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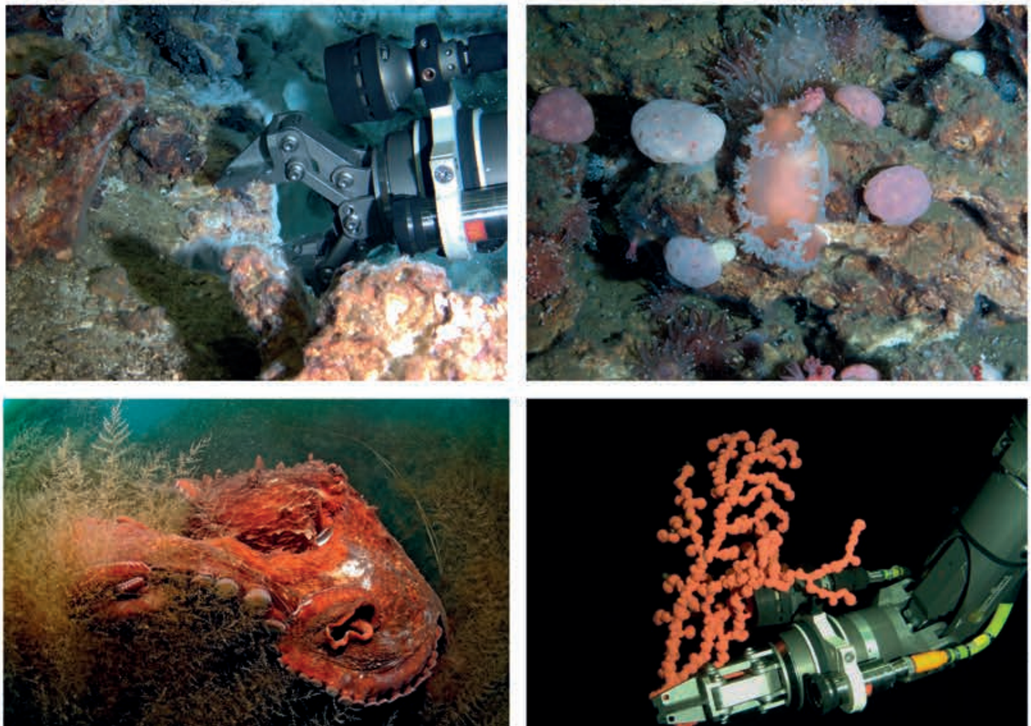
Marine Biology and Biodiversity Science in the 21st Century

Abstracts of the Russia-China Bilateral Workshop

September 23–24, 2025, Vladivostok, Russia



Vladivostok
2025

Ministry of Science and Higher Education
Far Eastern Branch of the Russian Academy of Sciences
A.V. ZHIRMUNSKY NATIONAL SCIENTIFIC CENTER OF MARINE BIOLOGY

Chinese Academy of Sciences
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The abstract book of the Russia-China Bilateral Workshop *Marine Biology and Biodiversity Science in the 21st Century,* September 23–24, 2025, Vladivostok, Russia contains materials presented during the workshop and dealing with various aspects of marine biodiversity and related issues of marine biology and ecology, environment, ocean health, aquaculture, etc. The book contains 27 abstracts of presentations by Russian and Chinese scientists. The workshop is the 7th meeting jointly organized by the NSCMB FEB RAS (Russia) and the Institute of Oceanology CAS (China) (six previous meetings were held in Qingdao in 2007, 2010, 2017, 2023 and in Vladivostok in 2012, 2019).

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Морская биология и наука о биоразнообразии в 21 веке : тезисы докладов российско-китайского билатерального совещания, 23–24 сентября 2025 г., Владивосток, Россия / составитель К.А. Лутаенко. – Владивосток : ННЦМБ ДВО РАН, 2025. – 71 с. – Текст. Изображение: непосредственные.
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Сборник тезисов докладов Российско-Китайского билатерального совещания «*Морская биология и наука о биоразнообразии в 21 веке*», 23–24 сентября 2025 г., Владивосток, содержат тезисы докладов, доложенных во время проведения совещания и посвященные различным аспектам изучения морского биоразнообразия, преимущественно на примере северо-западной части Тихого океана, и связанным с этим вопросам морской биологии и экологии, окружающей среды, здоровья океана, аквакультуры и т.п. Сборник тезисов включает 27 тезисов докладов российских и китайских участников. Совещание является 7-м мероприятием, организованным совместно ННЦМБ ДВО РАН (Россия) и Институтом океанологии КАН (Китай) (четыре предшествующих совещания прошли в г. Циндао в 2007, 2010, 2017, 2023 гг. и в г. Владивостоке в 2012, 2019 г.).

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Russia - China Bilateral Workshop
MARINE BIOLOGY AND BIODIVERSITY SCIENCE IN THE 21ST CENTURY
September 23–24, 2025,
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ПРИМОРСКИЙ ОКЕАНАРИУМ
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STUDYING PHYSIOLOGY OF MARINE MAMMALS

Andrey V. Boroda, Daria N. Kamenskaya, Alina V. Komkova, Veronika A. Yachmen, Maia N. Dyagileva, Daniil D. Malyshev, Elizaveta A. Selivanova, Daria A. Golovko, Polina V. Esipova
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Marine mammals are a unique group of animals that have partially or completely switched to an aquatic lifestyle. There are about 130 different species of marine mammals worldwide, of which 46 species live in Russian waters, most of which are protected by international and Russian laws. The degree and types of adaptation of their organisms to life in water vary among different orders. The main focus of our group's research is the physiological peculiarities of marine mammals caused by living in an aquatic environment. We have collected "live" biological material of various tissues from more than 30 individuals belonging to 14 species of marine mammals. Viable cell cultures were successfully isolated from most of the samples for genetic, cellular biological, ecotoxicological studies to reveal interspecies functional characteristics of cells. Analysis of hematological and biochemical values of the blood of marine mammals was the basis for establishing their dependence on species, sex, age, season and habitat conditions, as well as predicting diseases progress. A comprehensive study was conducted on the blood composition and morphological characteristics of the Commander Islands harbor seal subspecies *Phoca vitulina*, spotted seal *Phoca largha*, beluga whale *Delphinapterus leucas*, Baikal seal *Pusa sibirica*, Pacific white-sided dolphin *Sagmatias obliquidens*, and bottlenose dolphin *Tursiops truncatus gilli*. The diets of spotted seals *Phoca largha* were studied under conditions close to natural, which allowed us to assess the degree of seasonal changes, annual dynamics of body weight and changes in biological rhythms on the food motivation of individuals during a 7-year period of maintenance and to

supplement the available information on the biology and ecology of the species. Research on the diets of beluga whales kept in both stationary conditions in oceanarium and in open sea enclosures has commenced recently. The initial steps of searching for interspecies differences in the sensitivity of marine mammal and human cells to anthropogenic toxicants (heavy metals, petroleum products and detergents), as well as, decoding the complete genome of the Commander beaked whale *Mesoplodon stejnegeri*, sea otter *Enhydra lutris*, beluga whale *Delphinapterus leucas*, walrus *Odobenus rosmarus* and spotted seal have been taken in collaboration with “Biotechnological Campus” LLC.

The research has been completely funded by the state budget project for youth laboratories “Study of the physiological features of marine mammal cells caused by living in an aquatic environment”, № FWFE-2024-0009. The authors express their sincere gratitude to the collaborators in the Center of Oceanography and Marine Biology “Moskvarium”, A.N. Severtsov Institute of Ecology and Evolution of the Russian Academy of Sciences, “Biotechnological Campus” LLC and “Green Sakhalin” fund.

BOUNDARIES IN THE DEEP SEA – THE ROLE OF SEAMOUNTS IN FAUNA DISPERSAL

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Seamounts are areas of high biological productivity in terms of both benthic and pelagic communities, including commercial resources of aquatic organisms; many of these are supporting commercial fishing. These bottom elevations not only create additional substrates for bathyal fauna but also provide topographic conditions for the accumulation of zooplankton and suspended matter, which serve as a food base for bottom animals and fish. Furthermore, the seamount complexes may serve as a stepping stones for dispersal of deep-sea fauna. The Emperor Seamount Chain (ESC) is one of the largest seamount complexes in the northwestern Pacific, containing more than 50 seamounts, a part of the Hawaiian-Emperor chain – the longest contiguous chain of islands, guyots and seamounts in the world, whose edges are located in contrasting climatic and biogeographic zones. Based on the data obtained during research cruises of the NSMB, it was concluded that the boreal-temperate deep-sea species (including corals, sea stars ans brittle stars, black corals, radiolarians and diatoms) spread along the Emperor Chain southwards, while benthic species of tropical genesis spread northwards. The first finding of the biogeographic boundary between the faunistic assemblages in the ESC area was made for the 37°–39° N. Future detailed research may bring new data on the Spongia of the ESC, but presently it is not discovered clear zoogeographic boundary based on the distribution of Hexactinellidae sponges in the area. The Ministry of Science and Higher Education of Russian Federation provided the RV Akademik M.A. Lavrentyev for the research cruises and the support of the research including the laboratory processing of the samples (grant 13.1902.21.0012, contract No 075-15-2020-796).

DEEP DIVE: EXPLORING ISOPOD DIVERSITY IN THE NORTH PACIFIC TRENCHES WITH HOV *FENDOUZHE*

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Deep-sea trenches act as geographic barriers for abyssal fauna dispersal and also serve as drivers of speciation, requiring organisms to adapt to the extreme conditions of hadal depths.

The Kuril-Kamchatka (KKT) and Aleutian (AT) trenches are the northernmost trenches in the Pacific Ocean (PO), bordering the abyssal plain of the NW Pacific Basin from the northwest and north. They reach maximum depths of 7679 m (AT) and 9717 m (KKT) respectively, and are separated by a junction with depths of ~6000 m.

The KKT and AT were previously studied during several expeditions aboard the RV *Vityaz* (1949–1976), the German-Russian expedition KuramBio II (2016) in the KKT, and the German expedition AleutBio (2022) in the AT. These expeditions employed various trawls and grabs for sampling, including gears specifically designed for macrofauna sampling (such as epibenthic sledges). Thus, the region, particularly the KKT, has been relatively well covered by sampling efforts, although the use of trawls and grabs has certain limitations. E.g. their deployment is restricted or impossible in areas with complex topography (steep slopes, rocky outcrops). Given that these relief features are widely distributed along the slopes of both trenches, some deep-sea biotopes remain unexplored.

Therefore, the next important step in studying the hadal ecosystems of the KKT and AT was the 2024 Chinese-Russian expedition aboard the RV *Tan Suo Yi Hao* (42nd cruise), organized by the Institute of Deep-Sea Science and Engineering CAS in collaboration with the NSCMB FEB RAS. Sample collection and video observations were conducted during dives of the HOV *Fendouzhe* at depths ranging from 5628 to 9580 m. The use of an HOV enables *in situ* community research, selective sampling according to habitat patchiness, and investigation of previously inaccessible locations to address knowledge gaps in hadal fauna.

