* Linnaeus and *Ulva intestinalis* Linnaeus. In contrast, a species that was genetically indistinguishable from *Ulva compressa* Linnaeus never exhibited the expected branched tubular morphology of the type material and formed always sheets instead. Cultivation trials revealed that sporelings of the later species only form reduced attachment tissue, which possibly explains the fact that this species occurs nearly exclusively unattached (19 out of 21 samples), contributing 38 % of all drifting specimens from the area that were investigated. Two species that were for the first time detected in the Baltic Sea are *Ulva rigida* C. Agardh and *Kornmannia leptoderma* (Kjellmann) Bliding, with the later exhibiting the typical life cycle in laboratory culture. The most abundant species within the genus *Blidingia* was a cryptic species, genetically different from *B. minima* (Nägeli ex Kützing) Kylin and *B. marginata* (J. Agardh) P. J. L. Dangeard. *Ulva lactuca* Linnaeus, *Ulva prolifera* O. F. Müller, *Gayralia* sp. and *Ulvaria* sp. were expected, but not detected in the area.

# SEA ANEMONE NEMATOCYSTS STORED AND TRANSPORTED IN CNIDOSACS AND CNIDOPHAGE CELLS IN NUDIBRANCHS

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The nudibranchs *Aeolidia papillosa* (Linnaeus, 1759) and *Aeolidiella glauca* (Alder and Hancock, 1845) were fed with the sea anemones *Metridium senile* (Linnaeus, 1759) and the small anemone *Sagartiogeton viduatus* (Muller, 1776). Aeolid nudibranchs are known for storing nematocysts for self-defence from cnidarian preys in their numerous dorsal papillae or cerata. The nudibranchs possess a specific sorting mechanism to sequester these nematocysts. In each cerata tip a divertriculum of the gut opens into a cnidosac. Unfired nematocysts are stored in cnidophage cells inside the cnidosacs. One, two, three or more anemone nematocysts, of the same or of different types, could be present inside one cnidophage. Cnidophages, filled with nematocysts, were pressed out through the cnidosac pore. *A. glauca* and *A. papillosa* seemed to have a certain preference to store the most potent, large penetrating nematocysts; the large and medium p-amastigophores. They were relatively more numerous in some cnidosacs than in the anemones. Large p-amastigophores were often more abundant than large b-mastigophores, the most common acontia nematocysts. Small nematocysts were more abundant in the nudibranch faeces compared to in the cnidosacs. The adhesive spirocysts, which are not useful for self-defence for the nudibranchs, were not found in the cnidosacs or in the cnidophages. Spirocysts were ejected with the faeces. Stored nematocysts might partly mirror which anemone structure the nudibranch had eaten. The larger nematocysts, from the acontia of the anemones, dominated in many cnidophage cells. Expect for in the acontia, medium b-mastigophores were the most common sea anemone nematocysts. In some cnidosacs medium b-mastigophores were the most abundant nematocysts. *A. glauca* cnidophages had the structure of an elongate bag, with an opening apically, through which nematocysts were ejected. The cnidophages were parallel oriented, with their apical end towards the longitudinal