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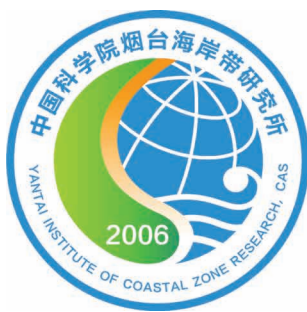
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MARINE BIODIVERSITY FOR A HEALTHY OCEAN – BIODIVERSITY, FUNCTIONAL GROUPS AND OCEAN HEALTH

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Russia-China Bilateral Workshop
Marine Biodiversity for a Healthy Ocean –
Biodiversity, Functional Groups and Ocean Health
October 10–11, 2019, Vladivostok, Russia

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Genetic variation and symbiotic associations in sea urchin *Strongylocentrotus intermedius*: an integrative approach for marine biodiversity analysis, monitoring, and conservation

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Developing genetic markers for the identification and analysis of recently diverged groups, such as incipient species, close species, or species complexes, still remains a challenge due to the usually low level of genetic divergence. *Strongylocentrotus intermedius* (A. Agassiz, 1863), inhabiting the Northwest Pacific region of Asia, is a commercially valuable sea urchin used as a target species for fisheries and aquaculture and a model organism for biological, pharmacological, and biotechnological research. The taxonomic identification of this species is uncertain due to its high morphological variation between different localities. The northern Primorye (Sea of Japan) populations of *S. intermedius* consist of two sympatric morphological forms, “usual” (U) and “gray” (G). The two forms are significantly different in morphology and preferred bathymetric distribution. We previously analyzed the genetic composition of the *S. intermedius* forms using nucleotide sequences of mitochondrial gene *COI*, nuclear gene *bindin*, and complete mt genomes to evaluate the possibility of cryptic species within *S. intermedius*. We also investigated the presence of symbiont microorganisms by means of 16S rRNA sequences. The present work summarizes the analysis and the main results of the previous studies. Particularly, the patterns of polymorphism and divergence, haplotype structure, linkage disequilibrium, neutrality tests, and microbiome composition and structure are considered in comparative manner for the U and G forms of *S. intermedius*. The gene *bindin*, evolving under positive selection, and bacterial symbionts reveal statistically significant differences between the morphological forms. These markers are expected to be most sensitive for monitoring the *S. intermedius* populations. The results confirm the unique evolutionary trajectories for the U and G forms, which might be considered as incipient species that necessitate considering them separately when making harvesting or biodiversity conservation decisions. Some methodological aspects of the conservation genetics are also discussed in connection with the issues of conservation, monitoring, and sustainable management of marine biodiversity.

Evaluation of the influence of biologically active microorganisms on the Far Eastern sea cucumber *Apostichopus japonicus*

***Elena A. Bogatyrenko*¹, *Sergey I. Maslennikov*², *Tatiana I. Dunkay*^{1, 2},
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Probiotics are widely used both in medical practice for the treatment and prevention of various human infectious diseases, and in veterinary medicine. The use of probiotics in aquaculture is a relatively new direction in biotechnology, however, the probiotic properties of a wide range of microorganisms have already been studied: gram-positive (*Bacillus*, *Enterococcus*) and gram-negative bacteria (*Aeromonas*, *Pseudomonas* and *Vibrio*), yeast (*Phaffia*, *Saccharomyces*), microalgae (*Tetraselmis*) which are successfully used to control the incidence and increase the productivity of hatcheries and marine farms. Using various objects (fish, shellfish, crustaceans) as an example, it is shown that the use of probiotics leads to an increase in the survival of hydrobionts by 20–62% and to an increase in their growth rate by 8–115.3%.

In the framework of our studies, out of 134 strains of cultured heterotrophic bacteria isolated from the digestive system of Far Eastern sea cucumber *Apostichopus japonicus*, 3 strains with the properties of potential probiotics were selected. These microorganisms have demonstrated the ability to synthesize a spectrum of digestive enzymes, as well as inhibit the growth of pathogenic vibrios and potentially dangerous bacteria such as *Staphylococcus aureus*, *Yersinia pseudotuberculosis*, *Pseudomonas aeruginosa* and *Escherichia coli*. The aim of further studies was to assess the ability of the selected bacterial strains to influence the growth rate of the mass of juvenile holothurians. To do this, bacteria cells of a certain concentration were added to sea cucumbers daily for 4 weeks. All experiments were repeated three times. Sea cucumbers, whose feed did not contain bioadditives, were used as control. As a result of the work performed, it was found that, despite the negative growth of all the studied animals, including control ones, a small positive effect was observed when cells of the *Arthrobacter* sp. Strain were added to the feed A16. To obtain optimal results, it is necessary to select the most effective concentration of bacteria and adjust the conditions for growing holothurians.

The study was carried out with the financial support of the Russian Federal Property Fund in the framework of the scientific project no. 18-34-00693.

Frozen collection of viable biological material from marine species

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The extinction of species is a natural and inevitable evolutionary process, but today it prevails over speciation: destruction of natural habitats, industrialization, unsustainable use of natural resources, etc. The conservation of every single species is required to maintain biodiversity, because eliminating any species may result in malfunction of whole ecosystems. Correctly cryopreserved cells and tissues from the species of interest contain information of diverse parameters, both of a particular organism and its population. They could be stored for decades, transported worldwide and recovered anytime, even from a small quantity of thawed biological material. Therefore, the technology for cryopreservation of marine hydrobiont cells and tissues need to be developed for increasing the extent of their integrity and functional activity after thawing. We succeeded in cryopreservation of marine mammal cells and tissues (from 20 individuals belonging to 10 species), salmon sperm (*Onchorynchus masou*), unicellular algae (15 clones from 11 species), marine invertebrates (35 unique samples of embryonic cells, hemocytes, gonad and digestive gland cells from 6 species). All samples have been tested to be viable and functionally active after storage at cryogenic temperatures by means of light, electronic and confocal microscopy, molecular biological methods and flow cytometry. The complex of developed methods for cryopreservation and assessing the state of biological material from marine hydrobionts could be of a great use for researchers in cryobanks worldwide.

The study was supported in part by the Russian Foundation for Basic Research (grant no. 19-04-00752).

The work was partly performed at the “Far Eastern Electron Microscopy Center” (A.V. Zhirmunsky National Scientific Center of Marine Biology FEB RAS, Vladivostok, Russia).

Harmful algal blooms significantly reduce the resource use efficiency in a coastal plankton community

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Plankton diversity plays vital roles in the global biological and geochemical processes. The relationship between species diversity and ecosystem functions is thus a central issue in ecology. Harmful algal blooms (HABs) have been investigated for their catastrophic effects on public health and aquaculture intensively, but rarely the intrinsic functions of the plankton community. We therefore investigated the shifts of plankton diversity via pyrosequencing during and around a natural dinoflagellate (*Prorocentrum donghaiense*) bloom and analyzed the effect of *P. donghaiense* abundance on the operationally-defined resource use efficiency (RUE) of plankton community to test our hypothesis about the relationships among blooming intensity, species diversity, and the RUE of plankton community. We found that the species diversity of eukaryotic plankton community was significantly lowered during the bloom, as reflected in OTU (operational taxonomic unit) richness, Shannon-Wiener and Gini-Simpson Indices. Principal coordinates analysis exhibited significant difference in plankton community structure between blooming and non-blooming periods. As hypothesized, the species richness was positively correlated to RUE (defined as the ratio of phytoplankton biomass to total phosphorous, TP), and more importantly, the cell density of *P. donghaiense* exhibited significant negative correlation with RUE. Our results explicitly demonstrated HABs reduce RUE by reducing species richness, providing field evidence for a trophic niche partitioning mechanism explaining why ecosystems with higher diversity have higher RUE, a key ecosystem function. Also, our work provides striking evidence for the relationship between plankton species richness (or diversity) and community function (resource use efficiency) via studying on HABs, a natural but exceptional phenomenon, in addition to revealing a profound consequence of HABs.

Harmful algal blooms mitigation using natural polysaccharide xanthan and local materials

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Red tide is a global marine disaster. How to safely and effectively control the multiplication and diffusion of the red tide microalgae in coastal environments is an important focus in marine environmental sciences. The process of flocculation-sedimentation is considered to be a promising method for the prevention and control of red tide. Xanthan, a commercial capsular polysaccharide, is produced by fermentation of the bacterium *Xanthomonas campestris*. It can effectively trap and wrap many typical microalgae in seawater, due to its super characteristics of high flocculating activity and electrolyte stability. The removal effect of xanthan was enhanced by the addition of appropriate calcium hydroxide that decreased the repulsive interaction between anionic xanthan and negatively charged algal cells. Local materials (soils or sands) was helpful in speeding up the kinetic process of flocculation and sedimentation. Moreover, the high molecular polymer structure of xanthan can also inhibit microalgae floating to the upper water from algal flocs. Xanthan attached microalgae could cause the destruction of algal cell membrane, which would reduce photosynthesis of microalgae and accelerate apoptosis of algal cells. Therefore, xanthan also has biological inhibition on microalgae after flocculation and sedimentation. It combines the flocculation process and the biological inhibition process together. This would provide a promising alternative for ecological controlling red tide in coastal environments.

Primary attempt using DNA metabarcoding to reveal macrobenthic community in Bohai Sea, China

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Metabarcoding surveys of DNA extracted from environmental samples are increasingly popular for biodiversity assessment in natural communities. Such surveys rely heavily on robust genetic markers. Therefore, analysis of PCR efficiency and subsequent biodiversity estimation for different types of genetic markers and their corresponding primers is important. Here, we test the PCR efficiency and biodiversity recovery potential of two commonly used genetic markers – nuclear small subunit ribosomal DNA (18S), mitochondrial cytochrome c oxidase subunit I (COI) and nuclear large subunit ribosomal DNA (28S) – using 454 pyrosequencing of a zooplankton community collected from Bohai Sea, China. We found that biodiversity detection power and PCR efficiency varied widely among these markers. All tested primers for COI failed to provide high-quality PCR products for pyrosequencing, but 18S and 28S passed all tests. Furthermore, multiple analyses showed that primers for 18S recover more (38 orders) groups than 28S (10 orders) across all taxa, and four vs. two orders and nine vs. six families for Crustacea. Our results showed that the 18S primers, is an efficient and powerful tool for profiling biodiversity in largely unexplored communities, especially when amplification difficulties exist for mitochondrial markers such as COI. Universal primers for higher resolution markers such as COI are still needed to address the possible low resolution of 18S for species-level identification.

Community succession of macrobenthic fauna over 60 years in Bohai Sea, China

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Based on the historical data since 1950s and field surveys in Bohai Sea, we found that in the past 60 years, the macrobenthic assemblages of Bohai Sea have undergone some succession, including the changes of species composition, the key species, the biomass and abundance, as well as the spatio-temporal changes of distribution pattern; the dominant position of *K*-strategy species with large body, long life and high competitiveness are gradually lost and replaced by *R*-strategy species with small body, short life cycle, strong adaptability and high reproductive ability.

The integrated impacts both from the climate changes and anthropogenic disturbances happened in Bohai Sea over the past 60 years, such as aquaculture, coastal land reclamation and sewage discharge were suggested to be the trigger factors for these long-term community succession. Environmental changes have affected and altered the spawning grounds, feeding grounds, overwintering field, migration routes and population recruitment of biological resources, human activities such as overfishing reduce the trophic level of marine ecosystems, shorten the food chain, make the structure of food webs simpler, and ultimately lead to miniaturization of species.

First data on the composition and structure of vulnerable marine ecosystems of the Emperor Chain: key taxa, landscapes, biogeography

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Seamounts are areas of high biological productivity of benthic and pelagic communities, including accumulations of bioresources capable of supporting commercial fishing. Benthic seamount communities of the northwestern Pacific Ocean have become the subject of more active study over the past decade due to the development of deep-sea research using remote-controlled underwater vehicles.

For the first time, a multi-disciplinary comprehensive study of the deep-sea ecosystems of the seamounts of the Imperial Range (northwestern part of the Pacific Ocean), organized by the A.V. Zhirmunsky National Scientific Center of Marine Biology, Far Eastern Branch of the Russian Academy of Sciences (July–August 2019), was carried out using the remotely operated vehicle “Comanche-18”.

Distribution of typical underwater landscapes and key taxa of vulnerable marine bottom ecosystems (VMEs) of the Emperor Chain – Octocorallia and Hexactinellidae sponges – are studied in complex for the first time. New data on the macrobenthos biodiversity of that chain of seamounts and guyots are collected.

A biogeographic description of the dominant animals (deep-sea corals and sponges) is given. For the first time, a change in the coral fauna in the latitudinal direction is shown, and new data on the biogeographic boundary in the area of the Emperor Chain are obtained.

Comprehensive biological studies of VMEs (together with hydrophysical, geological, and other works) in the area of the Emperor Chain are urgently needed as soon as possible to obtain data on the state of biological and other resources of the North Pacific. This will make a significant contribution both to the work of the North Pacific Fisheries Commission (NPFC) and to international scientific cooperation in the region to solve a wide range of scientific issues and food problems in the region.

Biochemical diversity of fatty acids reflects the nutrition strategy of cold-water corals

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Corals are found everywhere from tropics to polar regions and contribute substantially to the biodiversity of both tropical shallow waters and cold-water communities from bathyal depths. Ecology of coral communities and trophic relationships of corals are always in a focus of numerous investigations. Lipids and their fatty acids (FAs) are important biochemical markers and indicators applied in such investigations. Lipids serve as long-term energy stores and are involved in the majority of biochemical and physiological processes in corals. The primary characteristic of lipids is the composition of their FAs included in lipid molecules as acyl groups. At the higher taxonomic levels, the distinctions between coral groups are caused by differences in FA biosynthesis. Some FAs are transferred from food sources. Probably, both biosynthesis and food sources are responsible for the specificity of FA profiles of coral orders or families. A successful application of FAs for chemotaxonomy of coral taxa on the level of class and family was demonstrated. Nevertheless, there is no definitive understanding of the role of FAs biosynthesized and FAs consumed from food sources for chemotaxonomic distinction between cold-water coral (CWC) and hydrocoral species.

All species of CWC and hydrocorals cover their energy needs by heterotrophy. Heterotrophy includes the uptake of particulate organic matter (POM). The POM supply is comprised of phytoplankton, zooplankton, bacteria, and organic detritus. The specific FAs of POM are mainly determined and can be used as biochemical markers to estimate an influence of food sources on FA profiles of corals. The FA marker concept is based on the observation that marine primary producers lay down certain FA patterns that may be transferred conservatively to, and hence can be recognized in, primary consumers. Plankton as an important dietary intake of heterotrophic cold-water corals. In the present study, lipid class and FA signatures of fifteen species of cold-water soft corals and hydrocorals were determined for the first time.

CWC and hydrocorals were collected at depths 27–620 m near the Kamchatka Peninsula and a zone around Simushir Is. and Urup Is. (the Kurile Islands and the Sea of Okhotsk). The eleven soft coral species (Anthozoa) belonged to four families: Nephtheidae (alcyonarians), Paragorgiidae, Primnoidae, and Acanthogorgiidae (gorgonians). Four hydrocoral species (Hydrozoa) are from the family Styliasteridae.

Our study showed no significant difference in the lipid class content between specimens of the same species from different depths. The lipid profile characterizes cnidarian subclass as a whole, and the difference between FA profiles of soft coral families probably depend on their feeding behavior. PUFAs of cold-water phytoplankton and herbivorous zooplankton are rich in 20:5n-3. The high level of 20:5n-3 found in Primnoidae indicates that phytoplankton and/or herbivorous zooplankton is a major food source for all Primnoidae species investigated. The main source of 20:5n-3 in

the phytoplankton is diatoms, whereas dinoflagellates produce more 22:6n-3 and 18:4n-3. The ratio of 22:6n-3/20:5n-3 was applied to estimate an intake of diatoms. The low 22:6n-3/20:5n-3 ratio and the low level of 18:4n-3, which is observed in Primnoidae corals, supposes that C20-22 PUFAs may originate rather from diatoms (or herbivorous zooplankton) than from dinoflagellates. The presence of 20:5n-3 alone cannot indicate whether this FA originates directly from diatoms or it is conserved in herbivorous zooplankton prey. The 16:1n-7/16:0 ratio and C16 PUFAs are additional indicators of diatoms. The 16:1n-7/16:0 ratio < 0.3 (on average) and trace amount of C16 PUFAs indicate that herbivorous zooplankton makes the main contribution to nutrition of the cold-water Primnoidae corals from the Sea of Okhotsk.

Other investigated cold-water coral families (Nephtheidae, Paragorgiidae, and Acanthogorgiidae) were also characterized by low values of the diatom indicators but higher 22:6n-3/20:5n-3 ratios. Probably, these cold-water coral families assimilate less herbivorous zooplankton than Primnoidae.

Contrary to a dietary predomination of herbivorous zooplankton supposed for Primnoidae, opportunistic feeding on various food sources is suggested for other cold-water coral families investigated. The presence of 20:4n-6 in cold-water hydrocorals may be also explained by diet origin, whereas the presence of 22:5n-6 in tropical hydrocorals is caused by different FA biosynthesis

FA biomarkers indicate that trophic relationships of Primnoidae differ from those of other cold-water soft coral families (Nephtheidae, Paragorgiidae, and Acanthogorgiidae). Possibly, different feeding types of Primnoidae and other cold-water soft corals allow them to occupy different ecological niches at the same biotope. The character of feeding type or food source might be attributed to morphological features of coral polyps of taxonomic units compared.

Study of life in the Sea of Japan: reproduction and development

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The Sea of Japan is the richest of all the seas of Russia in its biodiversity. The sea is characterized by warm waters and monsoons; it has very high potential to develop fishery and mariculture. In the Peter the Great Bay, there are many bays suitable for mariculture farms. From the first days of the foundation of the Institute of Marine Biology, the institute staff began to study the biological bases of the rational use and the reproduction of commercially valuable species. In the early years, special emphasis was made on studying reproductive cycles of mass species of mollusks and echinoderms. It was necessary to reveal the features of gametogenesis and the time of spawning of various sea species. At the histological level, annual gonadal cycles were studied for a few dozen of mollusks and echinoderms. The results of the work were published in numerous articles, which were summarized in 1980 in a monograph (Kas'yanov et al., 1980).

The life cycles of most commercial species of marine invertebrates consist of two periods: a short settlement stage, represented by a planktotrophic pelagic larva, and a long benthic stage, represented by adult forms. The benthic stage includes the annual gamete formation, spawning and fertilization, resulting in formation of larvae feeding on phytoplankton. Species identification of planktonic larvae has practical importance for determination of the time of settling and metamorphosis of the sea organisms. Besides, species identification has zoological meaning since it allows identification of cryptic forms. It often happens that planktonic larvae are during surveys detected the first, and only afterwards – new benthic adult forms are found. The results of studies on biology of larvae were published in many articles and summarized in a monograph (Kas'yanov et al., 1983).

The staff of the Laboratory of Embryology actively studies the mechanisms of embryonic and larval development of a number of groups of sea hydrobionts inhabiting the Sea of Japan. Major research studies are carried out at the Biological Station “Vostok”, where the aquarium equipment is suitable for keeping adult animals, obtaining gametes from them, and growing larvae. An aquarium installation well-equipped for experimental embryological research is also available in the laboratory building in Vladivostok.

The model objects of developmental biology are representatives of the three main groups of coelomic animals: Ecdysozoa, Lophotrochozoa, and Deuterostomia. With ecdysozoans, our interests are focused on representatives of Artropoda (Cl. Crustacea and Nematoda). Crustaceans are a very commercially important group – it is suffice to mention the king crab *Paralithodes camchaticus*. Nematode is also an important group in practical relation, while many nematodes parasitize sea animals and plants. Sea nematodes are mostly free-living; they are an ecologically important component and make the bulk of marine meiobenthos. Mollusks and polychaetes are typical representatives of lophotrochozoans Protostomia; echinoderms and ascidians are typical representatives of Deuterostomia.

The embryonic development begins with formation of a zygote, resulting from fusion of gametes. Gametes are very diverse: they are mostly sperm cells, and they are species specific, since they determine the initial level of the post-copulatory reproductive barrier. Numerous studies on the ultrastructure of gametes of marine hydrobionts (sponges, hydrozoans, nematodes, crustaceans, polychaetes, mollusks, echinoderms, fish etc.) performed by the researchers of the Laboratory of Embryology have been published in many scientific journals and summarized in reviews and monographs (Drozdov, Ivankov, 2000).

Protostomia and Deuterostomia, the two evolutionary lineages of coelomic animals divided around 700 million years ago. They have a determinative (mosaic) and regulative development. These types of development are distinguished by five main features: the nature of eggs cleavage, the way of mesoderm formation, the fate of the blastopore, the type of larva, and the organization of the nervous system. Besides, the skeleton of Deuterostomes is mesodermal and the skeleton of Protostomes is ectodermal. The skin of deuterostomes is bilayer (ectodermal epithelium and mesodermal connective tissue cutis). Embryogenesis of Protostomes has no tendency towards regulation, which is well developed in Deuterostomes. This difference was demonstrated by many experimental embryological studies, surgical and other experiments.

There are significant differences in the functional organization of the cytoskeleton morphology of unfertilized eggs and blastomeres of mollusks and sea urchins. Unlike sea urchins, the cortical cytoskeleton in mollusks is not rearranged during fertilization. The morphogenetic role of the cortex in the regulatory development of Deuterostomia and deterministic (mosaic) development of Protostomia is being discussed.

Sperm morphology also differs in the structure of the cytoskeleton, which is most developed in echinoderms and is capable of significant restructuring during the acrosome reaction. Ecdysozoic sperm cells are practically devoid of the cytoskeleton, they are mostly immobile, or completely immotile.

Of particular interest for embryologists are echinoderms. These animals are evolutionarily close to chordates, whose name deuterostome means “mouth is second”. Their relatively early evolutionary isolation, accessibility and free development in sea water made it possible to use echinoderms, in particular sea urchins, as model objects in order to answer many key questions of developmental biology, evolutionary biology, biochemistry, and cell and molecular biology. Owing to their abundance, large size and the ease of maintenance in the laboratory, sea urchins of the family Strongylocentrotidae have become the objects of many early studies on developmental biology. Because of the high life expectancy of some sea urchin species, these organisms have been used as a model for studying aging processes. Annotation of the genome of some species of sea urchins allowed us to obtain information about regulatory gene networks that determine embryonic development. Repetitive non-coding DNA remains the least studied part of the eukaryotic genomes.

Research on hatching and development of red king crab larvae under controlled conditions

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Red king crab *Paralithodes camtschaticus* Tilesius, 1815 belongs to the order Decapoda, sub-order Anomura, family Lithodidae (craboids). Red king crab is the most important object of crab fishing; in the USA and Japan, red king crab is also an object of intensive fishing. The importance of red king crab is the high commercial value of this species.

The goals and objectives of this work are:

1. Find out the total duration of hatching of larvae from eggs in females of the red King crab.
2. Find out the total duration of development of red king crab larvae in artificial conditions.
3. Find out the overall survival of red king crab larvae from the stage zoea 1 to the stage of glaucotoe.
4. Find out the optimal density of planting red king crab larvae in the growth capacity.
5. Find out the optimal feed composition for red king crab larvae.

Place of work: Marine Biostation “Zapad” of the A.V. Zhirmunsky National Scientific Center of Marine Biology of the Far Eastern Branch of the Russian Academy of Sciences, Vostok Bay, Sea of Japan.

Aquatic center is equipped with a constant flow of sea water. Red king crab females were kept in containers filled to a volume of 3 tons. Female red king crab was fed by the mussels *Crenomytilus grayanus*. Red king crab larvae were fed 3 times per day. Feed for red king crab larvae was obtained on site.

The total duration of hatching of red king crab larvae was from 19 to 31, on average 24 days. The total duration of the development of red king crab larvae was from 33 to 55, on average 45 days. The survival rate of red king crab larvae for the entire development period ranged from 5.6 to 79.2, on average 33.2%. The highest proportion of survival was observed at an initial landing density of 48 ind./l. The optimal type of food for red king crab larvae is a mixture of *Artemia* + *Tetraselmis*.

Paedomorphosis in deep-sea isopods (Crustacea: Malacostraca)

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Paedomorphosis is a type of heterochrony in which mature individuals retain larval characters that can be achieved by neoteny (delaying somatic development) or progenesis (acceleration of reproductive development). This phenomenon was recorded for different taxa of deep-sea animals (e.g., Echinodermata, Ascidiacea, Gastropoda, Cephalopoda, Polychaeta, Sipuncula, Picnogonida, Cirripedia), and the effects were obvious in different reductions of body systems and morphological simplifications. Obviously, these are no deep-sea-specific adaptations, but they are useful for the colonization of the extreme deep-sea environments. The crustacean order Isopoda is one of the most frequent and diverse taxa at all depths of the World Ocean from the intertidal to hadal zones. At great oceanic depths they are one of the dominant macrobenthic taxa, mostly due to the contribution of the suborder Asellota, which includes 20 primarily deep-sea families. Isopod females carry their offspring in a brood chamber (marsupium). The postmarsupial development of Isopoda in general includes three manca stages with rudimentary pereonite 7 lacking appendages or bearing rudimentary pereopods VII. Within Isopoda, paedomorphosis was observed independently in some suborders. Among the suborder Anthuroidea the absence of pereopods VII was described for adult females of some species. The reduction of the posterior pereonite is a distinguishing feature within the parasitic family Gnathiidae (Cymothooidea) in which adult individuals possess only five pairs of pereopods. In the parasitic superfamily Cryptoniscoidea the free-swimming last larval stage (cryptoniscium) is a functional male, which finds and fertilize a female and then develops into a female. The reduction of the last pereonite and its appendages in mature specimens has also been described for some deep-sea families of the suborder Asellota including the Dendrotionidae (the genus *Dendromunna* and a species of *Dendrotion*), the Haplomunnidae (the genera *Munella* and *Abyssaranea*), the Ischnomesidae (some species of the genera *Stylomesus* and *Haplomesus*), and the dominant deep-sea family Munnopsidae (the subfamily Lipomerinae). In other subfamilies of Munnopsidae, varying degrees of reduction of body segments and articles of appendages can be traced. The Paramunnidae is a large and diverse shallow-water asellote family “that lives on the edge of the deep sea and has entered it often” (Wilson, 1980). Until now, three genera and four species have been reported from the abyssal depths of the Atlantic and the South Pacific. Multiple entrances of the paramunnids into the deep sea yielded morphological diversification, while the deep-sea paramunnids are highly modified compared to their shallow-water relatives. During the expedition KuramBio (2012) a new unusual deep-sea species representing new genus of the Paramunnidae, *Reductogonium* Golovan and Malyutina, was found in the abyssal of the NW Pacific. The new genus is distinguished from other paramunnid genera by its reduced pereonite 7 that lacks appendages in adult individuals. Paedomorphosis as an adaptive strategy associated with more efficient energy consumption at great depths where food

resources are limited, and competition is lower than in shallow waters. Shortening of the ontogenetic stages leads to a reduced body size, faster succession of generations, and, consequently, accelerated evolution. These biological characteristics seem to be successful strategies for deep-sea inhabitants. In addition, neoteneic features may appear as an adaptation for a specific lifestyle. Thus, the reduction of the last pereonite and its appendages in haplomunnids and *Reductogonium* was suggested to be related to their long-legged ambulatory habits that require a more compact body.

Emulsification characteristics of crude oil and its influence on normalized radar cross section

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The emulsification of crude oil is caused by the oil flowing into the water, resulting in the increase of oil film tension, viscosity, water content, and volume, which brings great harm to the marine ecological environment and difficulties for the cleanup of marine emergency equipment.

A laboratory method developed in Russia based on measuring the damping coefficient and the length of parametrically generated gravity-capillary waves is applied to a 50% emulsified oil films and to crude oil films. Measurements of wave damping were carried out in a range of surface wave lengths, corresponding to Bragg waves of X- to Ka-band radars. The obtained dependences of wave damping coefficient on emulsified oil films thickness have demonstrated the existence of a damping maximum at thicknesses of about 1–2 mm, and the maximum is approximately twice the one for crude oil films, the damping maximum for emulsified oil films is located at larger film thicknesses than for crude oil films. Theoretical calculations of wave damping have been performed and viscoelastic parameters of emulsified oil films have been estimated from comparison between theory and experiment.

We set up crude oil emulsification samples to study the physical property in laboratory and conducted radar measurements at different incidence angles in outdoor (China). The radar is C band in resolution of 0.7 m by 0.7 m. A fully polarimetric scatterometer (HH, VV, and VH/HV) is mounted at 1.66 m (minimum altitude) height at an incidence angle between 35° and 60°. The asphalt contents of less than 3%, 3%–7% and more than 7% crude oil and the filtered seawater were used to the outdoor emulsification scattering experiment. It is the first time to find that the emulsification of crude oil results in an increase of the normalized radar cross section and the maximum increase is 2 dB.

DNA-barcoding: from modern general biology paradigm verification to sea food mislabeling detection

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Literature and own data on the consistency of the latest molecular sequence data with the main modern paradigm, Neo-Darwinism are considered along with other relevant data on molecular markers (MM) usage, e.g. food sources mislabelling determination, etc.

There are 5 main items of the report:

1. A combination of nuclear DNA (nDNA) and mitochondrial DNA (mtDNA) MM best suits the hybrid identification and estimation of the genetic introgression (gene flow).

2. Evidence that available for both nDNA and mtDNA diversity seemingly make the hybrid occurrence among many taxa of animals and plants obvious. Although even in the wide hybrid *Mytilus* spp. zones, for example, the genetic introgression may be quite restricted or asymmetric, thus holding at least the “source” taxon intact.

3. If admit that a sexually reproducing species in marine and terrestrial realms is introgressed, as it is still evident for many cases, then we should recognize that the orthodox Biological Species Concept (BSC), in terms of complete lack of gene flow among species, is inadequate due to the fact that many wild nature species are not biological species yet. However, sooner or later they definitely become biological species, thus returning validity to BSC. This conclusion is supported by the genetic distances, that are minimal intraspecies and increasing with taxa ranks, as evident for bulk single mtDNA genes, for complete mitogenomes, and for abundant representative nDNA observations.

4. The investigation recently made on fish taxa divergence by the author using vast BOLD data, shows that gene trees investigated for taxa up to the family level are basically monophyletic, and interspecies reticulations are rare.

5. There are many other applications for MM in basic and applied science fields, like DNA barcoding of global biodiversity, forensics, international trading control that are included in the report.

Main outcomes from 5 above listed items have impact on the paradigms of evolutionary genetics, molecular systematics and phylogenetics, iBOL science policy and on the practice of species/specimens delimitation in particular. Common successful species delimiting, based on a widely applied barcoding technique, and reliable phylogeny reconstructions based on MM are possible due to the vast predominance of species origin throughout the geographic speciation mode and data fit to BSC.

Cold seep ecosystem in the South China Sea

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Since the discovery in 1983 on the Florida Escarpment in the Gulf of Mexico, cold seeps are recognized as important pathways of element cycling on Earth, representing areas that are typified by a series of biogeochemical reactions and commonly sustaining some of the richest ecosystems on the seabed. “Jiaolong methane reef”, which was first discovered by GMGC and IMF-GEOMAR joint survey in the South China Sea, is one of the largest known seep deposits in the world. The “Site F” of the Jiaolong Reef is an active seep site with a typical cold seep chemosynthetic ecosystem. Between 2013–2018, with support of strategic priority project “West Pacific Ocean System: Structure, Dynamic, and Consequences”, the Institute of Oceanology, Chinese Academy of Sciences performed 6 expedition cruises, more than 100 ROV dives on the “Site F”. The deep-sea research team of the IOCAS have developed deep-sea geological mapping system, in situ Raman spectrometry system, long time deep-sea observation system, versatile deep-sea sampling system, and onboard deep-sea macro-fauna cultivation system. With the facility of these deep-sea equipment’s, the IOCAS studied the biodiversity, tropical structure of the cold seep, profiled the microbe diversity of the seep microbe community, studied the genomics and transcriptome of deep-sea macro-fauna, and finally studied the chemosynthetic symbiosis of the deep-sea animals. We are looking forward to cooperating with our Russian colleagues, to joint force to explore cold-seeps and other deep-sea ecosystems.

**Spatio-temporal patterns
of subtidal macrobenthic assemblages
in Longkou Artificial Island areas
in the Bohai Sea, China**

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To evaluate the status and changes of macrobenthic communities related to construction of the Longkou Artificial Island (LAI) in the Bohai Sea, China, four annual surveys were conducted from 2010 to 2013. Significant changes on environmental variables and macrobenthic communities were observed in 2013 after the LAI construction a couple of years later. The changing environment was primarily presented by lower values of pH, DO, organic material (OM) percentage and higher values of salinity, suspended particulate matter (SPM) concentration and oil concentration. The main dominant species shifted from Polychaeta taxa in 2010 to Mollusca taxa in 2013 due to the changes of environmental variables. An apparent miniaturization tendency in body size of macrobenthic species was presented from 2010 to 2013. The biodiversity indices increased by years from 2010 to 2013. However, inter-site homogenization was observed in both the community structure and health status. M-AMBI analysis showed that the health status of stations changed depending on its original status and distance to the LAI. However, no significant differences were found in the spatial distribution of either environmental variables or macrobenthic communities. All the results will provide a basis for the long-term ecological assessment of reclamation.

Diversity and distribution of tintinnid ciliates along salinity gradient in the Pearl River Estuary in outhern China

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Tintinnid community structure in the Pearl River Estuary were investigated six times (10, 29 October 2014; 11, 30 June 2015 and 15 March, 1 April 2017) from upstream freshwaters to polyhaline waters. A total of 43 tintinnid species in 15 genera were identified. Freshwater, brackish and marine species occurred in sequence along salinity gradient. *Tintinnopsis mayeri*, *T. tubulosa* and *Tintinnidium fluviatile* were freshwater species. Fourteen and 15 tintinnid species were considered as brackish and marine species, respectively. The preferred salinity of freshwater species was < 3, abundance of freshwater species decreased along salinity gradient. Preferred salinity of brackish species ranged in 3–23. High abundance of brackish species occurred at mesohaline regions and decreased both towards oligohaline and polyhaline regions. Marine species abundance dropped sharply with the decrease of salinity, and seldom appeared when salinity was < 15. Tintinnid species richness was low at low salinity areas. With the increase of salinity, tintinnid species richness showed different variation patterns at different seasons. Tintinnid abundance showed bimodal-peak along salinity gradient. The first abundance peak was mainly contributed by brackish species and occurred where salinity was lower than 15. While the second abundance peak appeared where salinity was around 25 or higher than 30, which was mainly contributed by marine species. Low salinity, brackish water and coastal tintinnid communities were divided based on the abundance percentage variations of different tintinnid types. Complexities of those communities increased along salinity gradient.

Evaluation on short- and long-term performance of the red drum, *Sciaenops ocellatus*, a potential biological invasive species in China

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As an important fishery resource, the red drum, *Sciaenops ocellatus*, is originally distributed in the southeastern coast of the United States and the coast of Mexico. *S. ocellatus* was firstly introduced to Taiwan in 1987 and to mainland China in 1991 for aquaculture. With the development of reliable culture techniques, the commercial production of this species has expanded to eastern and southern coast of China because red drum is a popular food fish, relatively hardy and adapts well to aquaculture conditions. Based on a rough estimate, the aquaculture production of the red drum has reached to 68000 t/year. In recent years, more and more wild populations of this species have been found in Chinese coastal waters because of farming escape and being released artificially. This introduced species may cause potential threaten to the local natural zoology and the native biodiversity because of lacking well studying on their biological and ecological characteristics. Combined with the data collected in the past, we used the multi-methods technologies including transcriptome with high-throughput analysis, oxygen isotope analysis as well as stomach content analysis to estimate the performance of potential biological invasion of *S. ocellatus* in the coast of China. The *S. ocellatus* occupied the ability with characteristics of fierce appetite, fast swimming, low DO tolerance and euryhaline adaptability to compete against the local fishery species (such as drum fishes of Sciaenidae, hairtail fishes, etc.) in the coast waters of China. Therefore, the invasion of exotic marine creatures has attracted great attention from government and scientific community all over the world. The way to solve the biosphere of “foreign marine invasive species” problem and prevent they form any hazard towards a foreign country is a concern topic for ever.

Sea of Japan: a hotspot of molluscan biodiversity

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In an effort to estimate species richness of bivalves of the Sea of Japan, we have undertaken compilation of a catalogue of bivalve mollusks of the entire Sea. First, we compiled a list of bivalves separately for the western and eastern parts of the sea based largely on published literature including our own data for Russia and Korea. There are many taxonomic problems and various treatments of species validity and synonymy among Russian, Korean and Japanese malacologists that prevent future work and publication of the catalogue but we will try to resolve these problems in due course. This effort at making full catalogue of bivalves of the Sea of Japan is done for the first time in regional studies although there are some databases by American workers not freely available.

According to our preliminary data, western part of the Sea of Japan is inhabited by 371 species and subspecies of bivalve mollusks. Among them, 316 species are known for South Korea (SK), 50 species for North Korea, and, in Russia, 163 species for southern Primorye (Peter the Great Bay, SP), and 130 species for middle/northern Primorye, the area of the continental coast of the sea from Cape Povorotny to Tatarsky Strait (MNP). The South Korean fauna is quite rich, and is comparable with that of the East China Sea, which has 337 species (Xu, Zhang, 2011). In the eastern part of the sea (excluding Sakhalin shelf), 546 species and subspecies of bivalves are known. At least, ten families of bivalves are not known in the western part but present along the Japanese coast: Tindariidae, Nucinellidae, Cucullaeidae, Malleidae, Sportellidae, Tridacnidae, Cardiliidae, Pholadomyidae, Parilimyidae, Verticordiidae.

Currently, we suggest that about 600 species of bivalves inhabit the entire sea, a first estimate of total bivalve species richness for the Sea of Japan. This is sufficiently higher than in neighboring seas: 87 and 175 species are known for Bohai and Yellow seas, respectively (Xu, Zhang, 2011), about 288 species of bivalves were found in all Russian Far Eastern seas (Lutaenko, 2013), and 337 species are identified for subtropical East China Sea. The richest bivalve fauna in the world, in the South China Sea, is estimated at the level of 1200–1500 species. In Taiwan, 759 species of bivalves are known, in all Chinese seas – 1104, in Japan – 1472, in eastern Australia – 911, in western Australia – 658, in Vietnam – 812. Among these biodiversity-rich areas, Sea of Japan is one of the world molluscan biodiversity hotspot despite its large part lies in temperate waters. This can be explained by a regional oceanography.

A search of mollusks from some Russian seas (Sea of Japan, White Sea and Barents Sea) with abnormal hemocytes

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The common inhabitants of the Russian seas such as mussels are key elements of marine ecosystems and, in addition, they have a great economic importance. Today it is known (Metzger et al., 2015) that clonally transmissible cancer (CTC) broadly meet in marine Bivalvia, crossing taxonomic boundaries. Populations of *Mytilus trossulus* in northern Europe could be considered as a possible source of CTC spreading in populations of *Mytilus edulis* in western Atlantic. Our ultimate goal is to participate in the unfolding race of CTC studies. We would like to develop a technique of CTC identification and formally test regional populations of these mollusks for its presence-absence. To reveal CTC in Russian seas and try to understand this phenomenon, we tested hemocytes of mollusks (*Mytilus* sp.) from the European and the Pacific coasts. Mollusks were analyzed using conventional methods including flow cytometry and histological assays. We found only one specimen of *M. trossulus* from polluted area in the Sea of Japan (pretty close to the radioactive waste repository) in which about 40% of hemocytes had enlarged lobed or otherwise pleomorphic nuclei and unusual cytoskeleton. Chromatin was granular and no nucleoli were observed. Nucleus to cytoplasm ratio was high, although PCNA staining, a DNA synthesis marker, was absent in these cells (confocal microscopy). In comparison to normal hemocytes, abnormal hemocytes did not spread on a glass or plastic substrate. All specimens from northern Russian seas (the White Sea and the Barents Sea) did not demonstrate any hemocyte disorders. Perhaps we did not find seek mollusks from northern seas due to insufficient sample size or fairly young age of the analyzed mussels. We are just starting to elucidate some of the issues and in future, plan to continue this study using genetic methods for analysis.