The focus of our investigation in this project – the crustacean order Isopoda – represents one of the most abundant and diverse taxa of deep-sea macrobenthos in most explored regions of the World Ocean, mostly due to the contribution of deep-sea families of the suborder Asellota. According to published data, approximately 100 species from 34 genera and 9 families of isopods have been recorded in the KKT at depths from 6000 to 9600 m. Among these, 48 species are described (mainly based on the RV *Vityaz* collections), while 54 species are potentially new to science, collected during subsequent expeditions. In the AT, 13 species from 9 genera and 4 families of Asellota have been reported at depths ranging from 6000 to 7286 m (5 described and 8 potentially new species). Asellota account for 98% of all recorded species.

In the samples collected during the RV *Tan Suo Yi Hao* expedition, isopods were presented in material from 22 HOV *Fendouzhe* dives, including: 12 dives in the KKT (depth range: 5954–9580 m), 8 dives in the western AT (6608–6989 m), and 2 dives at the junction between the trenches (5573–6017 m). A total of 33 isopod species were identified, representing 15 genera, 9 families, and 2 suborders.

In the KKT samples, Isopoda were represented by 20 species from 12 genera and 8 families of Asellota. Among these, 10 species were previously known, while the remainder are presumed to be new to science. Nearly all known species were collected within their previously established distributional and bathymetric ranges. The exception was *Haplomunna* cf. *kurilensis* Golovan and Malyutina, 2023, which we had previously described from the PO abyssal adjacent to the KKT (5222–5380 m).

In the AT samples, Isopoda were represented by 13 species from 11 genera and 7 families, predominantly belonging to the suborder Asellota (12 species). Additionally, one species of Antarcturidae (suborder Valvifera) was found. Four species were previously known from the adjacent PO abyssal plain, while the remaining species are presumed to be new to science.

The AT yielded first records of several asellote taxa: families Haplomunnidae, Ischnomesidae, Janirellidae, and Macrostylidae; genera *Eurycope*, *Ilyarachna*, and *Bathyopsurus* (Munnopsidae); and the family Antarcturidae. Our findings doubled the known hadal isopod diversity in the AT from 13 to 26 morphospecies.

In addition to physical collections, video observations provided valuable insights into isopod diversity and distribution patterns in the hadal zone. Notably, giant isopods of the nektobenthic subfamily Bathyopsurinae (Munnopsidae) were frequently observed – often in large numbers – across all study areas: the AT, the KKT (down to 7292 m), and the abyssal junction between the trenches. Their repeated appearances in dive videos were particularly surprising, as Bathyopsurinae had never been recorded in the well-studied KKT. These skilled swimmers proved exceptionally difficult to capture, actively avoiding sampling gear by adjusting their swimming altitude and direction.

Antarcturidae are distinctive isopods characterized by a sedentary lifestyle, typically occurring as epifauna on sessile organisms. In the AT, we found *Chaetarcturus* sp. in large numbers inhabiting a community of epibenthic suspension feeders ("hadal garden") that had colonized a vertical rock wall at ~6,650 m depth. This discovery would not have been possible without HOV or ROV technology.

In summary, the HOV surveys have significantly enhanced our understanding of hadal isopod fauna in both the KKT and AT. However, several important questions remain open:

1. Approximately 35% of species in each trench, the KKT and AT (based on combined literature data and our findings) are shared with the PO abyss, while 7 species were recorded in both trenches. It should be noted that current molecular methods have repeatedly revealed complexes of morphologically similar but geographically or bathymetrically separated species in the study area. Therefore, reports of species distributions extending beyond a single trench or a depths zone require verification.
2. A major challenge for data synthesis at this stage is that a large proportion of the species list consists of undescribed species. Taxonomic work to describe these species is necessary and is planned as the next phase of our research.

A MARINE MOLLUSK-DERIVED PROTEIN MKC1QDC AS AN EFFECTIVE CANDIDATE FOR GYCOSYLATION-SPECIFIC DETECTION AND SUPPRESSION OF GIOMAS AND CARCINOMAS

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C1q domain-containing (C1qDC) proteins are widely distributed among invertebrates, with a particularly high abundance of their coding sequences identified in bivalve mollusk genomes and transcriptomes. As members of the TNF/C1q superfamily, these proteins display relatively low amino acid sequence homology but exhibit striking structural conservation in their C1q domains, including similarities to the human complement C1q protein. Most C1qDC proteins function in immunity as pattern recognition receptors, while their soluble forms act as agglutinins and opsonins by binding to carbohydrate pathogen-associated molecular patterns (PAMPs) on microorganisms.

The C1qDC protein from *Modiolus kurilensis* hemolymph (MkC1qDC) contributes to the mollusk’s immune defense, demonstrating antibacterial activity against different types of bacteria. It exhibits the strongest affinity for acidic galactans, mannans, and sialic acid – structures found not only in microbial PAMPs but also in the altered glycans of many tumors, particularly gliomas and carcinomas. Fluorescent staining with MkC1qDC-FITC conjugate revealed high binding affinity to colorectal, breast, and cervical adenocarcinomas, as well as to various brain tumor lines, including primary glioma cultures derived from patients at the Far Eastern Federal University

Medical Center. In contrast, non-tumorigenic cell lines showed either minimal nonspecific surface staining or none at all. When applied to patient biopsy sections, MkC1qDC-FITC selectively labeled brain tumor structures without staining normal brain tissue. Similar specificity was observed in proliferation assays: over 96 hours of exposure to MkC1qDC (2–8 μM), carcinoma and brain tumor cell lines exhibited dose-dependent growth suppression, while patient-derived glioma and neuroblastoma cells showed significant cell death at 8 μM. Non-tumorigenic lines, however, remained unaffected. Further analysis of MkC1qDC's cytotoxic properties revealed that tumor cells treated with the protein (2–16 μM) underwent a rapid, dose-dependent increase in cell death, detectable as early as 6 hours post-treatment.

The authors are grateful to the personnel of the Vostok Marine Biological Station and the Primorsky Aquarium Shared Equipment Facility of the A.V. Zhirmunsky National Scientific Center of Marine Biology, Far Eastern Branch, Russian Academy of Sciences.

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SIMULATING MARINE ECOSYSTEM HEALTH ON CHINA'S COAST

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Global climate change and extensive human activity put compounding pressure on coastal marine ecosystems, resulting in habitat degradation, a reduction in ecosystem services, and an increase in marine ecosystem disasters. Therefore, simulating the response of ecosystem health conditions to climate change and different human activity scenarios can provide direct and effective information to improve ecologically sound management strategies for the sustainable use and development of coastal areas. In the present work, we set up a scenario simulation model. Climate change and human activity impact scenarios were designed and individually applied and integrated to predict the possible responses of marine ecosystem health conditions.

The study was supported in part by the International Science Partnership Program of the Chinese Academy of Sciences (grant No. 133137KYSB20200002).

DEGRADATION OF POLYETHYLENE AND POLYPROPYLENE IN DIGESTIVE TRACTS OF ECHINODERMS

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An increasing number of papers are being published on plastic detected in dozens of marine species and its possible negative impact on various aspects of their lives. On the other hand, not only the impact of the plastic on organisms is important, but also the effect of organisms on plastic. Filter feeders and detritivores may not always distinguish microplastic from their usual food; other animals may mistake plastic particles covered by fouling organisms (microalgae and bacteria) for food. Plastic ingestion has been reported for 233 marine invertebrates such as echinoderms, arthropods, including amphipods, and mollusks. There are organisms such as amphipods, wax moth larvae, worms, etc. that ingest plastics in case of a lack of their natural food.

Our experiments have demonstrated that sea urchins, *Strongylocentrotus intermedius*, can consume films of such widely spread plastics as polyethylene and polypropylene not covered by fouling organisms. They crush and modify it in their digestive tracts, increasing the quantity of microplastic particles in the surrounding environment. It was reported earlier that digestive carboxylesterases in the gastric fluid of *Cancer pagurus* exhibit a high potential for hydrolyzing certain biodegradable plastics. Since esterases are common in digestive tracts of organisms, it seems likely that other invertebrates possess the ability to hydrolyze not only biodegradable plastics.

As indicators of polyethylene degradation, we used changes in the Raman spectra, including the level of crystallinity, calculated by the formula: $Xc = I_{1420}/I_{1296} *0.46$, where I_{1420} is the region of CH_2 stretching vibrations related to the crystalline phase of the polymer, and 0.46 is the scale factor determined for fully crystalline polyethylene. After baseline correction, each spectrum was normalized according to a reference peak known to be constant regardless of polymerization or degradation. For polyethylene, the 1296 cm^{-1} mode was used, reflecting the total intensity of CH_2 stretching vibrations independent of the crystallinity level and taken as an internal standard.

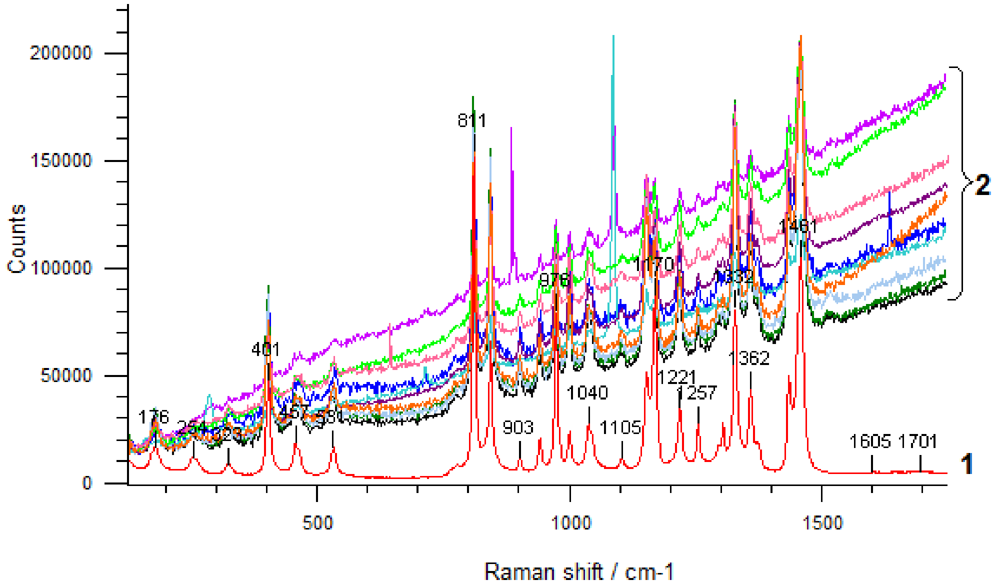

Fig. 1. Raman spectrum of reference polypropylene and polypropylene in sea urchin fecal pellets: 1 – polypropylene spectrum; 2 – spectrum taken from various parts of animal fecal pellets. The abscissa axis shows the Raman shift (cm^{-1}), and the ordinate axis shows the signal intensity in relative units.