centre of the cnidosacs. In its broad base a large nucleus and cytoplasm were present. The cnidophage narrowed from its broad base towards its apical end. Inside the cnidophages the elongate, mostly closely packed anemone nematocysts were parallel oriented. Their openings pointed all towards the apical cnidophage end with the opening. *A. glauca* cnidophages were slightly longer than the longest nematocysts of the favorite prey of the nudibranch, the *S. viduatus* anemone. Large *M. senile* nematocysts, too long to fit inside the cnidophages of *A. glauca*, were ejected with the nudibranch faeces. In light squash preparations of *A. papillosa* cerata, narrow strings of undamaged cnidophages could be pressed out of the cnidosac. *A. papillosa* cnidophages varied in size and shape, and the number of their stored nematocysts varied from 1–5 up to 15–20. No opening was visible in the apical cnidophage cell. Basally, the large nucleus and some cytoplasm were visible. Inside the larger, most common cnidophages, nematocysts were closely packed, and their number was not possible to count, as long as the cnidophage was intact. Nematocysts too long to fit inside the smaller cnidophages had only their apical capsule ends inside the apical cnidophage. Their basal capsule ends, outside the cnidophage, were sometimes spread apart in the squash preparations. However, the undischarged nematocyst capsules were still kept together by the apical cnidophage. The smallest cnidophages were of the size of the smallest *A. papillosa* nematocysts. Often they contained one single or 2–4 small nematocysts. The somewhat larger cnidophages contained 2–4, or more nematocysts of different sizes, the largest capsules with their basal end outside the cnidophage. Empty cnidophage cells, presumably representing different developing stages, were of different sizes and irregular shapes. Some cnidophages were connected to each other. A big nucleus was visible in the cytoplasm. The cytoplasm surrounded the inner cell wall, leaving an inner canal free of substance. In mucus strings, excreted from the nudibranch anus, cnidophage cells filled with nematocysts, small packages of free nematocysts fitting in size into the cnidophages, and strings of closely packed, abundant, free nematocysts were present. Nematocysts in the packages and in the strings were parallel oriented, with their apical capsule end pointing in the same direction. In both *A. glauca* and *A. papillosa* cnidae, less useful in self-defence for the nudibranchs, were rejected with the nudibranch faeces. In some faeces discharged or undischarged spirocysts were by far the most abundant cnidae. Small nematocysts were more common in the faeces than larger nematocysts, except for the largest *M. senile* b-mastigophores in the faeces of *A.glauca*. Large p-amastigophores were rare or missing. Additional observations and conclusions: Immature nematocysts, early in development, were not found in the cnidosacs. Only a few elongate p-mastigophores, late in development, with the same capsule structure as mature ones were indentified here. Obviously most nematocysts did not complete their maturation in the cnidosacs as proposed by Greenwood and Mariscal