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Deep-sea swimming isopods Munnopsidae (Crustacea: Asellota) from the Kuril-Kamchatka Trench area, Northwest Pacific

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Since 2010, the NSCMB FEB RAS together with German institutions fulfilled 4 deep-sea expeditions to study of benthic biodiversity and biogeography of different adjacent deep sea basins of the NWP: the SoJaBio expedition, 2010 sampled the semi-enclosed Sea of Japan; KuramBio, 2012 worked in the open abyssal plain adjacent to the Kuril-Kamchatka Trench (KKT); SokhoBio, 2015 – in the Kuril Basin of the Sea of Okhotsk and KuramBio II, 2016 – in the KKT hadal. Since the famous *Vityaz* expeditions (1949–1966), it was the first extensive biological investigations in the region with using modern sampling gears. Crustaceans of the order Isopoda was one of the dominant macrobenthic taxa and the family Munnopsidae was the most abundant and diverse isopod family, comprising 49% of all Isopoda. A list of the Munnopsidae species known for the region we enlarged from 39 species of 14 genera of to 157 species of 35 genera. Subfamily Lipomerinae with 5 genera and other 9 genera from 4 subfamilies were firstly recorded for the NWP/Pacific. In all sampled areas only 20 previously known NWP species were re-sampled, therefore, ~87% of the collected Munnopsidae were new to science.

Differences in species richness and composition of the Munnopsidae were revealed between the ocean abyssal plain (101 species of 28 genera were sampled) and the KKT hadal fauna (41 species of 15 genera), the abyssal basins of the Sea of Okhotsk (39 species of 20 genera) and the Sea of Japan (4 species of 4 genera). The subfamily Eurycopinae with the main genus *Eurycope* dominated in all areas. In the abyssal plain the Eurycopinae (56% of all ind.) followed by the *incertae sedis* genus *Microcope* (16%), then Ilyarachninae (10%), Betamorphinae (4%) and *Munneurycope* (4%). In the hadal zone Eurycopinae (42%) followed by Betamorphinae (33%), Storthyngurinae (17%), *Microcope* (7%) and Ilyarachninae (3%). In abyss of the Sea of Japan 99% of all munnopsids belonged to one species of the Eurycopinae. Only in the abyssal Kuril Basin the Eurycopinae (27%) followed the Ilyarachninae (39%), though it was the most specious subfamily there.

Like a numbers of species the taxonomic composition of the munnopsid fauna of the KKT hadal, the Kuril Basin and the Sea of Japan was also declined comparing to the richest fauna of the KKT abyssal area. Subfamilies Betamorphinae, Syneurycopinae and Storthyngurinae were not recorded in the Kuril Basin, though they were found at the KKT hadal depths. Two subfamilies, Lipomerinae and Acanthocopinae and five genera occurring the Kuril Basin were not sampled at the KKT hadal. Most of munnopsid (92%) of the KKT belong to three subfamilies: Eurycopinae (42%, 15 species), Betamorphinae (33%, 4 species) and Storthyngurinae (17%, 2 species). The subfamilies Ilyarachninae (3%), Munnopsinae (2%), Syneurycopinae (0.1%) and *incertae sedis* genera all together comprise 8% of all munnopsids. Eight most numerous species from 3 main genera, *Eurycope*, *Betamorphina* and *Rectisura* consisted 78% of all munnopsids individuals.

Only 3 from 36 NWP genera, *Eurycope*, *Ilyarachna* and *Munnopsis* were common in all four studied areas; 5 more genera were common for 3 areas besides the Sea of Japan. There are no common species between the Sea of Japan abyss and other studied areas, however, 10 species were common for the KKT hadal, abyssal plain and the Kuril Basin; 29 species were common for hadal and abyssal zones.

A study of the settlement of juvenile Far Eastern sea cucumber (*Apostichopus japonicus*) on a collector in cages in Possjet Bay

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Far Eastern sea cucumber – *Apostichopus japonicus*, is valuable commercial species. This species is successfully cultivated on a large industrial scale in the north of China, Korea, Japan. In recent years, the scale of sea cucumber has been growing in Russia, on the coast of the Sea of Japan.

The first and most important stage of the technological cycle is obtaining a viable planting material. There are two ways to obtain juveniles for subsequent commercial cultivation of trepang:

1. Factory.
2. Collecting on artificial collectors.

The plant growing method is the most expensive, as it requires large capital investments and compliance with strict biosafety rules. The method of collecting juveniles for artificial collectors in the natural habitat is currently rarely used due to low productivity. At the same time, the collector method is the cheapest to use and allows you to get immediately viable and adapted to natural marine conditions, juvenile sea cucumber. Another advantage of the method is its complete environmental safety.

The conducted experiment is aimed at modernizing the collector method. The basis of the method is the use of macrotanks – large cages placed in a natural habitat. At the same time, the state of planktonic organisms is partially controlled in cages through the use of a fine mesh nylon mesh.

To carry out work in the water area of Novgorodskaya Bay (Possjet Bay, Peter the Great Bay, Sea of Japan), 25 cages 5x5x5 m in size with nylon net walls were mounted within the aquaculture section of Hyperion LLC. Then in cages were placed 1650 adult individuals of sea cucumber, ready for spawning, with an average weight of 310 g. After spawning of adults, the trepang was removed from the cages in which the artificial collectors were mounted.

In early August, a selective survey of the collectors for sedimentation of trepang larvae was carried out. At the first cage, the average sedimentation density of juvenile trepang was 188.6 ± 51.6 ind./m². In the second cage, the average sedimentation density of juvenile trepang was 1271.5 ± 579.5 ind./m². The average sedimentation density of juvenile sea cucumber for the third cage is 2244.9 ± 1103.2 ind./m². The average total sedimentation density of juvenile trepang for all three cages was 1235.0 ± 466.7 ind./m². Taking into account the area of all collectors in cages, the total number of settled juveniles is 18673450 individuals for all collectors.

In addition to individuals of trepang, young sea anemones, polychaete worms, sea acorns, gastropods and bivalves, as well as ascidians.

Marine biobank of the NSCMB FEB RAS: the first lessons learned and prospection

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Coastal and deep-sea regions are offered as potential marine biological resources (MBR) and especially blue biotechnologies (technological applications that use marine biological systems, living organisms or derivatives to produce or modify products or processes for a specific use, as defined by the Convention on Biological Diversity) to create and promote employment, economic and regional development conducive to growth and cohesion. MBRs are one of the main services provided by marine ecosystems.

MBR culture collections are the key to a systematic study of interesting and unique genes, bioactive and marine biomaterials with potential for commercial development and job creation in coastal regions. The bioresource collections consisting of biological samples and associated data, have gained great significance for fundamental research and biotechnology.

Bioresource collection Marine Biobank “MBRU” (<http://marbank.dvo.ru>) was established in 2017 on existing unique biological collections located at the A.V. Zhirmunsky National Scientific Center of Marine Biology of the Far Eastern Branch of Academy of Sciences of Russia (NSCMB FEB RAS) in Vladivostok. MBRU is intended for storing, studying and implementing the results of a wide range of marine biological samples. MBRU is a new generation biorepository that combines the capabilities of the ultramodern robotic cryostorage of marine biomaterial, advanced information technologies for organizing open access to the stock collections, high-tech cellular technologies, and molecular genetic and biochemistry studies.

MBRU will set the basis for the common operation of the distributed marine biobanking facilities by:

1. Setting up technological tools and common procedures for the ex-situ maintenance of MBRs.
2. The application of best practice guidelines throughout the NSCMB FEB RAS collections to ensure compliance with regulatory framework that sets the rules on access and benefit sharing on the use of marine bioresources for commercial and academic research.
3. The development of innovation use cases involving industrial end users and administrations for the production of a set of best practice guidelines for using MBRs for innovation purposes. The MBRU will ultimately facilitate sustainable access to marine biodiversity, its associated data, and extractable products for local and international academia and industry users.

While biobanks are increasingly recognized as a crucial infrastructure for research, at the same time the widely varied practices in biobanking regarding for collection, storage and consent procedures may be a barrier to cross-border research and collaboration by limiting access to samples and data. In this regard, the current state and prospects for the development of the Russian marine

biobank are presented. The prospects of creating a bank of Marine Genetic Resources on the basis of Marine Biobank NSCMB FEB RAS is discussed.

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Spawning capabilities of mitten crab *Eriocheir japonica* under laboratory conditions

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Japanese mitten crab *Eriocheir japonica* (de Haan, 1835) is a cadastral species widespread in the north-western part of the Pacific Ocean. Representatives of the genus *Eriocheir* are considered to be valuable food objects in the countries of Southeast Asia. In 2014, the production of Chinese mitten crab worldwide amounted to 796621 tons.

To date, migrations and breeding of Japanese mitten crab in nature have been studied, where the phenomenon of repeated spawning of one female per season is described, but there are no data on direct observations of similar processes. The data on the time and season of mating are also insufficiently introduced in the literature; therefore, in our work, we investigated these processes in females of mitten crab under controlled conditions.

Within the framework of our research, in April 2019, two groups of specials were selected. The first group, consisting of 9 females, was caught with eggs. The second group of specials included 9 females and 3 males. Mating in this group started on 30.05.2019 and lasted until 10.06.2019. The temperature regime was maintained in the range from +12.1°C to +20.5°C. Salinity was within 29.9–32.4‰.

In the first group, 33.3% of the females didn't live up to spawning, the remaining 66.7% had post spawning death. In the second group, 22.2% of the females did not live up to spawning, another 22.2% didn't set down eggs. 11.1% of the females recorded post-spawning death, 22.2% of the females spawned once, 22.2% of the females spawned twice.

In the first group, the first spawning was recorded on 26.05.19 in one female. The number of larvae obtained was up to 100000. The second spawning took place from 28.05.19 to 06.06.19, 4 females were spawned. The number of larvae received was 13000. The third spawning was noted from 07.06.19 to 09.06.19, 50900 larvae were obtained from one female.

In the second group, the first spawning was recorded from 25.06.19 to 27.06.19, one chipped female no. 643093400042858 was spawned; the number of larvae was 294480. In the second spawning of 29.06.19 one female no. 643093400042850 was also spawned, the number of larvae obtained was 378000. The third spawning was recorded on 30.06.19. One female no. 643093400042849 gave 180000 larvae. The fourth spawning took place from 08.07.19 to 09.07.19.

One female was spawned, 107000 larvae were obtained. The fifth spawning took place on 28.07.19, the same female no. 643093400042858 was again spawned. The number of the larvae was 118000. On 29.07.19 the sixth spawning took place in which only one female took part (without a chip). 168000 larvae were received. And on 01.08–02.08.18 the seventh spawning took place. Female no. 643093400042850 was spawned for the second time. 245400 larvae were obtained.

This research shows that the females of Japanese mitten crab were spawned 1–2 times during the period of the studies. The minimum amount of larvae received from one female is 3250, the maximal amount is 378000, the average amount – 165478.

Taxonomic composition and distribution of meiofauna communities from the intertidal zone in Sishili Bay, Yellow Sea coast (northern China)

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The present work provides a preliminary baseline study of meiofauna communities in Sishili Bay, Yellow Sea coast (northern China) for the first time. The main goal is to study the density, species diversity, and structure of meiofauna communities from the intertidal zone in this area. Sishili Bay is a 130 km² embayment on the Yellow Sea coast with an average water depth of 8–9 m. The intertidal zone is mainly represented by sandy beaches, though a mudflat near the scallop and mussel farms exists. The tidal regime in the bay is semidiurnal with a maximum tide range from 1 to 3 m. The meiofauna was studied at 14 stations; these were located in three transects (A, A' and A'') in muddy zone and two transects (B and C) in the sandy zone; triplicate samples in each transect were randomly taken for meiofauna. During the study period, salinity in Sishili Bay changed slightly, ranging from 21 to 28‰. The surface-water temperature (18.1 to 19.2°C), and oxygen concentrations (4.88 to 8.67 ml l⁻¹). Organic matter in all sediments was generally low, ranging from 0.0028 to 0.152%. The density of meiofauna communities in the tidal zone of the Sishili Bay, both in silted and sandy areas, was relatively low and had uneven distribution. The highest density was found in the middle tidal zone at all transects, except only for the transect C where it was recorded in the low tide level. At least 11 meiofaunal taxa were identified. The most common taxa were nematodes, harpacticoids, ostracods, and polychaetes, which on average accounted for 95% of the meiofauna. The meiofaunal community was clearly dominated by the nematodes (80%), followed by the harpacticoid copepods (9%). Polychaetes had higher numbers than ostracods and formed a third dominant group. Representatives of such groups, as Turbellaria, Gastropoda, Amphipoda, Bivalvia, Isopoda, Amphipoda, Oligochaeta and Cumacea were non-abundant (≤ 0.10 ind./10 cm² on average). Highest density and diversity levels were reported for the transect A' (430±150 ind./10 cm²). A total meiofauna density was the lowest at the transect B (175±44 ind./10 cm²). The density of meiofauna was correlated with the average grain size (r Pearson = 0.379, $p < 0.05$). We believe that the structure of meiofauna on sandy beaches is affected by various physical parameters, such as temperature, salinity, oxygenation, and others. However, we consider the grain size of the sediment the main influencing factor.

High-speed calcium *in vivo* imaging to determine the neuronal and neurogenic activity of brain cells of salmonids

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Calcium ions play a vital role in the biology of neurons, regulating various processes, in particular, the exocytosis of presynaptic vesicles, synaptic plasticity and gene transcription. The overall level of calcium in neurons is determined by the final ratio between the influx of calcium ions and its release through channels on the cell membrane and receptors located along the entire body of the cell, dendritic branches and synaptic endings. Calcium concentration at rest in fish neurons is 50–100 nmol, however, when generating electrical activity, the concentration of calcium ions can increase many times. Such a change in the intracellular calcium concentration can be detected by introducing into the cell calcium-binding proteins or other calcium-sensitive molecules conjugated to a fluorophore. When such a protein or molecule binds calcium, there is a change in its luminescence or fluorescence, which can be visualized using fluorescence microscopy or other optical methods. Indicators can also be endogenously expressed in cells after genetic modification, as a result of the introduction of viral vectors, or in transgenic animals. Among the latest achievements in the field of vital imaging of calcium indicators in the brain of vertebrates using viral vectors should include innovative technology of miniaturized fluorescence microscopy. With the appearance of this type of microscopy, it became possible to carry out an *in vivo* study of neuronal activity using calcium imaging in intact cells, and also with various experimental effects. Vital microscopy has now reached a wide distribution in neurology, but the limitations of conventional microscopes prevent large-scale brain imaging experiments. In order to improve the availability, quality and throughput of research to identify neurogenesis events in the brain of salmon fishes, it is planned to use a miniature integrated fluorescence microscope with a design that allows vital monitoring and high-speed tracking of neural dynamics and neurogenic activity. The principles of micro-optics and semiconductor optoelectronics form the basis of a miniature microscope having a mass of 1.9 g and easily held with fingertips. In addition to creating dynamic high-speed images of the brain, it is necessary to note a significant expansion of new digital applications, which are provided through the miniaturized integration of a light microscope, in particular, portable diagnostics based on images and high-performance screening. Thus, the use of vital miniature microscopy will allow a fundamentally new approach to the physiological studies of mature functional multineuron complexes in different parts of the brain of salmon fishes, as well as to monitor neuronal/glial/immune activity in cells during traumatic brain damage.

High level of eicosapentaenic acid in total lipids of amphipods from northeastern Sakhalin Islands shelf as an indicator of Western gray whale’s food quality

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Eicosapentaenic acid (EPA; 20:5n-3) has an important role to play in supporting vital activity of the living organisms. This fatty acid is “essential fatty acids” and must be obtained from food because the most of marine organisms cannot synthesize these fatty acids in their body. The main producers of EPA are considered diatom microalgae. Marine consumers feeding microalgae accumulate EPA in their lipid content and pass it up the food chain. Therefore EPA concentration in total lipid of the forage animal can be considered an indicator of food quality for animals of higher trophic levels. In this work the investigation of the fatty acids composition from the total lipids of amphipods that are considered the main Western gray whale’s preys, was performed. These amphipods occur in the gray whale’s feeding area on the northeastern Sakhalin Island shelf. The main purpose was to assess the EPA concentrations in total lipid of these animals as an indicator of the quality of gray whale’s food resource and as an indicator of the diatom contribution to amphipod feeding. There were studied 6 amphipod species, some of which (*Ampelisca eschrichtii*, *Monoporeia affinis*, *Eogammarus schmidtii*) are dominant, other (*Maera loveni*, *Anonyx nugax*, *Onisimus derjugini*) are

Fatty acids (FA) concentration (%) of major amphipods

FA	<i>A. eschrichtii</i> (9)	<i>M. loveni</i> (1)	<i>A. nugax</i> (12)	<i>M. affinis</i> (10)	<i>E. schmidtii</i> (10)	<i>O. derjugini</i> (3)
14:0	3.8±0.1	5.0	1.8±0.3	5.7±0.9	2.8±0.3	2.0±0.5
16:0	9.7±0.2	11.0	13.7±1.0	17.6±0.6	15.7±0.4	16.4±0.5
16:n-7	17.9±1.6	14.0	13.5±1.1	19.1±2.6	13.8±1.5	10.8±0.9
18:1n-9	6.0±0.5	8.1	27.7±2.5	18.7±2.0	20.1±1.6	34.8±2.9
18:1n-7	5.8±0.7	7.1	6.4±0.8	2.2±0.9	4.0±0.5	3.7±0.1
16:2n-4	2.0±0.2	1.6	0.7±0.2	0.7±0.2	0.9±0.2	0.3±0.0
16:3n-4	2.2±0.2	1.9	0.6±0.1	2.4±0.3	1.2±0.3	0.7±0.1
16:4n-1	5.0±0.6	5.5	0.7±0.2	3.7±1.0	2.6±1.5	0.5±0.2
18:4n-3	3.5±0.2	3.3	1.2±0.3	2.2±0.3	1.8±0.3	0.1±0.0
20:4n-6	0.6±0.0	0.9	0.9±0.2	0.4±0.3	0.6±0.1	1.0±0.1
20:5n-3	27.7±0.7	28.0	18.2±1.6	15.4±2.0	21.5±1.1	13.5±0.7
22:6n-3	3.7±0.2	3.3	5.0±0.6	2.9±1.3	4.5±0.6	5.5±0.7

Note. The numbers of analyzes indicate in parentheses.

less abundant, but also contribute as potential food for gray whale. According to the results of FA analysis, maximum EPA concentration were identified in total lipids of the suspension-feeding amphipods *Ampelisca eschrichtii* (27.7%) and *Maera loveni* (27.8%) (see Table). The lowest concentration of EPA was showed for predator *Onisimus derjugini* (13.5%). The intermediate amounts of EPA were detected in total lipids of deposit-feeding amphipods *Monoporeia affinis* (15.4%), *Eogammarus schmidtii* (21.5%) and necrophagic amphipod *Anonyx nugax* (18.2%) from this area. Generally, the high levels of EPA (diatom marker) were found in all investigating amphipod species and along with others diatom marker fatty acids (16:n-7, 16:4n-1) point to a large contribution of fresh diatom-derived organic matter to amphipod feeding. Consequently, amphipod preys are a valuable source of EPA for the higher trophic level animals and especially gray whales on the northeastern Sakhalin Island shelf.

Sulphated steroids derived from marine sources and their biological activity

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Sulphated compounds, including steroids are widely distributed in nature. Sulphated steroids are found in many animals, reptiles and humans. In addition, they are present in extracts of plants and some shrubs, are produced by fungi, and also found in many marine invertebrates such as brittle star, starfish, sponges, ascidian, snails and algae.

One of the known and studied functions of sulphated steroids is that they are like a storehouse of biologically active steroid hormones. As is known, sulphated steroids are biologically inactive molecules in cells and acquire activity under the action of steroid sulfatase (STS) enzyme, which removes the sulphate group in steroids. STS inhibitors are potential therapeutic drugs for treatment of steroid-dependent cancers such as breast, prostate, endometrial cancer, as well as melanoma cells SK-MEL-28, SK-MEL-5 and RPMI-7951.18,22-26. Recently, various groups of scientists have shown that sulfonated steroids can perform the functions of endogenous neuromodulators.

Currently, more than 150 sulphated steroids have been found in marine invertebrates and algae. We selected about a third of the steroids that are of potential interest for practical and clinical medicine.

This presentation is devoted to sulphated steroids that are produced by brittle star, starfish, sponges, ascidian, snails and algae. Mono sulphated steroids have the pharmacological potential on anti-hypercholesterolemic, anti-neoplastic, and anti-inflammatory activity estimated with a confidence of 88 to 92%. Di-sulphated steroids that produced by marine starfish are predicted as having anti-neoplastic, anti-inflammatory and anti-hypercholesterolemic activity with a confidence of 78 to 89%. In addition, they may have potential immunosuppressant and hepatoprotective inhibitors estimated with a confidence of 73 to 83%. Tri-sulphated steroids exhibit anti-inflammatory and antineoplastic activities with a confidence level of 74 to 82%.

Seasonal cycles in the somatic and reproductive growth of the Yesso scallop in a polluted area

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Growth of the shell height, total weight, weights of shell, all soft tissues, muscle adductor, digestive gland and gonad of the Yesso scallop *Mizuhopecten yessoensis* was studied under the seasonal changes of environmental factors and reproductive activity of the scallop in the polluted Amursky Bay. The bay is exposed to anthropogenic impacts. The main source of pollution is domestic and industrial sewage from Vladivostok and the Razdolnaya River. This watercourse, in addition to the terrigenous runoff and the surface runoff from agricultural land, located in the catchment area, brings domestic and industrial wastewater discharged from Ussuriysk and Suifenhe (China). The coastal zone of the bay bears the greatest load by receiving a multicomponent mixture of pollutants of mineral and organic origin. The degree of water and sediment pollution has changed during last 30 years. The degree of water and bottom sediment pollution has changed during last 30 years. Prior to the early 1990s, there was an increase in pollution of the Bay due to the development of economic activities in the bay and river coasts. Later, due to a significant decrease in industrial production and agricultural activity in Russia, pollution of coastal areas decreased, the state of the benthic community improved. Studies of the somatic and reproductive growth of the scallop were conducted in comparative terms for these two periods of biotope development. Scallop collection was carried out in different seasons 1994–1995 and 2015–2016.

It was found that a food quantity and quality are not a governing (limitative) factor for the scallop growth. It appeared the main exogenous factors causing the seasonal changes in the scallop growth rates, the water temperature, too high in July–August and low in December–March, and the water salinity which falls below the optimal range for this stenohaline species in summer, as well as summer lowering of the water oxygen concentration.

The fluctuations of the scallop growth rates are also determined by such endogenous factor as reproductive cycle. Spawning results in the severe loss of the mass of the gonad and somatic tissues. The energy reserves of organism are redistributed in behalf on reproductive efforts, as the energy, which is required for the scallop gametogenesis, is covered, in particular, by the expense of the reserves that are accumulated not only in the muscle adductor, but also in the digestive gland. It testifies to the stress state of the population in the investigated polluted bay.

The ontogenetic stages of organism development also bring an amendment in the annual fluctuations of the scallop growth rates. Immature individuals do not have a decline of their organs' masses in summer. In contrast, muscle adductor mass even increases at this season. At the first gametogenesis, the gonad mass increases not so intensively, as somatic tissues. Later, reproductive efforts increase with age, again decline to old age of scallop.

At the different degree of environmental pollution, the somatic and reproductive growth lasts during all scallop life, but the lower growth rates occur under the higher pollution.

Challenges and strategies in the ecosystem-based management. A lesson from macroalgae bloom

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In the summer of 2008, the world's largest green macroalgae blooms (green tide) caused by *Ulva prolifera* occurred in Qingdao, a city at the west coast of the Yellow Sea and the host city of 2008 Olympic sailing events. The green tide caused damages to the tourism, marine transportation and brought environmental problems. The “green monster” led to the costs of billion of Chinese Yuan while ten thousand of people were involved in combating the green tide. Since then, green tide has been visiting the west Yellow Sea every summer, bringing big troubles to the central and local marine environment managers.

In the last ten years, one of the popular topics is that where the massive *U. prolifera* come from, what cause the green algae bloom, and the most important: who should take responsibility of the green algae bloom, so it is not only a scientific problem, but social and it concerns local governments. Scientist must tell people the truth and the systematic solution to prevent or reduce the damage of the green algae bloom. On the other hand, some people do not want scientists to reveal the truth, because it will affect the local economy and some people should take responsibility, they will continue to ask scientists to offer “more data and details”, it is a new challenge for the ecosystem-based management, because the problem occurred in one area but it affect other areas, to prevent and reduce the affection, it need investment and cost a big money. From 2015–2018, a comprehensive “Green Tide” Project has been conducted to find out the origin of the tides in Shandong and Jiangsu provinces. This project focuses on the disaster mitigation of green tides (induced mainly by *U. prolifera*) in the south Yellow Sea. Significant progress has been made on the mechanism of formation and the strategy of mitigation of the green tides in multidisciplinary studies, during which more than 20 cruises in the southern Yellow Sea were conducted and multiple research methods applied, including on-site investigation, satellite remote sensing, and simulation experiment, etc. The results show that the massive floating *U. prolifera* could be traced back to the offshore aquaculture areas in Subei Shoal, North Jiangsu. A proposal how to prevent the green algae bloom happen in Qingdao was submitted to the central government before the Shanghai Cooperation Organization summit, this proposal was accepted and carried out along the coast of Yellow Sea, it was very successful; it is a lesson for the Ecosystem Based Management, challenges and solutions.

The “seamount effect” of phytoplankton in the tropical western Pacific Ocean

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The tropical western Pacific is not only a typical oligotrophic ocean, but also one of the most concentrated areas of seamounts. Studying the phytoplankton of seamount in this area is very important for us to understand the primary production processes and characteristics of seamount ecosystem in oligotrophic sea.

The phytoplankton biomass (measured as chlorophyll *a*) of four seamounts (Y3, M2, M4, Magellan-Seamount) in the tropical western Pacific was investigated. Our results showed that, in tropical western Pacific, pico-phytoplankton is the dominant group, and the concentrations of chlorophyll *a* (Chl*a*) in surface water were very low (about 0.05 mg/m³), and chlorophyll *a* maximum layers were deeper than 75 m at all seamounts.

The “seamount effect” was found only in the seamount M4, where the isotherm was obviously elevated near the peak, and the water-column-integrated Chl*a* near the peak (14.18 mg/m²) was significantly higher ($P < 0.05$) than the surrounding sea area (12.17 mg/m²). In addition, the uplifted isotherm also existed in the seamount M2, and the highest value of Chl*a* appeared near the peak of the mountain, but there was no significant difference from the surrounding water. The tops of the seamount Y3 and Magellan-Seamount are deeper (Y3: 300 m; Magellan-Seamount: 1300 m), and the isotherms were unchanged in upper water (above 200 m), and their Chl*a* were same with surrounding water. The top of the seamount M2 and M4 are relatively shallower (M2: 34 m; M4: 57 m), their interactions with currents are more likely to break the stratification of the upper layer, and allowing the mixed layer water to enter the euphotic layer, providing nutrients for phytoplankton growth near the peak. Compared with the seamount M2, the landform of the seamount M4 (north-south extension) is more strongly influenced by the east-west sea current, which is the main reason for the “seamount effect” appears in the seamount M4 instead of M2. In addition, the peak of seamount M4 is a basin, and the organic matter is more likely to deposit on the top of the mountain, which could be one of the drivers of the phytoplankton biomass enhancement.

Investigation of deep-sea ecosystems by the use fatty acids marker

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Abyssal seafloor ecosystems cover more than 50% of Earth's surface. Being comprised of mainly heterotrophic organisms, they depend on the flux of organic matter produced in the surface layer of the ocean through photosynthesis. This results in pronounced food limitation and periodicity, which lead to development of specific deep-sea communities. As the organic matter falls from the euphotic zone to the abyssal zone, the content of polyunsaturated fatty acids is reduced, and the trophic value of the organic matter decreases. Abyssal and hadal invertebrates consume and accumulate sinking particulate organic matter (sestonophages and mobile surface deposit feeders). Other invertebrates use food that has undergone a trophic upgrade, when C20-C22 polyunsaturated fatty acids are synthesized from saturated and monounsaturated fatty acids. For example, Foraminifera can synthesize arachidonic acid and some barophilic bacteria produce eicosapentaenoic and docosahexaenoic acids. Analysis of FA of invertebrates collected in deep sea areas demonstrated presence many new and uncommon fatty acids, like 21:4(n-7), 22:4(n-8), 23:4(n-9), and 22:5(n-5). These FA are absent from different FAME standards. Only modern techniques of GC and GC-MS of FAME, using pyrrolidide and DMOX derivatives, allow rapid and reliable identification of FA in very complex mixtures of natural origin. The high levels of bacterial FA (odd- and branched-chain and 18:1(n-7) and the presence of a number of FA characteristic of abyssal foraminifera (an elevated level of ARA and, especially, the markers 21:4(n-7), 22:4(n-8), 23:4(n-9), and 22:5(n-5) can explain the FA composition of these of invertebrates by the transfer of FA through the food chain.

Influence of Liaoning Hongyanhe Nuclear Power Plant on zooplankton community

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In order to evaluate the impact of the Hongyanhe Nuclear Power Plant on the east coast of the Liaodong Bay on the zooplankton community in the surrounding sea area in summer, this paper investigated and analyzed the environmental factors such as temperature, salinity and chlorophyll and the distribution of zooplankton community on the east coast of the Liaodong Bay in the summer of 2017. Based on these, redundancy analysis (RDA) was employed to analyze the linearity of the influence of temperature, salinity and chlorophyll on zooplankton community. The results showed that: from July to September, the abundance of zooplankton and chlorophyll concentration in the eastern coast of Liaodong Bay increased first and then decreased. In August total abundance of zooplankton was 8116.70 ind./m³, Shannon-wiener index had a downtrend from July to September, the average value fell from 1.65 in July to 1.50 in September. The *Calanus sinicus*, *Paracalanus parvus*, copepod larvae and bivalve larvae are dominant species in these three months. The impact of the outfall of the nuclear power plant on environmental factors was mainly reflected in the increase of seawater temperature. The results of RDA analysis showed that the zooplankton community was affected by temperature, salinity and chlorophyll, and the degree of impacts varied every month. In which, the impact of the temperature was relatively strong and the impact of the salinity was relatively weak. The impact of Hongyanhe nuclear power plant on the structure and distribution of zooplankton community in its surrounding sea area in summer was the rising seawater temperature caused reduced dominant species abundance.

Taxonomic composition and distribution of recent benthic Foraminifera from the intertidal zone in Sishili Bay, Yellow Sea coast (northern China)

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The present work provides a preliminary baseline study of Foraminifera in Sishili Bay, Yellow Sea coast (northern China) for the first time. The main goal is to study the density, species diversity, and structure of benthic foraminiferal assemblages from the intertidal zone in this area. Sishili Bay is a 130 km² embayment in the Yellow Sea coast with an average water depth of 8–9 m. The intertidal zone is mainly represented by sandy beaches, though there is a mudflat near the scallop and mussel farms. The tidal regime in the bay is semidiurnal with a maximum tide range from 1 to 3 m. The Foraminifera assemblages were studied at 14 stations; they were located in three transects (A, A' and A'') in muddy zone and two transects (B and C) in the sandy zone; triplicate samples in each transect were randomly taken for the Foraminifera fauna. During the study period, salinity in Sishili Bay changed slightly, ranging from 21 to 28‰. The surface-water temperature changed from 18.1 to 19.2°C, and oxygen concentrations from 4.88 to 8.67 ml l⁻¹. Organic matter in all sediments was generally low, ranging from 0.0028 to 0.152%.

In the studied area, 37 species of Foraminifera belonging to 21 genera and 12 families were found. Among them, 28 species were collected from muddy tidal flat. At sandy tidal flat, 20 (area B) and 21 species were (area C) found. Among them, carbonate tests predominated (29 species), and only 8 species had agglutinated tests.

Distribution of Foraminifera on the muddy and sand intertidal areas was uneven. An increase in the number of species and the density of the Foraminifera populations at stations from the upper horizon to the lower horizon has been revealed. The smallest number of species (6 to 11) is found in the upper horizon. In the middle horizon, this parameter varied from 12 to 16 species. In the lower horizon, the number of species increased to 16–19 species per station. The density of the Foraminifera populations also increased from 12–120 ind./10 cm² in the upper horizon to 140–414 ind./10 cm² in the lower horizon. Living individuals comprised from 32 to 52% of the total Foraminifera complex at the muddy flat and sandy flat B. The smallest proportion of live individuals was found in the tidal flat C and was 10–15% of the total foraminiferan abundance.

Ammonia beccarii was the dominant species at all stations of the muddy intertidal, *Cribronion subincertum* and *Ammonia parkinsoniana* were subdominant. In sandy tidal flats, no clear dominance of any species was detected. Several species with equal abundance dominate over others, including *Ammonia beccarii* at all stations, except for the lower intertidal horizon of the area C. In this area, *Buccella frigida* and *Elphidium advenum* were abundant.

Seaweed flora of coral reefs in Sanya Bay (Hainan Island, China) at extremely polluted site from fish farm

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At the end of the rainy season in 2016 and at the end of the dry season in 2017, we conducted a floristic study of marine macrophytic algae in the intertidal and subtidal zones in moderately and heavily polluted areas at Luhuitou reef, Sanya Bay, Hainan Island, China. A total of 109 species of marine macrophytes were found during these samplings. At the end of the rainy season, 72 species of macrophytes (50% reds, 19% browns, and 31% greens) were found. At the end of the dry season, we found and identified 92 species of macrophytes (46% reds, 20% browns, and 34% greens). Seasonal changes in species diversity, species composition, and the structure of algal communities at differently polluted sites exhibited common features as well as specific characteristics. By the end of the dry season, the diversity of macroalgal species was increased, and the composition of dominant and accompanying species of macrophytes in polydominant communities was changed in moderately and heavily polluted areas. Seasonal changes in the marine flora of differently polluted areas were characterized by specific features as follows: less changes in species diversity of heavily polluted area compared with moderately polluted area during the change from the rainy season to the dry season; significant increase in the biomass of green algae and their projective coverage in the middle and low intertidal zones of heavily polluted sites in the dry season; and the increase in the numbers of mono- and bidominant communities in the middle and low intertidal zones of heavily polluted sites by the end of the dry season.

Investigation of mussel's byssus formation system in *Mytilus trossulus* Gould, 1850 (Bivalvia: Mytilidae) from the Sea of Japan

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Many bivalves save their byssus which attaches them to the surface of substratum in adult. Among of them, such genera of mollusks as: *Dreissena*, *Perna*, *Modiolus*, *Septifer*, and many other, including *Mytilus*. It is noted than many species of these genera are species-invaders. They are able to form strong connection with any anthropogenic substrates using byssus. Our previous study of the process of reattachment to various substrates in some mytilids have showed, that the most successful anthropogenic substrates (concrete, wood and iron) colonization by *Mytilus trossulus* among another species. Despite, that at the present time there are many papers about the morphological structure of byssus in the species of family Mytilidae in scientific literature, any information concerning byssus structure and its formation in mussel *M. trossulus* is limited.

Mytilus trossulus is common species of the benthic communities of the Sea of Japan. Also, this species is an important object of mariculture in Primorsky region of Russia. Note, that also *M. trossulus* is attached by byssus to the piers and offshore facilities, to the bottom of ships, slowing down their move. It is harmful and brings huge damage for government.

Therefore, the aim of this study was to investigate the morphological structure of byssus and structure of the pedal groove in details in *Mytilus trossulus* from the Sea of Japan. The obtained results are discussed with the point of view the process of the influence of anthropogenic load on the mussel invader.

The byssi and mussel's foots were isolated and its morphology examined using light and scanning electron microscopy (SEM). For SEM all samples were prepared using standard method. The specimens were photographed with Sony 5x Optical Zoom camera. For SEM we used a scanning electron microscope Carl Zeiss, Evo 40. All images prepared using graphic program Adobe Photoshop CS6.

Our results show that the byssus in *Mytilus trossulus* has the same morphological structure, which is characterized for the species of family of Mytilidae in general. The peculiarities of byssus structure in *M. trossulus* can be explained by the process of byssus formation in a pedal groove in the mussel. The results showed that in laboratory aquarium, the process of byssal threads formation has began with the stage when mussel has crawled and groped by distal end of foot a surface before attach to substrate and form the first byssal thread. During this process the mussel elongated a foot in 3–5 times from original length. The length of contracted mussel's foot was 1–1.5 cm in the samples with shell length 3 sm.

The SEM results showed that the groove is situated on ventral side of the mussel foot in central part and its length is approximated to the length of foot. The width of foot is 1428 mkm. At the distal

end of foot is situated the narrow distal fossa (transverse width 428 mkm). Here the foot is narrower. During process of byssal thread formation, the attachment disk is formed in the distal fossa. The measurement showed that the length of foot is 6000 mkm. The width of groove is 286 mkm. The deep of the groove is 70–250 mkm. The bottom of ventral pedal groove has plicated surface. The width of these folds is ranged from 100 to 200 mkm. The surface of these folders is covered by numerous pores. During the chemical process of byssal thread formation the secrets of five glands effluent using these pores in the pedal groove. The surface of ventral groove of mussel foot is covered by the fine clublike papillae (length 3.4 mkm). All secrets are mixed in the pedal groove of mussel using these papillae.

Common oysters and their distribution in China

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Oysters are important intertidal species, they are widely distributed in the world. The meat is delicious, rich in nutrition, with high economic value. Its production is the largest for aquaculture in China and the world at present. There are many kinds of oysters in coastal China, and the shell morphology of oysters is plastic and subject to environmental variation, it adds the difficulty for classification. With the development of molecular biology, molecular biology techniques have been applied to the phylogeny and classification of different species.

Based on this situation, we collected and analyzed a large amount of oysters from different sites along the coast of China. DNA sequences were analyzed. Compared their genetic relationships of all samples, combined with morphology and ecological environment analysis, our results indicate that the common oysters are: *Crassostrea gigas gigas*, *C. ariakensis*, *C. nippona*, *Talonostrea talonata*, *Ostrea denselamellosa* in northern China; *C. gigas angulata*, *C. sikamea*, *C. hongkongensis*, *C. iredalei*, *Planostrea pestgris*, *Saccostrea kegaki*, *S. echinata*, *S. mordax*, *D. folium*, *D. crenulifera*, *C. ariakensis*, *C. nippona*, *Talonostrea talonata*, *Ostrea denselamellosa* in southern China. We found some important oyster reefs in China, *C. ariakensis* was decreased on the reef.

This finding correct the oyster speciation and phylogeny system in China, suggest the high oyster diversity in China. It will contribute greatly to the oyster classification and phylogeny, as well as to the management and protection of oyster resources in China.

Vertical distribution of oceanic tintinnid (Ciliophora: Tintinnida) assemblages from the Bering Sea to Arctic Ocean through Bering Strait

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Knowledge on the distribution of plankton species is fundamental to understand planktonic ecosystem structure and function. We report the vertical distributions of tintinnid assemblages from the Bering Sea to Arctic Ocean. Dominant Bering Sea species (*Codonellopsis frigida*, *Ptychocylis obtusa*, *Parafavella* spp., *Acanthostomella norvegica*) had abundance peaks in the upper 50 m. In the Arctic Ocean, abundance peaks of dominant species (*P. urnula*) occurred in surface and deep chlorophyll *a* maximum layers. *Salpingella acuminata* and *S. faurei* occurred from 50–80 m in Bering Sea and Arctic Ocean oceanic waters. Bering Strait dominant species (*P. acuta*, *Parafavella* spp., *A. norvegica*) occurred from the surface to the bottom. Both *S. acuminata* and *S. faurei* were absent in Bering Strait at depths shallower than 120 m. Dominant Bering Sea species (*C. frigida*, *P. obtusa*, *Parafavella* spp., *A. norvegica*) disappeared successively with northerly progression. *P. urnula* occurred in the northern part of Bering Strait at depths exceeding 50 m. The size of *P. acuta* (only occurring in Bering Strait) was between that of *P. urnula* and *P. obtusa*. Dominant Bering Sea species had wide temperature but narrow salinity ranges (32.7–33.3‰); their successive northward disappearance might reflect salinity changes. *P. urnula* had a wide salinity but narrow temperature range in the Arctic Ocean; its distribution through Bering Strait is likely limited by temperature (–1.8 ... +1.2°C). The vertical distribution of *S. acuminata* and *S. faurei* might correlate with depth. Our results contribute to a better understanding of the vertical distribution of the microbial food web.