Another indication of plastic degradation was the decrease in band intensities, band disappearance, or the appearance of new bands and baseline drift in the Raman spectra. The band intensities decreased as the baseline drift increased, which was primarily caused by the luminescence generation within the sample as a polypropylene spectrum demonstrated (Fig. 1). The baseline drift is clearly visible, caused by the increased background of parasitic luminescence associated with the rupture of polymer chains on the plastic surface. This phenomenon is usually observed in the presence of conjugated double bonds or simple unsaturations, which are directly related to the rate of chain scission. The effect generating luminescence and creating baseline drift was probably due to the presence of terminal vinylidene and carbonyl groups and was a good indicator of polymer chain scission, and, therefore, it was caused by the degradation of the sample material. The greater the baseline drifts, the more the overall band intensity decreases, indicating a higher rate of polymer chain scission. Raman spectroscopy can indicate changes in polymer molar mass, but it primarily detects vibrational modes related to chemical structure rather than polymer chain length.

Using Raman microspectroscopy, we have experimentally shown that “non-biodegradable” plastics such as polyethylene and polypropylene undergo degradation or chemical changes in the digestive tract of sea urchin, *S. intermedius*, and its homogenate, as well as in the homogenized digestive glands of starfish, *Patiria pectinifera*. The Raman spectrum of polyethylene, after passing through the digestive tract of a sea urchin, shows a significant drift of the baseline associated with an increase in the level of parasitic luminescence of the polymer. With an increase in the luminescent background, the amplitude of the characteristic peaks of the polyethylene modes decreases. The crystallinity of polyethylene, after passing through the digestive tract of a sea urchin, also changes compared to the reference polymer. All the above findings indicate the initial stages of degradation. The same result (a drift of the baseline associated with an increase in the level of parasitic luminescence of the polymer) was obtained in a study of polypropylene after passing through the digestive tract of a sea urchin. The homogenate of the digestive tract of a sea urchin also led to a drift of the baseline in the Raman spectrum of polypropylene. It was caused by an increased background of parasitic luminescence associated with the rupture of polymer chains on the plastic surface. In addition, it should be noted that the peak (approximately 1640 cm^{-1}), corresponding to the carbonyl group C=O, was absent in the control spectrum, which also indicated rupture of polymer chains on the surface of the experimental polypropylene sample. Polypropylene from the homogenate of the sea urchin digestive tract and polypropylene from the homogenate of the starfish digestive glands were characterized by the same changes. In the Raman spectrum of polypropylene after incubation in the homogenate of the starfish digestive glands, the modes of 1619–1768 cm^{-1} appeared, corresponding to the carbonyl group C=O, which indicated a rupture of polymer chains on the surface of the experimental plastic sample. These modes were absent in the control.

Thus, our studies have shown that two of the most common plastics can be crushed by certain echinoderms and undergo degradation in their digestive system. However, no signs of a negative impact of plastic on sea urchins were observed. The most likely cause of plastic changes in the digestive system of these animals may be their symbiotic microflora, which is presumably more diverse than that of the surrounding water. Although not all changes that occur to plastic under the effect of digestive enzymes and gut microflora of echinoderms can be described in detail, it is assumed that these enzymes enhance the effect of abiotic environmental factors, making plastic less durable, leading to its faster degradation. The coating of plastic by fouling can lead to its more intensive destruction by animals, as compared to clean, unfouled plastic.

In general, the ability of free-living and symbiotic microorganisms to decompose or recycle plastic, along with the ability of animals to shred it, suggests that the biosphere has a potential to control the accumulation, spread, and harmful effects of plastic.

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CHEMOSYMBIOTIC BIVALVE MOLLUSCS PLIOCARDIINAE (VESICOMYIDAE): TRACES OF PAST HABITATS AND DYNAMICS OF RANGES

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Bivalve clams of the subfamily Pliocardiinae (Vesicomyidae), comprising about 100 Recent species, are one of the most successful groups of chemosynthesis-based ecosystems. They have a worldwide distribution inhabiting in areas of cold seepages, hydrothermal vents, and accumulations of decaying organic matter at depths from 100 to more than 6000 m. All known pliocardiines live in a symbiosis with sulphur-oxidizing gamma-proteobacteria, from which they receive their nutrition. Distribution of pliocardiines reflects a fragmented distribution pattern of reducing conditions on the ocean floor, where populations of the same species can be separated by thousands of kilometers. Such patterns of distribution are natural models for studying the pathways of population connectivity and the history of habitat colonization. To explain the extensive geographical ranges of fragmentary distributed chemosymbiotic species within those ranges and genetic homogeneity of distantly located populations, the following assumptions are usually discussed: the high dispersion ability of larvae and the presence of intermediate populations in not yet discovered reducing biotopes. Another non-mutually exclusive explanation is the assumption of reducing biotopes that are now extinct or changed but have existed in the past and supported pliocardiine populations (Krylova, Janssen, 2006).

Reducing conditions are known to change over time (Tunnicliffe et al., 2003), and local reducing biotopes may cease to exist after they have played the role of «stepping stones» for the dispersal of certain species. However, subfossil shell accumulations help to locate areas of past reducing biotopes inhabited by pliocardiines. The large size of pliocardiines and usually numerous settlements contribute to the rather frequent findings of shells on the seabed. Many of the subfossil valves were collected by trawls, often before the discovery of deep-sea reducing biotopes. Paleo records, some of which have been dated, are known for more than 10 extant pliocardiine species. Overall, our data show that ranges of pliocardiine species can vary significantly over a relatively short time. Pleistocene records of presently existing species are often located beyond the boundaries of their modern areals. For example, currently there is only one pliocardiine species on the Mid-Atlantic Ridge (MAR), *Abyssogena southwardae*. Nevertheless, in the extinct hydrothermal vents on the MAR, besides *A. southwardae,* subfossil valves of two other pliocardiine species have been found (Lartaud et al., 2010). Presently, these both species were not found at the MAR but live in the eastern Atlantic. The type of biogeographic range of the species may have changed from the panthalassic in Pleistocene to a near-continental type at present. However, paleo populations may also occur within the current range of the species between spatially separated populations, indicating possible pathways of population connections.

Studies of biogeographic ranges and connections of fragmented populations are particularly important in our time, when anthropogenic disturbances at sea are increasing together with the need to find rational solutions for the protection of marine communities.

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BIOENGINEERED CELL-BASED MODELS AND MOLECULES FROM MARINE ORGANISMS FOSTERING THE DEVELOPMENT OF PERSONALIZED ANTICANCER DRUGS

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Despite active research, gliomas, some carcinomas and sarcomas remain among the most incurable malignant tumors, primarily due to the lack of chemotherapeutic agents, among which first-line drugs often have high toxicity and insufficient efficacy. Using genetic and cellular engineering technologies, as well as methods for constructing a bioartificial extracellular matrix and creating 3D tumor growth models, we have developed a set of cell-based experimental systems that provide for the study of specific mechanisms of carcinogenesis and the search for drug candidates with selective action on individual cancer cells.

In order to search for drugs that are effective against individual glioma subtypes, we have developed a set of cell-based models obtained by various techniques of genetic and cellular engineering. Preliminary transcriptome analysis of single stem cells isolated from gliomas carrying IDH1 R132H and TP53 R248Q allowed us to identify promising molecular targets. Gene editing technology based on CRISPR/Cas9 with cytidine deaminases provided the generation of isogenic cell lines with IDH1 R132H and TP53 R248Q alleles, as well as their combination. A collection of early-passage cell cultures from

tumors of patients with different genotypes was also obtained for independent evaluation of the drug action and study of the mechanisms of gliomagenesis. Another system for searching for specific drugs was the HT1080-HAC/dGFP fibrosarcoma cell line with a human artificial chromosome carrying the green fluorescent protein gene. This model provides a quantitative assessment of the level of chromosomal instability and the search for drugs that cause its extreme level in cancer cells with their subsequent death. Also, these cell-based systems were additionally modified to express a construct with mCherry fused through the T2A translation separator with two IDH1 sequence variants and six TP53 variants. Using all of the above models independently, we were able to show that drugs that cause chromosomal instability in tumor cells are the most promising for the treatment of gliomas carrying IDH1 R132H. The presence of IDH1 R132H is associated with a high level of chromosomal instability, and the action of these drugs increased chromothripsis and provided a more pronounced cytotoxic effect compared to temozolomide. Another model cell lines expressing reporter constructs based on HIF-1 in glioma cells with different genotypes were developed, that provides screening of drug candidates suppressing the resistance of glioma subtypes to hypoxia. The prospects of the obtained models formed as three-dimensional systems in the extracellular matrix and their application for in vivo studies with intravital visualization of tumor growth in laboratory animals using two-photon microscopy were demonstrated. Applying recently developed cell-based models promising drug candidates with differential activity against cancer subtypes were isolated from marine biota.

This study was supported by the Ministry of Science and Higher Education of the Russian Federation (FZNS-2023-0017, FWFE-2024-0008).

HYDROCHEMICAL AND HYDROLOGICAL ENVIRONMENTAL FACTORS AND BIOLOGICAL PRODUCTIVITY OF COASTAL WATER AREAS OF PETER THE GREAT BAY, SEA OF JAPAN

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The aim of this work is to investigate the content and interannual dynamics of dissolved forms of macrobiogenic elements in the habitats of marine coastal plant communities in the waters of Peter the Great Bay (Sea of Japan/East Sea) and the influence of the upwelling–downwelling velocity in the shelf zone of Peter the Great Bay on their change to assess the hydrochemical regime and biological productivity of the explored coastal water areas.

A study of changes in the content and interannual dynamics of dissolved biogenic elements (carbon, nitrogen and phosphorus) was conducted in the coastal water areas of the Amur and Ussuri Bays and the Stark Strait. Hydrochemical and statistical analysis methods were used.

In marine coastal ecosystems, changes in the content of dissolved macrobiogenic elements primarily affect the functioning of primary producers communities — autotrophic organisms of the benthos, periphyton and plankton. It was found that the average level of dissolved organic carbon (DOC) in coastal water areas adjacent to the coast of Vladivostok — in the Amur Bay and the Ussuri Bay — is 3.5 mg/l (290 mkM) and 2.1 mg/l (175 mkM), respectively, which allows these water areas to be classified as highly productive marine waters [Skopintsev, 1979; Agatova, 2017].Coastal waters in the Stark Strait with an average DOC content of 2.0 mg/l (170 mkM) can be classified as medium productive marine waters. These data demonstrate the operation of a biological pump in the studied coastal water areas, responsible for the circulation of organic matter formed by autotrophic organisms during photosynthesis — the soft tissue pump. In the studied coastal water areas of the Amur Bay, the average level of total dissolved phosphorus (DTP) is 0.051 mg/l (1.6 mkM) and total dissolved nitrogen (DTN) is 0.3 mg/l (21 mkM). The average levels of DTP and DTN in the coastal water areas of the Ussuri Bay and the Stark Strait are even lower: 0.55 mkM and 14 mkM in the Ussuri Bay, 0.45 mkM and 14 mkM in the Stark Strait. Comparison with the average level of DTP and DTN in the ocean (0.074 mg/l or 2.4 mkM and 0.538 mg/l or 38.4 mkM, respectively) shows that all the studied water areas are phosphorus- and nitrogen-deficient ecosystems to varying degrees, which may be manifested in a decrease in the potential for secondary production.

Analysis of the data obtained for 2017–2024 showed that deviations from the average level in the interannual changes in the studied dissolved forms of biogenic elements are not random and can be represented as periodic functions (Fig. 1).