(1984). The shape and size of the cnidophages seemed to have an important roll in the transportation of nematocysts. No hydrozoan and scyphozoan nematocysts have been found in the cnidosacs. The rounded to oval size of these nematocysts might inhibit their storage in the cnidophages and cnidosacs. Hydrozoan and scyphozoan nematocysts were found in the nudibranch faeces. The sorting and rejecting mechanisms and the transportation of the nematocysts in the nudibranchs are still unknown but must be regarded as a masterpiece.

# ROUND TABLE

## *Marine science today: strategy, challenges and practical opportunities*

### SICILIAN FISHERMEN DISAGREE WITH THE NEW EU FISHERIES REGULATIONS: ARE THEY RIGHT?

**P. Consoli[1], L. Castriota[2], M. Falautano[2], P. Battaglia[1], V. Esposito[1], T. Romeo[1], M. Sinopoli[2], P. Vivona[2], F. Andaloro[2]**
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In 1999, after the collapse of the small pelagic's stocks in the Strait of Sicily (central Mediterranean), Italian Ministry authorized the trawl fishery to 13 Lampedusan fishing boats in order to mitigate the crisis of the fishery sector in this small island. This temporary fishing license, renewed, from year to year, by means of an Italian Ministerial Decree, was also justified by the high abundance of demersal cephalopod resources (i.e.: *Octopus vulgaris*) in the area, already exploited by the Italian fleet as well as by other European and extra-European vessels. Such a fishery has produced high yields when the 24 mm square mesh codend was used. After the application of the 40 mm diamond-mesh (regulation CE 1626/94), Sicilian trawl fishermen operating in the area reported decreases in catches that became unprofitable after the adoption of the 50 mm diamond-mesh, as established by the new regulation CE 1967/2006. Pressed by fishermen complaints, Fishery Department of Sicily Region promoted a research aiming at comparing the catch composition and yields of both retained and discards species, obtained with two different mesh sizes in the continental shelf bottom trawl fishery off Lampedusa Island: i) the previously used square mesh codend (24 mm) and ii) the current legally employed 50 mm diamond mesh codend. For this reason, twenty-one hauls were performed with an experimental 24 mm square mesh codend and 27 with the 50 mm diamond mesh codend at depths between 40-80 meters off the coasts of Lampedusa Island (Strait of Sicily). Total catches were sorted into the retained and discarded components by fishermen and catch data (kg and number of specimens of each species) were standardized to km$^2$. Finally, a permutational analyses of variance was used to perform univariate analyses in order to compare biomasses and abundances obtained by both mesh sizes (24 and 50 mm). A total of 55 taxa were retained whereas 120 were discarded. The retained fractions, represented a small part of the total catch in weight (23% and 21% with 24 and 50 mm mesh size, respectively) and cephalopods represented the most abundant group reaching the 58% in weight of the retained fractions by both mesh sizes. Most of the discard, instead, was made up by rhodoliths and macrophytes which reached, with the 50 mm mesh size, almost 90% in weight of the entire fraction. Fishes represented the second discarded group in term of % weight whereas all other groups recorded irrelevant weight percentages. The most common species encountered in the retained fraction were *Eledone moschata*, *Merluccius merluccius*, *Mullus surmuletus*, *Pagellus erytrhynus*, *Loligo vulgaris* and *Octopus vulgaris* which recorded the highest yields with both mesh sizes: 24 and 50 mm. These target species and all main taxonomic groups, caught by the 24 mm mesh size, always recorded mean CPUEs higher than 50 mm mesh size. Because of high values of standard deviations, in most cases, the univariate Permanova was not able to detect significant differences ($p<0.05$) between biomass indexes recorded by the two used mesh sizes. Moreover, the mean number of immature specimens (or below the minimum landing size) was higher with the illegal mesh size for all the main target species. According to the results obtained, the present research proved that fishermen are not right to refuse the new EU restrictions imposed by the regulation CE 1967/2006; in fact, the legal mesh size, even if not always significantly, reduces the number of immature specimens and yields of target species. What is more, this study, even if based on a quite obvious initial hypothesis, gave us the opportunity to gain an insight into the macrobenthic assemblage of the area. The discarded fraction, which represented almost the 80% in weight of the total catch, was mainly compose by rhodoliths or Maërl (calcareous red algae) which constitute a priority habitat according to the SPA/BIO protocol (Barcelona Convention). Moreover, according to the regulation CE 1967/2006, fishing with trawl nets, dredges, shore seines or similar nets above mäerl beds are prohibited. Based on the obtained results, the trawl fishery carried out in the area could not sustainable, both from an economic and ecosystem point of view. For these reasons, in our opinion, and according to the precautionary approach to fishery, further studies should be carried out in order to map this priority habitat, identify its boundaries, and then give precious information for the fishery management in the area.

## DEMO OF THE LIFEWATCH DATA SERVICES: ONLINE DATA PROCESSING TOOLS FOR BIODIVERSITY RESEARCH

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European and global biodiversity facilities, such as observatories, data bases and data systems, are often distributed and not linked to each other. Furthermore, the current availability of and access to biodiversity data at species level can be rather poor. Therefore, scientists who want to solve a certain scientific question first have to figure out which data can be found where, then they have to go to each facility separately and request the data, and, in case the data were indeed available, they have to face the challenge of piecing together all data to come to a coherent answer.

LifeWatch, a new e-infrastructure launched within the European Strategy Forum on Research Infrastructures (ESFRI) aims to integrate observatories, databases, web services and modelling tools, and thus act as a virtual laboratory to support and encourage scientific research on biodiversity and ecosystem functioning.