Biodiversity and distribution of deep-sea vent polynoids (Annelida: Polynoidae) in the Western Pacific Ocean

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Polynoid worms are one of the most representative group in the deep-sea hydrothermal vent faunas. They have a high species diversity among the vent polychaetes and various kinds of sexual dimorphism. Our investigation of polychaete specimens collected from deep-sea hydrothermal vents and cold seeps in the Western Pacific Ocean revealed seven genera and 14 species including five new ones. As the most diverse, widely distributed, and abundant polychaete group in hydrothermal vents, polynoids serve as a good model to evaluate the biogeographic division of hydrothermal vent faunas. By combining reliable data on *Branchinotogluma*, *Branchipolynoe*, *Lepidonotopodium* and *Levensteiniella*, the four most diverse polynoid genera occurring in hydrothermal vents, we evaluated their distribution pattern and recognized seven major hydrothermal biogeographic provinces throughout the world: Indian Ridge, Okinawa Trough and Izu-Ogasawara Arc, Mariana Trough, Southwest Pacific, Northeast Pacific, East-Pacific Rise (northern and southern) and Mid-Atlantic Ridge. Our analysis indicates that the Western Pacific is geographically complex and may have played an important role in the dispersal and speciation of vent polynoids.

Seamount megabenthic communities: isolated or connected?

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Seamounts, as characteristic deep-sea habitats, have been known to support higher biomass and higher diversity of marine life than their surrounding deep-sea floors. So far, our knowledge of seamount animals remains very limited, resulting in controversial explanations on their biodiversity and distribution. There have been several hypotheses on seamount benthic communities, but none has been widely accepted, largely due to the different groups used for analyses and the bias of under-sampling. We explored three seamounts up to 300 km apart from each other in sea areas of the Yap Trench and Mariana Trench and investigated the diversity and distribution of megabenthos collected by remotely operated vehicle (ROV). A total of 312 megabenthic species including a new genus and roughly 20 new species were obtained. The megabenthic communities showed clear distribution pattern along the altitude of seamounts and water depth gradients. Higher biomass and diversity of megabenthos occurred on hard substrates, where soft corals and sponges together with attached crustaceans and echinoderms frequently occur, while a “dessert” scene was observed on soft substrates. Among the 312 species obtained, no more than 5% of the total species were common to all the three seamounts, indicating the megabenthos communities are distinctly isolated. Our analysis indicates that different water currents, topography and substrate types might be the main factors structuring the spatial distribution of megabenthos communities in this area. Moreover, undersampling and the different assemblages used for analysis may affect the evaluation of seamount biodiversity.

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Health of coastal marine ecosystems associated with the impacts of harmful algal blooms

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Coastal marine ecosystems offer many services for the welfare of human-beings. However, under multiple stressors like global warming, land-based pollution, eutrophication, unordered aquaculture, over-fishing, land reclamation etc, the ecosystems exhibited significant changes in their structures, functions and services. The China Seas are mainly shallow continental shelf sea, and liable to the impacts of anthropogenic activities and global changes as well. The most significant changes in the China Seas are the occurrence of harmful algal blooms. Over the last 3 decades, intensive HABs have been recorded in different regions of the China Seas, and posed significant impacts on the health of marine ecosystems. Brown tides formed by pelagophyte *Aureococcus anophagefferens* have been recorded in the Bohai Sea and lead to significant impacts on the aquaculture industry of scallops. In the Yellow Sea, the blooms of macroalgae *Ulva prolifera* (green tides) and *Sargassum horneri* (golden tide) have been recorded for 13 years, massive floating green algae led to significant concerns on marine environmental qualities and fishery productions, but no effective mitigation measures have been developed so far. Large-scale red tides of dinoflagellates in the East China Sea led to many different disruptive impacts on the health of marine ecosystems, including ecosystem structure, hypoxia and contamination of seafood products. In the South China Sea, red tides of haptophyte *Phaeocystis globosa* posed significant threats to facilities like nuclear power plant. The implementation of protective and adaptive measures for coastal marine ecosystems requires a combination of ocean observations with analysis and prediction tools.

Phytoplankton is the main environmental factor influencing the reproduction of the sea urchin *Strongylocentrotus intermedius* in the northwestern Sea of Japan

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According to some assessments, marine invertebrates with external fertilization (so called broadcast spawners) and feeding (planktotrophic) larvae constitute at least 70% of all marine invertebrate species. It is generally believed that the spawning period of such animals is timed with the season when the sets of most important abiotic and biotic conditions are favorable for offspring development and survival. In temperate waters broadcast spawners usually exhibit annual reproductive cycle which ends with massive synchronous spawning. Synchronisation of spawning between females and males is very important for reproductive success in these animals, that is determined by the short longevity of gametes and rapid gamete dilution.

The concept of seasonality and synchrony of reproduction in marine invertebrates with planktotrophic larvae suggests that the animals are capable of perceiving certain environmental cues to determine if the environment is appropriate for spawning. Identification of these cues is necessary to understand the environmental and physiological mechanisms involved in triggering spawning activity in broadcast spawners. Sea urchins are widely used as model organisms to study different aspects of the reproductive biology of broadcast spawners both in the laboratory experiments and under field conditions, but despite intensive studies, the environmental factors that synchronize sea urchin reproductive cycle and trigger spawning are not yet fully understood.

Here we report the results of long-term studies of the reproductive biology of the sea urchin *Strongylocentrotus intermedius* in wild populations of this species located in the north western Sea of Japan along 400 km of the coast of the Primorye region of Russia and differing by the level of anthropogenic pressure.

The main purposes of our work were:

1. To study the reproductive cycle of the sea urchin in different locations.
2. To clarify the relationships between environmental factors such as phytoplankton, temperature, salinity, dissolved oxygen, moon cycle, tide level, time of the day and anthropogenic pressure and the timing of spawning in sea urchin populations.

An analysis of seasonal dynamics of gonadal condition showed the timing of spawning to be different in different sea urchin populations. We distinguished three types of sea urchin populations that differed from each other in the proportions of individuals with different spawning schedules. Sea urchin populations with a pronounced late spawning (autumn) were referred to the first type. Sea

urchin populations with a pronounced early spawning (early summer) were referred to the second type. The major part of sea urchin populations belongs to the third type, which is characterized by approximately equal proportions of individuals with early and late spawning.

We found that sea urchin populations with a predominant early spawning were located close to Vladivostok city, which is the main source of marine pollution in Peter the Great Bay. Sea urchin populations with a pronounced late spawning were located from Vostok Bay north to Rudnaya Bay. Thus, our results showed that the reproductive cycle of *S. intermedius* in the study area was desynchronized both within one population and between the populations. We found also that, in some years, despite the seasonal maturation of gonads, spawning did not occur for 20–90% of *S. intermedius* individuals from the populations located from Vostok Bay north to Rudnaya Bay. We proposed that spawning failure is attributable to the absence of natural signal/signals necessary for induction of sea urchin spawning.

It is important to note that marine environment pollution is associated with eutrophication of waters; thus, the effects of anthropogenic pollution on the reproductive cycle of the sea urchin are likely to be indirect and conditioned by great concentrations of phytoplankton. Based on the analysis of the structural, temporal and quantitative characteristics of phytoplankton of Peter the Great Bay, the waters adjacent to Vladivostok in the Amursky Bay were characterized as extremely eutrophic whereas the open waters of Amursky and Ussuriisky bays as well as Vostok Bay were attributed to the eutrophic type. Thus our hypothesis suggests that sea urchins, due to their high phenotypic plasticity synchronize their spawning with conditions favorable for food supply for the larvae, that is, availability of phytoplankton.

The studies of the role of phytoplankton as a natural regulator of sea urchin spawning helped us to understand the mechanisms determining the timing of the reproductive cycle of *S. intermedius*. These studies were conducted in Kievka Bay and adjacent area which are characterized by a very low level of human impact. To test this hypothesis, we developed a complex methodological approach that included video recording of sea urchin spawning behaviour (at 1-min intervals) in combination with automatic datalogging of environmental variables (tide level, temperature, salinity, and chlorophyll *a* and oxygen concentrations) in the habitats of the study animals (at 10-min intervals). The study was conducted in two bays, Kievka Bay (42.830° N, 133.691° E) and Alekseev Bay (42.981° N, 131.730° E), differing by levels of primary production. A significant positive correlation ($p < 0.001$) was found between chlorophyll *a* concentration and the average hourly frequency of *S. intermedius* spawning events, as assessed through video recording, whereas there were no such correlations for temperature, salinity, dissolved oxygen or tidal activity.

Our studies revealed the following hierarchy of biotic and abiotic factors influencing *S. intermedius* spawning:

1. Increasing the phytoplankton concentration induces spawning in males.
2. Both an elevated phytoplankton level and the presence of sperm stimulate spawning in females.
3. Circadian and lunar rhythms are additional factors affecting this process.

Assessing coral diversity in the Kocebu Guyot seamount using environmental DNA

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Deep-sea corals are an important source of biodiversity and habitat supporting diverse assemblages of marine life. Although traditional visual surveys are widely used to identify deep-sea corals, the diversity estimates are hampered by the high expense, complexity inherent to working in the deep marine environment and morphological variation. Environmental DNA (eDNA) metabarcoding offers a powerful molecular tool capable of surveying biodiversity from many ecosystems. The present study tests an eDNA metabarcoding protocol for assessing coral diversity from water samples collected from the Kocebu Guyot seamount. The molecular diversity result matches well with that of the visual surveys. Furthermore, the molecular method can complement traditional visual surveys by finding more rare species. By overcoming the difficulty in traditional visual surveys, the eDNA metabarcoding method will be broad applied in the identification of deep-sea octocorals.

Population genetic structure and evolutionary history of the seagrass *Zostera japonica*

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The dwarf eelgrass *Zostera japonica* Asch. et Graebn is a native species in the Northwestern Pacific, but was introduced to the Pacific coast of North America through oyster transport from Japan in the early 20th century. Its success in colonization and rapid expansion in North America has caused confusions in management. On the contrary, *Z. japonica* has suffered declines in its native range, and thus calls for conservation and restoration is rising. Population genetic structure is essential for species conservation and management strategies, which is, however, a gap for *Z. japonica*. This study is based on 22 typical microsatellite markers to fully clarify the population genetic structure of the native and invasive *Z. japonica* populations and explore its evolutionary and invasion history, which is expected to provide scientific basis for conservation, restoration, and management of this species.

A total of 593 individuals of 23 populations from the Northwestern Pacific were genotyped. All analysis on genetic structure showed that populations in the Northwestern Pacific diverged into three groups (Northern China group, Japan group, and South group). Exchange among most populations were extremely low, and relatively higher migration rates (> 0.1) mainly occurred at local scales (km ~tens of km). The history geographic events, such as the isolations between the marginal sea during the last glacial maximum (LGM), probably be responsible for the divergence among the three groups. In addition, the limited dispersal of propagules, increasing habitat fragmentation, and coastal currents have maintained the effects of LGM. Populations in DY, WH, and FC should get priority in later conservation, and they can be as the best donor for restoration in local areas.

A total of 267 individuals of 7 populations from the Pacific coasts of North America were genotyped. The invasive populations strongly clustered with populations of Japan and were nearest with the population in Tokyo, which proved invasion from Japan. Except the population in Humboldt Bay, genetic diversity of other invasive populations were not significantly lower than those of original populations, which indicated multiple invasions. Significant divergence have been detected between

invasive and original populations and within invasive populations. The population in Humboldt Bay revealed an extremely low allelic richness and a sign of bottleneck, which correspond to a pioneer population. The relatively high genetic diversity of the invasive populations indicated their strong potential to expand northward or southward.

This study filled the gap of population genetics of global *Z. japonica* populations. These results would provide scientific and useful information for later conservation and restoration projects.

Biogeographic and co-occurrence patterns of microbial eukaryotes from surface water to abyssal sediment in the Western Pacific Ocean

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Microbial eukaryotes include single-celled protists, an assemblage of highly diverse and phylogenetically distant groups, whose diversity and distribution in deep oceans are largely not known. Here, we investigated the vertical profiles of microbial eukaryotes throughout the deep-ocean water columns down to abyssal sediments and their horizontal distribution in the Western Pacific Ocean by high throughput DNA sequencing. Our study indicated both pelagic and benthic microeukaryotes exhibit a restricted distribution, whereas the extent to which is various. The variations in dispersal limitation among different taxonomic groups were further detected in surface water: a significant distance-decay relationship in Dinoflagellata and Radiolaria communities was detected, while no such relationship was observed for ciliates. Along vertical gradients, a distinct stratification was detected within the microeukaryotic communities, which could be clearly clustered into the euphotic, aphotic and sediment communities. However, nearly half of operational taxonomic units (OTUs) in the sediments could be also found in the overlying waters, with the abundant OTUs in the sediments often present in the overlying waters but generally in low abundance. These data highlighted significant variations but an intimate link between pelagic and benthic communities, and suggested that abundant benthic microeukaryotes might recruit from or could resuspend into and then transfer by the overlying water. Overall, our study sheds new light on the distribution patterns of microeukaryotes from seasurface to abyssal sediment in open oceans, and indicates a frequent species exchange between water and sediment, like that observed in prokaryotes.

Sea urchins of the genus *Mesocentrotus* as a model for studying animal longevity

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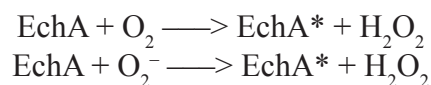
Echinoderms belong to deuterostomes and as such are closer relatives to vertebrates than other invertebrate taxons. Sea urchins are used as a convenient model for developmental biology, evolutionary biology, biochemistry, as well as cellular and molecular biology (Kondo, Akasaka, 2012). The life expectancy of different species of sea urchins ranges from 2 to 3 to 100 years or more. Due to the high life expectancy of some species of sea urchins, these organisms have become a model for studying aging processes (Brey, 1991; Davidson et al., 2002; Ebert et al., 2008). The most long-lived is the red sea urchin *Mesocentrotus franciscanus* (formerly known as *Strongylocentrotus franciscanus*), which lives up to 200 years or more. In this regard, the study of the features of its biology, physiology, and biochemistry attracts many researchers (Ebert, 2008; Bodnar, 2009).

Aging is a complex destructive, multifactorial, almost universal and yet incomprehensible process, the study of which is carried out by the science of gerontology. So far, gerontologists have found that one of the possible molecular mechanisms that promote aging is oxidative damage to biological macromolecules, including nucleic acids, by free radicals. Of these, free radicals, superoxide and peroxide, involved in intense intracellular metabolism, are especially dangerous. Active forms of oxygen (ROS) cause oxidative stress as a result of an imbalance between the production of ROS in the mitochondria and the elimination of damage due to the work of antioxidant systems and the mechanisms of repair or utilization of damaged biomolecules. Antioxidants can stop unwanted oxidation. Currently, an effective “cure for aging” does not exist, therefore, the interest of researchers in studying the metabolism of long-lived animals is understandable.

The presence of naphthoquinone pigments is one of the characteristic biochemical synapomorphies of sea urchins caused by the genes encoding polyketide synthase enzymes, which are required for the spinochrome biosynthesis. In regular globular sea urchins, for example, *Strongylocentrotus purpuratus*, naphthoquinone pigments appear at the stage of blastula (Drozdov et al., 2017). Naphthoquinone pigments of sea urchins (echinochrome A and its analogs, spinochromes A, B, C, D and E) have significant antioxidant activity, higher than the known antioxidant tocopherol acetate. They stop the chain reactions of lipid peroxidation in cells in several ways. In particular, they are able to inhibit the enzyme aldose reductase, the excessive activity of which is one of the causes of complications in diabetes mellitus, including the development of cataracts. Probably echinochrome A and spinochrome A appeared to be inhibitors of tyrosine hydroxylase and dopamine-b-hydroxylase, which are targets for treatment of hypotension. Except they have antimicrobial activity, that higher than that of their hydroxylated analogues.

Life expectancy may depend on a small number of regulatory genes. The genome of the purple sea urchin *S. purpuratus* is the first well-annotated sea urchin genome (Sodergren et al., 2006). This made it possible to structure information on regulatory gene networks that determine embryonic development (Oliveri et al., 2008; Peter, Davidson, 2017). Nowadays, the draft genome assemblies of *M. franciscanus* and *Lytechinus variegatus* are obtained and they compare the sequence of their proteins related to longevity with longevity related proteins of other species including with data of previously published complete genomic sequence of a purple sea urchin, *S. purpuratus* (Sodergren et al., 2006). The genome of sea urchins *S. purpuratus* contains more than 400 genes associated with the protection of these aquatic organisms from various stress factors that occur in the environment and lead to a reduction in average life expectancy. These genes encode detoxifying proteins and enzymes, as well as transcription factors, heat shock proteins, nuclear hormone receptors, etc. Also in the genome there are genes for aryl receptor (AHR), peroxisome (PPARs), hypoxia inducing factor (HIF) and others. Antioxidant protection is provided by the enzyme superoxide dismutase (SODs), catalase (Cats) and peroxidases (GPX3 and TXNS).

Polyhydroxynaphthoquinones, characteristic only for sea urchins (Hou Yakun et al., 2018), are the corresponding ligands of the above receptors and nuclear factors, which trigger their functioning in cells. One of the representatives of polyhydroxine naphthoquinones – echinochrome A (EchA) – has the ability to interact with all types of oxygen (O_2 , superoxide anion O_2^- and singlet oxygen) and turn them into hydrogen peroxide (H_2O_2) (Lebedev et al., 1999; Novikov et al., 2018).



EchA* is an oxidized form of echinochrome A.

As can be seen from the equations, echinochrome A performs an important function of the dismutation of superoxidation to H_2O_2 , which is catalyzed by the enzymes SOD1, SOD2 and SOD3 in the body.

An increase in the number of superoxide dismutases (SODs) and their functional mimetics suppresses oxidative stress in organisms and contributes to an increase in the lifespan of sea urchins and other animals.

Earlier we studied the skeleton in seven sea urchin species of the family Strongylocentrotidae by scanning electron microscopy (Vinnikova, Drozdov, 2011). The studied species can be divided into three groups:

1. *Strongylocentrotus intermedius* and *S. pallidus*.
2. *S. droebachiensis*, *S. polyacanthus*, and *Allocentrotus fragilis*.
3. *Mesocentrotus franciscantus*, and *M. nudus*.

Species of the genus *Mesocentrotus* are readily distinguished from the other species by the structure of their spines. Therefore, a comparative study of the biochemistry, genetics, and physiology of red sea urchin *Mesocentrotus franciscantus* and black sea urchin *M. nudus* is very promising for understanding the nature of the longevity of sea urchins.

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Sea urchins of the genus *Mesocentrotus* as a model for studying animal longevity

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The presence of naphthoquinone pigments is one of the characteristic biochemical synapomorphies of sea urchins. These substances have significant antioxidant activity: they stop the chain reactions of lipid peroxidation in cells in several ways. The most long-lived is the red sea urchin *Mesocentrotus franciscanus*, which lives up to 200 years or more. A comparative study of the biochemistry, genetics, and physiology of red sea urchin *M. franciscanus* and black sea urchin *M. nudus* from the Sea of Japan is very promising for understanding the nature of the longevity of sea urchins.

Octocorallia as a key taxon in the vulnerable marine ecosystems of the Emperor Chain (Northwest Pacific): diversity, distribution and biogeographical boundary

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Seamounts and guyots are of interest to the scientific community because not only numerous mineral resources occurrences are associated with them, but also areas of increased biodiversity (Rogers, 1994; Samadi et al., 2007; Morato et al., 2010). Sea floor elevations can be both reference points for the settlement of deep-sea fauna, and refuges and faunistic centers, and can also serve as biogeographic barriers and have a significant impact on the formation of the ocean fauna (Zezina, 1984; Rogers, 1994).

In the Northwestern Pacific, the transfer of species through currents meets the Emperor Chain of seamounts and guyots, but its biogeographic role in this area is unclear. There is only one publication devoted to the biogeography of the ridge, which shows the differences between the fauna complexes of the brittle stars inhabiting the northern and southern parts of the chain, as well as suggesting the existence of a biogeographic border near 37° N at the chain (Sirenko, Smirnov, 1989). Meanwhile, long-lived and important representatives of deep-sea communities, such as corals and sponges, can expectedly make a significant contribution to understanding the deep-sea species dispersal in the Northern Pacific being a marker of the distribution of bottom organisms in the latitudinal direction and in depth.

Against the background of climate change, the activity of exploitation of biological resources in neutral waters is also increasing, including in the northern part of the Pacific Ocean, where significant biological resources are concentrated in the area of the Emperor Chain (Boretz, Darnitskiy, 1983). Fisheries in seamounts and guyots doubled in recent decades (Watson et al., 2007). In different zones of high seas, international regional fisheries management commissions operate in order to develop quotas for fisheries and establish restrictive measures in areas of fishery activity near seamounts, and to prevent damage to vulnerable marine ecosystems of seamounts (VME).

In the Atlantic, in particular the North Atlantic Fisheries Commission (NEAFC) established a limited fishing in some zones, and introduced a complete ban on bottom fishing in several areas. Deep-water corals and sponges were taken as indicator groups of VMEs (NEAFC, 1982). North Pacific Fisheries Commission (NPFC) acts basing on the Convention on the Preservation of Biological Resources of the High Seas, to which the countries fishing in this zone are parties. The Commission and Convention focus on deep-sea bottom VMEs (including coral gardens, soft coral and gorgonians) in the seamounts and guyots of the Emperor Chain as sources (and, at the same time, indicators) of high productivity of the region. At a meeting in March 2018 (Yokohama, Japan),

the Commission recognized the lack of information on the location and population status of corals in the region and the urgent need for their research in seamounts. Indeed, so far there have been only two publications dedicated to the Octocorallia of the chain. Miyamoto et al. (2017) give a general list of Octocorallia genera of the southern part of the chain, obtained during trawl gatherings, but do not characterize the fauna of each seamount separately. Cairns et al. (2018) gives a list of 6 species of Primnoidae gorgonians, based on materials from trawl charges in the southern part of the chain. In connection with the above-discussed, the A.V. Zhirmunsky National Scientific Center of Marine Biology FEB RAS (Vladivostok, Russia) organized a comprehensive multidisciplinary expedition to the Emperor Chain in July–August 2019. The expedition, financially supported by the Ministry of Science and Higher Education of the Russian Federation, was carried out with the participation of a number of institutes of the Russian Academy of Sciences and Far Eastern Federal University. The main goals were planned in order to comprehensively study the VMEs of the chain – their biodiversity, the structure of planktonic and benthic communities, genetic, geological, hydrological and geochemical characteristics in a wide geographical range (Fig. 1).

Research methods included collection of bottom fauna, visual observations, photo and video filming using the remotely operated vehicle (ROV) Comanche 18. Visual observations were accompanied by continuous video recording, selective photographing and targeted sampling. During a series of dives, video transects were performed, which allowed for the first time to quantify the abundance of the leading groups of hydrobionts. A laser scale of 10 cm was used to estimate the population

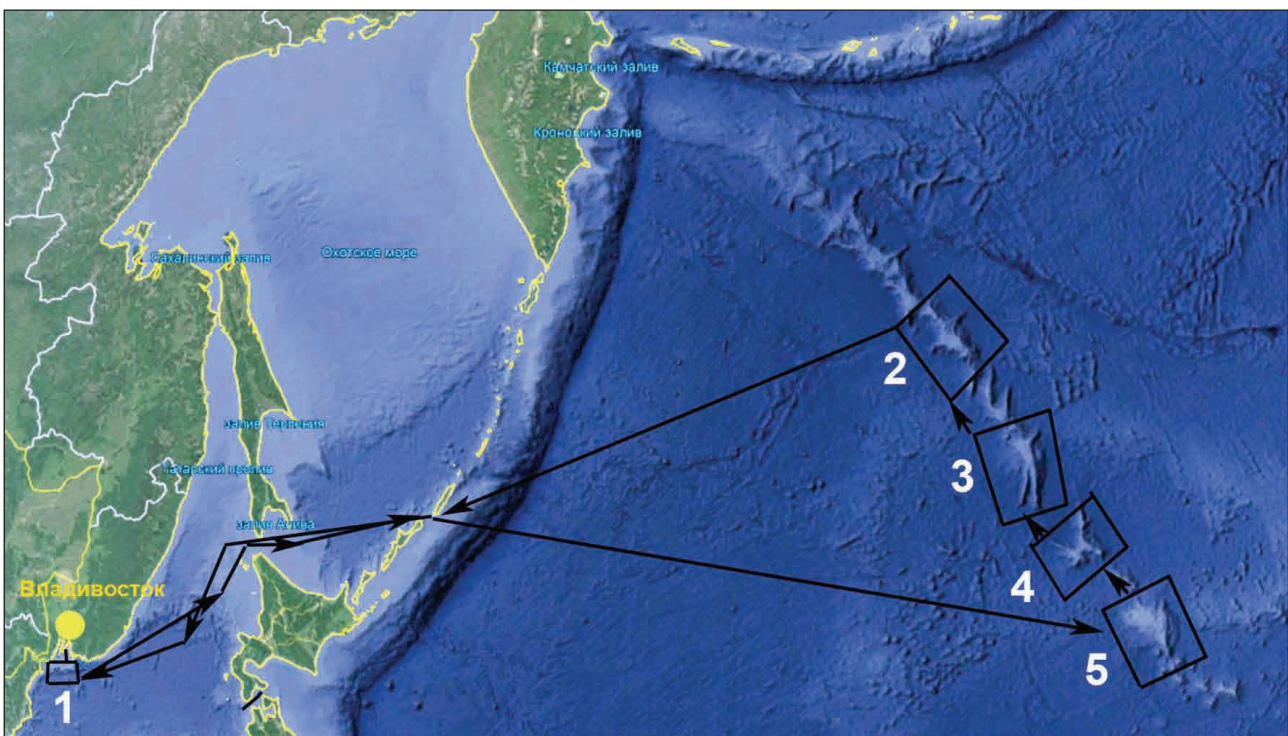


Fig. 1. Map of the working areas explored in the frame of the expedition of the A.V. Zhirmunsky National Scientific Center of Marine Biology FEB RAS jointly with other institutes of the Russian Academy of Sciences and the Far Eastern Federal University to the Emperor Chain (July–August 2019, RV *Akademik M.A. Lavrentiev*). **1** – starting site, Peter the Great Bay, Sea of Japan; **2** – guyot Suiko; **3** – guyot Nintoku; **4** – guyot Ojin and Jingu seamount; **5** – guyot Koko.

density of bottom animals. About 2000 photographs and 50 hours of video recording were obtained and analyzed. The landscape-ecological situation and the bottom fauna were studied in the depth range from 2182 to 338 m.

Preliminary results: coral distribution and a biogeographic boundary

Representatives of the several Anthozoa classes (Hexacorallia corals Scleractinia and Antipatharia, Octocorallia, sea anemones, and Ceriantharia) and Hydrozoa (Fam. Stylasteridae) were found in the studied areas (see Table). Of these, the most noticeable were Octocorallia and Scleractinia,

Preliminary data on the distribution of deep-water coral genera on the studied seamounts and guyots of the Emperor Chain in comparison with some areas of the temperate Northern Pacific

Coral genera (and <i>Paragorgia</i> species found)	¹ Alaska and Aleutian Islands	² Ojin, the Emperor Chain	³ Jingu, the Emperor Chain	⁴ Koko, the Emperor Chain	⁵ Hawaii
Hydrozoa, Anthoathecata					
<i>Stylaster</i>		+	+	+	+
Hexacorallia, Scleractinia					
<i>Caryophyllia</i>	+	+	+	+	+
<i>Falbellum</i>	+	+	+	+	+
Hexacorallia, Antipatharia					
<i>Leiopathes</i>				+	+
Octocorallia, Alcyonacea					
<i>Acanthogorgia</i>		+	+	+	+
<i>Calcigorgia</i>	+				
<i>Cyclomuricea</i>					+
<i>Muricella</i>					+
<i>Anthomastus</i>		+	+	+	+
<i>Bathyalcyon</i>					+
<i>Heteropolypus</i>	+				
<i>Pseudoanthomastus</i>					+
<i>Anhotela</i>					+
<i>Chrysogorgia</i>		+			+
<i>Iridogorgia</i>					+
<i>Metallogorgia</i>				+	+
<i>Pleurogorgia</i>					+
<i>Radicipes</i>					+
<i>Rhodaniridogorgia</i>					+
<i>Clavularia</i>	+	+		+	+
<i>Sarcodictyon</i>	+				
<i>Telestula</i>					+
<i>Corallium</i>				+	
<i>Hemicorallium</i>	+				+
<i>Acanella</i>					+
<i>Bathygorgia</i>	+				
<i>Isidella</i>		+		+	+
<i>Keratoisis</i>				+	+
<i>Lepidisis</i>		+	+	+	+
<i>Keroeides</i>				+	+

TABLE (Continued)

Coral genera (and <i>Paragorgia</i> species found)	¹ Alaska and Aleutian Islands	² Ojin, the Emperor Chain	³ Jingu, the Emperor Chain	⁴ Koko, the Emperor Chain	⁵ Hawaii
<i>Gersemia</i>	+				
<i>Siphonogorgia</i>				+	+
<i>Paragorgia</i>	+	+	+	+	
<i>P. arborea</i>	+	+	+		
<i>P. coralloides</i>				+	
<i>P. regalis</i>		+			
<i>Sibogorgia</i>	+				
<i>Echinomuricea</i>			+	+	
<i>Alaskagorgia</i>	+				
<i>Anthomuricea</i>					+
<i>Bebryce</i>					+
<i>Cryogorgia</i>	+				
<i>Muriceides</i>	+				+
<i>Paracis</i>					+
<i>Paramuricea</i>					+
<i>Placogorgia</i>					+
<i>Swiftia</i>	+	+		+	+
<i>Thesea</i>					+
<i>Villogorgia</i>					+
<i>Arthrogorgia</i>	+				
<i>Callogorgia</i>				+(+)	+
<i>Calyptrophora</i>	+				+
<i>Candidella</i>				(+)	+
<i>Fanellia</i>	+			+(+)	+
<i>Narella</i>	+			+(+)	+
<i>Paracalyptrophora</i>					+
<i>Parastenella</i>	+				+
<i>Plumarella</i>	+			+	+
<i>Primnoa</i>	+				
<i>Thouarella</i>	+			+	+
Pennatulacea					
<i>Anthoptilum</i>	+				+
<i>Calibelemnon</i>					+
<i>Echinoptilum</i>					+
<i>Halipteris</i>	+				+
<i>Kophobelemnon</i>				+	
<i>Pennatula</i>				+	+
<i>Ptilosarcus</i>	+				
<i>Umbellula</i>	+			+	+
<i>Cavernularia</i>	+				
<i>Stylatula</i>	+				
<i>Virgularia</i>	+	+		+	+
Total genera number	28	9	5	22	47

Note. Sources for different regions: 1 – Heifetz et al. (2005); Stone, Cairns (2017); Wing, Barnard (2004); Herrera et al. (2010); 2–4 – results of the present expedition of the NSCMB FEB RAS to the Emperor Chain (2019, RV *Akademik A.M. Lavrentiev*) with using the additional data from Dautova (2012) and Cairns (2018) (these are shown in parentheses); 5 – Cairns, Hourigan (2017); Parrish et al. (2017).

which were found in the entire range of studied depths and on all types of substrate, including soft sandy grounds (Fig. 2), calcareous outcrops (Fig. 3), rocky biotopes (Fig. 4B) and old lava flows (Fig. 4C). The greatest coral diversity was recorded on the Koko guyot in the southern part of the ridge – 22 genera of Octocorallia (4 genera – Pennatulacea, Fig. 2B, 22 genera – Alcyonacea). Only 5 to 8 genera of Octocorallia have been found on the Ojin, Nintoku and Jingu. Only on the guyot Ojin, 1 genus of Pennatulacea was observed, and the remaining 8 genera of Octocorallia discovered here belong to Alcyonacea – 7 genera of gorgonians, most of which are also found in the Aleutian Islands, and 1 genus of soft corals *Anthomastus* (Fig. 4A) (see Table). Scleractinia of the genera *Caryophyllia* and *Flabellum* were found almost everywhere and do not bring information for biogeographic conclusions. However, the discovery of the black coral of the genus *Leiopathes* on the Koko, previously noted only in the southern latitudes, is very remarkable (see Table).

The fauna complex Octocorallia on Koko can be characterized as very close to that of the Hawaiian Ridge, with a noticeable participation of the bamboo corals (gorgonians Isididae, Fig. 2A) and Chrysogorgiidae (including *Iridogorgia* and *Metallogorgia*, Fig. 4B), characteristic of the tropical and subtropical regions of the Pacific (see Table).

In Koko, there are three species of the genus *Chrysogorgia*, which was not previously observed north of the Hawaiian Islands, including *C. stellata* Nutting, 1908 (previously only observed in Hawaii, Cairns (2001)) and *C. ramosa* Versluys, 1902 (previously noted only in the Philippines, Cairns (2001)). Also noteworthy is the presence of the gorgonaria *Paragorgia coralloides* Bayer, 1993, previously found in the Pacific only near the Palau (Philippine Sea, Sánchez (2005)). On Ojin and Jingu, the composition of chrysogorgiids is depleted, *Iridogorgia* and *Metallogorgia* are absent, only *C. stellata* is noted (see Table). The discovery of the *Paragorgia arborea* in Ojin and Jingu extends its range in the northwestern Pacific and seems quite expected in connection with previous records near the eastern Kamchatka and the Aleutian Islands (Heifetz et al., 2005). The fauna of the Octocorallia of the Aleutian Islands, seamounts, and guyots on the west coast of North America and the Hawaiian Chain is much better documented (see Table). Summarized data show the significant role of gorgonians in communities – the families Plexauridae and Primnoidae contain 28% of species recorded along the American coast and 46% recorded on the mountains of the Hawaiian Ridge (Cairns, Hourigan, 2017; Stone, Cairns, 2017). On the Emperor Chain, we also noted the predominance of gorgonians in terms of the number of genera, primarily fam. Primnoidae, which were found in a wide range of depths – from 330 to 2200 m (see Table). Based on the above findings, the Emperor Chain can be considered as a chain of oceanic risings, where a faunistic complex of tropical and subtropical species of deep-sea corals meets with a complex of boreal Pacific species. The biogeographic boundary between the coral fauna in the area of the Chain obviously runs between 37.5° N and 39° N (i.e., in the region of the Ojin guyot and Jingu seamount, Fig. 1). This observation fully coincides with the assumption about the position of the biogeographic boundary between the boreal and the West Pacific biogeographic regions in the Emperor Chain region, made by Sirenko and Smirnov (1989) based on the data on the echinoderm bathyal fauna (materials of the 33rd cruise of the TINRO RV *Odyssey*). The Far East seas and the Emperor Chain are a biogeographically important region of the Pacific Ocean, on the fauna of which so far there were only a few data of trawl catch (Cairns et al., 2018; Dautova, 2018, with an overview of studies in the region; Miyamoto et al., 2017). As a result of the use of the modern deep-sea TPA during the expedition, we significantly expanded the list of Pennatulacea genera of the chain, made unique and biogeographically important findings of the genera and species of Octocorallia.

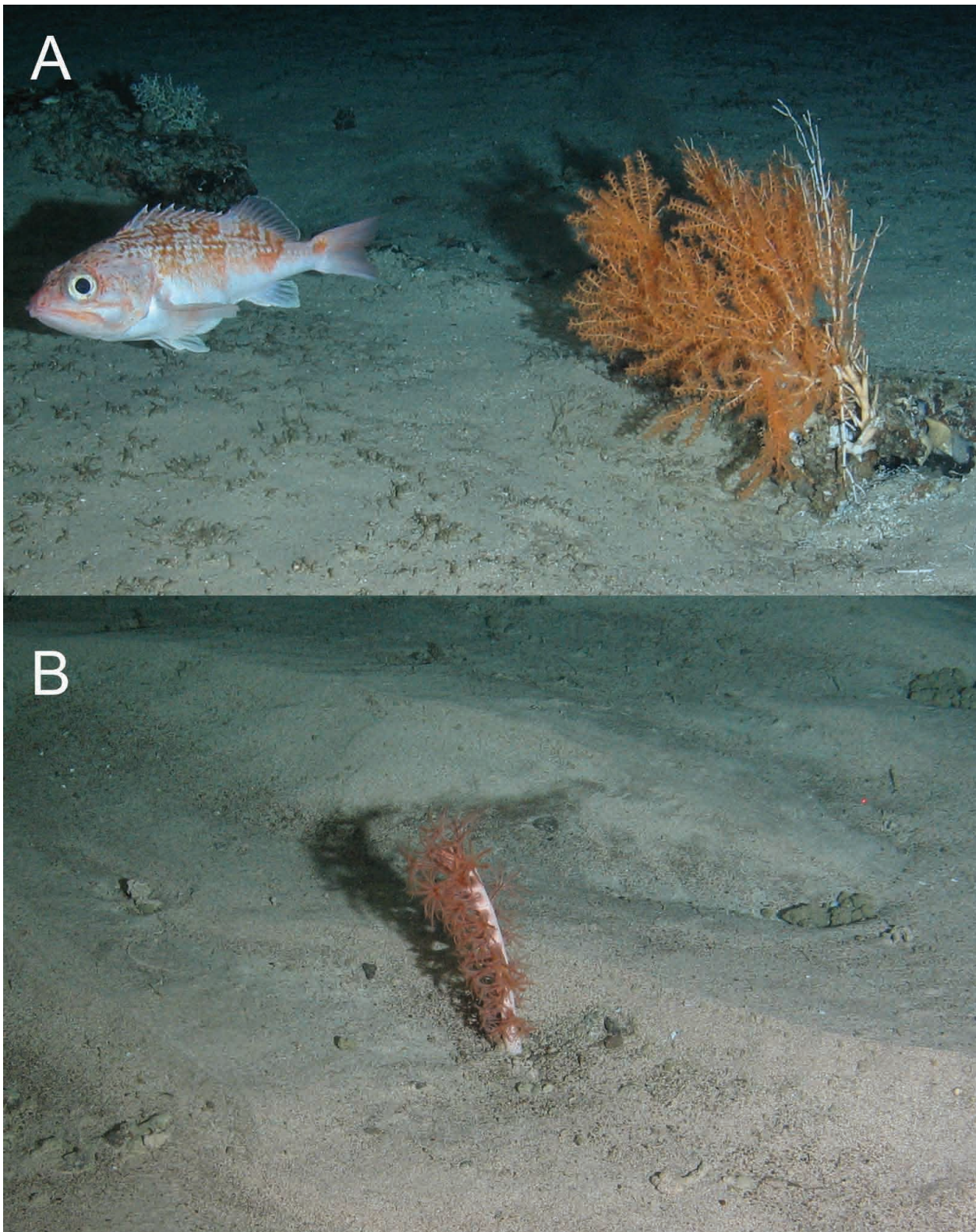


Fig. 2. Typical soft-bottom landscapes and inhabitants of the studied guyots. **A.** Bamboo coral (*Octocorallia*) and fish. Silty-sand bottom, Koko, 356 m depth. **B.** Sea pen (*Pennatulacea*) among the sandy dunes. These dunes show the influence of the strong currents. Koko, 1880 m.