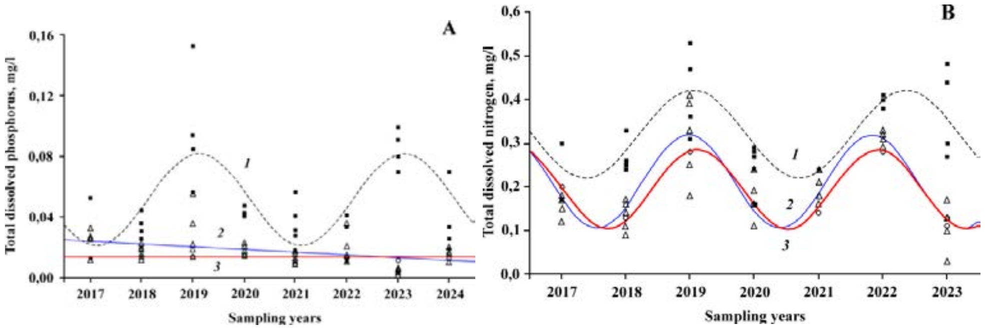

Fig. 1. Year-to-year dynamics of total dissolved phosphorus (A) and total dissolved nitrogen (B) in the macrophyte growth zone in 2017–2021 (with extrapolation): (1) – in the Amur Bay (●); (2) – in the Ussuri Bay (Δ); (3) – in the Stark Strait (○).

The primary role of coastal upwelling in the delivery of nutrients to estuarine bays, including the marginal seas of the northwestern Pacific Ocean, has been reliably established [Prego, 1993; Mackas and Harrison, 1997; Colbert and McManus, 2003]. To characterize in detail the role of this process in the biology, hydrology and hydrochemistry of Peter the Great Bay, there is a need to create models that describe the dependence of changes in the content of dissolved forms of biogenic elements on the dynamics of upwelling–downwelling. We studied the dynamics of the average monthly and average annual upwelling velocity in the shelf zone of Peter the Great Bay and described its influence on the change in the content of total dissolved phosphorus in the coastal water areas of the Amur Bay through a functional model using statistical analysis methods. Data for the analysis of the upwelling–downwelling process in the shelf zone of Peter the Great Bay (Japan/East Sea) from August 2014 to July 2022 were obtained using the ERDDAP server:

[http://coastwatch.pfeg.noaa.gov/erddap/ru/griddap/erdQBstressmday_LonPM180.html].

The Ekman vertical velocity values were calculated from satellite data at the Physical Sciences Laboratory of the National Oceanic and Atmospheric Administration (NOAA, USA). Data processing was carried out using the Ocean Data View (ODV 5.8.2) software package [Schlitzer, 2024. http://odv.awi.de].

The dependence of the influence of the average annual upwelling velocity on the content of total dissolved phosphorus for Amur Bay can be described by the equation:

$$Z = 0.034\times((\exp((Y/0.0734)3)-1)\times\exp(-0.5\times((X-0.0734)/(0.073/\exp(1))4)2)+1)$$

and is presented in the form of three-dimensional graphics (Fig. 2).

Thus, it has been shown that Ekman upwelling–downwelling in the shelf zone of Peter the Great Bay, with a certain combination of average annual velocities of this process in the two preceding years, leads to a significant (4.5-fold) increase in the content of total dissolved phosphorus in the studied coastal waters of the Amur Bay compared to the minimum average level of 0.034 mg/l (1.1 mkM), which remains constant over the next three years. Periodic changes in the content of total dissolved phosphorus, in turn, can affect the periodicity of fluctuations in the production indicators of the coastal ecosystems of the Amur Bay.

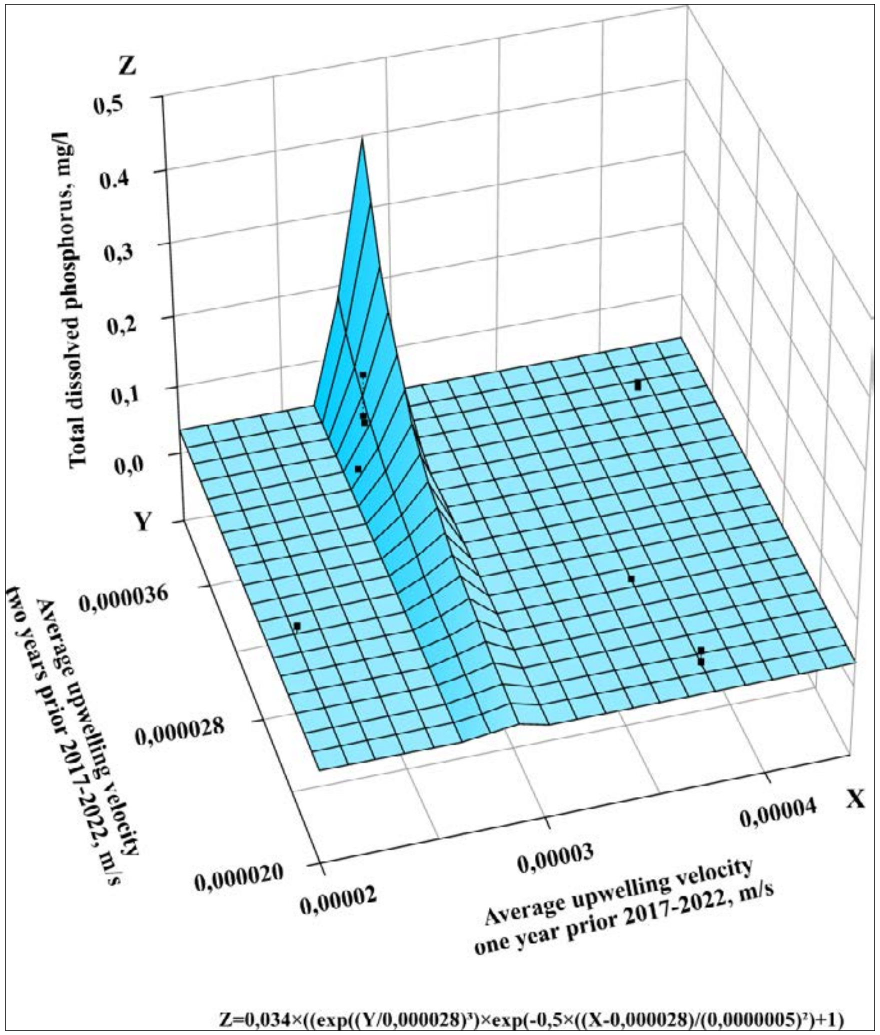

Fig. 2. Model describing the dependence of total dissolved phosphorus content on the average annual upwelling velocity in the studied coastal water areas of the Amur Bay in 2017–2022.

The work was carried out within the framework of the State assignment "Dynamics of marine ecosystems, adaptation of organisms and communities to environmental factors". Registration number: 124021900009-6.

DEVELOPMENT OF THE SHELL FIELD IN THE POLYPLACOPHORAN MOLLUSK (CHITON) *ACANTHOCHITONA RUBROLINEATA*

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The serially arranged shell plates of polyplacophoran mollusks (chitons) are a unique feature within the phylum, making them a crucial model for understanding molluscan evolution. While previous studies identified several cell populations, the morphogenesis of the shell field and the underlying molecular mechanisms have remained largely uninvestigated. In this study, we investigated the shell field development in the chiton *Acanthochitona rubrolineata* through detailed morphological and molecular analyses. Our results reveal a complex organization, where the shell field comprises not only the central plate fields and ridges but also a surrounding girdle precursor tissue, which we term the shell field margin. This margin exhibits a concentric organization, with spicule formation restricted to its outer domain. Analysis of dynamic *engrailed* expression and F-actin distribution revealed a highly complex morphogenetic process. The repeated units — the plate fields and ridges — are established gradually, through a process seemingly distinct from the canonical segmentation mechanisms of arthropods or vertebrates. To elucidate the underlying mechanism, spatio-temporal analysis of Notch-related molecules was performed, which suggested that the Notch signaling pathway is likely involved in this morphogenesis. Critically, functional experiments using small- molecule inhibitors confirmed that this pathway regulates key developmental events essential for the formation of the repeated units. Collectively, these findings provide a comprehensive model for the structure and morphogenesis of the chiton shell field, offering a critical foundation for exploring the mechanisms of polyplacophoran shell development and molluscan evolution.

RUSSIAN-CHINESE COOPERATION IN MARINE BIODIVERSITY STUDIES: HISTORY AND MODERNITY

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Russian-Chinese cooperation in the fields of marine biology, ecology and biodiversity started in the 1950s with intergovermental agreements. In 1957–1961, Soviet and Chinese researchers cooperatively studied the coastal zone of the China seas. Marine biologists of the Zoological Institute, the then USSR Academy of Sciences, E.F. Gurjanova, D.V. Naumov, O.A. Skarlato, A.A. Strelkov, B.E. Bykhovsky, L.F. Nagibina, P.V. Ushakov, V.V. Khlebovich, and N.L. Tsvetkova took part in these studies. In 1957, an expedition of the IOCAS and Zoological Institute worked in the Yellow Sea near Qingdao and Yantai (Shandong Province). The bionomical and faunistic research was headed by the famous Russian marine biologist and carcinologist Evpraksiya F. Guryanova. Professors Tchang Si, Liu Ruiyu, Tsi Chun_yen, and Wu Baolin participated in the expedition on the Chinese party. In 1958–1960, Guryanova was the Soviet head of a marine zoology expedition to Hainan Island (South China Sea), which studied the biology of commercial invertebrates and the species composition and the horizontal and vertical distribution of the coastal zone fauna and gathered collections of marine animals and plants. For her work in those expeditions Prof. Eupraxie Gurjanova was awarded the People’s Republic of China Order of Friendship. At that period, the founder and the first Director of the Institute of Marine Biology in Vladivostok, Alexey V. Zhirmunsky, also worked in China. Zhirmunsky, then a researcher in the Leningrad’s Institute of Cytology, USSR AS, later an Academician, and a leading figure in the development of Russian Far Eastern science, spent four months in 1959–1960 in expeditions to Hainan and Qingdao. He published the results of these expeditions in several papers in the

Russian and Chinese languages on the physiological ecology of mollusks, jointly with Dr. Li-Chun Chu.

In the 1980s and later, several researchers from Institute of Marine Biology FEB RAS visited the IOCAS, and *vice versa*, and carried out joint research. Yu.M. Yakovlev and G.A. Evseev spent several months in Qingdao in 1989 carrying out cooperative research on the morphology and anatomy of oysters resulted in several publications. Joint works of the Laboratory of Autotrophic Organisms and scientists of the Institute of Oceanology CAS started in 1993 when Dr. T.V. Titlyanova and Prof. E.A. Titlyanov jointly with Dr. Xia Bangmei identified herbarium of marine plants collected during the German-Chinese marine biological expeditions to Hainan Island in 1991 and 1992; this work was continued later; main directions of the research were floristic changes of marine benthic green algal species (Chlorophyta) in Hainan between 1933 and 2009 in relation to environmental degradation and the intertidal marine macroalgae of Hainan Island. A book published jointly by Drs. E.A. Titlyanov, T.V. Titlyanova, Xiubao Li and Hui Huang under the title ***Coral Reef Marine Plants of Hainan Island*** (2016) was the first publication devoted to the description of marine plants of Hainan Island, described marine plants, including the role of their communities in ecosystems of coral reef, discussed seasonal and decadal changes in biodiversity and the composition of the marine flora of the island. Drs. I.M. Yakovleva, A.V. Skripsova Ti Feng Shan, Shao Jun Pang, Yu Rong Zhang jointly studied genetic diversity and relationships of major farmed cultivars and geographically isolated populations of Sacharina japonica (Phaeophyta) in the north-westeren Pacific.