As part of the Flemish contributions to LifeWatch, the Flanders Marine Institute is making available several databases and data systems: e.g. the World Register of Marine Species (WoRMS, http://marinespecies.org/), Marineregions (http://www.marineregions.org/), the (European) Ocean Biogeographic Information System ((Eur)OBIS, http://iobis.org/, http://www.eurobis.org/), etc., and is developing several data services to make these and many more European and global data systems interconnected and accessible in one place. These data services are available through an online interactive data portal (http://lifewatch.be/data-services), and assist scientists in data standardization, quality control, visualization, analysis and retrieval of additional data. As LifeWatch is still in its construction phase, the number of available data services will increase in the next years.

When used in a concatenated way (i.e. where the output of one data service is the input for another data service), these data services are currently already able to answer certain scientific questions: (1) For instance, the user uploads a list with marine place names (e.g. name of a sea or ocean) and wants to know which species have already been observed in these areas and how many times. To answer this question two data services were built: the first data service (Get lat-lon by name) matches these uploaded place names to the Marineregions gazetteer and translates these place names into MRGIDs (Marine Regions Geographic Identifier). The second data service (Taxon list of a certain region) checks how many species observations are linked to these MRGIDs in OBIS, and generates a species list per geographical area. (2) Or perhaps the user uploads a list with their own species observations (marine species name, latitude, longitude) and wants to know how many times these species were already observed in a certain radius (e.g. 1000m) around their observation points. To find the answer to this question, two more data services were developed: the first data service (Taxon match) matches the uploaded marine species names to WoRMS and translates them into an AphiaID (the unique identifier of Aphia, the database behind WoRMS). The second data service (Number of observations in a 1000m radius around a point) first defines a radius of 1000m around the uploaded latitude and longitude, and then, based on the AphiaIDs generated by the taxon match, determines the observation records for these species in OBIS, in this specific radius.

In the future, more European and global databases and data systems, containing both marine and terrestrial taxonomic, biogeographic, ecological and genomic data, will be linked to each other through additional LifeWatch data services. The final goal is to be able to answer scientific questions such as: (1) If I take a benthos sample in the North Sea, which species can I expect? (2) Which invasive pelagic species are known to occur in the Black Sea, (3) Give me the maximum and minimum salinity where organisms with DNA seq homology above x% with this DNA sequence (=seqA) have been found, etc.

## THE LIFEWATCH TAXONOMIC BACKBONE: SUPPORTING THE MARINE BIODIVERSITY AND ECOSYSTEM FUNCTIONING RESEARCH COMMUNITY

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To support and encourage scientific research on biodiversity and ecosystem functioning, Europe launched LifeWatch within the European Strategy Forum on Research Infrastructures (ESFRI). LifeWatch functions as a central virtual laboratory, integrating observatories, databases, web services and modeling tools distributed throughout Europe.

As part of the Flemish contributions to LifeWatch, the Flanders Marine Institute (VLIZ) is setting up a central taxonomic backbone (TB) to facilitate the standardization of species data and the integration of the distributed biodiversity facilities.

The TB includes species information services (taxonomy access services, a taxonomic editing environment, species occurrence services and catalogue services) and integrates different component databases and data systems. Next to taxonomic information (taxonomic databases, species registers and nomenclatures), the TB will also include biogeographical data (species observations), ecological data (traits), genomic data and links to the available literature.

An important contributing database to the LifeWatch TB is the World Register of Marine Species (WoRMS), which currently holds >222.000 accepted species. Taxonomic information is supplemented with synonymy, vernacular names, species attributes, etc. Furthermore, there is a strong link between WoRMS and the (European) Ocean Biogeographic Information System ((Eur)OBIS) (currently >17.300.000 distribution records of marine species). To further complement the marine species distribution data in EurOBIS, a close cooperation with the European Marine Observation and Data Network (EMODnet) was established. To standardize geographic names between all data systems, Marine Regions, a standard list of marine georeferenced place names and areas (currently >32.000) is used. All these data systems are updated on a daily basis. As the TB is being constructed, more component databases and data systems will be integrated. In the near future the FADA database (Freshwater Animal Diversity Assessment) will be incorporated into the TB. Furthermore the collaboration with FishBase and Catalogue of Life (CoL) is being intensified. LifeWatch is supporting all these communities with a central data management task force, which is providing technical, logistic and financial support for upgrading and expanding the component databases. The LifeWatch TB should be fully operational by 2016.