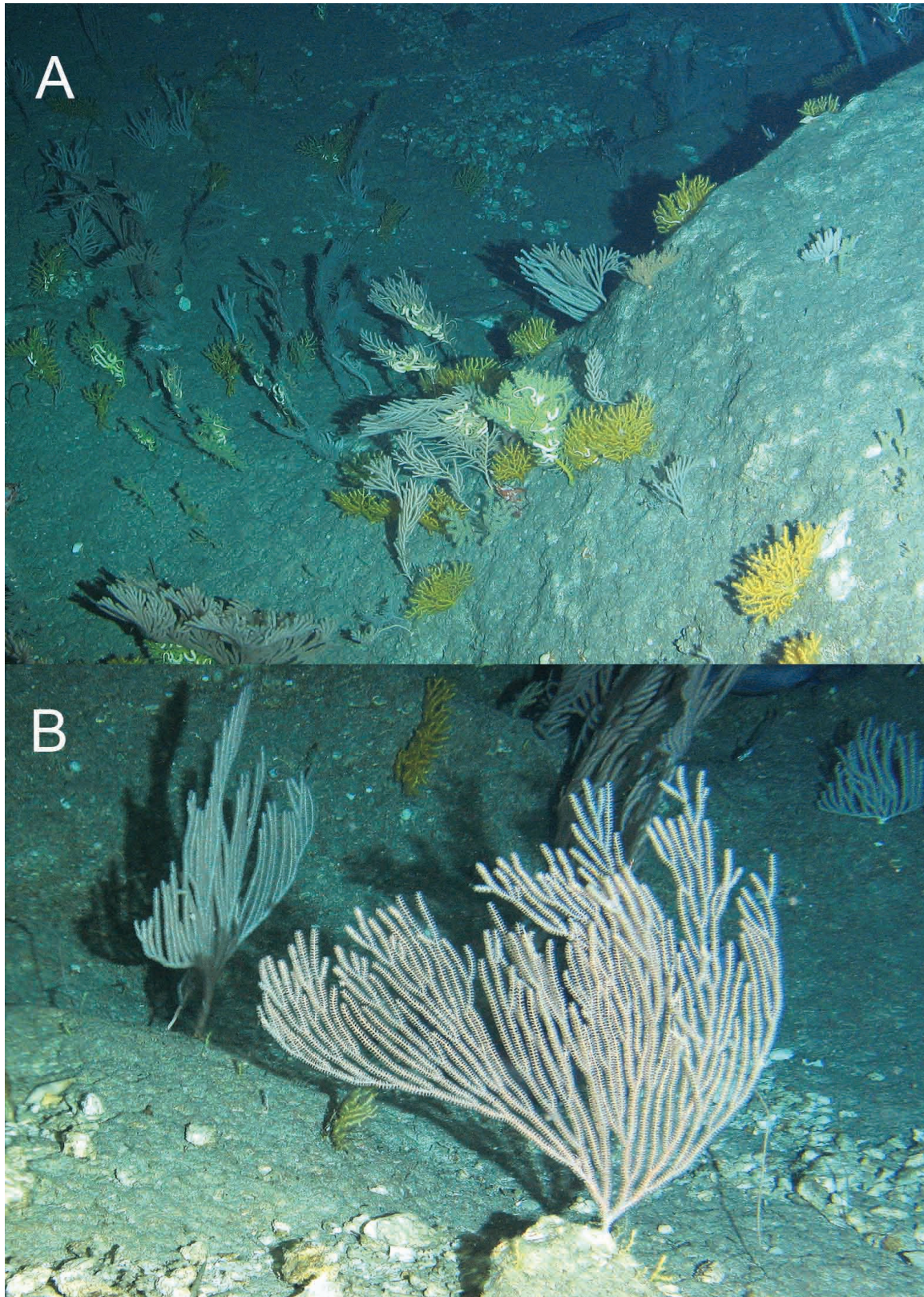


Fig. 3. Hard-substrata landscapes. **A.** Coral (*Octocorallia*) gardens on the hard substrata. Koko, 380 m depth. **B.** Gorgonian *Narella* on small stones. Koko, 378 m depth.

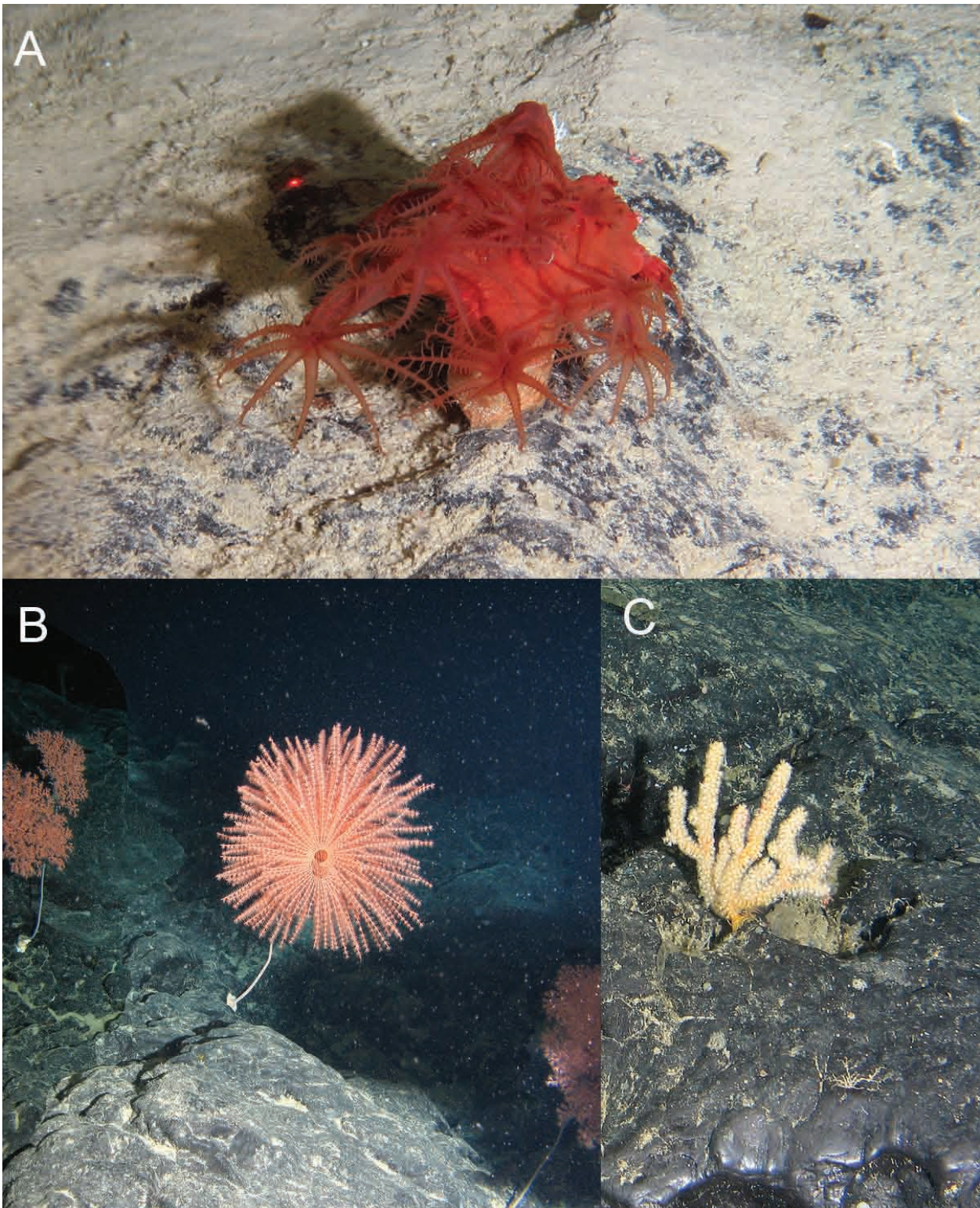


Fig. 4. Rocky landscapes. **A.** Soft coral *Anthomastus* settled on the old lava flow (covered by thin layer of fine sand). Koko, 2100 m depth. **B.** Settlements of the chrysogorgiid gorgonians (Octocorallia) – *Iridogorgia* sp. and *Metallogorgia* sp. on rocky substrata. Koko, 1431 m depth. **C.** *Acanthogorgia* on the old lava flow covered by manganese crust. Jingu, 1267 m depth.

Anthropogenic threats – loss of coral communities from heavy fishing?

Traces of trawls and anthropogenic trash were found in a number of areas on the top part of the Koko. These are clearly visible on calcareous outcrops in the shallow areas of Koko (350–550 m) which are more easily accessible for trawl fishing (Fig. 5C).

There is practically no bottom population. These subjects of anthropogenic origin includes not only plastic and metal dishes, but also scraps of fishing gear (Fig. 6).

In deeper areas (1000–2000 m) on the Koko slopes, no such traces of trawls were noted. In the shallow areas, Koko has a unique faunal coral complex as shown above. Therefore, damage or destruction of coral settlements here may be irreversible. Since there may be no similar settlements at great depths on this guyot and, therefore, there may not be a source for restoration of populations through larval settlement.

There are many studies of fishing impacts in shallow continental shelf environments demonstrated that recovery (of species richness, abundance, population biomass and production) can take several years and is dependent on both the type and extent of impact and the natural levels of disturbance that characterize a community (Collie et al., 2000, with a review). In contrast, only a few studies have examined impacts of fishing on the benthic communities of seamounts. In all these cases, the loss of coral populations and other microbenthic communities has been documented from heavily fished seamounts. Abundant scrape marks were visible, and the seamount rock surface was bare. For example, Clark and Koslow (2007) noted these facts in Tasmania; Clark and O’Driscoll (2003) noted out that effect of trawling by comparing areas subject to different intensities of fishing in New Zealand, while Watling et al. (2007) recorded the same situation in the North Atlantic.

Conclusions – trends and future research directions

The role of the Emperor Chain of seamounts and guyots (as part of the Emperor-Hawaiian Chain) in the distribution of corals in the northern Pacific Ocean can be very significant due to its extended length to the north in the meridional direction. Individual seamounts are believed to form biogeographic patterns and gradients of biodiversity, acting as “stepping stones” for settling species, like refugia or deep-sea speciation centers (O’Hara, Tittensor, 2010). However, it is still unclear how significant the connection between the neighboring mountains is. Genetic studies of fish fauna and free-living macrobenthos of seamounts have shown insignificant isolation (and even its complete absence) between neighboring mountains. However, for sedentary bottom organisms, both a high degree of isolation in some species and a high degree of genetic similarity in other representatives of benthos were revealed (Samadi et al., 2007; Cho, Shank, 2010; Tunnicliffe et al., 2010). The degree of interconnection between the faunas of neighboring mountains ultimately turns out to be specific species-specific and significantly depends on oceanographic conditions – especially currents that determine the range and distribution paths (Cho, Shank, 2010; Tunnicliffe et al., 2010). The use of ROV not only provides the opportunity for gentle non-contact monitoring of bottom communities, but also increases the possibility of targeted collection of bottom organisms. Conducting comprehensive hydrobiological studies of VMEs (along with hydrophysical, geological, and other works) in the area of the chain is urgently needed as soon as possible for study and conservation measures. It is extremely important to expand the data we obtained on the coral biodiversity of this region and compare them with the data on the current system that exists here. This possess new data on

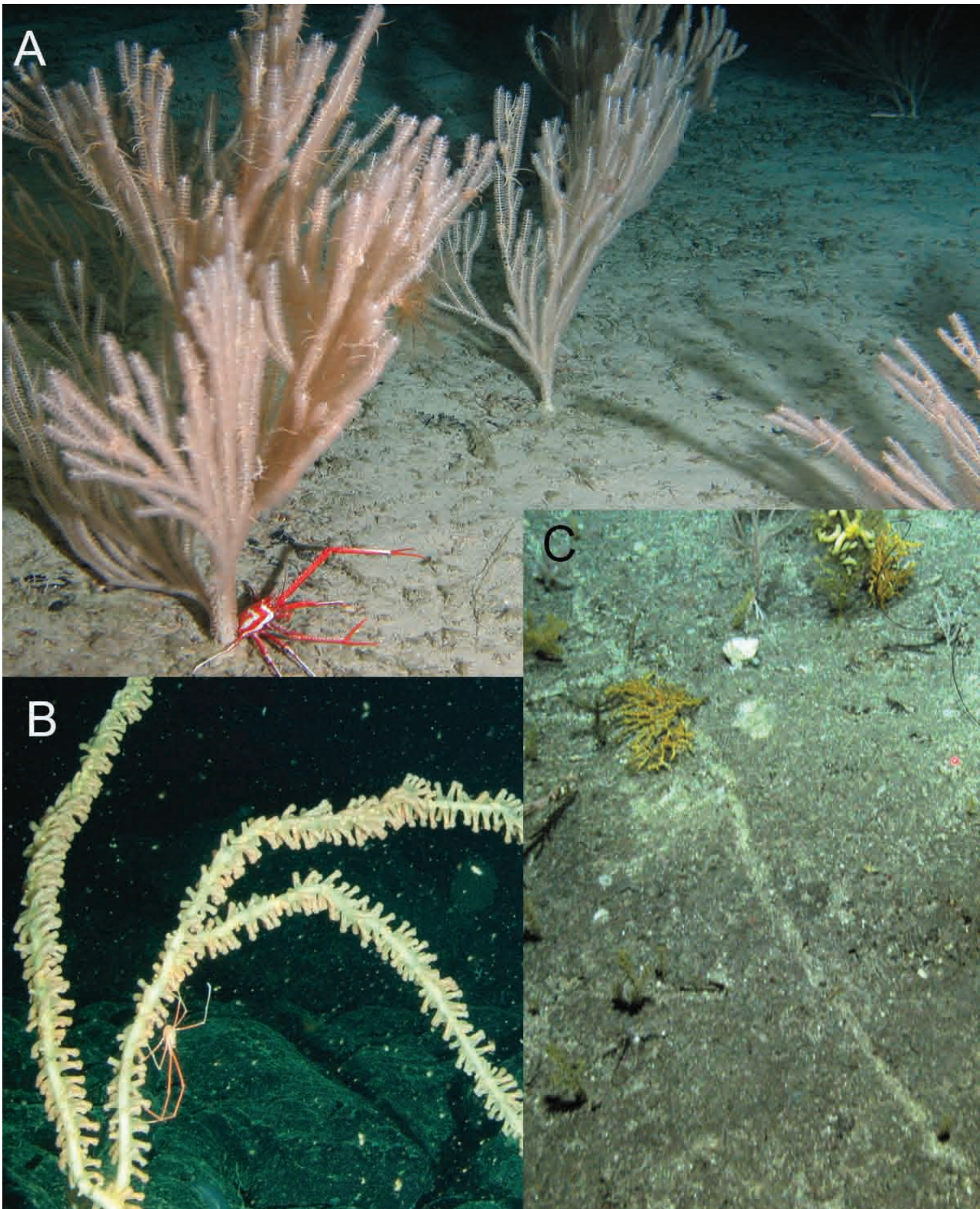


Fig. 5. Protecting role of Octocorallia. **A.** Crab among the *Narella* gorgonians, Koko, 380 me depth. **B.** Crab on the bamboo coral. Koko, 1431 m depth. **C.** Traces of trawls on calcareous hard substrata. One gorgonian *Isidella* is broken.

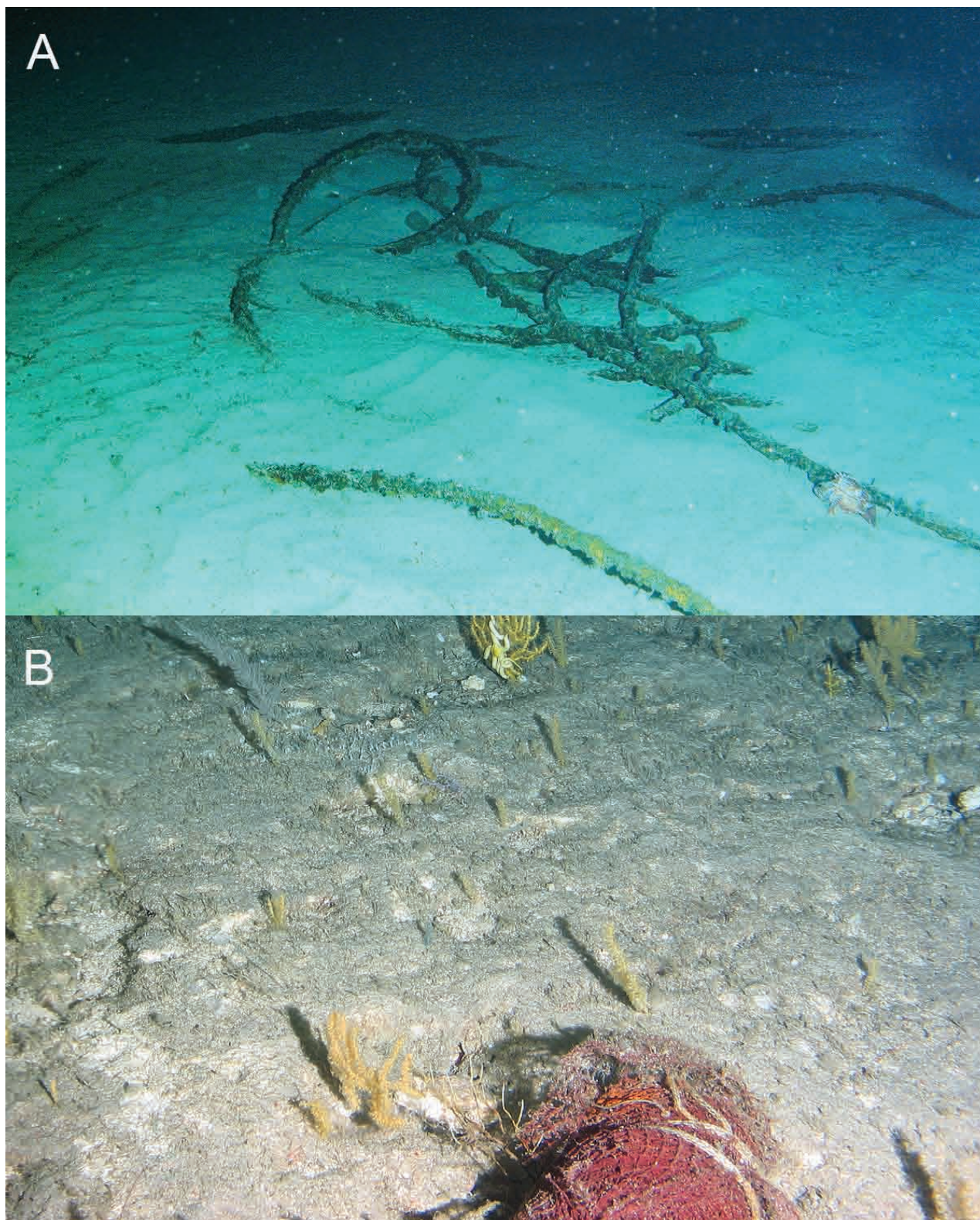


Fig. 6. Consequences of anthropogenic (fishery) activities noted at the Emperor Chain during the expedition (July–August 2019, RV *Akademik M.A. Lavrentiev*). Anthropogenic garbage. **A.** Metal cable, Koko, 760 m depth. **B.** Old fishery net, Koko, 380 m depth.

the biodiversity of the bathyal communities in the high seas of the North Pacific. It makes a significant contribution both to the work of the NPFC and to international scientific cooperation, and to the solution of food problems in the region.

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**Octocorallia as a key taxon in the vulnerable marine ecosystems
of the Emperor Chain (Northwest Pacific):
diversity, distribution and biogeographical boundary**

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A large-scale multidisciplinary expedition organized to the Emperor Chain (Northwestern Pacific) by the A.V. Zhirmunsky National Scientific Center of Marine Biology FEB RAS (Vladivostok, Russia) was held in July–August 2019. The expedition, financially supported by the Ministry of Science and Higher Education of the Russian Federation, was carried out with the participation of a number of institutes of the RAS and Far East Federal University. The main goals were planned in order to comprehensively study the vulnerable marine ecosystems (VMEs) of the Chain – their biodiversity, communities, geological, hydrological and geochemical characteristics in a wide geographical range. Research methods included collecting and video filming using the remotely operated vehicle Comanche 18. The deep-water corals Octocorallia, recognized in the area as the indicator benthic taxa of VMEs, showed differences in their diversity and distribution between the southern part of the Chain (guyot Koko, with tropical and subtropical deep-water corals) and the northern guyots. The intermediate position of the guyots Ojin and Jingu (with their mixed northern/tropical Octocorallia fauna, 37.5° N to 39° N) encourages implying a biogeographic boundary between the boreal and the West Pacific biogeographic areas. Traces of trawls and anthropogenic trash found in a number of areas should stimulate further studies of the chain's VMEs for the rational fishery and conservation measures.

Hydrological influences on amphipod abundances with depth in the gray whale feeding areas on the Northeastern Sakhalin shelf (the Sea of Okhotsk)

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Western Pacific gray whales (WGW from here on) of the eastern Sakhalin Island Shelf (Sea of Okhotsk) feed primarily on benthic gammaridean amphipods within a Nearshore area and an Offshore area that are separated by less than 40 km. The total area of the Nearshore survey area is approximately ~1100 km² and the total Offshore area is approximately ~2000 km² (Blanchard et al., 2019a, b). However, we are concerned with the portions of these feeding areas where significant biomass densities of amphipods occur. The approximately 71.1x5.4 km (384 km²) “Nearshore” amphipod polygon ranges in depths between 2 and 35 m and the approximately 39.7x33.7 km (1.338 km²) “Offshore” polygon ranges in depths between 20 and 65 m (Fadeev, 2012; Demchenko et al., 2016; Blanchard et al., 2019a).

Individual whales feed in both areas, which are separated by less than 40 km. The Nearshore benthic amphipod populations depend on phytoplankton production that is enhanced in spring and summer by flow from the Amur River and vertical ocean stratification of the Amur River plume (Rutenko et al., 2009; Zhabin et al., 2010; Rutenko, Sosnin, 2014). Winter production, and presumably Offshore amphipods, on the Sakhalin Shelf are dominated by vertical transport and downwelling of phytoplankton due to storm turbulence and the presence or absence of sea ice (Sorokin, Sorokin, 1999).

The ampeliscid amphipod, *Ampelisca eschrichtii* Krøyer, 1842 are the primary of Offshore WGW. Ampeliscid amphipods feed on the epi-benthic flow of organic matter composed mainly of settled phytoplankton (Coyle, Highsmith, 1994). In summer, the Offshore *A. eschrichtii* populations are beneath a 10 or 12 m deep surface water stratum that contains most of the phytoplankton biomass (Sorokin, Sorokin, 1999, 2002; Rutenko et al., 2009; Rutenko, Sosnin, 2014). Consistent with this pattern, the Offshore *A. eschrichtii* do not appear to grow in summer (Demchenko et al., 2016) and to starve, while absorbing their ova, by retaining their developing broods and by restricting their reproductive development (Durkina et al., 2018).

Demchenko et al. (2016) and Durkina et al. (2018) concluded, from the absence of summer growth and reproduction, that the Offshore Sakhalin Shelf *A. eschrichtii* populations must grow and reproduce in winter, when storm turbulence mixes the stratified water layers over the shelf and carries phytoplankton to all depths (Sorokin, Sorokin, 1999; Leonov et al., 2007; Prants et al., 2017). Winter sea ice cover and severe storms over the Sakhalin Shelf have thus far precluded winter benthic sampling of the Offshore area that is needed to directly test (Demchenko et al.'s (2016) and Durkina et al.'s (2018) winter growth hypothesis).

In contrast to the Offshore feeding area, the *Monoporeia affinis* of the infralittoral Nearshore feeding area (Demchenko, 2010) occur within the summer high phytoplankton biomass water stratum dominated by the Amur River plume (Rutenko, Sosnin, 2014). The Nearshore *M. affinis* growth and production are thus likely to be greatest in summer. Moreover, the reduced sea ice cover of the Nearshore area could permit significant primary production and consequent benthic community production in all seasons. Winter sea ice cover and severe storms over the Sakhalin Shelf and the 2–10 m depths of most of the Nearshore area, that are too shallow for large research vessels, have thus far precluded winter or summer benthic sampling of the Nearshore area that is needed to partially test Demchenko et al.'s (2016) and Durkina et al.'s (2018) winter growth hypothesis or to assess patterns and timing of most biomass production of WGW prey there.

Western gray whales feed in the Nearshore area where fine (Ps3 and Ps3Ps2) sands are associated with relatively warm, low salinity waters, and where *M. affinis* and *Eogammarus schmidti* are the dominant amphipods (Demchenko, Fadeev, 2009, 2011; Demchenko, 2010). The Nearshore *M. affinis* dominated community is predominantly confined to less than 10 m depths (Fadeev, 2007). However, nearly all benthic surveys have been restricted to 10 m and greater depths (Blanchard et al., 2019a, b) at the outer, eastern edge of the Nearshore feeding area. Benthic samples from 2–10 m depths of the Nearshore area, in winter or summer, needed to directly test the winter/summer Nearshore growth hypothesis are also insufficient.

Thus, Amur River flow may limit phytoplankton available for Nearshore benthic prey and benthic communities in less than 35 m depths in spring and summer (Tachibana et al., 2008), while, in contrast, phytoplankton availability and production of the greater than 35 m depth Offshore benthic communities may depend on deep vertical mixing (de-stratification) during winter storms (Leonov et al., 2007; Prants et al., 2017). The independent processes controlling availability of primary production to the Nearshore and Offshore western gray whale feeding areas therefore could be asynchronous. Nearshore biomass production in synchrony with summer primary production and Offshore biomass production in synchrony with primary production available to the benthos in winter are thus explicit predictions under the asynchronous production model. Direct tests for Nearshore and Offshore production synchrony will not be possible however, until these areas are directly sampled in winter and summer and possibly also before and after whale feeding occurs. We therefore attempted an indirect test of asynchronous production by comparing biomass from 2012, 2013 and 2014 summer and fall samples of the Nearshore and Offshore feeding areas. We assumed that high production in the Nearshore would result in high summer amphipod biomass in the year of sampling. We expected non-significant change in overall population biomass of *A. eschrichtii* with reduced juvenile recruitment during starvation events due to the low individual weights and relative numbers of juveniles (Demchenko et al., 2016, Fig. 5j). Due to the 2–3 year life cycle of *A. eschrichtii*, we variation in winter production in the Offshore would result in summer amphipod biomass changes in the following year.

Methods

Predictions of our three null hypothesis were that:

1. Offshore amphipod biomass production is out of synchrony with Nearshore amphipod biomass (of mainly *M. affinis*) within years.
2. Nearshore amphipod biomass is no greatest in summers of maximum Amur River flow, resulting in low salinity and relatively high temperatures.
3. Offshore amphipod biomass responses (of mainly *A. eschrichtii*), do not occur one year after assessed mild winters (and starvation events) when reductions of 2 year old population members are expected.

Our temperature and salinity data (Fig. 3B, D) are from August 2012 and October of 2013 and 2014 (Ivin, Demchenko, 2016; Blanchard et al., 2019a, b). We estimated winter severity from percentages of ice cover that we assessed from satellite images of the Sakhalin Shelf generated from the 0.645 μm to 0.859 μm range of a MODIS radiometer (Aqua and Terra satellites, radiometer MODIS) in May of 2011, 2012 and 2013. These images were calibrated, referenced, atmospheric corrected and pseudo-colored using SeaDAS software. A shoreline, coordinate grid and outline polygon was then superimposed on the images for comparisons that included pixels ice, minus pixels of fog and low clouds using the graphical editor, GIMP. We assumed mild winters when sea ice was absent in May and normal or severe winter years by expanded sea ice cover in May.

Our estimated Nearshore and Offshore amphipod densities and biomass totals, temperature and salinity with depth among years were from samples collected at 60 stations in 10–35 m depths adjacent to the Nearshore area and from 48 stations in 20–65 m depths within the Offshore area (in August of 2012 and in October of 2013 and 2014) (Blanchard et al., 2019).

We made monochrome contour graphs of the mean amphipod biomass in the Nearshore and Offshore areas for 2012, 2013 and 2014 to compare total amphipod biomass variations with the frequencies of amphipod density. For that purpose, we used the Surfer software package for Kriging interpolation as the gridding method and fixed ranges of biomass from 0 to 1300 g m^{-2} at 20 g m^{-2} contour biomass intervals for Offshore and 0 to 160 g m^{-2} at 1 g m^{-2} contour biomass intervals for Nearshore. Our analysis of the pixel intensity on the resulting graphs were made using the Wolfram Mathematica package. In accordance with the partition biomass scale, we found the dependence of biomass density on color intensity parameter RGB (x, x, x), where x varies in the range from 0 to 255 (from black to white). We used the number of pixels in colors corresponding to each biomass density color intensity to estimate area S_i , occupied by that average biomass density interval according to the relation:

$$S_i = S \frac{N_i}{N},$$

where S is the areas of the Nearshore and Offshore polygons, N is the number of pixels found in the polygon and N_i is the number of pixels of a given color intensity, calculated for each biomass density. We normalized the final pixel estimated area to actual area size and biomass per biomass interval to the average biomass per feeding area for each year.

WGW are likely to require high prey densities for feeding. The consistently greater prevalence of WGW over the Nearshore feeding area (Fadeev, 2012) is likely therefore to be adaptive for maximizing foraging rates. We therefore estimated the tonnes biomass in the 2012–2014 years at each amphipod density in the two feeding areas to assess quantities of potential prey biomass among areas and years.

Results

Nearshore and Offshore biomass were asynchronous (Fig. 1) as expected from the different processes controlling access to primary production in the two systems (Fadeev, 2012; Blanchard et al., 2019a). The greater Nearshore prevalence of WGW (Blanchard et al., 2019a) is also in contrast to the greater average biomass densities at Offshore sites (Fig. 1).

Amphipod biomass in the Offshore feeding area is greater than in the assessed Nearshore feeding area (Fig. 2) and highly aggregated (patchy) (Fig. 2A, C). The biomass occurring in high density aggregations, however, was dramatically greater in Nearshore in 2012 than in following years (Fig. 2B) and high density biomass was reduced in 2013 in Nearshore and Offshore compared to 2012 and 2014 (Fig. 2B, D). For WGW preferentially feeding on amphipods in high density patches, the greatest difference was in 2014 (Fig. 2B, D) when most Nearshore amphipod biomass occurred in less than 30 g m⁻² areas (Fig. 2B).

The 5–10 fold greater average Offshore biomass relative to Nearshore between 2012 and 2014 (see Table) are due primarily from the greater prevalence of amphipods in high density areas (Fig. 2B, D). Amphipod biomass changes are due primarily to the dynamics of the highest biomass populations (Fig. 2B, D). The 61% Nearshore and 17% Offshore amphipod biomass reductions in 2013 relative to 2012 (see Table) were therefore likely to have produced amplified effects on foraging WGW because they no longer had no access to the highest density prey that required less foraging energy per gram weight of prey in other years.

The 2012 samples were collected mostly in August while the 2013 and 2014 samples were collected in October.

The Amur River plume greatly influences salinity and primary production in the Nearshore area in summer (Tachibana et al., 2008; Bosin et al., 2010; Zhabin et al., 2010; Minervin et al., 2015). A large Amur River discharge in 2013 resulted in greater freshwater dilution (~28–30‰) in the Nearshore and Offshore to 35–40 m depths that persisted into October (Fig. 3). Salinity variation with depth among years however, was less in the Nearshore (Fig. 3B, D) and total Nearshore

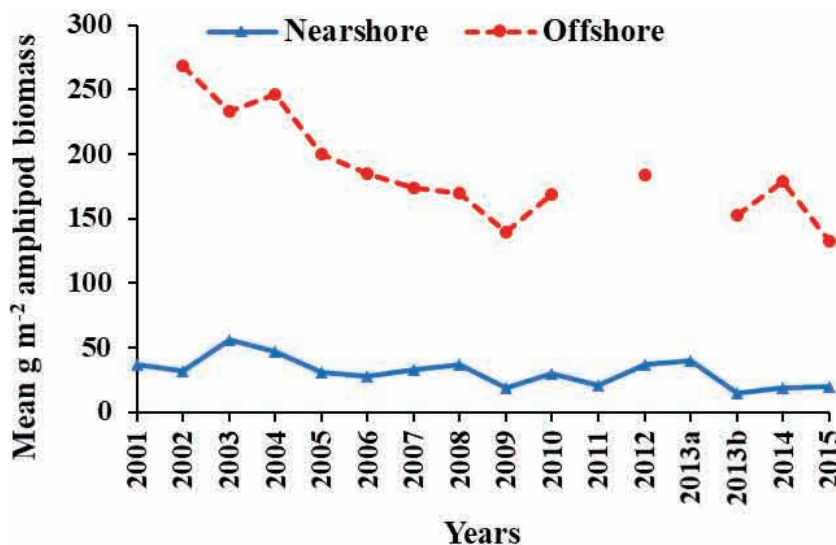


Fig. 1. Average Nearshore and Offshore biomass per m⁻² between 2001 and 2015 (from: Blanchard et al., 2019a). Note: 2013a, b – sampling in June and October of 2013.

amphipod abundances (sampled adjacent to the major populations occurring in less than 10 m depths) were greater in 2012.

The reduced Nearshore and Offshore amphipod biomasses between 18 m and 35 m depths (Fig. 3A, C) are consistent with a vertical transition in processes controlling the two areas as expected from the entirely different species that predominate in these two areas. Whether the decline of high density Nearshore populations in 2013 (Fig. 2B) was due to overall population declines, or to restricted migration from the adjacent and unsampled 2–10 m

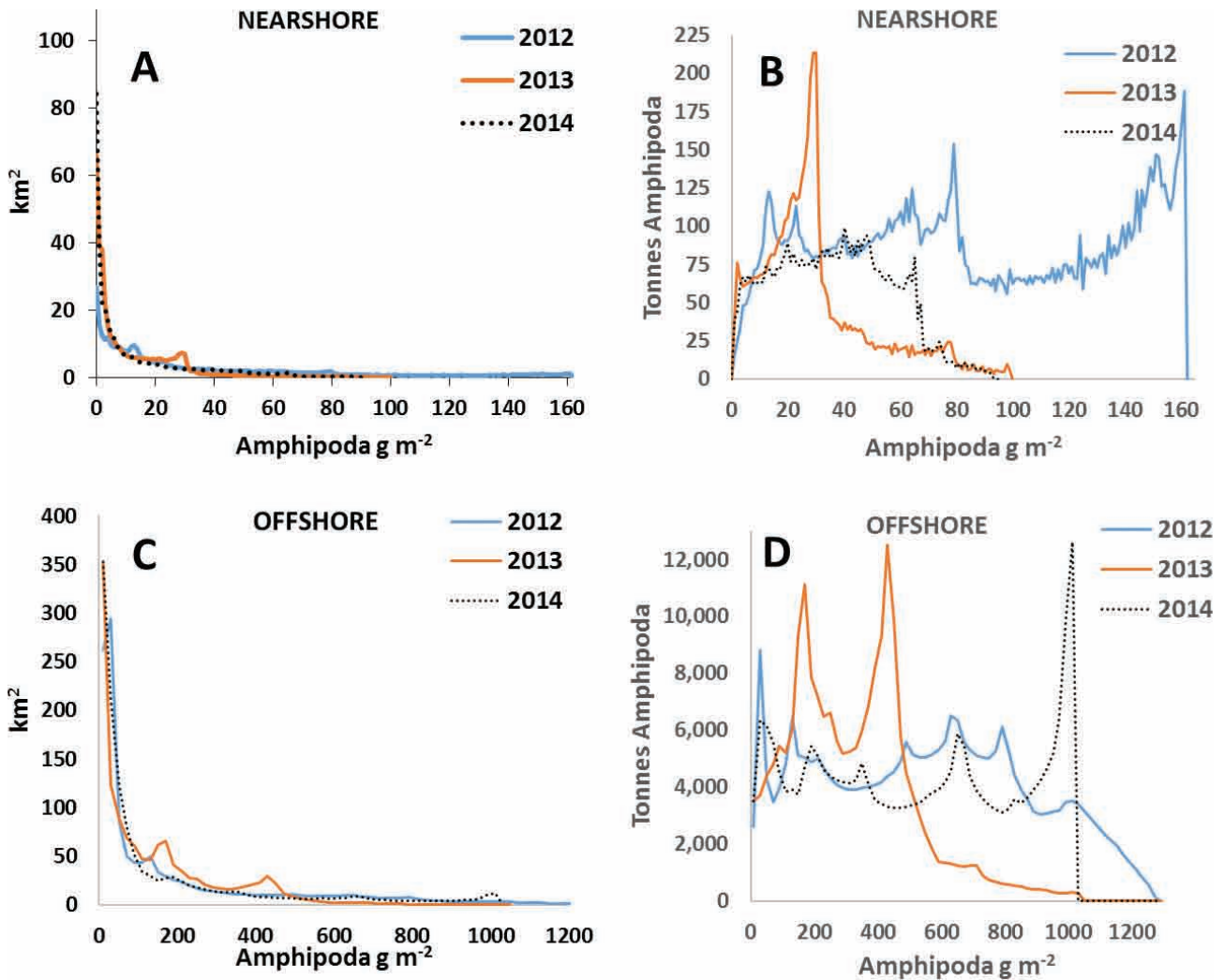


Fig. 2. Nearshore area per amphipod density Nearshore and Offshore (A and C) and tonnes of amphipod biomass per density of amphipods in Nearshore and Offshore (B and D) in 2012, 2013 and 2014.

Nearshore depths (where maximum shallow water production is likely), is unclear. The Nearshore salinities were reduced but similar with depth among years (Fig. 3B) despite the August timing of the 2012 survey and October timing of the 2013 and 2014 surveys. In contrast to the Nearshore, the lack of salinity variation below 40 m in the offshore in the Offshore area (Fig. 3D) and the increasing salinities with depth indicate restricted vertical mixing in summer.

Early sea ice retreat and mild winters over the Sakhalin Shelf were apparent in May 2012 and 2016 (Fig. 4). In contrast, variably severe winters were apparent from extensive sea ice remaining over the Sakhalin Shelf in mid and late May of 2011 and 2013–2015 (Fig. 4). Under the winter production hypothesis, 2013 and 2017 would be low offshore production years due to failed recruitment in the mild winters of the immediately preceding year.

The high 2012 average and maximum Offshore amphipod biomasses (Table; Fig. 2D) are consistent with the late sea ice retreat in 2011 (Fig. 4, top right panel) while the relatively low average and maximum biomasses of 2013 (Table; Fig. 2D) are consistent with early sea ice retreat in 2012 (Fig. 4, top center panel).

**Amphipod biomass in Nearshore and Offshore feeding areas:
with estimated sample areas, average biomass m^{-2} ,
maximum biomass m^{-2} , collection period
(midpoint of sample collection dates),
pixel based estimated tonnes biomass per feeding area and
with tonnes biomass in greater than 35 g m^{-2} areas of Nearshore
and tonnes biomass in greater than 100 g m^{-2} areas of Offshore**

Parameter	Year		
	2012	2013	2014
Nearshore (~384 km²)			
Mean g m^{-2} Biomass	36.6	14.4	19.0
Max g m^{-2} Biomass	161.6	103.2	104.3
Sample Period	08.29.12	10.12.13	10.09.14
Tonnes Biomass	13 953	5 475	7 241
> 35 g m^{-2} tonnes biomass	11 481	1 219	2 760
Offshore (~1,338 km²)			
Mean g m^{-2} Biomass	183.7	152.8	178.8
Max g m^{-2} Biomass	1289.9	1058.7	1026.2
Sample Period	08.21.12	10.12.13	10.13.14
Tonnes Biomass	240 768	200 256	234 394
> 100 g m^{-2} tonnes biomass	237 353	171 611	202 146

10 m depth Nearshore communities that were likely to have occurred within the highest phytoplankton production surface layer in 2013 were not sampled. However, the declines in Offshore amphipod populations in 2013 indicate that they did not benefit from high surface production that was likely in summer 2013.

Discussion

The asynchronous biomass densities among years in the adjacent Nearshore and Offshore western gray whale feeding areas, the transition of predominant amphipod species between the two areas and the depression of amphipod biomasses between the two areas corroborate Demchenko et al.'s (2016) and Durkina et al.'s (2018) proposals that production in the two areas results from different asynchronous mechanisms. The lack of correlation in the overall dynamics of the two areas is evidence that they are controlled by different mechanisms. The simultaneously low 2013 Nearshore and Offshore amphipod biomasses are therefore likely to have resulted coincidentally from different processes.

Nearshore benthic production thus appears to vary with Amur River flow and the intensity of summer and fall stratification that concentrates phytoplankton into the upper 10–35 m of the sea surface (Sorokin, Sorokin, 1999; Rutenko, Sosnin, 2014). The Nearshore received lower salinities and presumably received greater primary production in the upper sea stratum in 2013 than in 2012 or 2014. However, samples from the critical 2–10 m depths of the Nearshore area from late spring to early fall required to directly test for sea stratification effects, are lacking.

Offshore biomass from 2012 followed a mild 2012 winter where sea ice was absent by 13 May (Fig. 2) consistent with winter dependent growth. The greater 2014 biomass following a late sea ice retreat in 2013 (Fig. 2) and the greater Offshore biomass in 2015 (Fig. 1) following a late sea ice retreat in 2014 (Fig. 2) are consistent with winter dependent growth. Moreover, the high Offshore biomass stations (Fig. 4) occurred approximately where the winter ice edge occurred.