In 2006, the then Institute of Marine Biology FEB RAS and the Institute of Oceanology CAS under the leadership of Prof. A.V. Adrianov and Prof. Sun Song signed a new agreement of cooperation; the agreement was renewed in 2019 and 2023. Two institutes held six workshops/symposia on marine biology, biodiversity and ecosystem changes in 2007, 2010, 2012, 2017, 2019, 2023 in both Vladivostok and Qingdao leading to strengthening institutional and

personal ties. Several joint projects supported by CAS, NOWPAP UNEP and the APN (Asia-Pacific Network for Global Change Research) were conducted: *Regional Overview on Marine Invasive Species (MIS) in the NOWPAP Area (2009–2010); Marine biodiversity of the coastal zones in the NW Pacific: status, regional threats, expected changes and conservation (2007–2008); Atlas of Marine Invasive Species in the NOWPAP Region (2012–2013); Joint research of taxonomic study on common mollusks between China and Russian Far Eastern seas (2018–2019); Biodiversity Changes and Ecosystem Health Assessment in the Coastal Region of China and the Russian Far East under the Influence of Global Change (2021–2023).*

In 2014, a book, ***Marine Biodiversity and Ecosystem Dynamics of the North-Western Pacific Ocean*** (Editors: Sun Song, Andrey V. Adrianov, Konstantin A. Lutaenko, Sun Xiaoxia) was prepared and published jointly by the Institute of Oceanology, Chinese Academy of Sciences (IOCAS, Qingdao) and A.V. Zhirmunsky Institute of Marine Biology, Far Eastern Branch of the Russian Academy of Sciences (IMB FEB RAS, Vladivostok) as an outcome of collaboration in the field of marine ecology and biodiversity studies. It included comprehensive review papers on such topics as biodiversity in the Sea of Japan; status of marine biodiversity of the China seas; problems of environmental safety of the Far Eastern seas of Russian Federation; zooplankton functional groups in the Yellow Sea; diversity of potentially toxic microalgae on the east coast of Russia; etc.

A series of joint papers has been published on systematic malacology dealt with bivalve mollusks and chitons by the scientists of the IMB/NSCMB, Zool. Inst. EAS and IOCAS (Drs. Xu Fengshan, Zhang Junlong, K.A. Lutaenko, O.V. Yurchenko, A.V. Kalachev, B.I. Sirenko) for last twenty years. Dr. Yu.Ph. Kartavtsev and Dr. Hongtao Nie (Dalian Ocean University) have studied mitochodrial genome of some bivalves

Two projects on bentic ecology and biodiversity have been implemented since 2018 with the Institute of Coastal Zone Research CAS, Yantai under leadership of Drs. Li Baoquan, Chen Lin-Lin and K.A. Lutaenko. This resulted in publications on the meiofauna composition and trophic groups of the nematode communities studied at a sandy intertidal zone in Sishili Bay (Yellow Sea, China), description of a new species of nematode, composition and distribution of intertidal Foraminifera in Sishili Bay, and a taphonomic study on the transportation of bivalve shells by algae in Sishili Bay. A comprehensive review on long-term changes of marine subtidal benthic communities in North East Asia (Yellow and Japan seas) in a global change context was published (2020).

In 2024, the NSCMB FEB RAS started a very successful collaboration with the Institite of Deep-Sea Science and Engineering CAS (IDSSE CAS, Sanya) under the ledership of Dr. V.V. Mordukhovich, Xiaotong Peng and Mengran Du. An expedition to the Kuril–Kamchatka Trench and the western Aleutian Trench conducted in summer of 2024 led to the discovery of the deepest and the most extensive chemosynthesis-based communities known to exist on Earth using the manned submersible *Fendouzhe*. The communities dominated by siboglinid Polychaeta and Bivalvia span a distance of 2,500 km at depths from 5,800 m to 9,533 m, and these communities are sustained by hydrogen sulfide-rich and methane-rich fluids that are transported along faults traversing deep sediment layers in trenches, where methane is produced microbially from deposited organic matter, as indicated by isotopic analysis (Peng et al., 2025). These findings challenge current models of life at extreme limits and carbon cycling in the deep ocean (Peng et al., 2025).

Joint research makes science stronger and solid and the results obtained even more productive, diverse and integral. We believe that at this stage it is necessary to further develop and strengthen scientific ties in the field of marine biology between Chinese and Russian scientific institutions and universities and expand joint studies to other areas of the World Ocean. The 21st century is the century of the ocean and we should work together to study and preserve marine biodiversity and native ecosystems.

GHOSTS OF THE HADAL: GIANT ASELLOTES *BATHYOPSURUS* FROM THE ALEUTIAN AND KURIL-KAMCHATKA TRENCHES

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Deep-sea isopods are predominantly (98%) represented by the suborder Asellota. These typically small, cryptic crustaceans crawl along the seafloor and inhabit all aquatic environments - from freshwater systems and underground caves to every zone of the World Ocean, reaching their peak diversity in deep-sea habitats. Among the 22 deep-sea asellote families, Munnopsidae stands out as particularly remarkable, having evolved swimming capabilities. This family accounts for up to half of all deep-sea Asellota diversity. Most munnopsids are macrobenthic (1-10 mm in size), but the subfamily Bathyopsurinae includes the world's largest asellotes, with body lengths (excluding appendages) exceeding 65 mm. These giants exhibit a nektobenthic lifestyle, actively swimming in the water column above the bottom surface. They swim backwards on the dorsal side using modified paddle-like last three pairs of legs (pereopods V-VII). After landing, they move along the muddy bottom on long stilt-like anterior legs. Underwater imaging has frequently documented these swimming giants in various deep-sea regions, including Japan Trench, Monterey Bay, abyssal off the Galapagos and Peru, Puerto Rico Trench. However, reliable identification from imagery alone remains problematic without specimens, which are exceptionally difficult to collect. Since Beddard's (1885) initial work, only about a dozen specimens in poor condition have been caught and studied. Like many pelagic organisms, bathyopsurines possess delicate, translucent chitinous integuments that readily deform during capture, while their fragile appendages often broken off and lost.

The genus *Bathyopsurus* was described by Nordenstam (1955) based on *B. nybelini* from the western subtropical Atlantic's abyssal and hadal zones. Wolff (1962) later assigned specimens from the Tasman Sea and Kermadec Trench to this species. He also re-examined two similar *Eurycope* species: reclassified *E. abyssicola* (Beddard, 1885) as a *Bathyopsurus* species and established the new genus *Parapsurus* for *E. pellucida* (Beddard, 1885) and specimens from the Tasman Sea and Costa Rica, collected during *Galathea* expedition. Since these two genera did not correspond to any of the existing munnopsid subfamilies, Wolff established for them a new subfamily, Bathyopsurinae Wolff, 1962. Until now, the position of Bathyopsurinae within the family Munnopsidae was unclear due to missing morphological data (particularly pereopods II-VII and uropods). Recent studies have provided new insights: Peoples et al. (2024) examined *B. nybelini* from the Puerto Rico Trench, while Brandt et al. (2025) described a new species *B. sonnei* from the eastern Aleutian Trench. In the mentioned studies, despite the good condition of the few collected specimens, most of their legs were lost.

In 2024, during the Chinese-Russian deep-sea expedition in the Kuril-Kamchatka Trench and western part of the Aleutian Trench on the RV *Tansuoyihao*, using HOV *Fendouzhe* we managed to film and catch several *Bathyopsurus* specimens in good condition with preserved limbs. The morphological study allowed us to give a full description of the species, conduct a taxonomic comparative analysis of the characters and clarify the diagnosis of not only the genus, but also the subfamily. Initially, Wolff placed this subfamily in the family Eurycopidae and compared it with the superficially similar genus *Munneurycope*, also possessing a wide natasome. We found that several unusual characters of bathyopsurines were similar to those of some members of the specialized actively swimming subfamily Munnopsinae, which habitus weakly resembles Bathyopsurinae due to the narrow natasome. The following characters are common to both subfamilies: 1. Division of the body into ambulosome and natasome by the waist. 2. Massive mandibles with reduction of the molar and palp and a strong long condyle (as, for example, in *Munnopsis mandibularis*). 3. Absence of dactylus in swimming pereopods V–VII. 4. Short basis, ischium and merus of pereopods III and IV. 5. Elongated uropod with a long cylindrical protopod. 6. Opercular pleopods do not cover an anal operculum, which separate from the branchial chamber by a preanal ridge.

The three described species of *Bathyopsurus*, found across a remarkably wide geographic range in widely separated areas of the Atlantic and Pacific Oceans at depths ranging from 3886 to 7900 m, are morphologically very similar, making genetic comparisons particularly valuable. Genetic data have been obtained for the recently described new species *B. sonnei* from the abyssal eastern Aleutian Trench and *B. nybelini* from the Puerto Rico Trench. Our ongoing genetic analysis will help determine whether our specimens represent a known species (despite showing several morphological differences) or a new species.

Video and photographic evidence from HOV *Alvin* in the Puerto Rico Trench (Peoples et al., 2024) documented a swimming *B. nybelini* holding a piece of sargassum in its prehensile pereopods I. Morphological analysis of gut contents from two captured specimens revealed algal remains. The gut contents of our specimen contained remnants of diatom microalgae and crustaceans. In the food-limited environment of great depths, these active munnopsids - previously also documented as scavengers at baited traps containing fish remains (Brandt et al., 2004) - may employ multiple feeding strategies. They appear capable of capturing sinking organic matter (marine snow particles) from surface waters while also potentially hunting live aquatic organisms both in the water column and on the seafloor.

Our studies using novel technologies for observing and collecting these mobile hadal crustaceans have enhanced understanding of this rare taxon's biogeography and ecological adaptations. The new morphological and genetic data should help clarify its phylogenetic relationships.

PHYCOTOXINS IN THE FOOD WEB FROM THE RUSSIAN PACIFIC: THE FIRST EVIDENCE OF A POTENTIAL THREAT

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Microalgae are the base of the food chain in the marine environment, serving as the primary food source for filter-feeding organisms. The rapid proliferation of microalgae can lead to the dangerous natural phenomenon known as Harmful Algal Blooms - HABs. In recent years, the increasing trend towards global climate warming has led to significant changes in the frequency, intensity and geographical distribution of HABs worldwide, which pose a serious threat to marine ecosystems, fisheries, and coastal economies (Hallegraeff, 2004). During HAB periods, microalgae can produce and release secondary metabolites called phycotoxins, which are essential for the microalgae to provide their vital functions, such is defense, anti-stress, signaling and others. But some microalgal toxins can cause severe damage when they enter higher trophic levels, such as marine mammals, birds, and humans, causing mass mortality and/or adverse neurological and gastrointestinal effects when ingested in amounts exceeding safe thresholds (Vilarino et al., 2018). Mollusks, especially bivalves, are the main carriers of phycotoxins, but zooplankton and fish can also play an important role in the transmission of toxins to other animals. Phycotoxins have also been found in crabs, gastropods, and echinoderms (starfish and sea urchins), indicating that the toxins can affect both benthic and pelagic communities. It has been shown that some toxins persist in the environment (water, sediments) and in the food chain long after the HABs itself has ceased to exist. This suggests that there are various potential pathways and vectors through which toxins can affect higher trophic levels over time and space.