This central TB will be a valuable asset to the biodiversity and ecosystem functioning research community. Through the species information services, researchers can standardize and validate their own biodiversity data. These services, along with geographic and tidal services are available on the Flemish LifeWatch portal (http://www.lifewatch.be/data-services).

## ROV BASED DEEP-SEA INVESTIGATIONS OF THE A.V. ZHIRMUNSKY INSTITUTE OF MARINE BIOLOGY, FAR EASTERN BRANCH OF THE RUSSIAN ACADEMY OF SCIENCES

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In 2011 and 2013, two expeditions aboard the RV *Akademik Lavrentyev* (owned by FEB RAS) to the Sea of Okhotsk have been organized together with the Far Eastern Aquarium, FEB RAS. For the first time, complex investigations of the deep-sea ecosystems of the Derjugin Basin (1700 m) in the deepest zone of the sea were performed using underwater robotics, among them a ROV, which is capable of sampling bottom substrates and certain marine invertebrates. Biological diversity was examined in active gas emission zones with high methane concentrations and in heavy-hydrocarbon seep areas.

The so-called Barite Mountains or barite "smokers", which provide the substrate for numerous benthic invertebrates, were examined with the use of remotely operated robotics for the first time. The peculiarities of the bottom landscapes of the Derjugin Basin were for the first time described in detail with the use of high resolution video equipment. Unique bottom communities with high densities and biomass of sea organisms that are supported by bacterial chemosynthesis and methanotrophy were described. About 200 species of deep-sea organisms were recorded, which is indicative of the high biological diversity of these deep-water communities. Mass assemblages of Okhotsk Sea endemic mollusks that are maintained due to chemoautotrophic symbiotic bacteria were discovered. Aggregations of pogonophore worms that are also nourished by symbiotic bacteria were discovered. Remarkably, the most active zones marked by molluskan assemblages are characterized by the seeping of heavy hydrocarbons resembling petroleum or bitumen. A similar phenomenon is known for the low-temperature seep area in the California Bight.

The results obtained during these expeditions substantially change our knowledge of the biological diversity and marine biological resources at great depths of the Far Eastern seas of Russia. Taking into consideration that depths greater than 1 km comprise 95% of the area of the World Ocean, it is the oceanic depths that in the near future may become the largest source of new biological species and biological resources, and the more so because of the limited resource potential of the land and coastal waters.

## GUIDELINES SUPPORTING ENVIRONMENTAL STUDIES RELATED TO COASTAL DEFENCE WORKS

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In this paper we present the "Guidelines for environmental studies related to the construction of coastal defense works" published by ISPRA within the European project COASTGAP (MED) “Coastal Governance and Adaptation Policies in the Mediterranean” aimed to capitalize on 12 Best Practices derived from 9 previous European projects (as SHAPE, COASTANCE, PEGASO, etc). In particular, the Guidelines were developed within the European Project COASTANCE (MED) related to “Regional action strategies for coastal zone adaptation to climate change” (www.coastance.eu).

The Guidelines illustrate the methodological approach that led to the development of the matrix-system, named “structure/impact” vs “habitat/species”, that can be used as a support tool to assess the impacts generated by coastal defense works on habitat and flora and fauna species.

The matrix-system is organized in a hierarchical system of classification of the marine and coastal environments: starting from broad environmental categories (macro-environments) and with progressively increasing detail this hierarchical system reaches the highest level of analysis with the identification of habitats and species.