Additionally, winter polynya (areas of relatively open water surrounded by ice) formed over the shallowest (2–10 m deep) Nearshore in 2014 and 2015 (Fig. 4) that could have increase winter primary production and contributed to the subsequently increased Nearshore amphipod biomass in 2014 (Figs. 1, 2B; Table). The less than

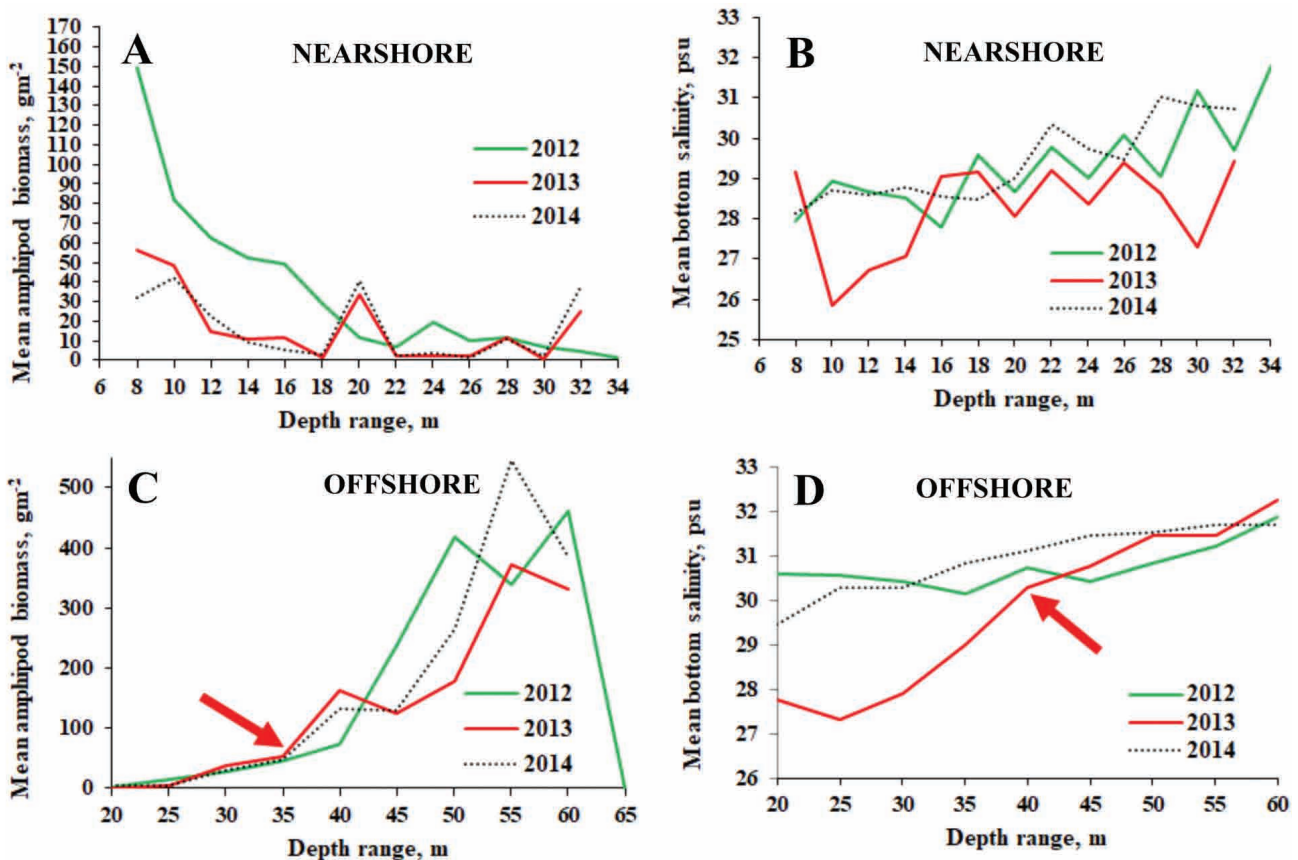


Fig. 3. Average Nearshore and Offshore amphipod biomass and salinity with depth (A and B) and (C and D) respectively among 2012–2014 surveys (August in 2012 and October in 2013 and 2014).

Production of the Offshore benthos appears to vary with winter and spring de-stratification and vertical mixing of phytoplankton to depths greater than 35 m. The reduced Offshore biomass in 2013 followed an early sea ice retreat in 2012. The normal or severe winters of 2011 and 2013 were thus likely to have mixed more phytoplankton biomass to the Offshore benthos than in 2012 and 2014 (Fig. 2D). Moreover, greater Offshore amphipod densities occur where the winter ice edges are likely to persist. These observations corroborate a winter mixing and production mechanism hypothesis. Winter samples of the Offshore required to directly test for de-stratification effects and winter production however, are lacking.

Surveys of the Nearshore and Offshore areas before and after WGW feeding commences are also needed. Our kriging and pixel analyses may provide a more accurate representation of biomass densities with area that WGW perceive but nevertheless remain similar to our estimates based on raw data (see Table). The influence of WGW grazing on the Nearshore and Offshore benthos is unknown. The mild 2012 winter could have enhanced Nearshore production in 2012. However, the 2013 and 2014 surveys were conducted after two more months of WGW grazing than in 2012.

Available data are insufficient to clearly test dependence of Offshore amphipod biomass and production on previous year winter storm driven vertical mixing or the dependence of Nearshore amphipod abundances on summer and fall concentrations of phytoplankton held in the sea surface

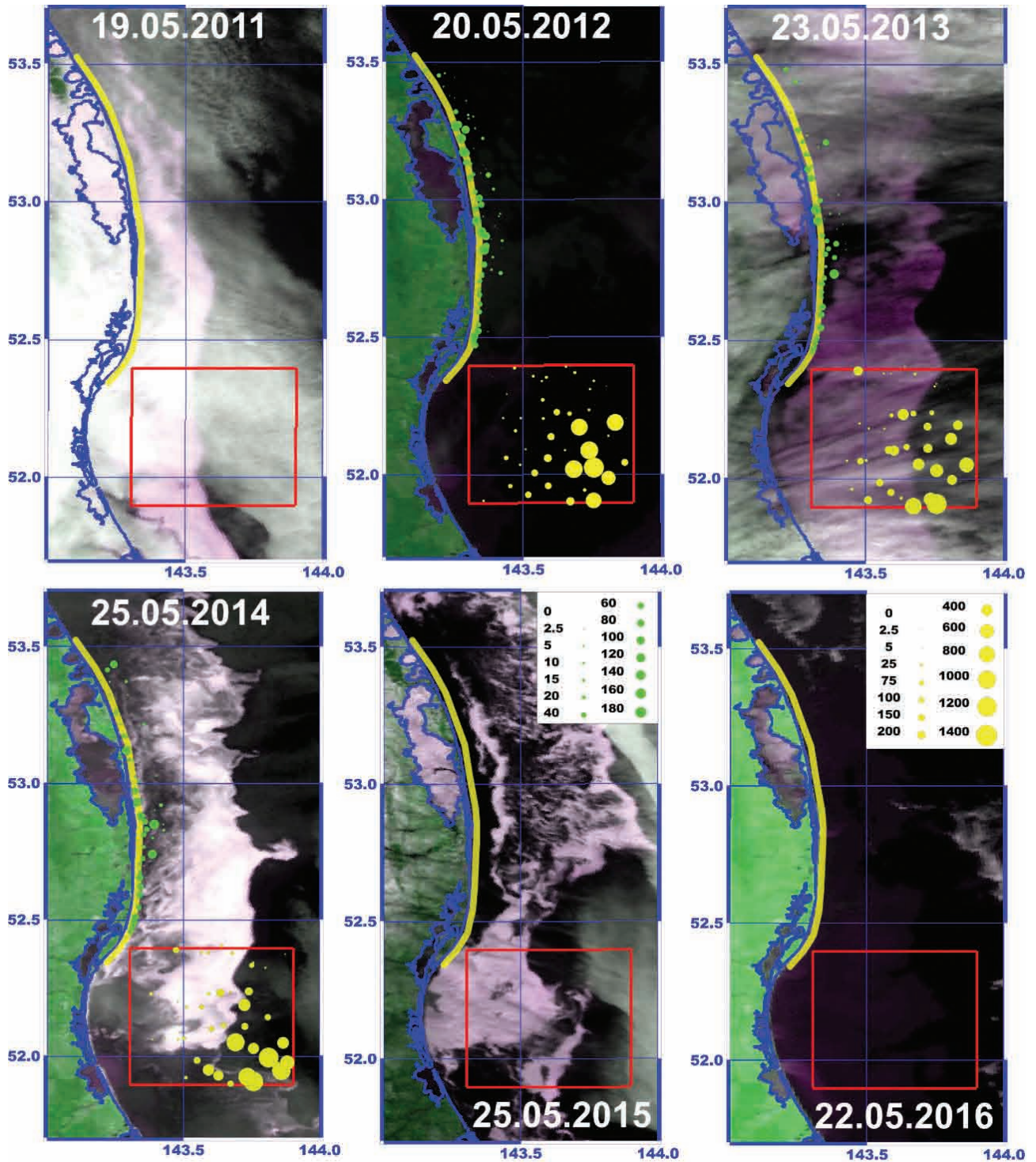


Fig. 4. Sea ice cover over the northeastern Sakhalin Shelf in mid to late May of 2011–2016, with the absence of sea ice (early ice retreat) apparent in 2012 and 2016, the approximate 2–10 m deep Nearshore shallows indicated by a yellow line, green bubbles corresponding to relative Nearshore amphipod biomass in 2012–2014 samples, yellow bubbles corresponding to relative 2012–2014 Offshore amphipod biomasses, Offshore survey perimeter out lined in red and shoreline highlighted in blue.

stratified layer. The asynchronous Nearshore and Offshore production hypotheses warrants direct tests from increased summer sampling of the 2–10 m deep benthos of the Nearshore area and winter sampling of the Offshore area.

Finally, despite massive efforts over the last two decades to assess WGW prey resources, the prey biomass required to feed existing WGWs aggregate and the importance of WGW access to their prey relative to prey abundance remain unexplored. Curiously, amphipod biomass has remained significantly greater in the Offshore area but WGW presence is greater in the Nearshore. The mixtures of echinoderms and other inedible prey in the Offshore could limit WGW access to a minor fraction of the Offshore amphipod populations present. In contrast, seasonally low salinities and constant sorting of Nearshore sands may limit refractory WGW prey, benefit optimal prey and maintain favorable sediment conditions for feeding. Moreover, prey populations in the two feeding areas could be greatly influenced WGW predation. Surveys beginning before and after the WGW arrivals in addition to samples from control areas, where WGW do not feed, would therefore be extremely useful for factoring out the dependence of prey density and biomass relative to prey availability on WGW predation.

Acknowledgements

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Hydrological influences on amphipod abundances with depth in the gray whale feeding areas on the Northeastern Sakhalin shelf (the Sea of Okhotsk)

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Ilya A. Shcherbakov, Sergey E. Dyakov, Victor V. Ivin, Evgeniy P. Dats*

Tests of a previous hypothesis of asynchronous benthic prey production in the Nearshore and Offshore western gray whale feeding areas on the Sakhalin Island Shelf are partially corroborated herein. Asynchronous amphipod biomass densities observed in the Nearshore and Offshore feeding areas is strong corroboration for differences in the controlling processes. Production of the Offshore benthos may depend on winter storms and sea ice-controlled phytoplankton transport to greater than 40 m depths and thus occur mainly in winter. Nearshore benthic production, in less than 35 m depths, appears to be controlled by summer/fall phytoplankton production enhanced by Amur River flow that is trapped in a stratified surface layer that does not mix to greater than 35 m depths. Greater benthic biomass (presumably due to greater production) occurred in the 20–65 m deep Offshore in 2012 and 2014, following large expanses of sea ice and severe winters in 2011 and 2013. In contrast, relatively low benthic biomass (presumably due to reduced production) of the Offshore area occurred in 2013, following a relatively mild winter and reduced winter sea ice in 2012. The low 2013 Offshore biomass occurred despite high Amur River flow and production conditions in less than 35 m deep waters in 2013. The relatively low Offshore biomass of 2013 was therefore consistent with winter production while tests of expected high summer production in Nearshore benthos in 2013 were precluded by a lack of sampling in 2–10 depths. The proposed asynchronous Nearshore and Offshore production remains open to question until summer/fall surveys of the 2–10 m deep Nearshore benthos and winter surveys of the Offshore benthos can be completed.

Glass sponges – unique animals with organosilica crystal-like composite skeleton as biomimetic model

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Biom mineralization is biochemical process by which available inorganic ions are extracted from marine water and are included to cellular structure. Marine organisms have calcium organic or silicon organic skeleton.

To date, there are around 600 species that belong to the classes of the so-named glass (Hyalospongia) or six radial (Hexactinellida) sponges. They are very ancient animals and highly unusual in that their major tissue component is a giant “syncytium” that ramifies throughout the entire body. The macrostructural organization of some of their spicules is a system of thin layers laid around the central cylinder containing a square canal filled with organic matter (Ehrlich et al., 2006). Some of them have the spicule as a system of the “cylinder-within-a-cylinder” type (Fig. 1).

The principal function of the spicules of hexactinellids is certainly a skeletal one. Still, their organizational traits imply the presence of other functions. Probably, the spicules may serve as waveguides transmitting optical, electric, or chemical signals and carry information on the state of the environment to cells within a sponge.

Organosilicic spicules of the glass sponges are composed of chemically inert materials. Mineralized remnants of siliceous spicules composed of chemically inert materials are preserved in sedimentary rocks and provide evidence of the ecological state of the ancient biosphere. The physic properties of organosilicic spicule materials (microdensity, Yung module, light transmission) are close with amorphous silica, but they have birefringence, that indicates their high ordered anisotropic crystal-like nature (Drozdov, Karpenko, 2011). Spicules demonstrate their capacity for thermoluminescence and triboluminescence.

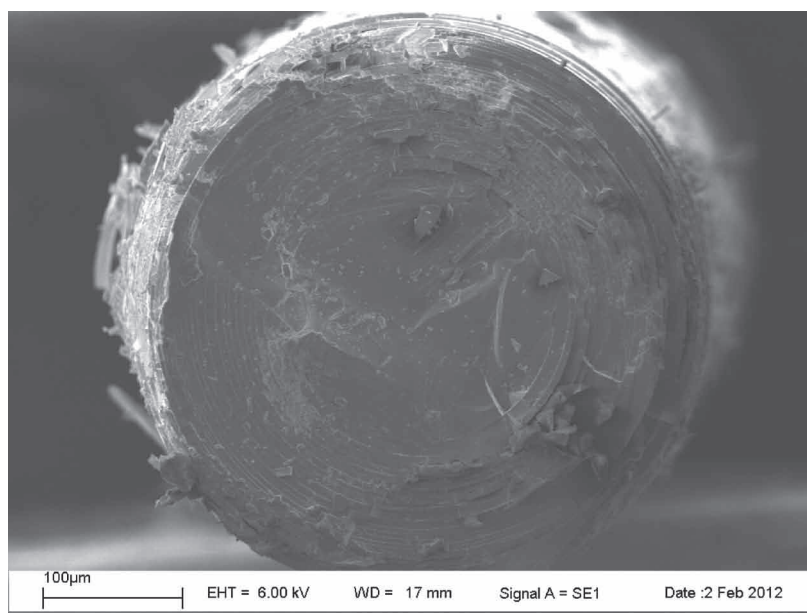


Fig. 1. A scanning electron microscopy of the basal spicule of *Hyalonema* sp. The cross-sections show the central cylinder, surrounded with 30 concentric layers. Scale 100 μm.

The spicules exhibited a capability of luminescence. The intensity of luminescence increases under the influence of 970-nm laser radiation (Fig. 2). The spicules can be destroyed by various methods. Local heating of a spicule was used in the present case.

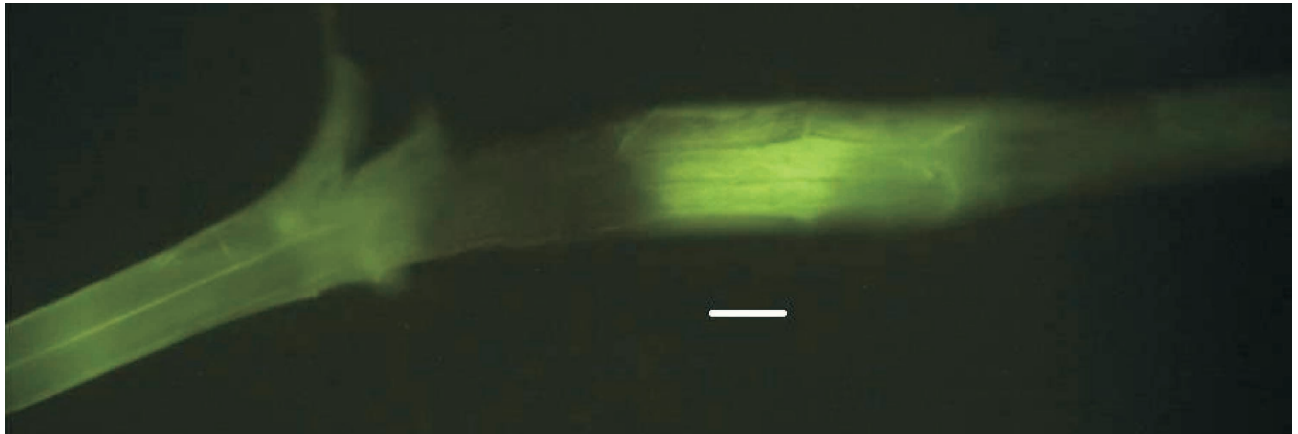


Fig. 2. Luminescence of the corporeal spicule of the glass sponge *Asconema setubalense* exposed to the heating effect of a 970-nm laser. Excitation wave length is 365 nm. Scale 1 mm.

The generated light emission may be used by symbiotic bacteria on the spicule surface (Drozdov et al., 2008).

Organosilicon spicules are dielectrics. However, multi-layered long and elastic spicules of six-ray sponges have a piezoelectric effect and condense charge. Short, thick and non-elastic spicules do not show the piezoelectric effect. Because of piezoelectric effect spicules of sponges, which inhabit in aphotic area, which lacks in light, can luminesce.

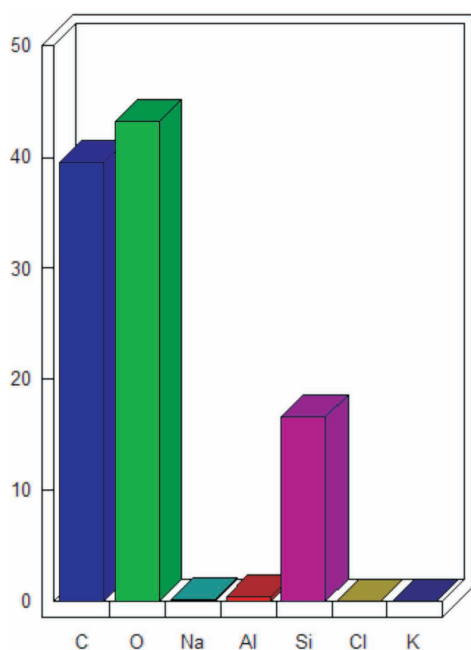


Fig. 3. Percent ratio of elements in spicule *Hyalonema sieboldy*.

Element	%
C	39.51
O	43.20
Na	0.13
Al	0.41
Si	16.66
Cl	0.03
K	0.05
In total	100.00

Spicules of six-ray sponges are formed by composite silicon organic material. It usually contains up to 80% of silicon.

Moreover, they contain admixture of ions of Na, Al, K, Cl, Mg, S, Ca, Cu. Impurity ratio in spicules from differ species varies (Fig. 3). Such micro elemental mixtures influence on electric qualities of spicules, allowing part of them to form piezoelectric effect. Our findings on the presence of the piezoelectric effect in composite organosilicon material of the hexactinellid spicules may contribute to the creation of biomimetic materials capable of generating light emission (Drozdov et al., 2018).

Piezoelectric properties of organosilicon spicules seems to be due to their complex multi-layered organization. There is mechanical tension between layers in different parts of spicules, which is removed upon destruction of the spicule (Fig. 4). The discovery of triboluminescence in spicules of deep-sea hexactinellid sponges suggests that the spicules may provide photons to the photosynthesizing symbionts living in them. It is likely that, under certain conditions, the sponge itself may provide its own symbionts with light energy. The discovery of piezoelectric effect in living composite organosilicon materials may contribute to the creation of biomimetic materials capable of generating light emission. This, in turn, may be used in various technical constructions for the transformation of energy.

The result obtained by us (Karpenko, Drozdov, 2019) in preliminary experiments shows that the natural material of silicone spicules of sponges can be re-formed as a result of self-assembly into three-dimensional or flat structures (Fig. 5). These data speak in favor of the assembly, or, at least, embedding, as on a matrix, of composite blocks of monoliths. Silica is dissolved in an alkaline medium (NaOH solution). In this case, organic components are released, on which silica can be adsorbed, forming materials in the form of plates and three-dimensional structures. This is largely a hypothetical “mechanism” that requires further research and the development of methods and technologies.

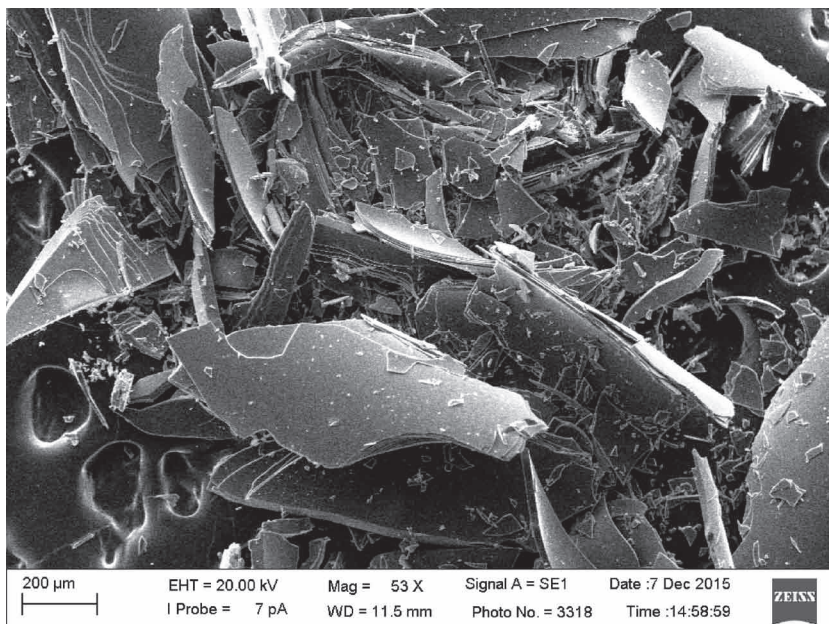


Fig. 4. The SEM images of a *H. sieboldi* basal spicule following its destruction at the inflexion point after a number of flexion-extension iterations. Scale 200 μm .

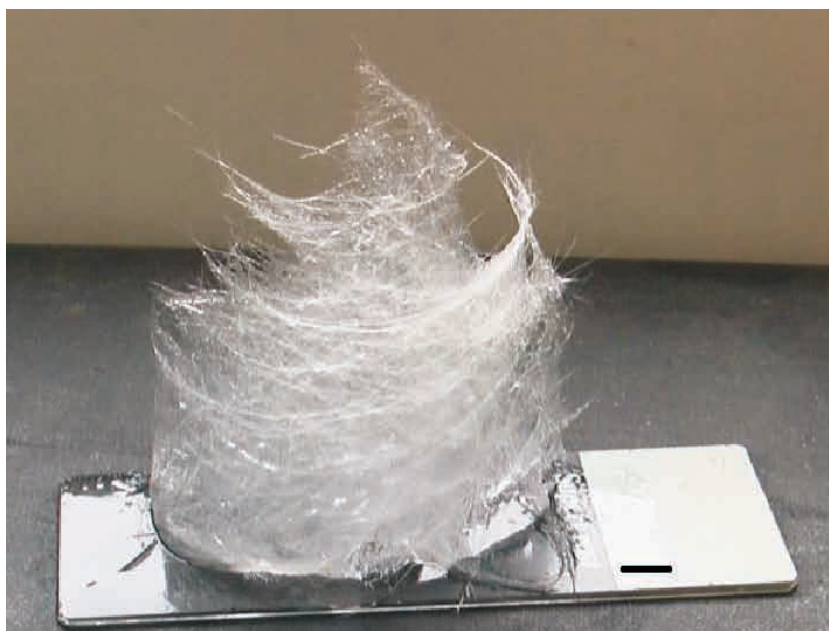


Fig. 5. Skeleton of glass sponge *Asconema setubalense*. Fused spicules after 90 days in a 1 M NaOH solution. Scale 10 mm (after Karpenko, Drozdov, 2019).

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Glass sponges – unique animals with organosilica crystal-like composite skeleton as biomimetic model

Anatoly L. Drozdov

Organosilicic spicules of the glass sponges are composed of chemically inert materials. They demonstrate their capacity for thermoluminescence and triboluminescence. The generated light emission may be used by symbiotic bacteria on the spicule surface. Organosilicon spicules of hexactinellids are dielectrics, however they have a piezoelectric effect and condense charge. Piezoelectric properties of organosilicon spicules seems to be due to their complex multi-layered organization. Their structure is a system of the “cylinder-within-a-cylinder” type.

The interannual growth variability of the Yesso scallop (*Mizuhopecten yessoensis* Jay, 1857) in hanging culture in Minonosok Bay (Possjet Bay, Peter the Great Bay, East Sea/Sea of Japan)

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The Yesso scallop is one of the important edible bivalves in East Asian countries including Russia, China, Korea and Japan. It has been denoted as a target resource that is managed using a more reasonable mollusk regimen in hanging culture that can maintain an optimal population size. For the propagation and management of the Yesso scallop, it is important to understand its population characteristics with regard to its mollusk growth.

In Northwestern Pacific Russian Federation the main mariculture areas are Primorsky Territory and Sakhalin-Kuril Region (Ivin et al., 2016), and some of the surrounding areas. In Possjet Bay, hanging culture areas occupy to about 110 km² (Fig. 1); they is carried out mainly in zones that extend from approximately 1 to 5 km offshore, at the depth of 10–20 m (Gavrilova, Kondratieva, 2018).

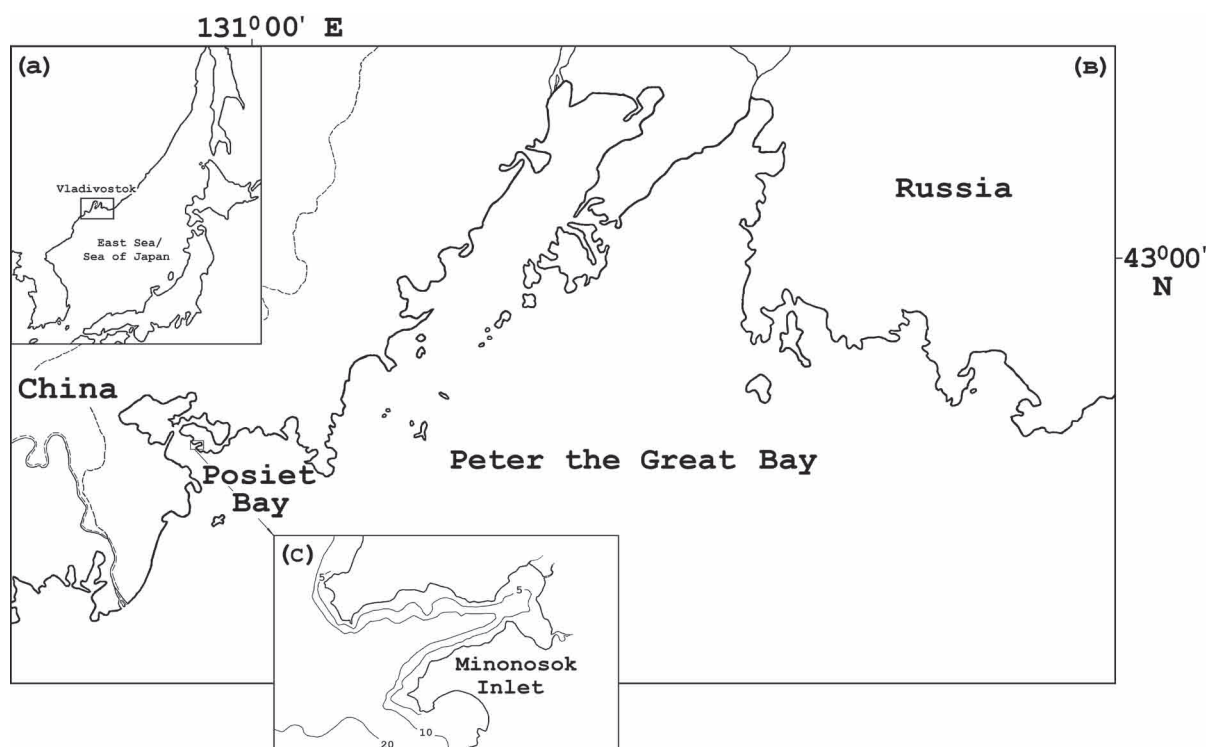


Fig. 1. The location of the sampling site: **a** – Sea of Japan; **b** – Peter the Great Bay and Possjet Bay; **c** – Minonosok Bay.

Previously, there have been many studies on aspects of reproductive ecology including propagation and rearing of *Mizuhopecten yessoensis* (Jay, 1857) (Belogradov et al., 1977), its larvae distribution, growth, and aquaculture. However, little information is available about Possjet Bay. Therefore, the main aim of this study is to describe the interannual growth variability of the Yesso scallop in hanging culture in Minonosok Bay during 1970–2011.

Materials and methods

The material for this study was collected during the last forty one years (1970–2011) from marine farm cultivating the Yesso scallop in Possjet Bay (Belogradov et al., 1977; Gabaev, 1990; Silina, 1994; Grigoryeva, 1999). In addition, data were used provided by N. Konovalova, G. Polikarpova, V. Regulev and T. Reguleva.

Results and discussion

Spawning of *M. yessoensis* in Peter the Great Bay occurs from May to July. Slight discrepancy in the spawning period between different areas are related to geographic differences in environmental conditions such as water temperature. In Possjet Bay larvae develop over a period of 22 to 40 days to 250–280 μm (Belogradov et al., 1977). Larvae settle on the mesh contained in the bags. Plastic monofilament packed in “onion” bags are strung from submerged, buoyed, horizontal longlines, and hang from 4–6 m below the water surface to 2–5 m above the sea bottom. Spat are harvested from the collectors in about 3–4 months after settlement. They are then transferred to intermediate culture in cages; this occurs in the autumn, in rare cases in the spring. Spat are placed into cages of 200–250 specimens (Kucheryavenko, Zhuk, 2011). Intermediate culture then continues to grow through winter until the following spring. One-year old scallops are transferred into separate cages of 20–25 individuals and two-year-olds scallops of 5–10 individuals. Scallops are harvested after 3–4 years of culturing.

In the our study, early juvenile scallops produced in June show an average in shell height of 3.3 mm in July (Fig. 2). The wide size range indicates that some individuals enter the surrounding area after the main settling. According to Fig. 2, Yesso scallops grow to an average of 17.4 mm in shell height in October. In April–May of the next year, they grow to an average of 31.7 mm in shell height. The shell height reaches 57.6 mm, 72.6 mm, 87.0 mm and 99.1 mm in October, in May, in the next October and in the next May respectively. By the end cultivation, Yesso scallops grow to an average of 11.2–11.4 cm in shell height. The standard deviation (SD) of the scallop shell heights analyzed in the present study varied from approximately 2.0 mm (spat) to 11.7 mm (2–3 ages). All the above growth characteristics are based on stocking the intermediate culture cages with the recommended number of specimens (Kucheryavenko, Zhuk, 2011). Growth is very dependent on stocking density, and the poor growth rates are probably due to deviating from the densities recommended by the research centres.

Also observable data indicated that water temperature changes, including frequent fluctuations, can be a primary environmental stressor affecting scallop growth. Thermocline in Possjet Bay is often influenced by the northern cold water mass in Peter the Great Bay, creating water temperature variations of up to 5°C within the same water layer (Grigoryeva, 2013), and the cultivation Yesso scallops framework is often laid in this layer.

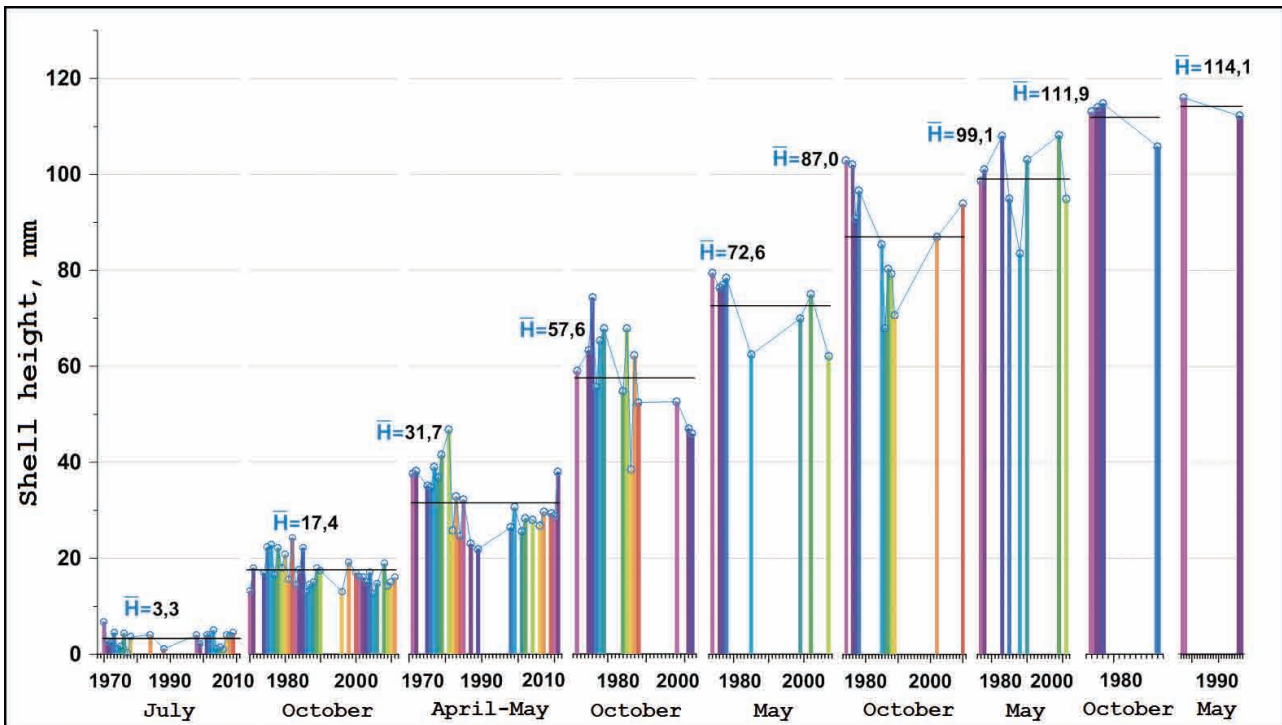


Fig. 2. Mean shell heights (mm) of Yesso scallop, *Mizuhopecten yessoensis* Jay, 1857), grown in hanging culture at different years.

The main environmental problem which the cultured scallops encounter is high temperature in the summer. After settlement in June in Minonosok Bay, temperatures increase rapidly (to 28–30°C) and the surface layers are above the survival threshold of > 23°C for scallop (Ventilla, 1982), although the tolerance range is from –2°C to 26°C (FAO, 2016). It is possible that water temperature changes related to scallops physiology and immunity is an important contributing factor to summer mortalities. In 2010 there was mass mortality of spat in Minonosok Bay caused by high water temperature. If temperatures continue to rise and scallop culture is carried out using the same methods used at present, mass mortality of the Yesso scallops will be unavoidable.

As indicated by Belkin (2009), the East Sea/Sea of Japan has been one of the most rapidly warming water bodies during the past decade. In general, the retreat of cold water species and colonization of warm water species will be apparent in Russian waters in the 21st century. Much evidence revealed that marine ecosystems, including the fish community in Korean waters, has been seriously affected by oceanographic changes (Kim et al., 2007). In Korean waters the southern limit of the scallop *M. yessoensis* has been shifted to about 1° northward for about 20 years from 36°04' N in 1980s to 37°13' N in 2000s (Jo et al., 2012). In Japan, previously, the scallop matured at more than 2 years old. More recently, the sexual maturation or differentiation has been seen to begin at 1 year (Kosaka, 2016). For *Mytilus edulis* along the western Atlantic, a range contraction of approximately 350 km in response to rising temperatures has already been documented (Jones et al., 2010). Increases in ambient temperature due to climatic change could therefore affect both small- and largescale distributions.

From an aquaculture point of view, the shift in biodiversity can be a new opportunity. The advantageous aspect might be a potential introduction of foreign species into aquaculture business. Although not all introduced species establish in the new environment with deleterious ecological

effects, many of them can cause certain concern. Introduced species can change populations, communities, and ecosystems in dramatic ways in a short period of time. These were known to be linked to loss of biodiversity (Jo et al., 2012). This is the most alerting aspect of introduction of foreign species for aquaculture purpose together with potential transmission of exotic pathogens.

There is no way to make a clear elucidation for the mechanism between climate change and biodiversity in the ecosystem, but there is a number of observations bridging the two parameters reasonably (Jo et al., 2012). In many cases the effect of climate change has been implicated in the decline and even collapse of several marine ecosystems. The loss rate of biodiversity has been identified by many authors as cause for an alarm (Soto, 2002). Species abundance and distribution are expected to change as a result of global climate change, potentially compromising the efficacy of marine protected areas as biodiversity conservation tool. Thus, climate change together with changes by anthropogenic variants such as increasing deposition of nitrogen and pollutants, and habitat disturbance and lower amount of dissolved oxygen, can affect species distribution and resource dynamics in aquatic ecosystems. The changes in oceanographic and biological processes and conditions triggered by global climate change will cause changes in abundance and distribution of many species, and consequently in biodiversity.

Conclusion

In Possjet Bay (Peter the Great Bay, East Sea/Sea of Japan) shell heights of the Yesso scallop (*M. yessoensis*) varied from an average of 3.3 mm in July to 111.9 mm in October after 3 years of hanging culture. The standard deviation (SD) of the scallop shell heights varied from 2.0 mm (spat) to 11.7 mm (2–3 ages) after 2–3 years. The effects of climate change on the growth rate and life expectancy of Yesso scallops were analyzed in order to come up with controlled measures for the reduction of summer mortalities associated with the rise of water temperatures, and other environmental stressors.

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Zonal-biogeographical structure of species composition of bivalve mollusks in the intertidal zone of the Far Eastern seas of Russia

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According to the materials of the hydrobiological expeditions (1966–2013) carried out mainly by the A.V. Zhirmunsky Institute of Marine Biology (FEB RAS) with the participation of the staff and students of several universities (FEFU, SPBU and MSU), the Botanical and the Zoological Institutes of the RAS and other institutions, as a result of studying 2 464 quantitative and qualitative samples of macrobenthos with bivalves, as well as with consideration of literature data, 95 bivalve mollusk species were identified in the intertidal zone of the Far Eastern seas of Russia. The species belong to 27 families, 22 superfamilies and 10 orders.

“A check-list of animals, plants and fungi from the intertidal zone of Far Eastern seas of Russia”, compiled earlier (Kusakin et al., 1997), was supplemented with 14 species of bivalve mollusks: *Arca boucardi* Jousseume, 1894, *Chlamys farreri* (Jones et Preston, 1904), *Limatula vladivostokensis* (Scarlato, 1955), *Astarte crenata* (Gray, 1824), *Trapezium liratum* (Reeve, 1843), *Serripes (Serripes) groenlandicus* (Mohr, 1796), *Serripes (Serripes) laperousii* (Deshayes, 1839), *Corbicula japonica* Prime, 1864, *Mysella ventricosa* Scarlato, 1981, *Macoma nipponica* (Tokunaga, 1906), *Macoma* sp., *Saxidomus purpurata* (Sowerby II, 1852), *Mya truncata* L., 1758, and *Barnea japonica* (Yokoyama, 1920).