Worldwide, there are close to 100 known marine phytoplankton species that can produce phycotoxins (Cembella, 2003), out of which 37 have been reported for Pacific coast of Russia (Orlova 2014). Toxigenic species belong primarily to the Dinophyceae and Bacillariophyceae. Phytotoxins are a common source of seafood contamination worldwide, and human effects are classified based on clinical symptoms, with the most common being paralytic shellfish poisoning (PSP), diarrhea shellfish poisoning (DSP), and amnesic shellfish poisoning (ASP).The causative agents of PSP are saxitoxins (STXs) produced by dinoflagellates *Alexandrium* spp. Causative agent of ASP is domoic acid (DA), produced by the diatoms *Pseudo-nitzschia* spp. DSP is the result of the lipophilic toxins production (ocadaic acid (OA) and dinophysistoxins (DTXs) by dinoflagellates of the genera *Dinophysis* and *Prorocentrum*. There is concern that the observed global expansion of HABs represents a significant threat to human health, food production, ecosystem services and wildlife populations (Anderson et al, 2022). There is therefore a need for an improved understanding of the trophic transfer, and persistence of toxins in marine food webs.

For the first time, the concentrations of three toxin groups of commercial and environmental importance, domoic acid (DA), saxitoxin (STX) and ocadaic acid (OA), were measured in cultures, seawater, sediments, mollusks, fish, echinoderms, and sea mammals from Russian Pacific. In total, 518 samples were analyzed, including samples for measuring STX (n =176), DA (n =193), and OA (n= 149) quantified using ELISA methods. In the studied samples (19 samples of sea water and cultural samples, 18 samples of bottom sediments, 3 species of mammals, 9 species of bivalve mollusks, 1 species of echinoderms, and 19 species of fish), the concentration of phycotoxins varied significantly: STX was detected in 72 % of the samples, among which prevailed bivalves, mainly filter-feeder mussels, bottom sediments, mammals, and pelagic predator. DA was detected in 50 % of the samples, mainly in mammals, and in fish, which feeds on plankton and cephalopods. OA was detected in 98% of the samples, which were dominated by mammals, followed by bivalves, primarily the filter-feeder. Relatively high concentrations of OA were also recorded in near-bottom predator flatfish, and in the pelagic predatory fish.

The detection of multiple lipophilic and neurotoxic toxins in such a diverse range of pelagic and benthic prey species suggests that marine predators, including higher trophic levels, may be simultaneously exposed to multiple toxins by different pathways. Risk assessment models to understand the impacts of exposure to HAB toxins on marine predators therefore need to consider how chronic, low- dose exposure to multiple toxins, as well as acute exposure during a bloom, could lead to potential long-term health effects ultimately contributing to mortalities. The potential synergistic, neurotoxic and physiological effects of long-term exposure to multiple toxins require investigation in order to appropriately assess the risks of HAB toxins to high predators.

Despite the fact that the measured concentrations of DA, STX and OA in biosamples (sea water, sediments, and internal organs/tissues) were in most cases significantly lower the Health Russia's permissible levels, their simultaneous presence indicates the need for monitoring and control of phycotoxins in the food web from the Russian Pacific.

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STUDIES ON POLYCHAETES (ANNELIDA: POLYCHAETA) IN PACIFIC ASIA: PATTERNS, TRENDS AND CONSEQUENCES

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Polychaetes are one of the most widespread and often mobile groups of meio- and macroinvertebrates in marine bottom communities around the world. Regular research on the morphology, anatomy, diversity, and systematics of polychaetes, like most other living creatures, began in Europe in the 18th century. The growing interest and close attention to the anatomy and systematics of this group in Europe occurred at the end of the 19th and the first half of the 20th centuries, while in the second half of the 20th century there was a definite decline. The history of biological research in other parts of the world is different from the history of biological research in Europe. Despite some differences between regions, it is possible to identify common patterns of these studies. These patterns and general current trends, as well as their consequences, are discussed here using examples from Pacific Asia.

There are three **patterns** of polychaete research, depending on the origin of the people who initiated them. Two of them were mainly carried out by Europeans, including ***travelers*** during long-term sea expeditions visiting Asian countries and ***visitors*** during short-term land trips to Asia, while the third research model, which can be called ***national***, includes professional taxonomists from local Asian countries who often grew up under the supervision of European fellows.

In accordance with the scale of interests of taxonomists, such as ***generalists*** who have studied the morphology and taxonomy of all polychaete groups in the past, and ***specialists*** focused on specific families in the present, two patterns of past and current polychaete research can be distinguished. Typical of these groups is that the old generalists mostly included professional fellows who had studied polychaetes all their lives, while modern specialists mainly include graduate students who cease their interests after defending their thesis.

A general **trend** characteristic of polychaete research worldwide is the shift from interest in the morphology and anatomy of polychaetes, which were very popular in the past, to molecular data, which have become popular now. While it takes 10-20 years of study to become a good morphologist, a geneticist can publish articles in highly ranked journals within one year. This is especially unfortunate, as new sampling and analysis methods have been significantly developed in recent decades, while research on the diversity and systematics of polychaetes has been discontinued not only in Asian countries, but throughout the world.

Historical patterns in the study of polychaetes in Asian countries and general modern trends in taxonomy have led to certain consequences. These include, first of all, the introduction of names of polychaetes, which were first described in European waters, for Asian species. This practice, common in the past, not only supported the idea of the “cosmopolitan” spread of many polychaetes, which I call the “*global European invasion*,” but also underestimated the local biological diversity in Asian countries.

Another consequence of the first period of research in Asia is that old specimens collected during 19th-century expeditions and visits can only be found in European museums. This has a definite advantage, since in some Asian countries museum collections are still in poor condition (what, frankly, is typical for most countries of the world).

The third important consequence of modern research on polychaetes, as well as some other invertebrates, is the massive creation of endless “phylogenetic” trees based on molecular data, without understanding the underlying morphological, reproductive, and other biological characteristics of organisms.

PUBLIC AQUARIUM: NEW MEANINGS AND NEW TRENDS IN ITS DEVELOPMENT, AND ITS CONTRIBUTION INTO RAISING ENVIRONMENTAL AWARENESS

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The Primorsky Aquarium Scientific and Educational Center is a branch of the NSCMB FEB RAS. It is located on the coast of Russky Island (Peter the Great Bay, Sea of Japan) and is the largest in Russia center for the study and conservation of marine ecosystems. Its exhibits not just display aquatic organisms, but also interpret them to the visitors through educational labels and texts on a range of lightbox displays, tablets, and kiosks. Immersive exhibits allow the visitors both to see the creatures inhabiting all the oceans of the Earth, and to get first-hand information from the Aquarium’s experts. The Aquarium houses a Shared Equipment Facility that carries out research projects in the following areas: the physiology of marine mammals, their behavior and nutritional requirements; bioactive compounds with antioxidant and antitumor potential isolated from marine organisms; determination of sex in Humboldt penguins and kinship in their colony, as well as assigning parentage in marine mammals by use of DNA-based molecular methods; environmental security of marine areas over the Russian Far East; the bioactivity and nutritional value of the microalgae that may be potentially useful as feed or dietary supplements for aquatic organisms. The results of the research activities have been presented at many scientific conferences and symposia conducted both in Russia and in other countries. They have also been published in more than 50 articles and used in MSc and PhD dissertations.

The Primorsky Aquarium seeks to educate its visitors on the diversity of species in the sea, to raise environmental awareness and to promote caring attitude towards living things, to connect people with nature and make their commitment to ocean conservation become an integral part of their everyday life. Our educational staff have learnt from secondary schools, scientists, and their own experience to become highly qualified professionals in creating unique programs for children of different ages. These include: programs for school children, laboratory sessions conducted in learning laboratories equipped with microscopes, as well as numerous environmental celebrations for a wide variety of visitors. All the Aquarium team members are engaged in educational activities: scuba divers, dolphin trainers, aquarists, and engineers take part in the programs for kids. The children participating in our educational events explore the fascinating world of the Ocean and learn about amazing creatures inhabiting it.

Over the last decade, even private-owned public aquariums have been evolving from being solely focused on profit-making to encompassing a social and environmental agenda. They provide environmental education activities for their visitors, create wildlife rehabilitation centers to help protect rare and endangered species, and build research laboratories. This is a global trend among public aquariums, and the Primorsky Aquarium stands out as one of the leaders in this field.

LIPIDOMICS OF MARINE ORGANISMS: MEMBRANE ADAPTATION, CORAL RESILIENCE, AND ECOLOGICAL APPLICATIONS

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Cell membranes, composed of diverse lipids and proteins, represent fundamental nanostructures in living organisms. Marine organisms are particularly valuable for research as they produce unique bioactive compounds, including ether lipids, which regulate transport, cell signaling, and differentiation while exhibiting anti-inflammatory and antioxidant properties. Advances in analytical techniques, such as high-performance liquid chromatography (HPLC) and mass spectrometry (MS), now allow for direct lipid analysis without extensive sample preparation, enabling deeper insights into membrane composition and function. The heterogeneous lipid makeup of biomembranes, combined with proteins and glycans, determines key properties like fluidity, phase behavior, and overall functionality. The precise distribution of lipids across cellular membranes plays a crucial role in processes ranging from cell survival to apoptosis and oncogenesis, making their study essential for biochemistry, pharmacology, and ecology.

Corals (Cnidaria), recognized as metaorganisms (holobionts), rely on symbiotic relationships with endosymbiotic dinoflagellates (Symbiodiniaceae) for growth and reef formation. However, rising ocean temperatures due to global warming disrupt this symbiosis, leading to coral bleaching—a major threat to reef ecosystems. Lipids are central to coral health, with phospholipids (PL) (e.g., phosphatidylcholine (PC), phosphatidylethanolamine (PE), phosphatidylserine (PS)), sphingolipids (e.g., ceramideaminoethylphosphonates (CAEP)), and glycolipids playing critical roles in membrane stability and metabolic regulation. This study, part of the state-funded project "Physicochemical methods for biomembrane research," employs HPLC, MS, and molecular biology techniques to investigate membrane structure and lipid dynamics.