In order to create the matrix-system, four main steps were followed:

1) Analysis of the main coastal defense structures and of their main physical effects;

2) Analysis of the potential environmental impacts of coastal defense structures;

3) Identification and classification of the protected marine and coastal habitats (sensu Habitats Directive) into physiographic categories;

4) Definition of the criteria to associate the protected flora and fauna species to the physiographic categories.

The proposed matrix-system represents a simplified and useful tool that can be used by technicians and Administrations involved in the drafting and/or assessment of environmental impact studies related to coastal defence works. By allowing to predict, assess and minimise the impacts of coastal defence works, the matrix-system is a valuable tool for the conservation and protection of biodiversity, sometimes difficult to assess in the marine environment.

## WHY WE NEED AN INTERNATIONAL ECOLOGICAL PROGRAM (IEP)?

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Ecological research plays a strategic role in ensuring a global transition to the path of sustainable development. Spontaneous «organic» evolution of ecological research is not sufficient for the timely resolution of a whole range of pressing issues. These issues call for organizational and financial support in the tried-and-true format of a dedicated international decade program.

It is crucial to set the right priorities for such an IEP. Programs previously supported through international effort include:

1) a program for exploration of global ecosystem productivity (International Biological Program (IBP): 1994—1974, UNESCO);

2) an intergovernmental UNESCO program for the study of human impact on the biosphere (MaB: established in 1971);

3) an international program for biodiversity conservation of the International Union of Biological Sciences (established in 1982).

However, like many other areas of ecological theory and practice, studies of ecosystem productivity and structure, anthropogenic pressures impacting the biota, or conservation of biological diversity have to rely on fundamental knowledge about the ecology of species, which is in catastrophically short supply.

Autecology still constitutes the foundation of ecology. Attempts to focus efforts on demecology or sinecology were rather productive, however, they were limited in terms of their ability to answer the key questions of ecology: why does a particular species occupy a particular habitat? what causes sudden explosions in the population of a particular species? what shapes the species composition of a particular ecosystem? Answers to these key questions would help successfully tackle the following issues: 1) maximum permissible exposure limits for organisms, species, and ecosystems; 2) ecosystem productivity projections, including potential crop yields; 3) limits to community resilience in response to various types of natural disturbances and anthropogenic stress.

Lack of knowledge about ecological specialization of species, or the nature of species' dependence on environmental factors on all stages of the life cycle, including intraspecies variability and norm of reaction, undermines the prospects of successful problem-solving in the various fields of theoretical and applied ecology.

An international program for ecology would help to encourage the much needed intensification of autecology research; coordinate systematization, integration and cataloguing of all available knowledge on the ecology of all known species; determine plans for further coordinated research with international support; facilitate intercalibration of methods; support aggregation and synthesis of knowledge in order to promote its dissemination and appropriate use in environmental education; set up ecological monitoring systems; improve systems of indicators and criteria for ecological characterization of species, populations and ecosystems; promote the compilation of data bases on the ecological 'preferendum' of species and permissible exposure limits.

It stands to reason that a special foundation should be established to provide international support for ecological research, including both large-scale comprehensive and costly studies and independent research projects on the ecology of selected species, conducted by small groups of scientists.