The intertidal zone of the Far Eastern seas of Russia belongs to the Pacific boreal biogeographical region. A zonal-biogeographical analysis showed the following structure of the species composition of bivalve mollusks of the studied area:

Widely distributed boreal (including amphiboreal) species: *Mytilus trossulus septentrionalis* Clessin, 1889, *Musculus minutus* Scarlato, 1960, *Solamen leanum* (Dall, 1897), *Pododesmus macrochisma* (Deshayes, 1839), *Cyclocardia crassidens* (Broderip et Sowerby I, 1829), *Cyclocardia crebricostata* (A. Krause, 1885), *Clinocardium californiense* (Deshayes, 1839), *Clinocardium nuttallii* (Conrad, 1837), *Serripes laperousii* (Deshayes, 1839), *Mysella kurilensis* Scarlato et Ivanova, 1974, *Mysella ventricosa* Scarlato, 1981, *Neaeromya compressa* (Dall, 1899), *Mactromeris polynyma* (Stimpson, 1860), *Macoma balthica* (L., 1758), *Macoma golikovi* Scarlato et Kafanov, 1988, *Macoma lama* Bartsch, 1929, *Macoma middendorffi* Dall, 1884, *Megangulus luteus* (Wood, 1828), *Protothaca staminea* (Conrad, 1837), *Turtonia minuta* (Fabricius, 1780), *Mya japonica* Jay, 1857, *Mya uzenensis* Nomura et Zinbo, 1937, *Penitella penita* (Conrad, 1837), *Bankia setacea* (Tryon, 1863), *Siliqua alta* (Broderip et Sowerby I, 1829). (Only 25 species account for 26.3% of the total).

Boreal-arctic species: *Musculus glacialis* (Leche, 1883), *Musculus discors* (L., 1767), *Musculus laevigatus* (Gray, 1824), *Astarte crenata* (Gray, 1824), *Serripes groenlandicus* (Mohr, 1796), *Mysella planata* (Krause, 1885), *Liocyma fluctuosum* (A.A. Gould, 1841), *Mya truncata* L., 1758,

Hiatella atctica (L., 1767) s.l., *Cyrtodaria kurriana* Dunker, 1861, *Panomya norvegica* (Spengler, 1793). (Only 11 species account for 11.6% of the total).

Highboreal species: *Musculus filatovae* Scarlato, 1955, *Vilasina vernicosa* (Middendorff, 1849), *Arvella manshurica* Bartsch ex Scarlato, 1960, “*Modiolus phenax* (Dall, 1915)”, *Mysella gurjanovae* Scarlato et Ivanova, 1974, *Kellia comandorica* Scarlato, 1981, *Macoma* sp., *Lyonsia cucumerina* Ivanova ex Scarlato, 1981. (Only 8 species account for 8.4% of the total).

Lowboreal species: *Crenomytilus grayanus* (Dunker, 1853), *Vilasina pillula* Scarlato, 1960, *Adula schmidtii* (Schrenck, 1867), *Arvella japonica* (Dall, 1897), *Chlamys swiftii* (Bernardi, 1858), *Mizuhopecten yessoensis* (Jay, 1857), *Cyclocardia isaotakii* (Tiba, 1972), *Kellia japonica* Pilsbry, 1895, *Spisula sachalinensis* (Schrenck, 1862), *Megangulus venulosus* (Schrenck, 1861), *Megangulus zyonoensis* (Hatai et Nishiyama, 1939), *Nuttallia ezonis* Kuroda et Habe ex Habe, 1955, *Callista brevisiphonata* (Carpenter, 1864), *Protothaca adamsii* (Reeve, 1863), *Protothaca euglypta* (G.B. Sowerby III, 1914), *Entodesma navicula* (A. Adams et Reeve, 1850), *Thracia itoi* Habe, 1961. (Only 17 species account for 17.9% of the total).

Subtropical-boreal species: *Modiolus kurilensis* Bernard, 1983, *Limatula vladivostokensis* (Scarlato, 1955). (The found 2 species account for 2.1% of the total).

Subtropical-lowboreal species: *Musculista senhousia* (Benson ex Kantor, 1842), *Arca boucardi* Jousseume, 1894, *Glycymeris yessoensis* (Sowerby III, 1889), *Crassostrea gigas* (Thunberg, 1793), *Corbicula japonica* Prime, 1864, *Maetra chinensis* Philippi, 1846, *Cadella lubrica* (Gould, 1861), *Macoma contabulata* (Deshayes, 1854), *Macoma incongrua* (Martens, 1865), *Gari kazusensis* (Yokoyama, 1922), *Nuttallia obscurata* (Reeve, 1857), *Felaniella usta* (Gould, 1861), *Ruditapes philippinarum* (A. Adams et Reeve, 1850), *Protothaca jedoensis* (Lischke, 1874), *Anisocorbula venusta* (Gould, 1861), *Potamocorbula amurensis* (Schrenck, 1861), *Teredo navalis* L., 1758, *Panopea japonica* A. Adams, 1850. (Only 18 species account for 18.9% of the total).

Subtropical species: *Mytilus coruscus* Gould, 1861, *Mytilus galloprovincialis* Lamarck, 1819, *Septifer keenae* Nomura, 1936, *Chlamys farreri* (Jones et Preston, 1904), *Macoma nipponica* (Tokunaga, 1906), *Macoma irus* (Hanley, 1844), *Irus ishibashianus* Kuroda et Habe, 1952, *Saxidomus purpurata* (Sowerby II, 1852), *Cryptomya busoensis* Yokoyama, 1922, *Barnea japonica* (Yokoyama, 1920), *Zachsia zenkewitschi* Bulatoff et Rjabtschikoff, 1933. (Only 11 species account for 11.6% of the total).

Tropical-subtropical species: *Trapezium liratum* (Reeve, 1843), *Barnea manilensis* (Philippi, 1847), *Laternula marilina* (Reeve, 1860). (Only 3 species account for 3.2% of the total).

Bivalve mollusks of the Bering Sea and the Pacific coast of Kamchatka are represented by only four identical biogeographical complexes (in spite of the fact that there are almost 2 times more species in the Bering Sea than in Kamchatka) (see Table). The intertidal zone there refers to the Bering Sea province of the Bering subregion (Kusakin, 1971). Both in the Bering Sea and on the Pacific coast of Kamchatka, most of the bivalve species are widely distributed boreal (48.4% and 76.5%, respectively). A large portion of boreal-arctic species of the Bering Sea constitutes 29%. The subtropical-boreal complex in both regions is represented by one species – *Modiolus kurilensis*.

The greatest number of species of bivalve mollusks (63) was recorded in the intertidal zone of the Sea of Okhotsk (see Table), because the species number includes both warm-water and cold-water complexes of the species (the biogeographical border between the high and low boreal subregions of the Pacific boreal region passes in the intertidal zone of the southern Kuril Islands and at the southern Sakhalin to the Terpeniya Bay) (Kussakin, 1971, 1975, 1976; Scarlato, 1956, 1981).

**Zonal-biogeographical structure of the species composition
of bivalve mollusks of the Far Eastern seas of Russia**

Species	BeringSea	Pacific coast of Kamchatka	Sea of Okhotsk	Islands of Lesser Kuril Ridge	Sea of Japan	Total for the Far Eastern seas
Widely distributed boreal, %	48.4(15)	76.5(13)	30.2(19)	38.7(12)	21.4(12)	26.3(25)
Highboreal, %	19.4(6)	5.9(1)	12.7(8)	–	–	8.4(8)
Lowboreal, %	–	–	22.2(14)	25.8(8)	25.0(14)	17.9(17)
Boreal-arctic, %	29.0(9)	11.7(2)	8.0(5)	12.9(4)	3.6(2)	11.6(11)
Subtropical-boreal, %	3.2(1)	5.9(1)	3.1(2)	–	1.8(1)	2.1(2)
Subtropical-lowboreal, %	–	–	19.1(12)	16.1(5)	25.0(14)	18.9(18)
Subtropical, %	–	–	3.1(2)	6.5(2)	17.8(10)	11.6(11)
Tropical-subtropical, %	–	–	1.6(1)	–	5.4(3)	3.2(3)
Total number of species	31	17	63	31	56	95

Note. Numbers in parentheses indicate the number of species identified.

Almost a third of the species number is widely distributed boreal (30.2%). The share of lowboreal (22.2%) and subtropical-lowboreal (19.1%) species is also significant (mainly owing to mollusks of the Kuril Islands). Besides, the largest number of highboreal species lives here (even in comparison with the Bering Sea). In the Sea of Okhotsk, two endemic highboreal species occur – *Arvella manshurica* and *Lyonsia cucumerina*.

In the intertidal zone of the islands of the Lesser Kuril Ridge, in spite of their small size, there occur as many species of bivalve mollusks (31) as there are in the intertidal zone of the Bering Sea (see Table). This is explained by the fact that in addition to the widely distributed boreal species (38.7%), the intertidal zone of the islands is inhabited by many lowboreal (25.8%) and subtropical-lowboreal (16.1%) species.

Many species of bivalve mollusks are found in the intertidal zone of the Sea of Japan (56), most of which inhabit the Peter the Great Bay. Some authors (Lutaenko, Noseworthy, 2014) attribute this area to the Japanese-Manchurian province of the Pacific boreal region (Ainskaya Province after Kusakin, 1971) and indicate that southwards from the Cape Povorotny, the number of subtropical bivalve species begins to prevail over the number of widely distributed boreal species. In our study, the share of boreal species (widely distributed boreal and lowboreal) in the intertidal zone of the Sea of Japan constitutes 46.4% (see Table), and together with the boreal-arctic species – even 50%.

The share of warm-water species (subtropical-lowboreal, subtropical and tropical-subtropical) constitutes almost a half (48.2%). Of the 9 tropical-subtropical species of bivalve mollusks known for Peter the Great Bay (Lutaenko, Volvenko, 2017), 3 species were recorded in the intertidal zone (*T. liratum*, *B. manilensis*, and *L. marilina*).

Thus, boreal bivalve species in the intertidal zone of the Far Eastern seas of Russia constitute more than a half of the number of bivalve mollusks (52.6%), of which widely distributed boreal (including amphiboreal) species account for 26.3%, lowboreal species – for 17.9%, and highboreal species – for 8.4% (see Table). Boreal-arctic and subtropical species account for 11.6% each, subtropical and lowboreal species – for 18.9%, and tropical-subtropical species – for 3.2% of the total number. There occur few bivalves with a wider range – subtropical-boreal species – just 2.1%.

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Zonal-biogeographical structure of species composition of bivalve mollusks in the intertidal zone of the Far Eastern seas of Russia

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The intertidal macrobenthic communities of Yuri Island (Lesser Kuril Ridge)

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Yuri Island is uninhabited, low, and woodless island of the Habomai Islands in the Pacific Ocean (Lesser Kuril Ridge). The territory of the island is included in the biological reserve “Small Kuriles” (part of the Kurilsky State Nature Biosphere Reserve). The coast of the island is influenced by the Oyashio Current, carrying cold, low-salinity waters. Sometimes in winter, Habomai Islands, including Yuri Island, are sea-ice-covered region. The sea surface temperature is 14–15°C in August and about 1°C in February (Sakurai, 2007; Fujikura et al., 2010). Irregular semi-diurnal tides are characteristic of Yuri Island (Atlas..., 1967), the tides reach 1.7 m.

In the 1940s–1950s, reconnaissance investigations of the intertidal zone were conducted on some of the Habomai Islands, but the results of these single surveys were not published, although materials on some groups of animals and plants were used in the taxonomic studies or floristic and faunal surveys. But there are few publications on various groups of macrobenthos where species are exactly indicated for the intertidal zone of Yuri Island: Algae (Rybakov, 1968; Vinogradova, 1974; Makienko, 1980), Polychaeta (Radashevsky, 1993; Khlebovich, 1996), Isopoda (Kussakin, Mezhev, 1979), Gastropoda (Golikov, 1963; Golikov, Gulbin, 1977, 1978). In addition, the listing of the intertidal macrobenthic communities and their biomass were previously given on some of the Habomai Islands, including Yuri Island (Tsurpalo, Kostina, 2017).

Material and methods

On Yuri Island, sampling was carried out at low tides in August 1987 (quantitative and qualitative samples) and in August 2013 (qualitative samples). Belt transects (perpendicularly to the coastline) were used to estimate the distribution of intertidal communities. The coastline along each transect was divided into three subzones: the upper, the middle and the lower subzones. The subdivision of the intertidal zone was done according to the Vaillant’s principle of vertical stratification in the intertidal zone (Vaillant, 1891). The boundaries of the upper, middle, and lower subzones were determined as the highest tide mark, the high water level of neap tide and the low water level of neap tide, and the lowest tide mark (0 m depths) respectively. The investigations were conducted in Shirokaya and Katernaya bays and on Cape Lomot’ (Fig. 1; Table 1). Metal 250 and 500 cm² frames were used for sampling on loose substrata and 100, 250, and 500 cm² frames on hard substrata. To remove bottom deposits from macrobenthic samples, we used a set of soil sieves. The collected samples were analyzed, all the organisms were registered and, after drying on a filter paper, weighed using pharmaceutical scales accurate to 10 mg; large plants were weighed on a technical balance accurate to 1 g. The obtained data were extrapolated for 1 m². The collections were fixed in 75% alcohol or 4% formalin.

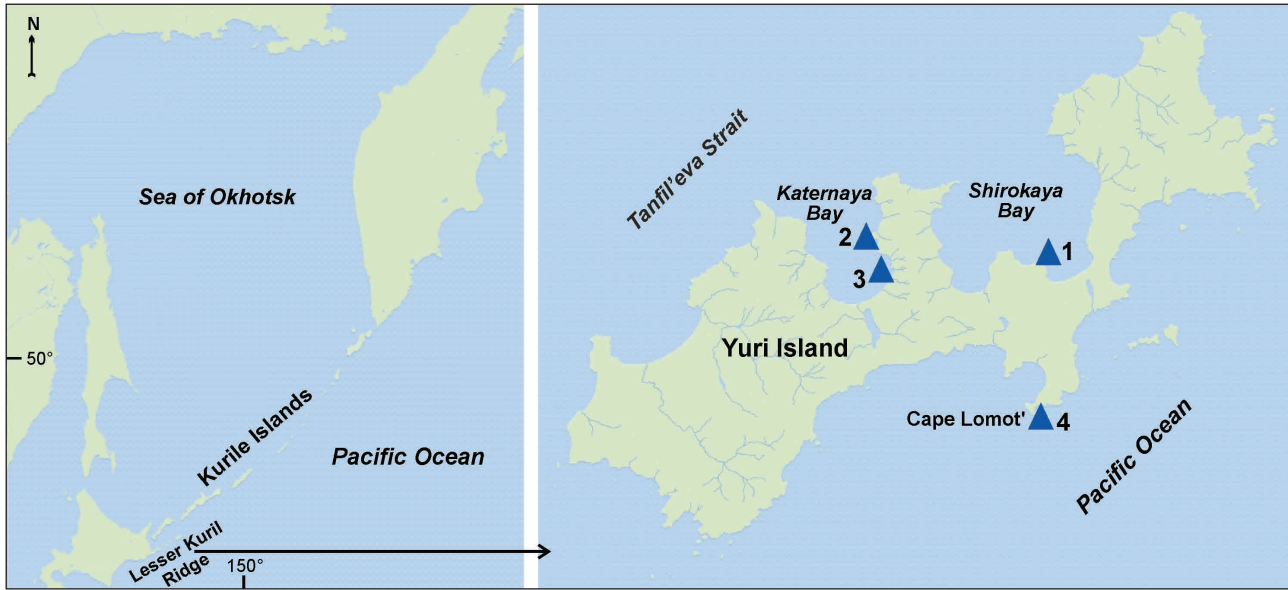


Fig. 1. Locations of sampling on Yuri Island (marked by triangles, 1–4 – transects nos.).

TABLE 1

Sampling locations in the intertidal zone of Yuri Island

No. transect	Location	Latitude, N°	Longitude, E°	Substratum	Number of samples
1	Shirokaya Bay	43.425827	146.080706	Rocky-bouldery with admixture sand in the lower part of the intertidal zone	15
2	Katernaya Bay, first right reef	43.426898	146.061973	Rocky reef	11
3	Katernaya Bay, second right reef	43.425579	146.063325	Rocky reef+silted sand	2
4	Cape Lomot', rock (kekur) 150 m from the cape	43.412355	146.081972	Rocky-bouldery	12

Distribution of the macrobenthic communities

The upper intertidal subzone (1.7–1.4 m over depths 0). There is the belt-forming community dominated by barnacle *Chthamalus dalli* in Shirokaya and Katernaya bays (Table 2; Fig. 2A). Sometimes the red alga *Gloiopeltis furcata* can be found among barnacles. While on Cape Lomot', community dominated by the shield limpet *Lottia pelta* is widespread and algae are not typical for these communities. The sea snail *Littorina sitkana* does not form a separate community in the upper intertidal subzone as on other Kurile Islands. In Katernaya Bay, community dominated by *G. furcata* is found on the boundary between the upper and middle subzones.

The middle intertidal subzone (1.4–1.1 m over depths 0). Fucoids are dominant in Shirokaya Bay (Fig. 2B). The upper part of the subzone is occupied by the *Fucus distichus* subsp. *evanescens* and *Silvetia babingtonii* communities with the patches of the green alga *Ulva lactuca*, the red algae *Corallina pilulifera*, *Bossiella compressa*, and *Neorhodomela aculeata*, the brown algae *Pylaiella*

TABLE 2
Vertical distribution of major intertidal macrobenthic communities on Yuri Island

Over depths 0, cm	Shirokaya Bay	Katernaya Bay	Cape Lomot'
170	<i>Chthamalus dalli</i>	<i>Chthamalus dalli</i>	<i>Lottia pelta</i> , <i>Chthamalus dalli</i> + <i>Semibalanus cariosus</i>
140			
110	<i>Fucus distichus</i> subsp. <i>evanescens</i> , <i>Silvetia babingtonii</i> , <i>Corallina pilulifera</i> , <i>C. pilulifera</i> + <i>Neorhodomela aculeata</i>	<i>Fucus distichus</i> subsp. <i>evanescens</i> , <i>Corallina pilulifera</i> , <i>C. pilulifera</i> + <i>Analipus japonicus</i> , <i>C. pilulifera</i> + <i>Neorhodomela aculeata</i>	<i>Silvetia babingtonii</i> , <i>Analipus japonicus</i> , <i>Corallina pilulifera</i> + <i>Mazzaella parksii</i>
	<i>Alaria</i> sp.+ <i>Saccharina gyrata</i> , <i>Zostera marina</i> , <i>Phyllospadix iwatensis</i>	<i>Saccharina gyrata</i> , <i>Zostera marina</i> , <i>Phyllospadix iwatensis</i>	<i>Saccharina gyrata</i>
0			

varia, *Scytosiphon lomentaria*, *Stephanocystis crassipes*, and *Analipus japonicus*. Species of gastropods *Littorina sitkana*, *Nucella freycinetii*, and *Falsicingula kurilensis*, barnacle *Chthamalus dalli* are the most numerous in the furoid communities. These communities are characterized by fairly high biomass of macrobenthos (up to 6 kg wet wt m⁻²). The belt-forming community dominated by the calcareous red alga *C. pilulifera* and its variations occur below the furoids. In the *C. pilulifera* community, species composition of algae is poorer than in the *F. distichus* subsp. *evanescens* and *S. babingtonii* communities (only the red algae *Mastocarpus pacificus* and *N. aculeata* often occur). Amphipoda, Polychaeta, species of gastropods *Buccinum percrassum* and *F. kurilensis*, and a bivalve mollusk *Mysella kurilensis* are the most numerous among animals.

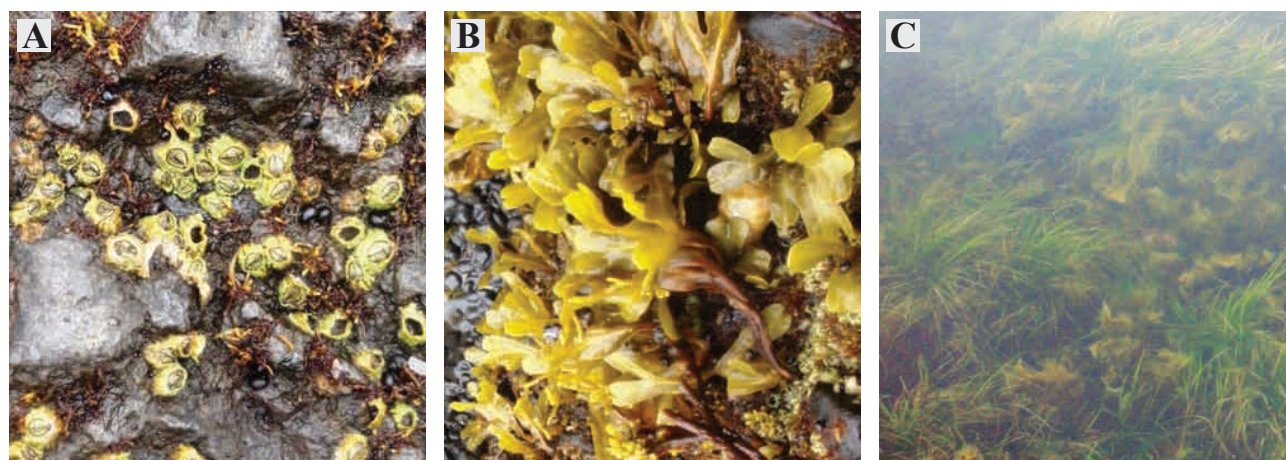


Fig. 2. The belt-forming intertidal communities dominated by *Chthamalus dalli* (A), *Fucus distichus* subsp. *evanescens* (B), and seagrasses (water level is ~0.4 m) (C) in Shirokaya Bay.

In Katernaya Bay, communities dominated by *C. pilulifera* are more widespread than fucoid community (Table 2). *U. lactuca*, *N. aculeata*, *Pylaiella littoralis*, the red alga *Mazzaella parksii*, and *L. sitkana* are conspicuous inhabitants among of *Corallina*. Sometimes the red algal community dominated by *N. aculeata*+*Vertebrata stimpsonii* forms separate patches in Katernaya Bay.

Unlike the Shirokaya and Katernaya bays well protected from wind and wave action, widespread in the middle intertidal subzone of the Far East seas the belt-forming seaweed *F. distichus* subsp. *evanescens* is not found on wave-exposed Cape Lomot'. Contrariwise, the communities dominated by the other brown algae *S. babingtonii* and *A. japonicus* are distributed on the cape, and sometimes *Gloiopeltis furcata* is found among them. These communities are poor in species composition (mollusks *L. sitkana* and *F. kurilensis*, and an isopod species *Cliamenella fraudatrix* often occur). Besides, the red algal communities *C. pilulifera*+*M. parksii* and *Porphyra ochotensis* with the rare patches of the green algae *Acrosiphonia duriuscula* and *U. lactuca* can be found in the middle intertidal subzone on Cape Lomot'. Chiton *Schizoplax brandtii*, an isopod species *Idotea ochotensis*, the hermit crabs *Pagurus middendorffii* and *P. brachiomastus*, and the shield limpet *Lottia pelta* are also common here.

The lower intertidal subzone (1.1–0 m depths). Communities dominated by large laminarian algae *Alaria* sp. and *Saccharina gyrata* form the dense beds in both the lower intertidal subzones and subtidal fringe of Yuri Island (Table 2). The biomass of macrobenthos is up to 14 kg wet wt m⁻², and the dominant species make up more than 99% of the community biomass. Among macrophytes, the red algae *Chondrus pinnulatus*, *Rhodomela sachalinensis*, *Bossiella compressa*, *Constantinea rosa-marina*, *Grateloupia divaricata*, and *Corallina pilulifera*, the brown algae *Leathesia marina*, *Dictyosiphon foeniculaceus*, and *Chordaria flagelliformis*, and the green alga *Acrosiphonia duriuscula* can be found in thickets of laminarian algae. *Pagurus middendorffii* and *P. brachiomastus*, sea snail *Margarites pilsbryi*, species of bivalves *Cyclocardia isaotakii*, *Protothaca euglypta*, chiton *Schizoplax brandtii*, ascidian *Aplidium glabrum*, sponge *Sycettusa* sp., species of gastropods *Buccinum mirandum*, *B. percrassum*, and *Lottia pelta*, the helmet crab *Telmessus cheiragonus*, sea urchin *Strongylocentrotus intermedius*, and diverse amphipod species are the most abundant invertebrates of the laminarian communities.

In Shirokaya and Katernaya bays, in sites where rocks are splited by spaces filled with sand, the community dominated by the eelgrass *Zostera marina* occurs with the total biomass of macrobenthos up to 10 kg wet wt m⁻². Surfgrass *Phyllospadix iwatensis* sometimes occurs (Fig. 2C).

On Yuri Island, the vertical distribution pattern of macrobenthos is typical for that of a low-boreal intertidal zone with a maximum tidal range about 1.6–1.7 m. At least, 169 species of macrobenthos (75 species of plants and 94 species of animals) are found in the intertidal zone of Yuri Island. Red algae dominate among plants (36 species) and species of gastropods (33 species) prevail among animals. According to preliminary data, the proportion of warm-water species (low-boreal and tropical/subtropical-low-boreal species) is quite small (about 15%), which can be explained by the influence of the cold waters of Oyashio Current on the intertidal macrobenthos of Yuri Island.

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The intertidal macrobenthic communities of Yuri Island (Lesser Kuril Ridge)

Elena E. Kostina, Alexandra P. Tsurpalo

Vertical distribution of the macrobenthic communities on Yuri Island (Lesser Kuril Ridge) is given. Communities dominated by the barnacle *Chthamalus dalli* and the gastropod species *Lottia pelta* with the poor species composition of the macrobenthos are typical for the upper intertidal subzone. The middle intertidal subzone is occupied by fucoid assemblages and communities dominated by the red alga *Corallina pilulifera*. The dense beds of laminarian algae dominate in the lower intertidal subzone on rocky-bouldery substrata and seagrass *Zostera marina* inhabits silted sand. The sea snail *Littorina sitkana* does not form a separate community in the upper intertidal subzone as on other Kurile Islands. The seaweed *Fucus distichus* subsp. *evanescens* is not found on wave-exposed intertidal zone. At least, 169 species of macrobenthos (75 species of plants and 94 species of animals) are found in the intertidal zone of Yuri Island. The red algae dominate among plants (36 species) and species of gastropods (33 species) prevail among animals. According to preliminary data, the proportion of warm-water species (low-boreal and tropical/subtropical-low-boreal species) is quite small (about 15%), which can be explained by the influence of the cold waters of Oyashio Current on the intertidal macrobenthos of Yuri Island.

**On the study of the avifauna
of marine and near-water birds
on the northeastern coast of Sakhalin Island
(Sea of Okhotsk)**

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Birds (Aves) are one of the main groups of animals that have occupied the World Ocean and playing an important role in coastal and pelagic ecosystems. In Russia, large nesting colonies are located on the islands and mainland coasts of the North Atlantic, Arctic, and Pacific. The rich and diverse avifauna of northern Sakhalin Island numbers almost 360 species (Nechaev, 1991; Tiunov, 2005). The coastal waters and shores of Sakhalin are inhabited by seabirds, water birds, and near-water birds. They use lakes on the coast for nesting, rest, feeding, and molting, as well as areas of the littoral zone exposed during low tides for feeding and rest (Tiunov, Blokhin, 2005, 2007). Compared to other groups, seabirds usually live longer, breed at an older age, and produce fewer chicks and, thus, can spend a significant part of their time for bringing them up. They feed on the sea surface or under water, and can also prey on each other. Some species live in the open ocean, far from coasts; others, only on the coast; there are also species that spend a part of the year far from sea (Biology..., 2001).

The goal of the study is to determine the composition of the summer seabird and shorebird avifauna in the area of Piltun Bay, northeastern coast of Sakhalin Island. The monitoring bird surveys were carried out in June–July 2018. The following research methods were used: counting along routes, comparative description, and faunistic analysis.

Short-term visual surveys of water birds were carried out during daylight hours. To identify species of birds, field binoculars with a resolution of 7x35 were used. All shorebirds and seabirds (sitting on the shore and on the water and flying over) within the full range of detection were recorded. Each survey day was divided into fixed 30-minute intervals, which were referred to as a unit of survey effort.

Below are data on seabird and shorebird species recorded from the Piltun Bay area, northeastern coast of Sakhalin Island (Sea of Okhotsk).

Family Phalacrocoracidae

1. *Phalacrocorax pelagicus* Pallas. Small in number, nesting, common, nomadic and transient species.

Family Anatidae

2. *Histrionicus histrionicus* (L.) (Fig. 1, A). Rare nesting bird, abundant during migrations; common during summer nomadic migrations. In the nesting season, distributed throughout the coast.

3. *Clangula hyemalis* (L.) (Fig. 1, B). Common transient and abundant wintering species. During seasonal migrations, it occurs in coastal waters.

4. *Melanitta deglandi* (Ridgway). Abundant transient species. It nests in northern Sakhalin, on the coasts of Nyisky, Chayvo, and Piltun bays.

5. *Mergus serrator* (L.) (Fig. 1, C). Rare, nesting, common transient species.

Family Accipitridae

6. *Haliaeetus albicilla* (L.). Rare, nesting, transient, and wintering species, tending to rivers, lakes, and the sea coast. Listed in the Red Data Book of Russia (The Red..., 2001).

7. *Haliaeetus pelagicus* (Pallas) (Fig. 1, D). Rarely nesting, transient, and wintering species, distributed on the coast of northern Sakhalin in the nesting season. Listed in the Red Data Book of Russia (The Red..., 2001).

Family Falconidae

8. *Falco peregrinus* Tunstall. Rare, nesting and transient species. Listed in the Red Data Book of Russia (The Red..., 2001).

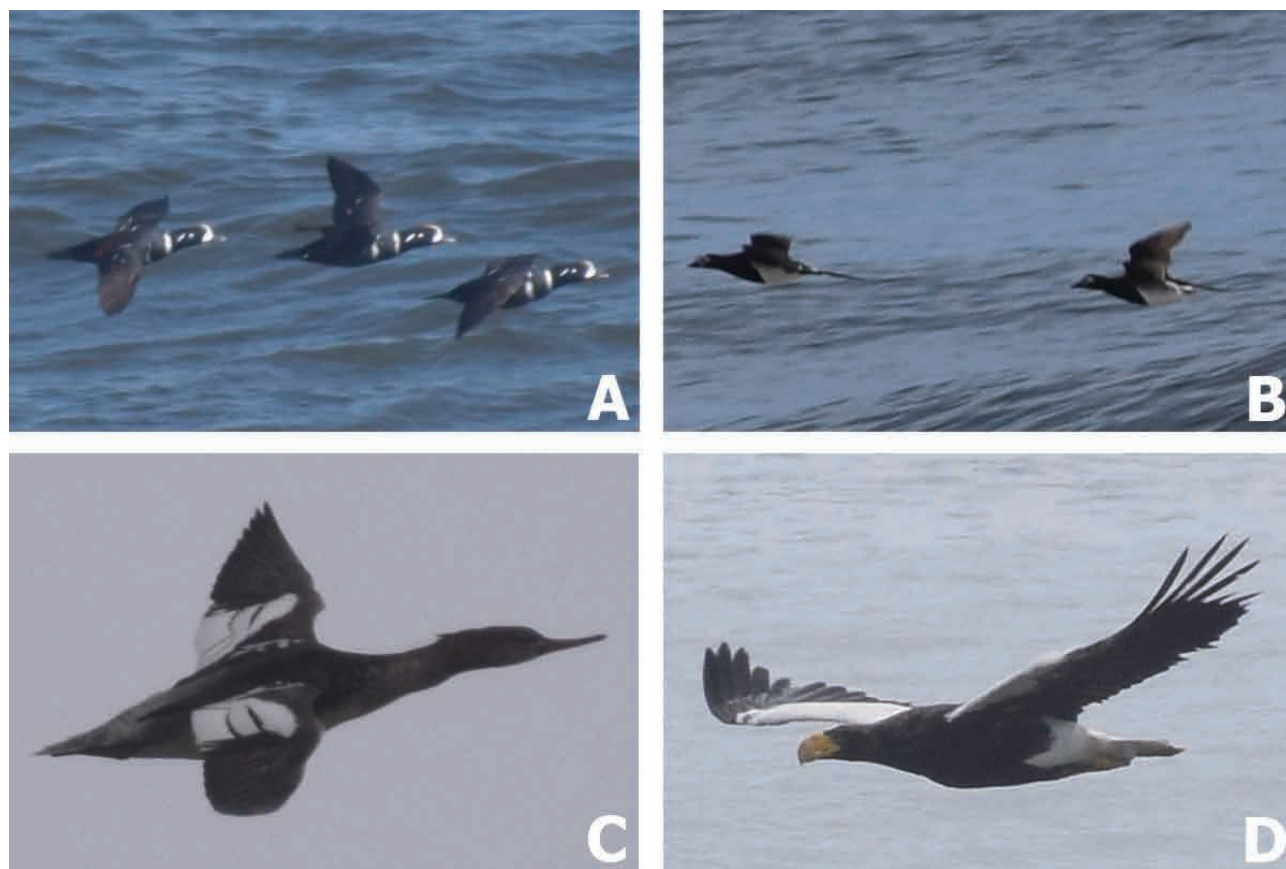


Fig. 1. The view of: **A** – *Histrionicus histrionicus*; **B** – *Clangula hyemalis*; **C** – *Mergus serrator*; **D** – *Haliaeetus pelagicus*.

Family Scolopacidae

9. *Tringa glareola* L. Small in number, nesting, and common transient species. It nests on lagoon coasts of northern Sakhalin.

10. *Numenius madagascariensis* (L.) (Fig. 2, A). Small in number, transient species. Listed in the Red Data Book of Russia (The Red..., 2001).

11. *Calidris minuta* Leisler (Fig. 2, B). A rare transient species (Tiunov, Blokhin, 2011). We observed the little flock only once, on July 28, 2011. Earlier, one bird was recorded here on May 21, 2000, and on August 22, 1999 a flock of 5 birds was observed.

Family Stercorariidae

12. *Stercorarius pomarinus* (Temminck). Rare species. It occurs during spring, summer and autumn migrations. On the Sakhalin coast, it is observed from May to October.

13. *Stercorarius parasiticus* (L.). Small in number, transient, and summer nomadic species. On the Sakhalin coast, it is recorded from May to October, singly and in flocks of 10 individuals each.

14. *Stercorarius longicaudus* Vieillot (Fig. 1, C). Small in number, transient, and summer nomadic species.

Family Laridae

15. *Larus ridibundus* L. (Fig. 2, D). Abundant transient and common nomadic species. It nests in northern Sakhalin. A common species in the study area.

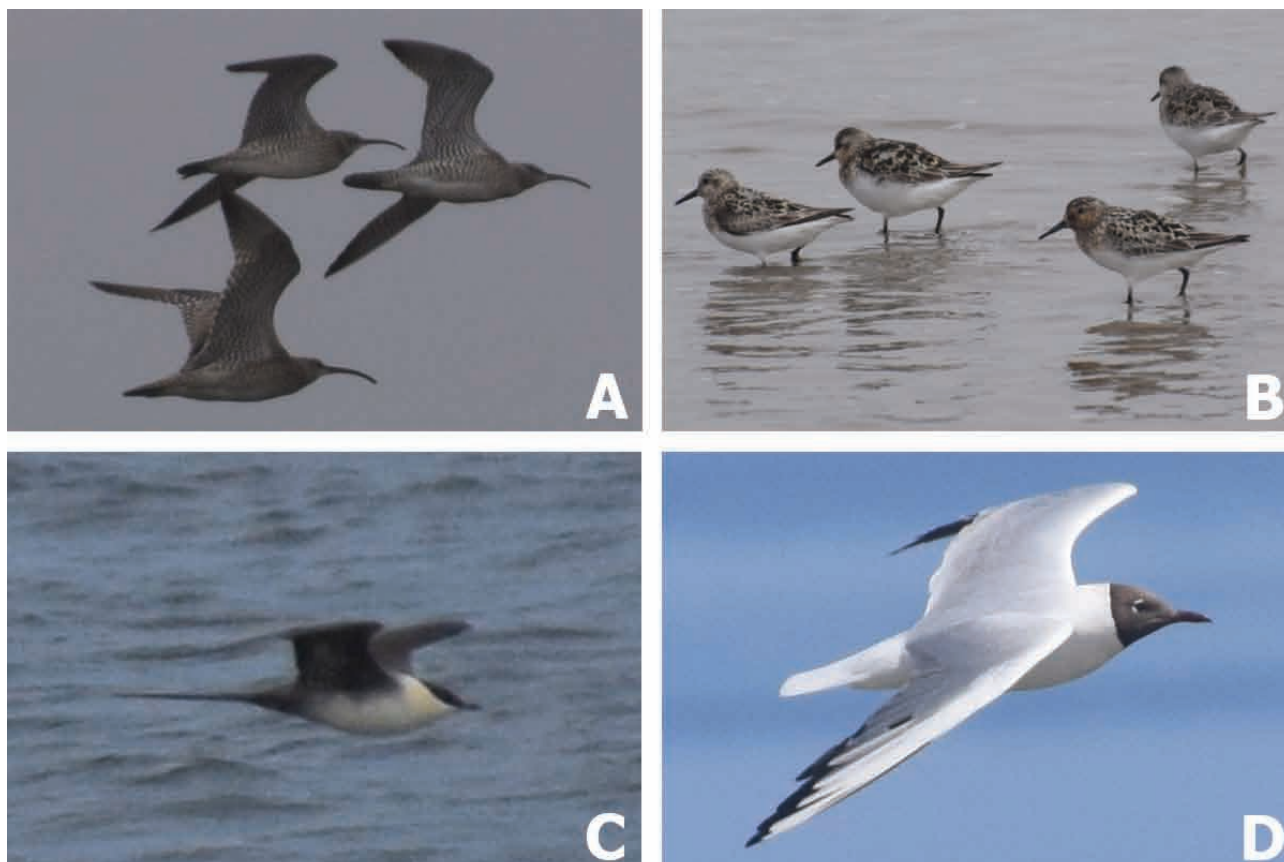


Fig. 2. The view of: **A** – *Numenius madagascariensis*; **B** – *Calidris minuta*; **C** – *Stercorarius longicaudus*; **D** – *Larus ridibundus*.

16. *Larus vegae* Palmen (Fig. 3, A). Inhabits marine and riverine shores, aggregating at sites with abundant fish. Common species in the study area.

17. *Larus schistisagus* Stejneger (Fig. 3, B). Overwinters in ice-free waters of the Far Eastern seas. Forms aggregations at sites with abundant fish. Breeds in colonies on rocky areas of the sea coast and islands, sometimes in tundra lakes, river estuaries, and inland bodies of water. The main breeding colonies are located on the mainland coast of the Sea of Okhotsk, eastern Kamchatka, and the Kuril Islands (Artyukhin, Burkanov, 1999). The most abundant species in the study area.

18. *Larus hyperboreus* Gunnerus (Fig. 3, C). Small in number, transient and summer nomadic species. Tends to sites with aggregations of fish. Sometimes forms flocks of up to 20 birds, but more frequently occurs singly in flocks of Slaty-Backed and Black-Headed gulls.

19. *Larus canus* L. (Fig. 3, D). Common transient and nomadic species in the study area. Found together with other species of gulls at sites with aggregations of fish.

20. *Larus crassirostris* Vieillot. In the summer of 2018 the species was very rare.

21. *Rissa tridactyla* (L.) (Fig. 4, A). Abundant nesting, common transient and summer nomadic species. It nests on Iony Island, Tyuleny Island, and Cape Terpeniya.

22. *Sterna hirundo* L. (Fig. 4, B). Abundant nesting and transient species. It nests in bays of northeastern Sakhalin, on islands of coastal lagoons.

23. *Sterna camtschatica* Pallas (Fig. 4, C). Common or small in number nesting species. Listed in the Red Data Book of Russia (The Red..., 2001).