The native composition of biomembrane lipids of marine invertebrates such as mussels *Crenomytilus grayanus* and *Mytilus trossulus*, sea urchins *Mesocentrotus nudus* and *Strongylocentrotus intermedius*, sea anemone *Exaiptasia diaphana*, and commercial crab species *Paralithodes camtschaticus* and *Eriocheir japonica* was studied. It was shown that the lifespan of mussels and sea urchins is associated with the composition of their membrane lipids. The sea urchins *M. nudus* and the mussel *C. grayanus* with longer lifespan were characterized by increased contents of PC, PE and PS with odd alkyl/acyl chains, as well as molecular species with arachidonic acid (20:4*n*-6), the higher contents of which may contribute to better adaptation of the mussel *C. grayanus* and the sea urchin *M. nudus* and thus to longer lifespan. By studying the dynamics of the molecular species profiles of storage lipids such as triacylglycerols (TG) and membrane lipids such as glycerophospholipids (PL), a more comprehensive model of the lipidomic patterns during embryonic and larval development of the two commercial crab species *E. japonica* and *P. camtschaticus* was provided. The obtained results indicate different requirements for PUFAs in *P. camtschaticus* and *E. japonica*, which should be taken into account when choosing optimal diets. The structure of biological membranes of corals and their symbiotic dinoflagellates was studied and it was shown that the lipidomes of the thylakoid and plasma membranes of dinoflagellates are characterized by features associated with their different thermal stability and unique membrane lipids. For the host organism of the coral, the transmembrane distribution of PS and CAEP was studied for the first time. They are localized on the inner side of the plasma membrane. The discovery was to detect the transmembrane movement of PE with a change in season. The dynamics of the profile of molecular species of membrane PL during bleaching under heat stress and subsequent recovery of soft coral was studied. It was shown that there is a restructuring of the profile of molecular species of PL, which is one of the adaptation mechanisms of the coral under stress. The sequences of the soft coral β-actin and 36B4 genes were determined and characterized and will be used for real-time PCR in studies of PL biosynthesis.

These insights not only advance fundamental membrane biology but also support conservation strategies, such as optimizing diets in aquaculture and predicting coral resilience under climate stress. By integrating lipidomics with ecological research, this work contributes to the development of effective monitoring tools for preserving marine biodiversity.

A NEW OBSERVATION AND ASSESSMENT SYSTEM IS NEEDED TO MAINTAIN THE OCEAN HEALTH AND ACHIEVE SUSTAINABLE DEVELOPMENT

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Healthy oceans and sustainable development are the core contents of the "Ocean Decade" plan put forward after the United Nations Ocean Conference. Maintaining the health of marine ecosystem is an effective guarantee for the realization of marine service and output functions, an important support for sustainable economic and social development, and a major issue of global concern. In many cases, we manage the ocean without understanding the ocean, because we do not really understand the past, present and future of the ocean, and the most important thing is that we lack the knowledge and hands to perceive, recognize and master the ocean. The health of the oceans depends largely on the state and safety of the organisms in the oceans. So, the theme of how to evaluate the health of the ocean should also be biology. We are concerned about marine eutrophication, because eutrophication can cause red tides and the increase of many harmful algae, which in turn will lead to the accumulation of algae toxins in shellfish that feed on algae, which will have a serious impact on human health and life when humans eat these shellfish. For a long time, our monitoring of the ocean emphasis on the environment, not the ecosystem, and the monitoring content is mainly chemical factors, with emphasis on pollutants, but the monitoring of organisms in the ocean is relatively weak, and the criteria we have long used to classify the state of the ocean are expressed by "several types of seawater", which is far from enough for the healthy ocean and sustainable development. Unable to meet the requirements of marine health assessment, we need to establish a marine health assessment system with marine organisms as the main body to monitor the ocean from the marine ecosystem The goal of measurement should be biological change and the environmental factors that lead to biological change.

VANT-GOFF'S LAW FOR VARIABLE TEMPERATURES

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According to this law, the rate V of an elementary homogeneous chemical reaction increases 2–4-fold each time when the temperature rises an additional 10°C. This relationship can be described by an exponential equation $V = \exp(Kt)$, where K is constant, and t is temperature, °C. This rate is expressed here in relative units for simplicity ($V = 1$ at $t = 0$°C).

The Vant-Goff's law is valid within a narrow temperature range from 0 to 100°C (liquid phase of water). The Arrhenius' equation works more accurately in a wider range. It has a thermodynamic basis, the Boltzmann's distribution. However, this equation uses the Kelvin scale for absolute temperatures, which starts at a threshold of –273.15°C. This temperature range is not "ecological" and is too wide to describe life on Earth.

In nature, temperature is rarely constant, varying in space and time. What should the average of reaction rate constant be in this case? In the present study, we attempted to find an answer to this question.

Variable temperature is characterized by frequency distribution (see Fig. 1). Temperature variations in space (the Sea of Japan stretches from southwest to northeast) and in time (all year-round seasonal observations combined over 20 years) are summarized here. Note the frequencies that fluctuate randomly near the same level of 0.04 in a wide range of temperatures, from 5 to 19°C.

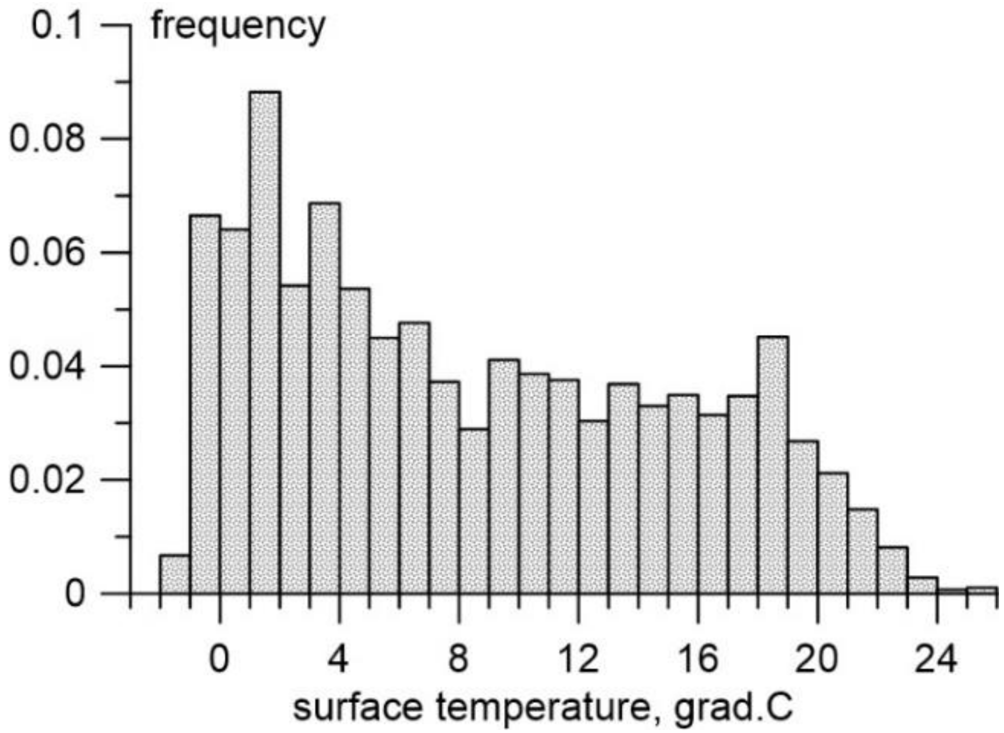

Fig. 1. Frequency distribution of surface temperature in the Russian economic zone of the Sea of Japan (Sukhanov, Ivanov, 2009).

The average constant of the reaction rate can easily be calculated by integrating with the known frequency distribution. However, separating the influence of arithmetic mean and temperature variability on this constant is a challenge. We here need a mathematical model.

We chose the simplest model of uniform (rectangular) distribution from the entire set of models (Hastings, Peacock, 1980). Its nonzero frequency remains unchanged in a temperature range from t_{min} to t_{max}. This distribution is characterized by two parameters: arithmetic mean M and standard deviation S:

$$M=(t_{min}+t_{max})/2, \qquad S=(t_{max}-t_{min})/\sqrt{12}. \qquad (1)$$

The average relative rate is found through integrating the chemical reaction rate $V = \exp(Kt)$ within limits t_{min} and t_{max}:

$$V = [\exp(Kt_{\max}) - \exp(Kt_{\min})] / [K(t_{\max} - t_{\min})].$$

Express the parameters $t_{\min}$ and $t_{\max}$ using M and S by Eq. (1).

As a result, the final exact solution is found by the following equation:

$$V = \frac{e^{K(M+C)} - e^{K(M-C)}}{2C}, \text{ where } C = \frac{S\sqrt{12}}{2}. \quad (2)$$

Estimate the parameter K from the definition of the Vant-Goff's law as an average of ln(2)/10 and ln(4)/10. Hence, $K = 0.10$. Plot the rate V as a function of M and S (Fig. 2): temperature, expressed as standard deviation S and mean M, respectively. Calculation was performed using by Eq. (2). The relative rate of the chemical reaction is equal to unity when $M = S = 0$°C.

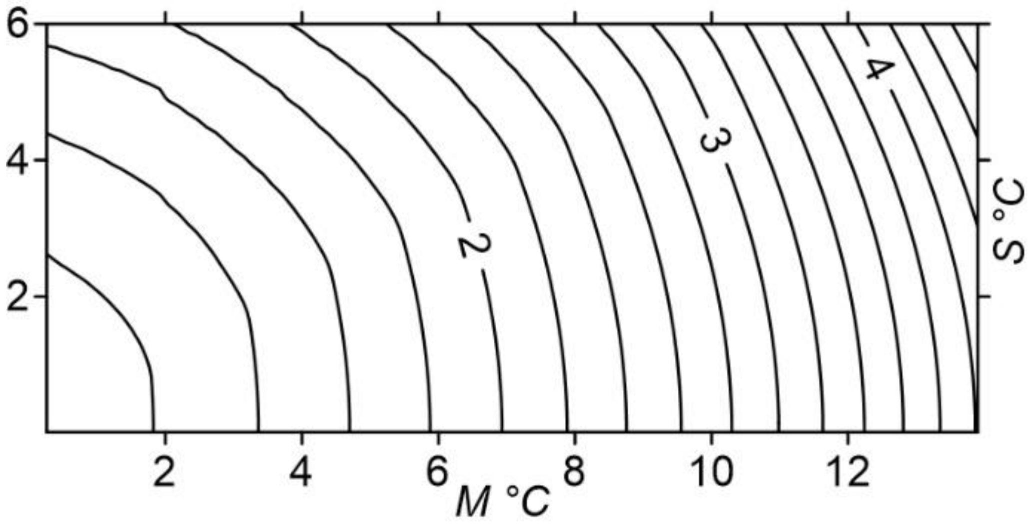

Fig. 2. Relationship of the average rate of chemical reaction with the variable

The graph in fFg. 2 illustrates an exact generalization of Vant-Goff's law for variable temperatures that show uniform distribution. Condensations of isolines on the right along the M axis means as follows. An increase in the mean temperature M has an effect on the average rate V in the exponential manner, as in the canonical Vant-Goff's law, which does not take into account temperature variability.

However, an additional effect is also clearly visible on the graph. The temperature scatter S is as exponential as the mean M: they work concordantly.

The effect of the standard deviation S is more pronounced at low temperatures. Other pasterns of distributions of variable temperature (dome-shaped, L-shaped, J-shaped, or polymodal) lead to the same phenomena as in the uniform distribution. This is caused by the greater contribution of the exponential Vant-Goff's function to the average reaction rate V at high temperatures.