## A DEEP-SEA SECTION FOR THE MARINE HABITAT CLASSIFICATION OF BRITAIN AND IRELAND

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The current Marine Habitat Classification for Britain and Ireland (MHCBI) describes seabed habitats from the intertidal zone down to depths of 200 m and is maintained by the Joint Nature Conservation Council (JNCC). It is essential to develop a deep-sea section for the MHCBI to allow the consistent classification of UK survey data acquired in waters deeper than 200m. A consistent approach across the UK will prevent numerous new deep-sea biotopes being proposed independently for similar data and promote cohesion within the classification community. A new list of over 30 UK deep-sea biotopes has been defined in collaboration with Plymouth University and Scottish Association for Marine Science (SAMS). These biotopes were identified based primarily on results of cluster analysis undertaken on JNCC survey data collected between 2005 and 2011, with some additional recognised biotopes included from the academic literature. Infaunal analysis was undertaken using grab sample data at 336 stations in Strategic Environment Assessment (SEA) area 4 in the Faroe-Shetland Channel and 337 in SEA area 7 in the Rockall region. A sub-sample of 2331 images from Rockall Bank, Hatton Bank, Rosemary Bank, Wyville Thomson Ridge, Faroe-Shetland Channel, Polygonal Faults, South-west Canyons, Anton Dohrn Seamount and Darwin mounds was analysed to identify epifaunal assemblages. Descriptions have been produced for each biological assemblage that specify characterising species and associated environmental characteristics. Each biological assemblage (e.g. *Lophelia pertusa* reef) is linked to one ‘parent’ broad community (e.g. cold water coral reef). Broad communities are considered to occupy a set niche and fulfil a certain functional role. A widely recognised problem with the current MHCBI is that, because sampling methods focus on epifaunal or infaunal communities, most biotopes describe either the epifaunal or the infaunal component of the biological community and not both. Past attempts to link epifauna and infauna into related biotopes have not been successful, with particular issues around the spatial distribution of these components. In the new deep-sea classification, epifaunal and infaunal broad communities and their ‘child’ biotopes are described separately and the user advised to select either one or the other depending on the sampling method. Analysis of species distribution and abundance data also informed the definitions of environmental categories used in the classification. The deep-sea assemblages were categorised based on biogeographic region, vertical biological zone, substratum, and whether a biogenic structure is present. Two biogeographic regions were proposed: Arctic and Atlantic. Three vertical biological zones were proposed (Upper Bathyal, Lower Bathyal and Abyssal) that relate to changes in water mass with depth. Zones should be selected primarily based on the biological community present if possible, but depth proxies representing water mass structure were also defined. Substratum categories were taken from the existing MHCBI and EUNIS to ensure compatibility. The deep-sea section of the classification will be made available on the JNCC website (jncc.gov.uk) along with guidance documents, background information and a database that allows users to search for biotopes based on characterising variables. Deep-sea biotopes in the MHCBI will be proposed for inclusion in the upcoming revision of EUNIS to ensure classification within the UK is consistent with the approach taken at the European scale.

## THE EUROPEAN OCEAN BIOGEOGRAPHIC INFORMATION SYSTEM (EUROBIS): ONLINE SOURCE FOR MARINE QUALITY CONTROLLED BIOGEOGRAPHIC DATA

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Knowledge on species occurrences in space and time is of the utmost importance in biological research. Although species occurrence information is highly relevant and often requested by scientists, this kind of data can be hard to find and sometimes even harder to access…

The European Ocean Biogeographic Information System – EurOBIS – helps filling this gap in our scientific knowledge, by making the largely scattered and very diverse biogeographic data on marine species freely available and easily accessible online. EurOBIS brings together biogeographic data that are either collected within European marine waters or by European researchers and institutes outside Europe, with a focus on taxonomy and distribution records in space and time and offers a number of online tools to easily query and visualize the data.

EurOBIS does however more than just putting the available data online. As an additional service to its users, all received data go through a series of quality checks. The aim of these quality control (QC) procedures is two-fold. First of all, it helps the data management team and data providers to check the quality and completeness of the submitted data and to detect (possible) errors. Secondly, the assigned quality flags can help users in selecting data that are fit for their use and purpose. The assigned quality control flags can be combined according to the required ‘fitness for use’ for the users, thereby creating specific filters on the available data within EurOBIS. The European Marine Data and Observation Network (EMODnet) Biology (http://www.emodnet-biology.eu/portal/) makes the EurOBIS data available through its data portal and is currently applying such a filter. EMODnet only makes available those distribution records from EurOBIS that comply with specific QC steps, including e.g. only records that were identified till genus or species level and locations within the marine environment. On the dataset level, users can see how many records have passed the postulated quality control procedures and are thus available through the portal.