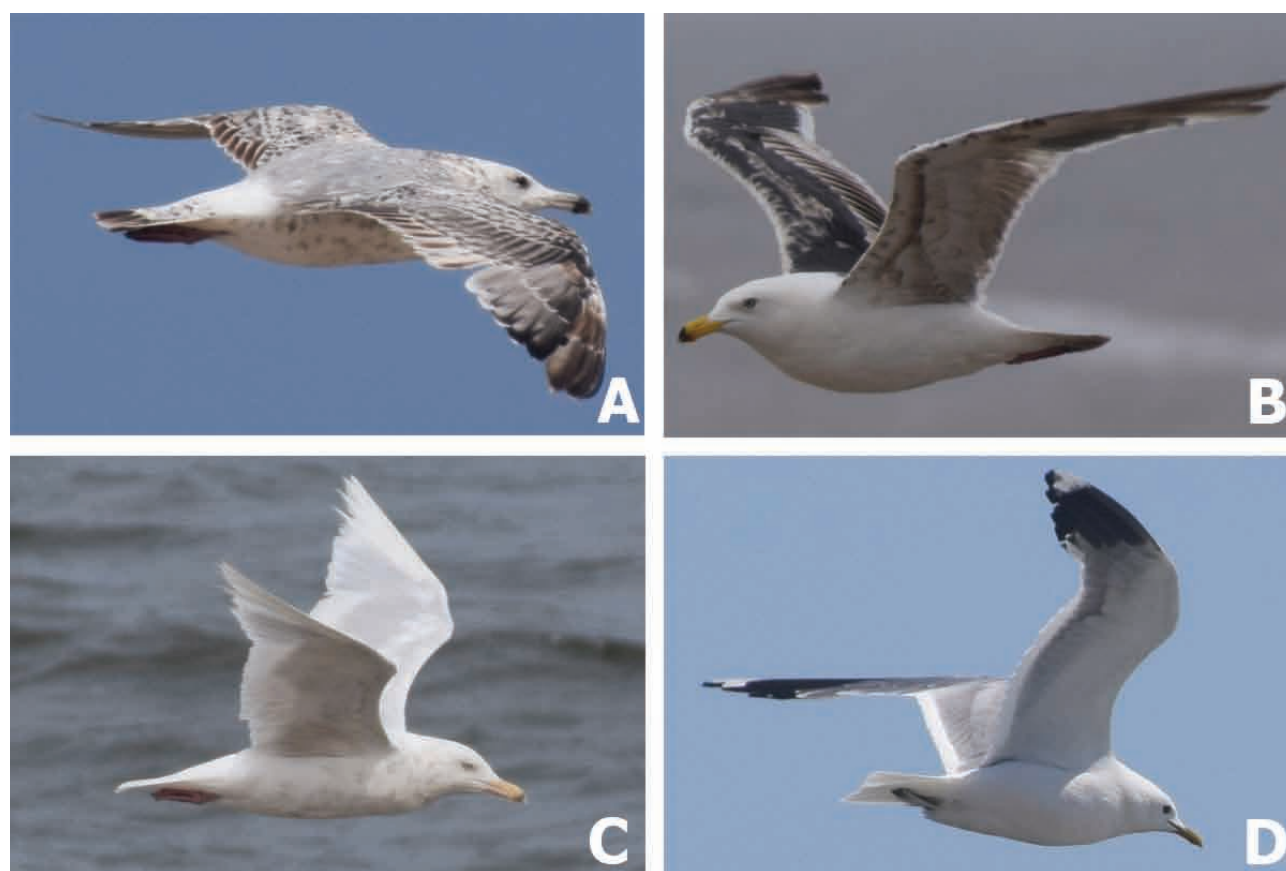


Fig. 3. View of: **A** – *Larus vegae*; **B** – *L. schistisagus*; **C** – *L. hyperboreus*; **D** – *L. canus*.

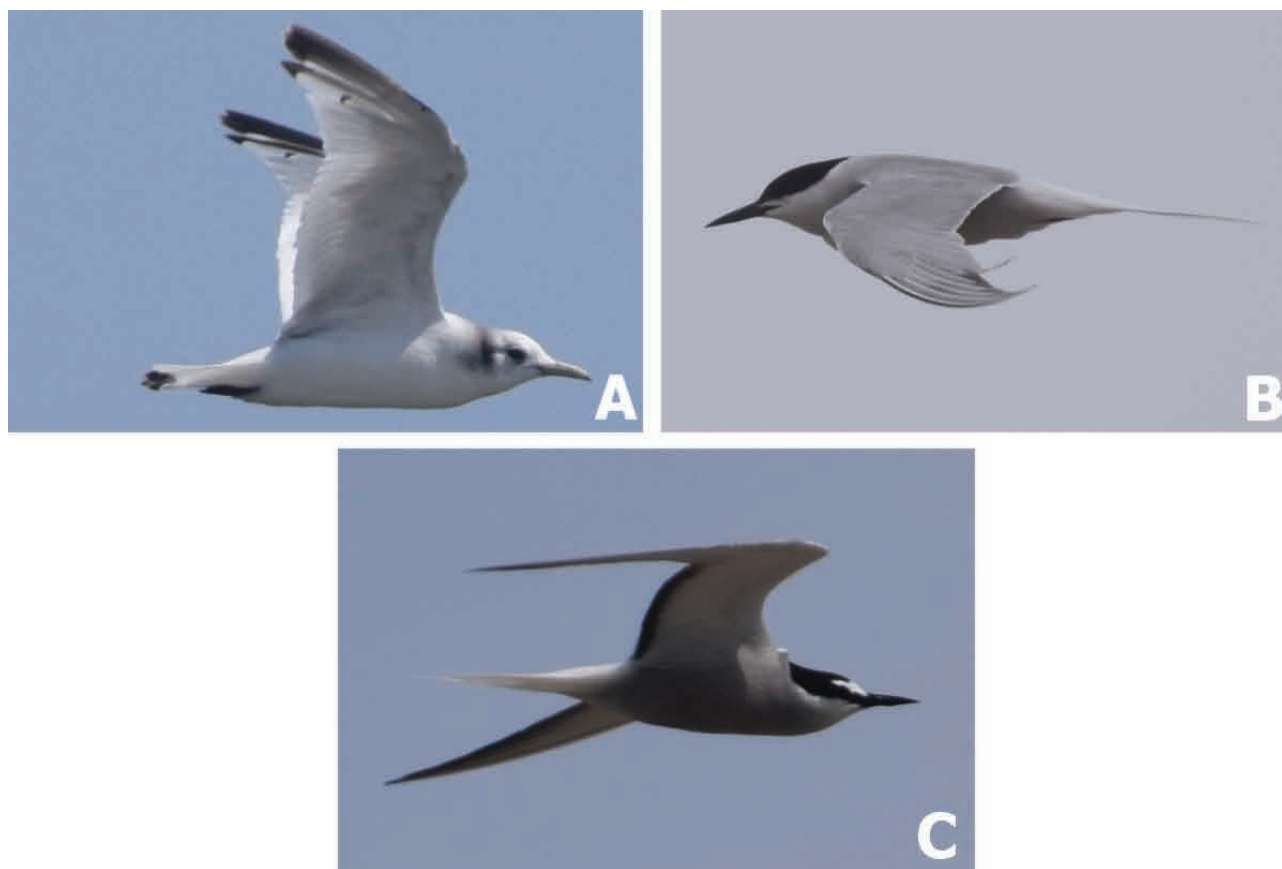


Fig. 4. View of: A – *Rissa tridactyla*; B – *Sterna hirundo*; C – *S. camtschatica*.

Family Alcidae

24. *Lunda cirrhata* (Pallas). Small in number, nesting, transient species.

Family Alaudidae

25. *Alauda arvensis* L. Abundant, nesting and transient species. Distributed throughout Sakhalin Island.

Family Motacillidae

26. *Motacilla lugens* Gloger. Abundant nesting and transient species. Distributed throughout Sakhalin Island.

Thus, the composition of summer avifauna in the Piltun Bay area has been studied. Of the 26 species encountered during visual surveys on the northeastern coast of Sakhalin Island in 2018, seagull species (Family Laridae) dominated: they accounted 35% of all the species recorded. The second largest group was duck species (Family Anatidae), 15%. The third groups were skuas (Family Stercorariidae) and sandpipers (Family Scolopacidae) had 11% each. Among the species entered in the Red Data Book, *Haliaeetus pelagicus* and *H. albicilla*, were found occasionally; the species *Falco peregrinus*, *Lunda cirrhata*, and *Larus crassirostris* occurred singly.

It has been established that the Slaty-Backed Gull *Larus schistisagus*, Common Gull *L. canus*, and Kittiwake *Rissa tridactyla* are common flocking species of marine avifauna in the area. It should be noted that most individuals of the species *L. schistisagus*, *L. hyperboreus*, *L. vegae*, and *L. canus* were immature and had intermediate plumage. In 2018, *Sterna hirundo* and *S. camtschatica* were common species nesting on small islands in lagoons.

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On the study of the avifauna of marine and near-water birds on the northeastern coast of Sakhalin Island (Sea of Okhotsk)

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The composition of summer avifauna of marine and near-water birds in the area of Piltun Bay, northeastern coast of Sakhalin Island, Sea of Okhotsk has been determined. The monitoring bird surveys were carried out in June–July 2018. Of the 26 species encountered during visual surveys, seagull species (Family Laridae) dominated: they accounted 35% of all the species recorded. The second largest group was duck species (Family Anatidae), 15%. The third group was skuas (Family Stercorariidae) and sandpipers (Family Scolopacidae) had 11% each. Among the species entered in the Red Data Book, *Haliaeetus pelagicus* (Pallas) and *H. albicilla* (L.), were found occasionally; the species *Falco peregrinus* Tunstall, *Lunda cirrhata* (Pallas), and *Larus crassirostris* Vieillot occurred singly. It has been established that the Slaty-Backed Gull *Larus schistisagus* Stejneger, Common Gull *L. canus* L., and Kittiwake *Rissa tridactyla* (L.) are common flocking species of marine avifauna in the area. It should be noted that most individuals of the species *L. schistisagus*, *L. hyperboreus* Gunnerus, *L. vegae* Palmen, and *L. canus* were immature and had intermediate plumage. In 2018, sea-gulls *Sterna hirundo* L. and entered in the Red Data Book *S. camtschatica* Pallas were common species nesting on small islands in lagoons.

Coastal marine biodiversity of Vietnam (South China Sea), its current problems and major threats

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The South China Sea, including its Vietnamese coast, is one of the richest regions of the World Ocean in terms of biodiversity. The sea is partially included into the *East Indies Triangle*, or the *Coral Triangle* (Hoeksema, 2007), a centre of maximum marine biodiversity. In total, more than **11000** species are found in Vietnamese marine waters including about 6000 zoobenthic species, 2458 fish species, 653 species of algae, 657 zooplankton species, and 537 phytoplankton species, among other taxonomic groups (Fourth Country Report..., 2008).

The A.V. Zhirmunsky National Scientific Center of Marine Biology, Far Eastern Branch of the Russian Academy of Sciences (Vladivostok; hereafter, the NSCMB; formerly, Institute of Marine Biology (1970–2016)) has been studying the marine biological diversity in coastal zones of Vietnam since the early 1980s, its status, threats, recent modifications due to global change and human impact, and ways of its conservation. Staff members of the NSCMB have also been involved in the international projects supported by the Asia-Pacific Network for Global Change Research (APN) (Lutaenko et al., 2012). We recently presented a synthesis of data and original research findings on coral reef modifications, biota of the intertidal zone, meiobenthic communities, species richness of rare groups of animals and economically important mollusks as a monograph (Adrianov, Lutaenko, 2016), and here we provide comments on some biodiversity problems in Vietnam. History of Russian marine biodiversity research along with bibliography was presented earlier (Lutaenko, 2016a).

Intertidal biodiversity

Recently, E.E. Kostina et al. (2016) summarized in details all available data about the biodiversity of the intertidal zones of Vietnam, from the Gulf of Thailand in the south to the Gulf of Tonkin in the north, including those published by earlier French workers, national Vietnamese studies and Russian researches from 1980–2005. According to this review, the macrobenthos of hard substrata is the richest in qualitative and quantitative composition, and the population of soft substrata is the poorest. Some **1664** species, subspecies or varieties of macrobenthic organisms (278 plant species and 1386 animal species) are found, with red algae dominating among plants (154 species), and gastropod mollusks (334 species) and decapod crustaceans (275 species) prevailing among animals.

The intertidal zone is most sensitive to any human-induced changes, e.g., overexploitation of biological resources, tourism pressure and pollution. One of the important intertidal ecosystems are mangrove systems, one of the most complex and productive world ecosystems, providing crucial livelihood support to coastal communities, but they are being degraded and lost in most countries (Fig. 1). The area of mangrove forests in Vietnam is estimated about 200.000 ha, and more than 60% of them are located in the coastal zone of southern Vietnam; they were heavily devastated during



Fig. 1. Mangroves in Vietnam under threat of aquaculture, salt farming and coastal erosion (after Tuan, Kuenzer (2012); photo belongs to GIZ (via IUCN)).

war times in the 1950s–1970s (Thanh, 1995). In Vietnam, the principal threat to mangrove ecosystems is their conversion to aquaculture (Orchard et al., 2015). Vietnam lost 69% of its 269000 ha of mangrove forests held in 1980, with an estimated 77% of this loss due to aquaculture (Hamilton, 2013). In the recent year, due to the rapid population growth and excessive aquaculture activities, mangroves have been seriously destroyed, so, the mangrove area in the Mekong River delta has decreased rapidly from 250.000 ha in 1950 to 72.000 ha in 1995 (Thanh, 2006).

A monitoring system should be implemented to record changes in the intertidal biotic communities, their biodiversity and environment. As this approach requires deep taxonomic knowledge and expertise for correct identification of animal and plant species, a collaboration between national and overseas researchers is strongly needed. Recently, several papers on mollusks of mangrove ecosystems of Vietnam were published by a team of zoologists from Russia and China presenting for the first time reliable data on this key invertebrate group (Zvonareva, Kantor, 2015; Zvonareva et al., 2016). Another team of researchers (L.A. Prozorova, K.A. Lutaenko, Quang Xuan Ngo et al.) currently studying mangrove mollusks of southernmost Vietnam.

Biodiversity of corals and coral reefs

As a result of more than 30-year studies of the reef-building scleractinians of Vietnam, **358** corals species belonging to 80 genera were found (Fig. 2), of which 153 species in 28 genera were recorded for the first time in the area (Latypov, 2007, 2011). The species diversity of Vietnam's reefs consists mainly of the members of five families: Acroporidae (98 species), Faviidae (42 species), Fungiidae (32 species), Poritidae (31 species), and Dendrophylliidae (26 species), making up altogether 64% of the total scleractinian species composition. The species composition and high diversity of Vietnamese corals are closely related to the Indonesia-Polynesian center of origin of the coral

faunas (Latypov, 2007, 2011). The species composition and high diversity of the Vietnamese coral fauna, as well as its close similarity to the southwest Pacific coral fauna, allow one to refer it to the Indonesia-Polynesian center of origin of the coral faunas of the tropical Indo-Pacific. The entire Vietnam coast is one biogeographical unit and is a part of the Indo-Polynesian Province of the Indo-Pacific Area (Latypov, 2016).

Based on various literature data, the survey of coral reefs in Vietnam during the last 15 years shows that the area of coral reefs has been reduced by 15–20%, mainly in coastal waters of the central part of Vietnam from Da Nang to Binh Thuan Province (Lutaenko et al., 2012). Along with the coral reef area reduction, the species richness also decreased. For example, the coverage of coral reefs in Bai Tien area (Nha Trang) was 30% (1984), with 60 species, and it reduced to 1% by 1998 and the number of species decreased to 30 (Lutaenko et al., 2012). Other organisms diversity and abundance also reduced significantly. Out of 200 coral reefs investigated over the past 10 years in Vietnam, only 1% have high coverage rate (covering > 75%) while 31% have low coverage rate (covering < 25%); the percentage of sites with average and above-average coverage are ranging at 41% and 26% respectively (Fourth Country Report..., 2008).

Biodiversity of bivalve mollusks

An example of high biodiversity is fauna of marine bivalve mollusks recently discussed by Lutaenko (2016b). The South China Sea itself has the most diverse bivalve fauna in the world from 1200–1500 species, and Vietnamese fauna contributes a significant portion to that species richness. Regional species biodiversity in the western sea area varies from 344, at Singapore in the south, to 822, southern mainland China in the north, more of an indication of sampling efforts and the state of knowledge of the fauna than real biodiversity gradients (Lutaenko, 2016b). Vietnam is among the world biodiversity-rich areas, and bivalve species richness of Vietnamese fauna is currently up to **812** species (Fig. 3). However, more and more species are described nearly every year from Vietnam and one may expect that species richness of bivalve fauna may be at level between 900 and 1000 species.

Problems in studying the region's bivalve biodiversity include inflated synonymy, a lack of trained, regionally-based taxonomists, good voucher collections, and a lack of funding for taxonomy. However,

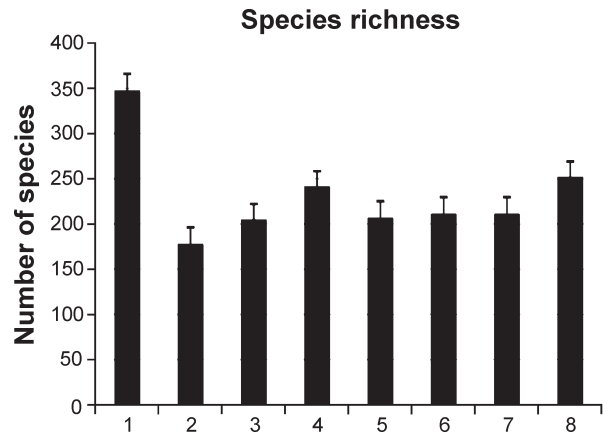


Fig. 2. The species richness of scleractinian species in different regions of Vietnam. 1 – total number of species (347), 2 – Gulf of Tonkin (177), 3 – Central Vietnam (204), 4 – South Vietnam (240), 5 – Thu Island (206), 6 – Con Dao Islands (210), 7 – Spratly Island (211), 8 – Gulf of Siam (251) (after Latypov (2016)).

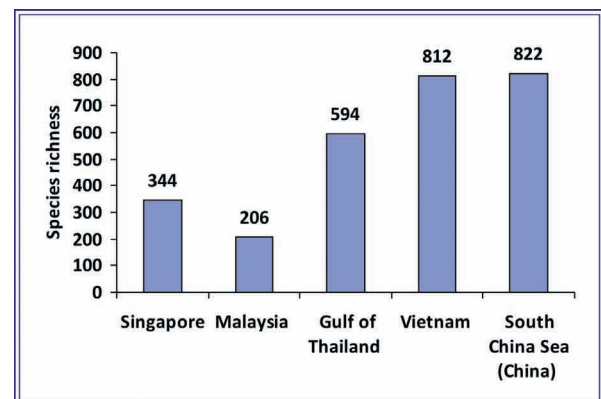


Fig. 3. Species richness of bivalve mollusks in major regions of the western South China Sea (Singapore, Malaysia, the Gulf of Thailand, Vietnam and Chinese (mainland) part of the South China Sea) (after Lutaenko (2016b)).

these problems are common in biodiversity researches of many other animal taxonomic groups. Monitoring of the Vietnamese national literature for last 30 years shows that economic growth in this country is not accompanying with increasing quality of taxonomic research.

Threats to marine biodiversity

Threats to marine biodiversity in the South China Sea and Vietnam may include habitat degradation, fragmentation and loss, especially mangrove forest destruction, loss of coral reefs, change in the landscape mosaic of wetland, estuary, and sand and mud flats; global climate change including sea level rise, storm events, rainfall pattern changes, and warming of the coastal ocean; effects of fishing and other forms of overexploitation, pollution and marine litter; species introduction/invasions, physical alterations of coasts, and tourism (Gray, 1997; Thanh, 2010; Lutaenko, Thai, 2014; et al.). Nationally recognized threats with regard to marine biodiversity can be summarized as follows: extending land for agricultural and industrial plantation, and aquacultural farming; infrastructure development; unsustainable fishing; illegal wildlife hunting and trade; introduction of new species and invasive alien species; environmental pollution; climate change; pressure from population growth; increasing consumption of natural resources (Fourth Country Report..., 2008).

Continued warming through the twenty-first century is inevitable and will likely have widespread ecological impacts (Serreze, 2009). In Vietnam, the Red (Song Hong) and Mekong rivers discharge into the sea, and the drainage systems of these two transboundary rivers cover parts of six countries, and their water and sediment discharges greatly influence the coastal seas of Vietnam. The impact of human activity includes changes in the quality of the coastal and marine environments due to the increased use and accumulation of pollutants, and the loss of habitat. These impacts have resulted in the increasing unpredictability and severity of coastal problems, such as floods, erosion, sedimentation, saltwater intrusion, environmental pollution, and the degradation of ecosystems, with an accompanying decrease in biodiversity and fishery productivity (Thanh et al., 2004).

The decline in quality of marine environment has resulted in habitat destruction of most marine organisms, causing changes in biodiversity (e.g., decrease in number of species, some being locally extinct); 236 aquatic organisms are listed as endangered, precious, rare ones, of which 70 species are listed in Vietnam Red Book whereas many of them are still objects for exploitation (Fourth Country Report..., 2008).

There are National Strategy and Action Plan on Biodiversity in Vietnam, several biodiversity laws were implemented, raising public awareness, biodiversity conservation measures, establishing national parks and reserves are all positive steps towards marine biodiversity conservation. However, more efforts in understanding and studying marine biodiversity are needed, in close cooperation with international scientific community. Russian contribution to marine biodiversity study in Vietnam shown here for selected groups and environments (intertidal, corals, mollusks) has been significant and would be continued due to high potential of national biological science.

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Coastal marine biodiversity of Vietnam (South China Sea), its current problems and major threats

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Main problems related to study and threats to coastal marine biodiversity of Vietnam are discussed on selected example of intertidal communities, coral reefs, and molluscan diversity and based on Russian researches. Threats to marine biodiversity in Vietnam include habitat degradation, fragmentation and loss (mangrove destruction, loss of coral reefs, change in landscape mosaic of wetland, estuary, etc.); global climate change including sea level rise, storm events, rainfall pattern change, warming of the coastal ocean; effects of fishing and other forms of overexploitation; pollution and marine litter; species introduction/invasions; physical alterations of coasts; tourism. More international and national efforts are needed to study marine biodiversity of Vietnam, including high quality taxonomic studies.

Dynamics of phytoplankton and chlorophyll “a” concentrations in Paris Bay (Russky Island, Sea of Japan) in 2014–2015

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The importance of phytoplankton communities for coastal water ecosystems can scarcely be overestimated because microalgae are their sources of bioenergy and the base of food web as well as an essential link connecting them with areas of the open ocean (Druzhkov, 1997; Tyukina, 2012). Interannual and seasonal changes constitute an integral part of temperate marine ecosystems and are most pronounced at the level of phytoplankton communities where succession of dominant species occurs (Lafanchuk, 2012). Chlorophyll “a” is a natural indicator allowing to assess the health of oceanic ecosystems. Since chlorophyll formation and destruction are related to overall plant metabolism, chlorophyll “a” concentrations can be used for identifying levels of phytoplankton growth and primary production (Sigareva, 1984; Mordasova, 2014). Detailed description of microalgal communities is especially needed in case of coastal waters which are designated as special protected areas or serve as spawning grounds and sites for aquaculture farms. Paris Bay, located off the northeastern coast of Russky Island, can be considered a water area of this kind, as it harbors the Center for the Study of Marine Mammals belonging to the Research and Education Center Primorsky Aquarium, NSCMB, Far Eastern Branch of Russian Academy of Sciences. The Center consists of several open net pens housing seven beluga whales.

The investigation of phytoplankton dynamics in the waters near the net pens will enable us to evaluate both the captive marine mammals’ impact on the aquatic environment and the ecosystem’s impact on the animals.

Material and methods

Quantitative samples of phytoplankton for this study were collected in 2014–2015 in Paris Bay near the Center for the Study of Marine Mammals of the Research and Education Center Primorsky Aquarium, NSCMB FEB RAS Paris Bay, a smaller subordinate bay in Peter the Great Bay, is located off the northeastern coast of Russky Island. This shallow bay has a depth of 14 m in the central part. The bay is 2.1 km long and 1.3 km wide; its area is 2.8 km². The waters of Paris Bay may be influenced by the adjacent waters of Amur and Ussury bays, connected through the Eastern Bosphorus Strait. In summer, water temperatures in Paris Bay reach their highest values in August, with surface waters warming up to 25.5°C. Significant amounts of rainfall are typical mainly for early and late summer. In the winter month of January, water temperatures of the area fall down to –1.8°C (Luchin et al., 2005). The waters of Paris Bay are regularly polluted with marine debris brought with waters transported from the Eastern Bosphorus Strait and Ussury Bay to the north-west. This water transfer

poses a high threat of pollution to such northern bays as Paris Bay. The phenomenon takes place mostly during periods of northwestern winds or calm sea (Kalinchuk et al., 2010).

Phytoplankton samples were taken with a 5-litre Niskin bottle from a depth of 0.5 m twice a month. One liter of sample water was fixed with Utermöhl’s solution until it turned pale-yellow. The samples were concentrated by reverse filtration, using a 2 µm polycarbonate filter membrane (Sukhanova, 1983), or by sedimentation (Utermöhl, 1958).

To determine chlorophyll “a” concentrations, one liter of sample water was filtered using a vacuum pump and Whatman glass microfiber filter GF/F. The air-dried filter was placed into 4 mL of 90% acetone. Chlorophyll “a” concentrations were determined with a Shimadzu UV-2600 double-beam spectrophotometer. Species identification was performed under an Olympus BX 41 light microscope. Algae were considered to be blooming at concentrations exceeding 10⁶ cells/L.

Results and discussion

Species composition. The analysis of the samples collected in Paris Bay from January 2014 to December 2015 showed the presence of 103 species and intraspecific taxa of microalgae from 4 classes.

The highest species diversity was recorded for diatoms – 49 species, of which, the genus *Chaetoceros* was the richest in species (8). Within the genus the most abundant species were *Chaetoceros debilis*, *C. decipiens*, *C. didymus* and *C. simplex*. Dinoflagellates were represented by 47 species dominated by species of the genus *Protoperidinium* (17). In addition, 6 species of *Ochromytha* and 1 species of *Euglena* algae were observed.

The interannual analysis of phytoplankton species composition revealed that 64.1% of the species and intraspecific taxa of microalgae were reported for both years of 2014 and 2015.

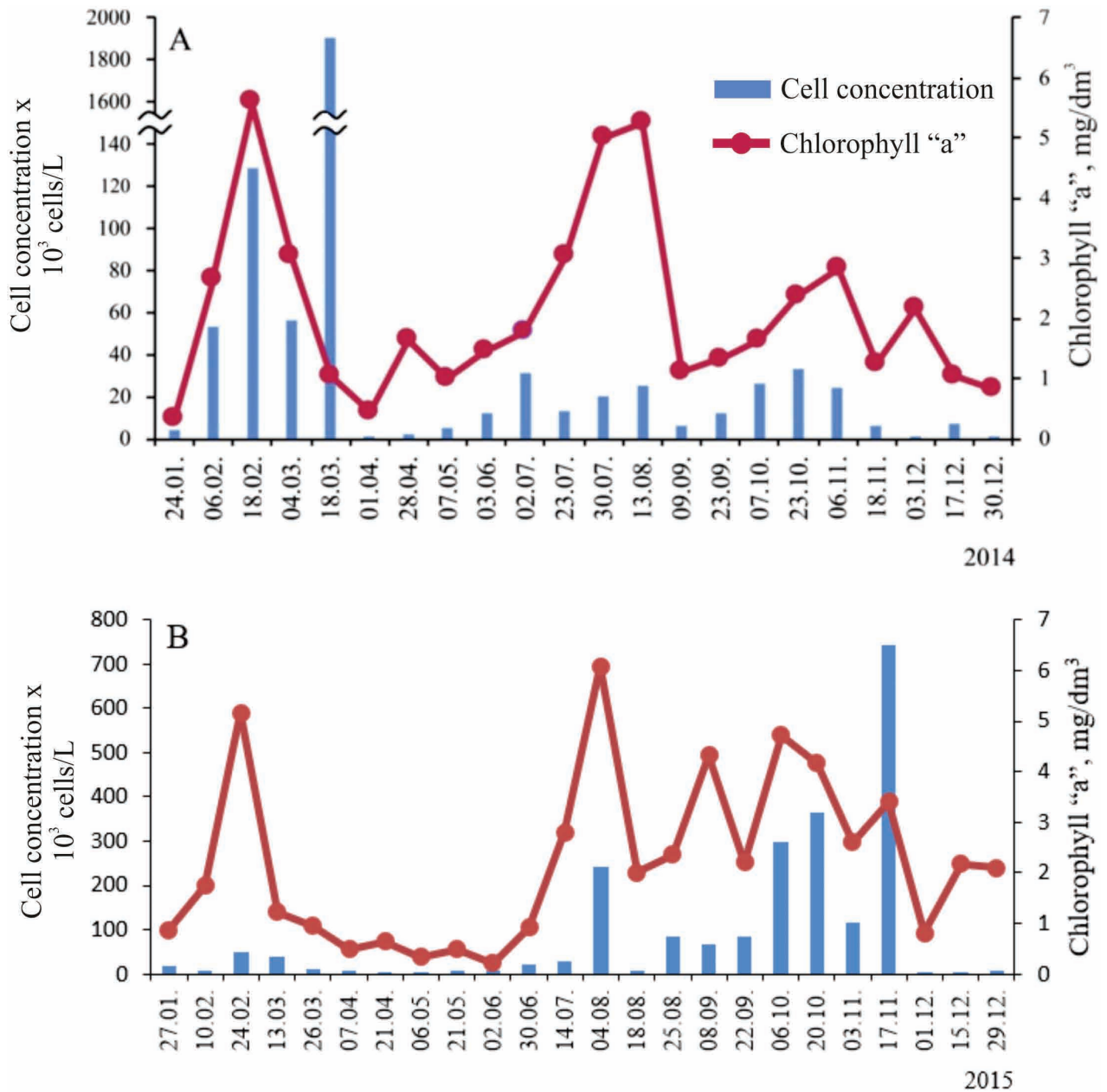
Having compared the data obtained and literature data, we found out that phytoplankton species composition of Paris Bay was identical to that of other areas in Peter the Great Bay (Konovalova, 1972; Morozova et al., 2002; Morozova, Orlova, 2005; Orlova et al., 2009).

Dynamics of phytoplankton concentrations. During the study period the phytoplankton concentrations increased from 1.3x10³ cells/L to 1.9x10⁶ cells/L, reaching their peak in March 2014.

During the first study year (2014) two peaks in microalgal density were observed – one in winter and the other in spring (see Figure). The most significant peak of phytoplankton abundance occurred on 18 March and was caused by mass growth of the diatom *Thalassiosira nordenskiöldii* which accounted for up to 99.6% of the total phytoplankton abundance. During the bloom of *T. nordenskiöldii*, diatoms *Melosira moniliformis* and *Odontella aurita* were also present in the phytoplankton community of the study area. The next samples taken on 1 April did not contain any cells of *T. nordenskiöldii*. The winter peak (128.6x10³ cells/L) induced by proliferation of the diatom *T. nordenskiöldii* was far lower than the spring one. Along with *T. nordenskiöldii*, small concentrations of the diatom *Pleurosigma formosum* were recorded.

During the second study year (2015) two peaks of phytoplankton abundance were observed – one in summer and the other in autumn (see Figure). In summer the phytoplankton density reached a maximum of 243.8x10³ cells/L. The peak concentrations resulted from mass growth of *P. triestinum*. The autumn peak, the largest in 2015, occurred in November and was induced by proliferation of *Skeletonema* species whose abundance was 744.1x10³ cells/L.

The analysis of the obtained data showed that dynamics of microalgal density changed within the study period.



Dynamics of microalgal (N, x10³ cells/L) and chlorophyll "a" concentrations in Paris Bay in 2014 (A) and 2015 (B).

The winter-spring period of the second study year was characterized by a reduced duration of ice-cover on the water area. The absence of ice and high illuminance level were probably the factors responsible for low phytoplankton growth rates.

According to Konovalova (1979) and Stonik and Orlova (1998), in water areas not exposed to anthropogenic pollution, autumn peaks of phytoplankton abundance are more common than those occurring in summer. In 2015 in Paris Bay the autumn peak concentrations were higher than the summer ones. In general, the phytoplankton density (except for March 2014) did not exceed 10⁶ cells/L; algal bloom was reported once within the study period. In view of phytoplankton parameters, the investigated part of Paris Bay can be regarded as an area with low human impact.

Dynamics of chlorophyll “a” concentrations. The analysis of the data obtained over the entire period of study in Paris Bay demonstrates that chlorophyll “a” concentrations in the upper water layer varied from 0.21 mg/dm³ to 6.08 mg/dm³. The highest pigment concentrations were observed in August 2015.

During the first study year two peaks in chlorophyll “a” concentrations were reported – one in winter and the other in summer (see Figure). The winter peak in chlorophyll “a” concentrations (5.59 mg/dm³) was reported in February; it resulted from/was induced by mass proliferation of *T. nordenskiöldii* (125.8x10³ cells/L) – the species typical of winter phytoplankton communities. The summer peak in chlorophyll “a” concentrations was recorded in August (5.26 mg/dm³). During that period the phytoplankton assemblages were dominated by *Skeletonema* species.

During the second study year two peaks in chlorophyll “a” concentrations were observed – one in winter and the other in summer, as in 2014 (see Figure). The February peak was slightly lower than that of the previous study year (5.15 mg/dm³). During that period the diatoms *T. nordenskiöldii* were dominant in the microalgal community. The 2015 summer peak in chlorophyll “a” concentrations was the highest one within the study period; like the previous summer peak, it took place in August, accompanied by mass growth of the dinophyta *P. triestinum* which accounted for 87.5% of the total phytoplankton density, with a concentration of 213.3x10³ cells/L.

The analysis of the data obtained over the study period showed a similarity in seasonal dynamics of chlorophyll “a” concentrations in 2014 and 2015 as well as their high values in winter and summer.

High rates of summer chlorophyll “a” concentrations at low abundance of chlorophyll-bearing phytoplankton in 2015 may have resulted from overestimation of chlorophyll “a” due to heavy showers just before the sampling date (2–3 August 2015). Some terrestrial organic substances, e.g. suspended sediments in runoff, can emit fluorescence at a wavelength of 640 nm (Dajum et al., 2010).

Conclusions

The analysis of the phytoplankton from Paris Bay revealed that the water area was not subjected to anthropogenic pollution. Algal bloom was reported only once over the entire study period. The highest concentrations of microalgae occurred in spring and autumn, while peak concentrations of chlorophyll “a” were observed in winter and summer. The research conducted in this study shows that maximum concentrations of chlorophyll “a” were induced by intense growth of diatom plankton, precipitation and coastal runoff.

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Dynamics of phytoplankton and chlorophyll “a” concentrations in Paris Bay (Rusky Island, Sea of Japan) in 2014–2015

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The article gives data on species composition and dynamics of phytoplankton and chlorophyll “a” concentrations in Paris Bay (Rusky Island, Sea of Japan). A total of 103 species and intraspecific taxa of microalgae from 4 classes have been identified. Annual dynamics of phytoplankton concentrations has been found to differ from that of chlorophyll “a” concentrations. During the study period, the highest phytoplankton density was recorded in spring and autumn, while peak concentrations of chlorophyll “a” were observed in winter and summer.

Lipidomic approach to the study of the zooxanthellae and polyp host contribution in total lipid composition of the soft coral *Sinularia siaesensis*

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One of the most important marine tropical ecosystems is coral reefs (Spalding, Grenfell, 1997). Colonies of reef-building corals (subclass Hexacorallia) have a solid exoskeleton built of calcium carbonate. Soft corals (subclass Octocorallia) are devoid of an exoskeleton and calcium carbonate inclusions (spiculae) spread over the colony volume. Alcyonacea is the most numerous order of octocorals.

Most of all tropical corals are symbiotic animals; their tissues contain intracellular microalgae or zooxanthellae (dinoflagellates of the *Symbiodinium* genus) (Davy, 2012). In the process of photosynthesis, zooxanthellae produce nutrients, providing for up to 90% energy required by the host species. Particular or complete loss of zooxanthellae by coral colonies at water temperature above 32°C is termed “coral bleaching” and leads to host organism death (Hoegh-Guldberg, 1999).

Alcyonaria are rich with lipids, which make up to 23% of dry weight of coral soft tissues (Yamashiro et al., 1999). Lipids play important functions in the coral organism (Treignier et al., 2008); neutral lipids serve as a major energy source, whereas polar lipids perform a structural function. Neutral lipids of alcyonaria, which include wax esters (WE), triacylglycerides (TG), monoalkyldiacylglycerides (MADAG), and sterol esters (SE), comprise over half of the total lipids in these animals (Imbs et al., 2010a). Total lipids of tropical alcyonaria contain 13–50% of polar lipids (Imbs et al., 2010a), including ethanolamine-, choline-, serine-, and inositolglycerophospholipids (PE, PC, PS, and PI, respectively), ceramide aminoethelphosphonate (CAEP), and lyso- PE, PS, and PC. In addition to 1,2-diacyl- glycerophospholipids, alcyonarians contain 1-*O*-alkyl-2-acyl- and 1-*O*-alkenyl-2-acyl-glycerophospholipids (plasmalogens) (Imbs et al., 2015a, b). MADAG is typical of cnidarians (Joseph et al., 1979), absent from zooxanthellae lipids (Imbs et al., 2010b), and hence, can be considered a marker of polyp tissues (host organism).

Several classes of glycolipids, i.e., sulfoquinovosyldiacylglycerol (SQDG), mono-, and digalactosyldiacylglycerol (MGDG and DGDG), typical of biomembranes of photosynthesis apparatus in plants, have been detected among zooxanthellae lipids (Awai et al., 2012). Galactolipids, as well as some polyunsaturated FA (PUFA), which comprise acyl groups of these lipids, are considered as lipid markers of zooxanthellae (Bishop, Kenrick, 1980).

Measurement of total lipids, major lipid classes, and FA composition is one of the main methodological approaches in study of the efficiency of reproductive strategy, the degree of damage and rate of restoration of partially bleached reefs, the trophic and symbiotic relationships of corals,

as well as transport of organic carbon between symbionts and the host organisms (Seemann et al., 2013; Mueller et al., 2014). Since first screening studies (Meyers, 1977), a large information about the total lipid and FA composition of corals has been accumulated (Imbs et al., 2010a; Imbs, 2016). We assume that studies on lipid molecular species (lipidome) of corals may develop new areas of biochemistry and the ecology of these organisms. Knowledge of alcyonarian lipidomes is limited to the description of the composition of molecular species of polar lipids of three tropical and a single cold-water species (Imbs et al., 2015a, b; Imbs, 2017). In the present work, we analyzed the total lipidome of the tropical soft coral *Sinularia siaesensis* by a combination of gas chromatography–mass spectrometry, HPLC, and tandem high-resolution mass spectrometry, to evaluate the contribution of zooxanthellae and the host in total lipid composition of the symbiotic coral.

Material and methods

Solvent of analytical grade were used for lipid extraction and TLC, and LC-MS grade – for HPLC. TLC was performed on ready-to-use Sorbfil PTSKh-AF-V plates, 10×10 cm (Russia). Lipid standards were obtained from Avanti Polar Lipids Inc. (USA).

Colonies of the soft coral *Sinularia siaesensis* Ofwegen, 2008 were collected by a diver at 4–6 m depths in the Nha Trang Bay (the South China Sea). Four different colonies were used for the lipid analysis; tables report average values of four measurements, deviations did not exceed 10% of the average value. Total lipids were obtained according to a modified Folch's protocol published recently (Sikorskaya, Imbs, 2018).

WE molecular species were analyzed according to Bosh and Long (2017). Briefly, WE were isolated by preparative TCL in hexane: benzene (70:30), analyzed by gas chromatography on a Shimadzu GC-2010 (Japan) equipment with flame ionization detector and an Equity-5 (Supelco, USA) quartz capillary column (0.25 mm×30 m, film thickness 0.25 µm). Structure of WE molecular species was determined by gas chromatography–mass spectrometry on a Shimadzu GCMS-QP5050A (Japan) equipment.

TG and MADAG molecular species were analyzed according to (Sikorskaya, Imbs, 2018). The sum of TG and MADAG were isolated by preparative TLC in benzene. The amounts of TG and MADAG in the total lipids were measured by densitometry of the images of analytical TLC plates. Molecular species of TG and MADAG were separated by supercritical fluid chromatography on a Nexera UC (Shimadzu, Japan) equipment on two sequential Shim-pack XR-ODSII (2.0 mm×150 mm) columns (Japan). To determine the amounts of TG and MADAG molecular species, a light scattering ELSD LT II (Shimadzu, Japan) detector was used. The structures of TG and MADAG molecular species were determined with a triple quadrupole mass spectrometer LCMS-8060 (Shimadzu, Japan). The analysis was performed under atmospheric pressure chemical ionization (APCI) at positive ion mode.

The polar lipid and glycolipid molecular species were analyzed as described earlier (Sikorskaya, Imbs, 2018). The amounts of phosphorus-contained total lipids and lipid classes were determined with a UV-1800 (Shimadzu, Japan) spectrophotometer based on the amount of inorganic phosphorus. The total lipids were separated by TLC in chloroform: methanol: 28% NH₄OH: benzene (65:30:5:10) and the amount of glycolipids was determined followed by densitometry of TLC plates with calibration using an external glycolipid standard. To analyze the content and structure of the molecular species of the glycolipids and phosphorus-containing lipids, the total lipids were separated on a Shim-Pack diol column (4.6 mm×50 mm, particle size 5 µm) (Shimadzu, Japan) using a Nexera-e

chromatography system (Shimadzu, Japan). To detect lipids, a high-resolution tandem mass spectrometer LCMS-IT-TOF (Shimadzu, Japan) was used. Analysis was performed under electro-spray ionization (ESI) mode with simultaneous registration of signals of positive and negative ions.

Results and discussion

Total lipid extract of *Sinularia siaesensis* contained WE (18.25%), TG (5.83%), MADAG (7.79%), PE (2.14%), PC (2.53%), PS (1.50%), PI (0.32%), CAEP (0.71%), MGDG (0.29%), DGDG (0.18%), and SQDG (0.82%). In the total lipids, the major nonpolar molecular species were comprised of 14.07% of WE (16:0/16:0, 16:0/18:0 and 18:0/16:0), 3.51% of TG (16:2/16:0/16:0 and 16:0/16:0/16:0), and 3.87% of MADAG (18:0e/16:0/16:0, 16:0e/16:0/18:0 and 16:0e/16:0/16:0). The major polar molecular species were comprised of 1.20% of 18:0e/24:5 PS, 1.06% of 18:0e lyso-PC, 0.91% of 18:1e/20:4 PE, 0.51% of 18:0e/20:4 PC, 0.43% of 18:2b/16:0 CAEP, 0.41% of 14:0/16:0 SQDG, and 0.20% of 18:0/24:5 PI.

Saturated 16:0/16:0 and 16:0/18:0 were indicated as the main components of WE in hydrocorals of the genus *Millepora* (Al Lihaihi et al., 2002). In *S. siaesensis*, saturated molecular species dominated WE, whereas unsaturated molecular species accounted for less than 6.8% of total WE. A similar distribution has been earlier found in two other species of symbiotic alcyonaria (Bosh, Long, 2017). In contrast, reef-building corals contained up to 47% of unsaturated WE molecular species (Bosh, Long, 2017). One can suppose that in alcyonaria, similar to solid corals, this main class of reservoir lipids is synthesized in the host organism (Patton et al., 1977; Chen et al., 2017), while domination of saturated molecular species in WE is a species-specific feature of tropical alcyonaria. WE of symbiotic coral species contain no FA markers of zooxanthellae. We assume that zooxanthellae do not synthesize WE themselves but may increase the content of saturated WE molecular species through transfer of saturated FA to the host organism (Patton et al., 1977).

The distribution of PUFA among the molecular species of TG and MADAG may indicate the origin of these nonpolar lipids in coral symbiotic association. The method of FA markers has been often used to characterize lipids of symbionts and the host, as well as to trace FA transfer between algal symbionts and animal host (Imbs et al., 2014). Several PUFA, such as 20:4, 22:5, and 22:6, are typical for animal tissues, and the presence of molecular species of TG and MADAG containing these PUFA residues is logical for cnidarians. Octocorals synthesize rare tetracosapolyenic acids (TPA, 24:5n-6 and 24:6n-3) (Vysotskii, Svetashev, 1991; Imbs et al., 2010a), and therefore, 18:0e/24:5/16:0 MADAG is without doubt a marker of the host organism. PUFA markers of zooxanthellae include 16:4, 18:3, and 18:4 (Treignier et al., 2008; Imbs et al., 2010b). Zooxanthellae synthesize no ether lipids, therefore detection of MADAG molecular species with residues of zooxanthellae markers (18:0e/18:3/16:0, 18:0e/18:4/16:0, and 16:0e/18:3/16:0) should be considered as a reliable evidence of PUFA transfer from symbionts to the host.

A comparison of the polar lipidomes of *S. siaesensis* and other tropical alcyonaria confirms that the majority of PE, PC, and PS molecular species of these animals is in alkylacyl form, while diacyl form is typical of PI molecular species. The main glycerophospholipids of zooxanthellae is PC in diacyl form (Awai et al., 2012). Hence, the most of glycerophospholipid molecular species of *S. siaesensis* can be attributed to the host lipids. In alcyonarians, TPA residues, chemotaxonomic markers of all octocorals (Vysotskii, Svetashev, 1991; Imbs et al., 2010a), concentrated in molecular species of PS and, partially, PI of tropical and cold-water alcyonarians (Imbs et al., 2015a, b).

Notably, 18:0e/24:5 PS containing the TPA residue is one of the key components of the soft coral *S. siaesensis*. The presence of molecular species with the TPA acyl groups in the soft coral lipidome is a consequence of the fundamental properties of lipid biosynthesis in octocorals.

In the lipidome of *S. siaesensis*, zooxanthellae are the origin of MGDG, DGDG, and SQDG, which are the main classes of lipids of thylakoid membranes in plants. SQDG 14:0/16:0 was found to be the key components of the *S. siaesensis* lipidome indicating the considerable input of zooxanthellae in the lipidome of symbiotic soft corals. The dominance of saturated waxes in reserve lipids, considerable amounts of MGDG, DGDG, and SQDG, as well as utilization of unique zooxanthellae FA in lipid synthesis of the host organism, indicate the importance of zooxanthellae in formation of the lipid profile of symbiotic soft corals.

Thus, the total lipidome of soft corals forms according to the species-specific features of lipid biosynthesis in this animal taxon, whereas symbiotic and associated organisms significantly modify coral lipid profiles.

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**Lipidomic approach to the study of the zooxanthellae and polyp host contribution
in total lipid composition of the soft coral *Sinularia siaesensis***

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The lipidomic analysis is a good alternative to the common lipid indicators, such as the content of total lipids and the composition of total fatty acids, to study the efficiency of reproductive strategy, the degree of damage and rate of restoration of partially bleached reefs, the trophic and symbiotic relationships of corals. Soft corals are an integral part of tropical and cold-water ecosystems of the World Ocean. The total lipidome of the tropical soft coral *Sinularia siaesensis* (Cnidaria: Anthozoa: Octocorallia: Alcionacea) containing intracellular symbiotic microalgae (zooxanthellae) was studied by chromatography–mass spectrometry. The structure and content of 144 molecular species of the main classes of acyl lipids of this alcyonaria were determined, including waxes (WE), triacylglycerides (TG), monoalkyldiacylglycerides (MADAG), ethanolamine-, choline-, serine-, and inositolglycerophospholipids (PE, PC, PS, and PI), ceramide aminoethylphosphonate (CAEP), sulfoquinovosyldiacylglyceride (SQDG), and mono- and digalactosyldiacylglycerides (MGDG and DGDG). Similar to other tropical alcyonarians, the dominance of saturated waxes in reserve lipids was observed in *S. siaesensis*. Detection of MADAG with residues of FA markers of zooxanthellae (18:0e/18:3/16:0, 18:0e/18:4/16:0, and 16:0e/18:3/16:0) confirms the transfer of PUFA from the symbionts to the host. Tetracosapolyenoic FA, the chemotaxonomic markers of octocorals, are concentrated in molecular species of PS and PI. Alkylacyl form dominated PE, PC, and PS molecules, diacyl form was characteristic for PI molecules. A significant part of MGDG, DGDG, and SQDG points to the importance of zooxanthellae in the formation of the lipid profile of symbiotic soft corals.

Generalisation of Bertalanffy–Gompertz model for multidimensional stochastic growth of organisms

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Mechanism of determined interaction between organism's characters is explained on the basis of analogy between an organism and biological community. This analogy has an old story and in due time has played an important role in formation of «organismic» concept of biocenosis (Clements, 1949).

Any biological community consists of the set of species populations connected with each other by matter-energy streams. The organism can be considered also as the set consisting of its various parts – bodies, morphological separateness, etc. These parts are connected to the uniform system by mutual internal environment formed by streams of liquids (blood, plasma, coelomic liquid in animals, xylem and floem juice in plants).

The substance and energy stream received by an organism from external environment always is limited – either by external conditions, or by the rate of it's processing by digestive organs or photosynthesis. Limitation of receipt rate of substances and energy in an organism lead to “competition” for these resources between growing organs. Thereof there should be interactions between them. Besides, there are also analogues of interactions of type “predator–victim” in an organism. For example, when a certain organ provides by its resources the growth of other organs.

This determined system of a developing organism exists in stochastic environment. Noise fluctuations have disturbing influence on a growth trajectory of each character included in this system. Moreover, these noise fluctuations for different characters can be correlated with each other, for example, because they are under the influence of the same stochastically fluctuating of environmental factor (Sukhanov, 1990).

The model is represented by the system of stochastic differential equations

$$dy_i/dt = \beta_i + n_i(t) - \sum_{j=1}^m \alpha_{ij} y_j, \quad (1)$$

where $i = 1, \dots, m$. This system represents the generalization of classical Bertalanffy's model (Mina, Klevezal, 1976) on a case of m quantitative characters co-operating with each other in the growth process of organism which lives in stochastic environment. Here t is the age of a cohort; $\alpha_{ij}, \beta_i = const$. The $n_i(t)$ is the white Gaussian noise in the sense of Ito. It describes stochastic influence of environment on the growth rate of i -th quantitative character indicated by y_i .

The system (1) generalises the model of Bertalanffy (Mina, Klevezal, 1976) to a complex from m quantitative characters which describe the age dynamics of a body size of an organism and its parts growing in stochastic environmental conditions.

Replacement $z_i = y_i - \bar{y}_i$ does the system (1) by homogeneous one. Here the vector $\bar{Y} = (\bar{y}_1, \dots, \bar{y}_m)^T$, where T is the operator of transposition, is decision of the system $\beta_i = \sum_{j=1}^m \alpha_{ij} \bar{y}_j$, $i = 1, \dots, m$. This vector describes the average definitive state of organism. Differently, \bar{y}_i represents the asymptotic mean of i -th character y_i for adult organism which stops its growth at $t \rightarrow \infty$.

Solution of model for a vector of characters $Z = (z_1, \dots, z_m)^T$ looks like m -dimensional normal distribution (Tikhonov, Mironov, 1977) with a vector of averages \bar{Z} and a matrix of covariations V , changing with the years t .

The vector of averages is defined by the equation $\bar{Z} = UEU^{-1}\bar{Z}_0$, where U is a matrix which columns are eigenvectors of matrix $A = \|\alpha_{ij}\|$ of coefficients of inter character interactions; \bar{Z}_0 is the vector of initial average values for characters Z at the age $t = 0$; E is a diagonal matrix with the elements equal to $\exp(-\lambda_i t)$. Here λ_i is the i -th eigenvalue of matrix A .

Matrix A is supposed by nonsingular and positively defined. For this purpose it is necessary, that in an organism's character set do not present any their linear combinations. So, it is impossible to use the sum of sizes of various characters, for example, when the length of a whole body is equal to length of a head plus length of the rest of a body.

The covariation matrix V of characters Z is defined by the equation $V = USU^T$, where S is the matrix with elements $S_{ij} = (g_{ij}/(\lambda_i + \lambda_j))(1 - \exp(-(\lambda_i + \lambda_j)t))$. Matrix $G = \|g_{ij}\|$ is equal to $G = U^{-1}B(U^{-1})^T$, where $B = \|b_{ij}\|$ is a symmetric matrix of diffusion coefficients which are looking like $b_{ij} = \rho_{ij}\sqrt{D_i D_j}$. Here ρ_{ij} is correlation coefficient between white noises $n_i(t)$ and $n_j(t)$; parameters D_i, D_j are the intensities (dispersions of increments) of these noises.

Return from z_i to variables $y_i = z_i + \bar{y}_i$, and then the transition in the space of characters $x_i = \exp(y_i)$ leads to the model of Gompertz described by m -dimensional lognormal distribution with a vector of averages and covariation matrix which change in the process of organism's ageing.

Developed by the author regular procedure of parameter Bertalanffy's model estimation generalising the method of Ford–Walford (Mina, Klevezal, 1976), can be used for multidimensional model. It is possible when characters do not co-operate with each other (that is, α_{ij} it is not equal to zero only for $i = j$) and when for any age class the condition of a constancy of an interval between two neighbour ages is satisfied: $t_{k+1} - t_k = \tau = \text{const}$. Then $M_{i,j,k+1} = p_{ij} + q_{ij}M_{i,j,k} + r_{ij}N_{i,j,k}$. Here k is the number of age class, $M_{i,j,k}$ is the second cross ordinary moment for (i, j) -th pair of characters, $N_{i,j,k}$ is the product of i -th and j -th averages. For the model of Bertalanffy these statistics are calculated to original characters, for model of Gompertz – to their logarithms. Calculation of the moments is realized for individuals of every age cohort. Unknown parameters p_{ij}, q_{ij}, r_{ij} are estimated by the least squares method for data points of regression line with the age index k .

Then parameters $\alpha_i, \alpha_j, \bar{z}_{0i}, \bar{z}_{0j}$ are calculated from symmetric matrices $H = \|h_{ij}\|$, $W = \|w_{ij}\|$, where $h_{ij} = -\tau / \log(r_{ij})$, $w_{ij} = p_{ij}(1 - r_{ij}/q_{ij}) / (1 - q_{ij})$ taking into account expressions $\alpha_i + \alpha_j = h_{ij}$, $\bar{z}_{0i} \bar{z}_{0j} = w_{ij}$. Diffusion coefficients are equal to $b_{ij} = -p_{ij}\tau / ((1 - q_{ij})\log(r_{ij}))$.

And, at last, we will result one more generalisation of multidimensional model of growth of organisms:

$$dx_i/dt = f_i(x_1, \dots, x_m) + n_i(t)g_i(x_1, \dots, x_m).$$

In comparison with the equations (1) this model basically can generate polymodal distributions, if functions $f_i(x_1, \dots, x_m)$ and $g_i(x_1, \dots, x_m)$ and sufficiently nonlinear. Therefore if we want to remain within the limits approximating Gaussian law it is necessary to state that intensities of stochastic noises $n_i(t)$ must be small enough values. Then the approximated relations for averages \bar{x}_i and noise

covariations v_{ij} , which can be deduced with the help of the integrated moments method (Tikhonov, Mironov, 1977), are described by the equations:

$$d\bar{x}_i/dt = f_i, \quad dv_{ij}/dt = \rho_{ij}g_i g_j \sqrt{b_i b_j} + \sum_{n=1}^m \left(\frac{\partial f_i}{\partial \bar{x}_n} v_{nj} + \frac{\partial f_n}{\partial \bar{x}_j} v_{ni} \right), \quad (2)$$

where $f_i = f_i(\bar{x}_1, \dots, \bar{x}_m)$, $g_i = g_i(\bar{x}_1, \dots, \bar{x}_m)$.

Generalised version of the model of multidimensional stochastic growth of organisms, presented here, can show a rich gallery of various dynamics types of age characters variability. Correlation ellipses can move along curvilinear trajectories in character's space. These trajectories even can look like spirals, threaded to some multidimensional point representing definitive state of organism. These spirals can represent stable self-supported limiting cycles.

At the same time, in the checking of a special case (1) of given models with the help of concrete materials (the bivalve mollusk *Mizuhopecten yessoensis* and the marine fish, Sakhalin population of pollack *Theragra chalcogramma*) it was found that the cross coefficients α_{ij} , $i \neq j$, describing determined interactions between various characters have appeared statistically uncertain differed from zero. Therefore presented model which was originally planned for a role of the general working model, it is necessary to consider as constructed "to allow for growth" for description, including difficult and rare cases which can meet in the future. Most likely, simpler variant (1) can apply for a role of basic multidimensional model, sufficient for the description of typical processes of stochastic growth of organisms.

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Generalisation of Bertalanffy–Gompertz model for multidimensional stochastic growth of organisms

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The mathematical model describing growth of a complex of characters in organism, existing in stochastic environment is discussed. It is based on a concept of the noise variability describing influence of fast unpredictable fluctuations influencing growth of organism. The model describes age dynamics of the multidimensional normal law. It is defined by the vector of averages and covariation matrix of characters.

The taxonomic and geographical diversity of benthic flora of Minonosok Bay, Possjet Bay (Peter the Great Bay, Sea of Japan)

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Reduction of species diversity of marine biota, including flora, is a natural and inevitable evolutionary phenomenon. As known, the rate of speciation currently lags behind the anthropogenic activity (Kafanov, Volvenko, 2001). Due to the degradation of the environment, pollution, and industrial development, the structure of benthic communities and coastal ecosystems is subject to disturbance (Levenets, Lebedev, 2015; Butov, 2016). Therefore, conservation of each species is crucially important for maintaining biodiversity. Vanishing of any of them can lead to unexpected consequences for the biota of the Ocean.

The goal of this study is to analyze the dynamics of the taxonomic and zonal-geographical composition of the benthic flora in Minonosok Bay, Possjet Bay, for the past 25 years. The material was collected by researchers of the A.V. Zhirmunsky National Scientific Center of Marine Biology and the Far Eastern Marine Reserve of the Far Eastern Branch, Russian Academy of Sciences, in the 1990s and 2010s. Sampling was conducted along five basic hydrobiological transects in different parts of Minonosok Bay. Macroalgae were collected directly from bottom sediments and from live mussels and scallops.

As a result of systematic processing, the taxonomic composition of the benthic macroflora of Minonosok Bay was determined. During the study years, we recorded a total of 120 species of algae (23 green, 30 brown, and 67 red), belonging to 3 phyla, 27 orders, 52 families, and 86 genera. In the 1990s, 104 species of algae and 4 species of sea grasses were identified. The species richness and taxonomic diversity were high. Red algae dominated in terms of number of taxa. The phylum Rhodophyta was represented by 4 classes, 16 orders, 30 families, 44 genera, and 58 species. Brown algae (class Phaeophyceae, phylum Ochrophyta) ranked second: 6 orders, 11 families, 20 genera, and 25 species. Green algae (phylum Chlorophyta) were represented by 1 class, 4 orders, 6 families, 11 genera, and 21 species.

In the 2010s, only 54 species of algae were recorded from samples. The species richness and taxonomic diversity of the flora declined. The phylum Rhodophyta was represented by 3 classes, 10 orders, 14 families, 25 genera, and 29 species. The following taxa disappeared: class Bangiophyceae, 6 orders (Acrochaetiales, Gigartinales, Gracilariales, Halymeniales, Hildenbrandiales, Bangiales); 17 families (Table 1), 24 genera, and 29 species.

TABLE 1
Dynamics of taxonomic richness of the phylum Rhodophyta at family level

Family	1990s	2010s	Family	1990s	2010s
Acrochaetiaceae	1	0	Hildenbrandiaceae	1	0
Bangiaceae	2	0	Hydrolithaceae	1	0
<i>Callithamniaceae</i>	0	3	Kallymeniaceae	2	0
Ceramiaceae	4	8	Lithophyllaceae	1	0
Champiaceae	1	0	Lithothamniaceae	1	1
Colaonemataceae	1	1	Lomentariaceae	1	0
Corallinaceae	4	3	Mesophyllaceae	1	1
Dasyaceae	2	2	Palmariaceae	1	2
Delesseriaceae	3	0	Peyssonneliaceae	1	1
Endocladaceae	1	0	Phyllophoraceae	1	0
Erythrotrichiaceae	1	1	Rhodomelaceae	12	3
Gelidiaceae	2	1	Rhodophysemataceae	1	0
Gigartinaceae	4	0	Rhodymeniaceae	2	1
Gracilariaceae	2	0	Stylonemataceae	1	1
Halymeniaceae	1	0	Tichocarpaceae	1	0
Hapalidiaceae	1	0			

Note. In tables 1–3, the families that have disappeared from the benthic flora of Minonosok Bay are highlighted in bold; the newly recorded families, in italics.

The family Rhodomelaceae reduced from 12 to 3 species (*Neorhodomela aculeata*, *N. munita*, *Laurencia nipponica*, *L. saitoi*, *Symphyocladia latiuscula*, *Chondria dasyphylla*, *Symphyocladia marchantioides*, etc. disappeared). The compositions of 7 families did not change. New species appeared in the families Ceramiaceae (*Ceramium cimbricum*, *Antithamnionella longicellulata*, *Campylaephora crassa*, and *Pterothamnion yezoense*) and Palmariaceae (*Devaleraea microspora*). The new family Callithamniaceae with 3 species (*Ptilota filicina*, *Tokidaea corticata*, and *T. hirta*) was recorded.

The class Phaeophyceae of the phylum Ochrophyta was represented by 6 orders, 10 families, 12 genera, and 16 species. One order, 3 families (Table 2), 8 genera, and 9 species disappeared. The families Acinetosporaceae (*Feldmannia irregularis*), Dictyotaceae (*Dictyota dichotoma*) and Pseudochordaceae (*Pseudochorda nagaii*) were not found by the end of the study period. The species lists of some large families reduced: Chordariaceae (*Coilodesme japonica*, *Chordaria flagelliformis*, *Leptonematella fasciculata*, and *Sphaerotruchia divaricata* disappeared) and Sargassaceae (*Coccolophora langsdorfii* and *Stephanocystis crassipes* disappeared). In the family Scytosiphonaceae, three species (*Colpomenia peregrina*, *C. sinuosa*, and *Petalonia fascia*) disappeared, but a new species (*Scytosiphon lomentaria*) appeared. The number of species in 4 families – Chordaceae, Laminariaceae, Ralfsiaceae, and Sphacelariaceae – did not change. The family Agaraceae was supplemented by a new species, *Agarum clathratum*. Two new families, Desmarestiaceae (with the species *Desmarestia viridis*) and Ectocarpaceae (with the species *Ectocarpus siliculosus*), appeared in the benthic flora.

TABLE 2
Dynamics of taxonomic richness of the class Phaeophyceae at family level

Family	1990s	2010s	Family	1990s	2010s
Acinetosporaceae	1	0	Laminariaceae	2	2
Agaraceae	1	2	Pseudochordaceae	1	0
Chordaceae	1	1	Ralfsiaceae	3	3
Chordariaceae	6	2	Sargassaceae	5	2
<i>Desmarestiaceae</i>	0	1	Scytosiphonaceae	3	1
Dictyotaceae	1	0	Sphacelariaceae	1	1
<i>Ectocarpaceae</i>	0	1			

The phylum Chlorophyta was represented by 1 class, 4 orders, 6 families (Table 3), 9 genera, and 9 species. The families Bryopsidaceae (*Bryopsis plumosa* and *B. hypnoides*) and Derbesiaceae (*Derbesia marina*) disappeared. The number of species in the Cladophoraceae decreased from 8 to 3 (*Chaetomorpha melagonium*, *Ch. moniligera*, *Rhizoclonium tortuosum*, *Cladophora opaca*, and *C. speciosa* disappeared). In the composition of the flora, species from the following 3 families were not found: Codiaceae (*Codium yessoense*); Ulotrichaceae (*Urospora wormskioldii*, *Acrosiphonia duriuscula*, and *A. saxatilis*); and Ulvaceae (*Ulva clathrata*, and *U. prolifera*). Two new families appeared: Monostromataceae (with the species *Monostroma grevillei*) and Ulvellaceae (with the species *Ulvella viridis*).

TABLE 3
Dynamics of taxonomic richness of the phylum Chlorophyta at family level

Family	1990s	2010s	Family	1990s	2010s
Bryopsidaceae	2	0	<i>Monostromataceae</i>	0	1
Cladophoraceae	8	3	Ulotrichaceae	4	1
Codiaceae	2	1	Ulvaceae	4	2
Derbesiaceae	1	0	<i>Ulvellaceae</i>	0	1

Thus, the changes in the taxonomic composition of the flora became most pronounced by the end of the observation period and were manifested in the form of impoverishment at the levels of species and super-species. The reduction in the taxonomic diversity of the Rhodophyta families and genera has become particularly noticeable.

To analyze the latitudinal distribution of the taxonomic richness of the benthic flora, its zonal-geographical composition was determined taking into account the pattern of phyto- and zoogeographic zoning (Perestenko, 1994; Kudryashov, Kafanov, 2000; Levenets, 2011). In the 1990s, it was represented by 7 species complexes (Fig. 1A).

As can be seen, the flora is characterized by a significant representation of relatively warm-water species (16). The contribution of the relatively cold-water wide boreal-arctic and wide boreal species is insignificant (a total of total of 4 Rhodophyta species). The low-boreal complexes are formed by boreal-(sub)tropical (total 25, including 5 green, 8 brown, and 12 red) and, to a lesser degree, by boreal species (5 species, of which 4 are red algae).

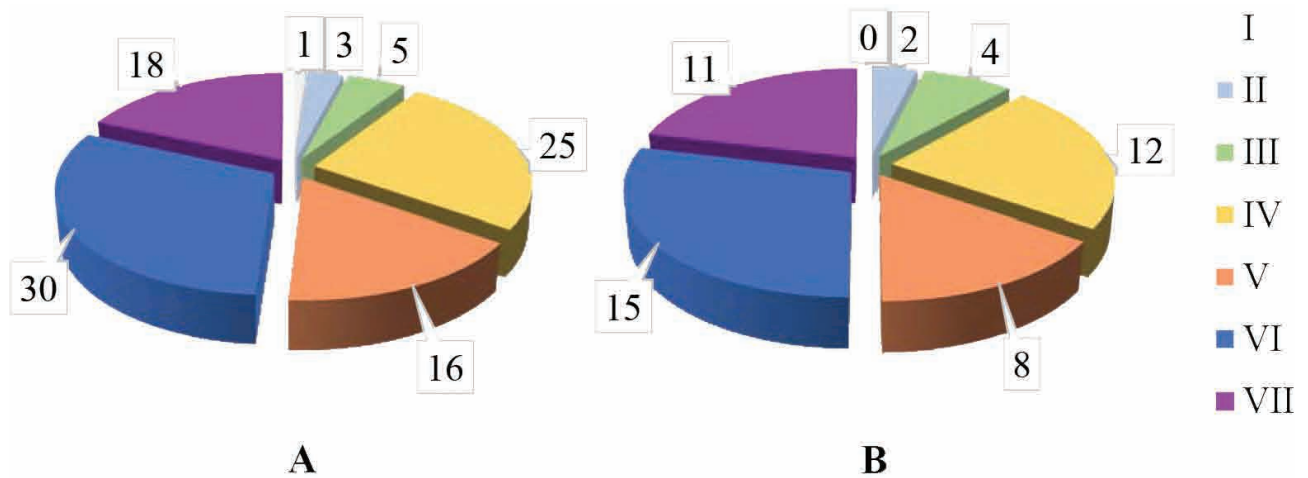


Fig. 1. Zonal-geographical composition of the benthic flora in the 1990s (A) and 2010s (B): (I) wide boreal-arctic species; (II) wide boreal; (III) low boreal; (IV) low boreal-subtropical and low boreal-tropical; (V) wide boreal-subtropical and wide boreal-tropical; (VI) widespread; (VII) multizonal. Arabic numerals show the number of species.

The complex of widespread species was represented by boreal-arctic-(sub)tropical, boreal-(sub)tropical-notal (14 Rhodophyta species), and boreal-arctic-notal species (total 30). The multizonal complex was formed by 18 species (of which 10 are from the Chlorophyta) which are distributed ubiquitously or almost ubiquitously in the World Ocean.

In the 2010s, the number of species complexes decreased from 7 to 6 (Fig. 1B). The boreal-arctic-notal species *Sphaerotrichia divaricata* (Phaeophyceae, Ochrophyta) was not found in the group of widespread species. The decrease in species richness affected all the zonal-geographical complexes, but it was especially noticeable in the low boreal-(sub)tropical, wide boreal-(sub)tropical, widespread, and multizonal ones.

The major part of the flora is formed by red algae (Fig. 2). In this group, the changes in zonal-geographical composition proved to be most significant. The number of species in each complex decreased 2-fold. The boreal-arctic species *Euthora cristata* and the wide boreal species *Hymenena ruthenica* and *Mazzaella parksii* disappeared; a new species, *Devaleraea microspora*, was recorded. Among low boreal species, *Porphyra inaequicrassa*, *Neorhodomela munita*, and *Nienburgella angusta* disappeared. New species also appeared in this complex: *Tokidaea hirta* and *Antithamnionella longicellulata*.

In the low boreal-(sub)tropical complex, the following species disappeared: *Gelidium elegans*, *Chondrus armatus*, *Ch. pinnulatus*, *Mazzaella japonica*, *Laurencia nipponica*, *L. saitoi*, *Symphycladia latiuscula*, *Botryocladia wrightii*, and *Tichocarpus crinitus*. Several species were newly recorded: *Tokidaea corticata*, *Campylaephora crassa*, and *Pterothamnion yezoense*. Among wide boreal-(sub)tropical species, the following species were not found: *Porphyra variegata*, *Gloiopeltis furcata*, *Neopolyporolithon reclinatum*, *Callophyllis rhynchocarpa*, and *Neorhodomela aculeata*. The species *Ptilota filicina* appeared. In the widespread group, the following species disappeared: *Acrochaetium humile*, *Champia parvula*, *Gracilaria vermiculophylla*, *Grateloupia divaricata*, *Lomentaria hakodatensis*, *Clathromorphum compactum*, *Ahnfeltiopsis flabelliformis*, and *Chondria dasyphylla*. One species, *Ceramium cimbricum*, appeared. Among multizonal species, *Corallina officinalis*, *Hildenbrandia rubra*, and *Pneophyllum fragile* disappeared.

The decline in the number of low boreal-(sub)tropical species was observed also among brown algae. Species *Coilodesme japonica*, *Pseudochorda nagaii*, *Coccophora langsdorfii*, and *Stephanocystis crassipes* were not recorded in 2010s (Fig. 3). The number of species of the low boreal complex did not change. In the wide boreal-(sub)tropical complex, *Analipus japonicus* disappeared. Many species of widespread group were not found: *Chordaria flagelliformis*, *Leptonematella fasciculata*, *Sphaerotrichia divaricata*, *Colpomenia peregrina*, *C. sinuosa*, and *Dictyota dichotoma*. Among multizonal species, *Feldmannia irregularis* and *Petalonia fascia* disappeared, while *Scytosiphon lomentaria* and *Ectocarpus siliculosus* appeared.

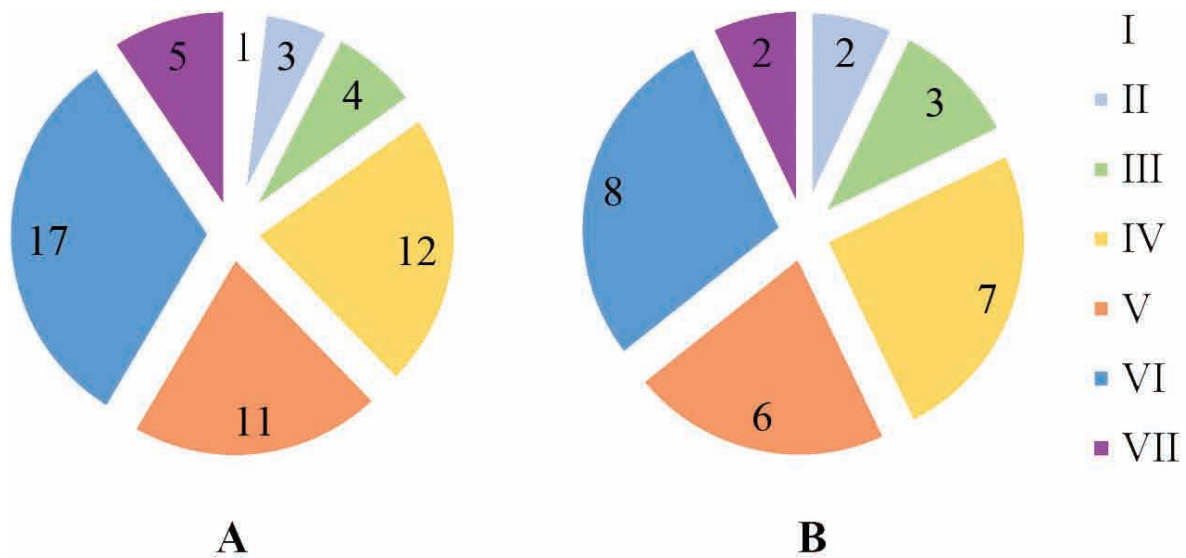


Fig. 2. Dynamics of the zonal-geographical composition of Rhodophyta during the 1990s (A) and 2010s (B). For explanation of Roman and Arabic numerals, see Fig. 1.

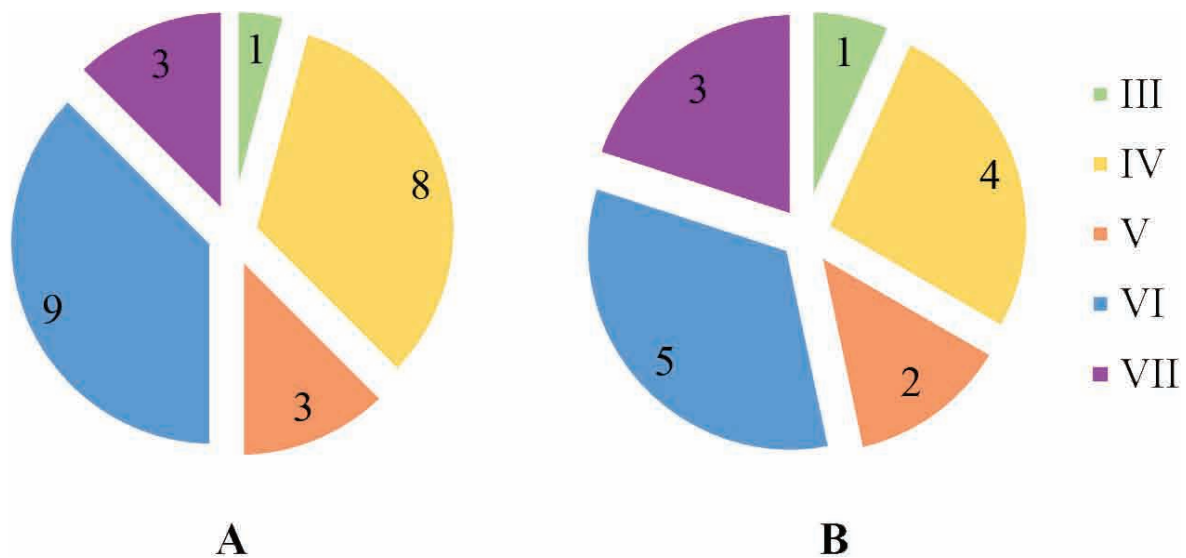


Fig. 3. Dynamics of the zonal-geographical composition of the class Phaeophyceae of the phylum Ochrophyta in the benthic flora during the 1990s (A) and 2010s (B). For explanation of Roman and Arabic numerals, see Fig. 1.

Among green algae in 2010s, the wide boreal-(sub)tropical species *Acrosiphonia duriuscula* and *A. saxatilis* disappeared (Fig. 4). In the low boreal-(sub)tropical complex, the following species disappeared: *Chaetomorpha moniligera*, *Cladophora opaca*, *C. speciosa*, and *Codium yezoense*.

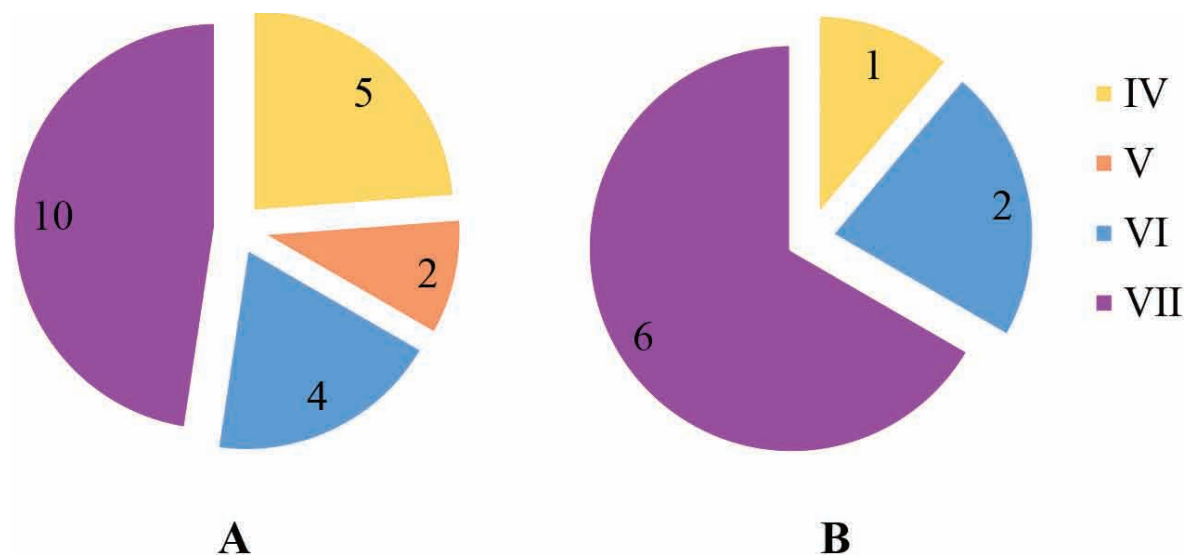


Fig. 4. Dynamics of the zonal-geographical composition of the Chlorophyta in the benthic flora during the 1990s (A) and 2010s (B). For explanation of Roman and Arabic numerals, see Fig. 1.

The widespread species *Bryopsis hypnoides* and *Urospora wormskioldii* were not found also. Six multizonal species disappeared: *Bryopsis plumosa*, *Derbesia marina*, *Chaetomorpha melagonium*, *Rhizoclonium tortuosum*, *Ulva clathrata*, and *U. prolifera*. Two new species, *Monostroma grevillei* and *Ulvella viridis*, appeared in the benthic flora.

Thus, the taxonomic and geographical composition of the benthic flora in Minonosok Bay for the past 25 years has been analyzed. A reduction in species composition and a decrease in the taxonomic diversity of the macroflora were revealed by the end of the study period. Despite the significant fluctuations in the number of species, the relative constancy of the biogeographic composition of the flora was observed throughout the study period.

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**The taxonomic and geographical diversity of benthic flora of Minonosok Bay, Possjet Bay
(Peter the Great Bay, Sea of Japan)**

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The taxonomic and geographical composition of the benthic macroflora in Minonosok Bay, Possjet Bay, Peter the Great Bay, for the past 25 years has been analyzed. Sampling was conducted along five basic hydrobiological transects in different parts of Minonosok Bay. Macroalgae were collected directly from bottom sediments and from live mussels and scallops. During the study years, we recorded a total of 120 species of algae (23 green, 30 brown, and 67 red), belonging to 3 phyla, 27 orders, 52 families, and 86 genera. In the 1990s, 104 species of algae and 4 species of sea grasses were identified. The species richness and taxonomic diversity were high. Red algae dominated in terms of number of taxa. In the 2010s, only 54 species of algae from three phyla were recorded from samples. The species richness and taxonomic diversity in all macrophytes groups declined. The changes in the taxonomic composition of the benthic flora influenced by long-term Japanese Scallop's mariculture were manifested in the form of impoverishment at the levels of species and super-species. The reduction in the taxonomic diversity of the Rhodophyta families and genera has become particularly noticeable in 1990th. Despite the significant fluctuations in the number of species, the relative constancy of the biogeographic composition of the flora of Minonosok Bay was observed throughout the study period.