EurOBIS is part of the central taxonomic backbone of LifeWatch, which aims at standardizing species data and integrating the distributed biodiversity data repositories and operating facilities. In this framework, the database structure of EurOBIS is being expanded, making it possible to not only capture presence or abundance of species but also to offer e.g. biomass data and length-measurements in a standardized and structured way. EurOBIS closely links with other ongoing European and international initiatives, such as the World Register of Marine Species (WoRMS, www.marinespecies.org), the most authoritative and comprehensive list of names of marine organisms. In addition, a link is being prepared between these distribution and taxonomic databases and ecological species traits. The documentation of species traits is currently ongoing within EMODnet Biology and WoRMS. Linking taxonomy, distribution and ecological information on a species level will open up a wide range of possibilities related to ecological research. Within EMODnet Biology for example, EurOBIS data will – amongst others – be used in the creation of spatially distributed data products with specific relevance for Descriptor 2 of the European Marine Strategy Framework Directive (MSFD), dealing with non-indigenous species.

Currently (April 2014), EurOBIS holds 544 marine datasets representing over 17.3 million distribution records, of which 87% or 15 million are available through the EMODnet Biology Portal. The development and maintenance of EurOBIS and the related quality control procedures is part of the VLIZ contribution to LifeWatch, and funded by the Hercules Foundation. The main goal is to facilitate the fitness for use of individual and integrated biogeographic data for scientists, by offering several tools that help in the assessment of the completeness and validity of distribution records.

# EMBS 49 TIME SCHEDULE AND SOCIAL EVENTS

| **DATE** | **TIME** | **EVENT** |
|---|---|---|
| 9 8 2014 | 8:00 – 18:00 | Registration |
| | 09:45 – 10:00 | Opening Ceremony |
| | 10:00 – 11:30 | 1st session |
| | 11:30 – 11:50 | Coffebracke |
| | 11:50 – 13:50 | 2d session сессия |
| | 13:50 – 14:40 | Lunch |
| | 14:40 – 16:00 | 3d session |
| | 16:00 – 16:20 | Coffebracke |
| | 16:20 – 17:40 | 4th session |
| | 18:30 – 20:30 | Icebracker Party |
| 9 9 2014 | From 9:00 | Poster mounting |
| | 10:00 – 11:30 | 5th session |
| | 11:30 – 11:50 | Coffebracke |
| | 11:50 – 13:50 | 6th session |
| | 13:50 – 14:40 | Lunch |
| | 14:40 – 16:00 | 7th session |
| | 16:00 – 16:20 | Coffebracke |
| | 16:20 – 18:00 | Poster session |
| | 19:00 – 23:00 | Round Table |
| 9 10 2014 | From 9:00 | Poster mounting |
| | 10:00 – 11:30 | 8th session |
| | 11:30 – 11:50 | Coffebracke |
| | 11:50 – 13:50 | 9th session |
| | 13:50 – 14:40 | Lunch |
| | 14:40 – 16:00 | Poster session |
| | 16:00 – 16:20 | Coffebracke |
| | 17:00 – 21:00 | City tour |
| 9 11 2014 | 10:00 – 11:30 | 10th session |
| | 11:30 – 11:50 | Coffebracke |
| | 11:50 – 13:50 | 11th session |
| | 13:50 – 14:40 | Lunch |
| | 14:40 – 16:00 | 12th session |
| | 16:00 – 16:20 | Coffebracke |
| | 16:30 – 18:00 | Yellow Submarine Competion |
| | 19:00 – 22:00 | Symposium Dinner |
| 9 12 2014 | 10:00 – 11:40 | 13th session |
| | 11:40 – 12:00 | Coffebracke |
| | 12:00 – 13:40 | 15th session |
| | 13:40 – 14:40 | Lunch |
| | 14:40 – 16:00 | 16th session |
| | 16:00 – 16:15 | Closing Ceremony |

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