The stimulating effect of variable temperatures on the vital activity of organisms was discovered long ago (Konstantinov, Zdanovich, Sholokhov, 1991). The presented model provides a theoretical basis for this economically important phenomenon.

One of the purposes of this paper was to explain the evolutionary patterns of marine bivalve mollusks living in the east of the Pacific coast. These patterns have been found through processing of materials (83 families, 302 genera, and 1306 species of Bivalvia) available in the Bernard's catalogue (1983).

USING BATHYMODIOLINAE MUSSELS AS MODEL ORGNISMS TO STUDY ADAPTATION AND EVOLUTION IN DEEP-SEA ENVIRONMENTS

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Deep-sea hydrothermal vents and cold seeps are submarine springs where reductive fluids emanate from the sea floor and support flourishing benthic communities based on chemoautotrophic primary production. Among the benthic animals, deep-sea mussels (Mytilidae: Bathymodiolinae) are of great ecological importance due to their high biomass and adaptive plasticity. *Gigantidas platifrons*, a deep-sea mussel endemic to the Northwest Pacific, is one of the few bathymodioline species capable of inhabiting two chemically distinct ecosystems: hydrothermal vents and methane seeps. They rely on nutritions provided by their methanotrophic (methane-oxidizing) endosymbionts housing in their gill bacteriocytes. Thus, *G. platifrons* is an excellent model for studying the variation of symbiotic microbes and their contribution to environmental adaption.

Herein, we conducted metatranscriptome analysis of *G. platifrons* collected from a methane seep at Formosa Ridge in the South China Sea and hydrothermal vents in the Mid-Okinawa Trough to study the adaptive strategies for different geochemical environments. The results revealed the active detoxification of sulfide in *G. platifrons* gills by both the symbiotic bacteria and host mussels. The Campylobacterota epibiotic bacteria were more abundant in vent mussels and contributed to environmental adaptation by active oxidation of extracellular H_2S. For endosymbionts, a key sulfide-oxidizing gene, sulfide:quinone oxidoreductase (sqr), was significantly upregulated in vent mussels, indicating the oxidization of intracellular sulfide by the

endosymbiont. In host mussels, genes involved in oxidative phosphorylation and mitochondrial sulfide oxidation pathway played important roles in the sulfide tolerance of the host mussels.

In addition, we conducted a fine-scale metagenomic analysis of endosymbionts to further distinguish their within-species variation in mussels from different environments. Strain-level genome assembly revealed the highly heterogeneous compositions of methanotrophic endosymbionts in vent and seep habitats. Phylogenetic analysis separated the assemblies into three distinct environment-linked clades. Their functional differentiation follows a mosaic evolutionary pattern. Core genes, essential for central metabolic function and symbiosis, were conserved across all clades. Clade-specific genes associated with heavy metal resistance, pH homeostasis, and nitrate utilization exhibited signals of accelerated evolution. Notably, transposable elements and plasmids contributed to the genetic reshuffling of the symbiont genomes and likely accelerated adaptive evolution through pseudogenization and the introduction of new genes.

In conclusion, our study uncovers the environment-driven evolution of deep-sea symbionts mediated by mobile genetic elements. Our findings highlight a critical role of heterogeneity in the symbiotic microbiome, providing new insights into the adaptive evolution of deep-sea symbiotic organisms.

DEEP-SEA OPHIUROIDEA (ECHINODERMATA) ON THE EMPEROR SEAMOUNT CHAIN IN THE NORTHWESTERN PACIFIC: SPECIES COMPOSITION, COMMUNITY STRUCTURE, BIOGEOGRAPHY

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More than 2,100 species of brittle stars have been found in the World Ocean, of which more than 1,409 species are found in the Pacific (Stöhr et al., 2012). Brittle stars are the largest and species-reach class of echinoderms, dominating benthic communities and often associated with typical benthic taxa on seamounts, i.e. corals and sponges (Boissin et al., 2016). The species diversity of brittle stars is underestimated, not all available data have been analyzed and many taxa presently need revision (O’Hara et al., 2019).

The distribution of echinoderm larvae, particularly brittle stars, is determined by oceanographic conditions and currents. The main environmental factors influencing distribution are salinity, temperature, and advection (Doll et. al, 2022). Seamounts are promising for the study of the fauna of brittle stars, as they serve as facilitators in the dispersal of bottom fauna over long distances as “stepping stones”, provide shelter from unfavorable conditions and promote speciation (O’Hara, 2007; O’Hara and Tittensor, 2010). Deep-sea ecosystems of the seamounts, including those of the ESC, are recognized as vulnerable, but interest in mining iron-manganese crust minerals from the sea is growing in the world and makes the issue of conservation their biodiversity more pressing than ever (Washburn et al., 2023).

The Emperor Chain, a part of Hawaiian–Emperor seamount chain, consists of more than 30 seamounts and guyots, extending from the Northwestern Hawaiian Islands and ending off the coast of the Kamchatka Peninsula. The Emperor Seamount Chain (ESC) is a long barrier capable of modifying the direction and nature of currents. It divides the Kuroshio current into a weak flow in the north and a strong flow in the south between 33º and 35ºN, moving northward to 38ºN before reversing direction. The physical-geographical characteristics, morphostructures, and geological history of the seamounts of the Emperor Chain may be important factors influencing biogeography, phylogeography, and evolutionary processes of Ophiuroidea, particularly in the Pacific Ocean, where the highest number of endemic species has been recorded in its eastern and northern parts (Greshanovich et al., 1977; O’Hara, 2007; Stöhr et al., 2012).

Representatives of the class Ophiuroidea were collected from the Koko Guyot, Ojin Guyot, Jingu, Nintoku,Yuryaku, and Kimmei seamounts during expeditions conducted by the A.V. Zhirmunsky National Scientific Center of Marine Biology of the Far Eastern Branch of the Russian Academy of Sciences (FEB RAS), in collaboration with the P.P. Shirshov Institute of Oceanology and other institutes of the Russian Academy of Sciences aboard the research vessel *Akademik M.A. Lavrentyev* in July–August 2019 (cruise LV86-2019) and in July–September 2021 (cruise LV94-2021). More than one hundred samples of ophiuroids were collected during 27 dives at depths up to 2235 m using the remotely operated vehicle (ROV) Comanche 18 (Sub-Atlantic, UK) and were placed in a sample container. The information on the ophiuroids occurrences were also documented through photographs and over 70 hours of video recordings. The photo and video materials were used to analyze the distribution of ophiuroids and the composition of their communities. All collected specimens were preserved in a 70% ethanol solution, while arm’s fragments were preserved in a 96% ethanol. The samples are stored in the Museum of the National Scientific Center of Marine Biology (MIMB, Vladivostok, Russia).

Specimens were identified based on morphological characteristics following the latest taxonomic system (O'Hara et al., 2018). For the identification of ophiuroid specimens, different literature sources were used (Djakonov, 1954; Fell, 1960; Goharimanesh et al., 2021; Martynov, 2010; Stöhr et al., 2010; 2012, O'Hara et al., 2017; Thuy and Stöhr, 2011; 2016). The Bray-Curtis similarity analysis was performed using the PRIMER 6 software package (Clarke and Gorley, 2006).

The present study focused on Ophiuroidea collected during expeditions in 2019 and 2021 in the area of the Emperor Seamount Chain. The aim was to provide data on the diversity of brittle stars on the seamounts, as well as their vertical distribution. Representatives of 29 species, 17 families, and 21 genera of the class Ophiuroidea have been identified, and their association with different types of substrate (sandy sediment with silt and basalt outcrops, solidified lava and rocky bottom) on the ESC have been revealed. Dominant species was found on different seamounts. The benthos of the ESC was found to contain a large number of brittle star taxa, which were dominant or significant components of the communities. A correlation between different brittle star taxa and specific substrate types was identified. Due to the spatial extent of the ESC, communities contain groups of brittle stars with very different biogeographical characteristics. The Bray-Curtis similarity analysis confirmed the presence of a biogeographical boundary around 37ºN, where the North Pacific ophiuroid set of species intersects with that of Central Pacific origin.

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COMPARATIVE PHYLOGEOGRAPHY AND ADAPTIVE GENOMICS OF TWO SYMPATRIC MANGROVE LUCINID CLAM SPECIES ALONG THE SOUTH CHINA SEA COAST

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We investigate the genetic diversity, population structure, and adaptive mechanisms of two sympatric lucinid clam species, *Indoaustriella scarlatoi* and *Rugalucina vietnamica*, distributed across intertidal mangrove zones along the South China Sea coast. By employing whole-genome resequencing, a total of 73,937,613 and 137,833,997 high-quality SNPs were identified for *I. scarlatoi* and *R. vietnamica*, respectively. Population genetic analyses revealed distinct clustering patterns in *I. scarlatoi*, forming two geographically defined groups: the Beibu Gulf group and the eastern Qiongzhou Strait group. In contrast, *R. vietnamica* populations exhibited weaker genetic differentiation with less-defined geographic structuring. Selective sweep analyses highlighted species-specific adaptations. In *I. scarlatoi*, genes associated with fatty acid metabolism were enriched, suggesting adaptation to desiccation stress in the upper intertidal zone. Meanwhile, *R. vietnamica* showed enrichment in genes related to protein degradation and recycling, indicating an adaptive advantage in utilizing dissolved organic matter in aquatic environments. These findings underscore divergent energy utilization strategies as a potential driver of species coexistence. This study provides genomic resources for lucinid clam research and offers insights into the conservation and utilization of resources in South China Sea mangrove ecosystems. The results enhance our understanding of the genetic architecture underlying environmental adaptation and historical population dynamics in these ecologically significant bivalves.

OBSERVATIONAL STUDY OF DEEP OCEAN CIRCULATIONS IN THE WESTERN PACIFIC

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The deep branch of the Pacific Meridional Overturning Circulation (i.e., Pacific deep circulation) is a crucial element of the ocean's climate and biogeochemical systems through carrying the Upper and Lower Circumpolar Waters from Antarctica. A thorough understanding of the pathways and volume transport of Pacific deep circulations is an important objective of the oceanographic and climate communities. We designed full-depth mooring arrays, developed new technologies to enable real-time transmission of deep ocean data, and established an observing network for deep ocean circulations in the western Pacific. Based on the deep mining of mooring observation and model data, we draw the first map for the structure and volume transport of deep circulations at depths below 2500 m in the western Pacific, revealed the pathway, volume transport, and variability of the western Pacific deep circulations, and deepened the understanding of the mechanisms governing energy interconnections and transfer across the entire water column of the open ocean.

CONSIDERATIONS FOR REDUCING HUMAN EXPOSURE TO MICROPLASTICS FROM CONSUMPTION OF FISH

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As global plastic waste production continues to rise significantly in the coming decades, microplastics (MPs) remain one of the most challenging pollutants in environmental contamination worldwide. MPs are widely distributed in the ocean and can be ingested by fish. Despite fish being a major source of aquatic protein for humans, no study has yet addressed how to reduce the risk of human exposure to MPs when consuming fish. This study investigated 1,075 fish from 37 species across representative fishing areas, analyzing MP presence in various tissues, including gills, intestines, and muscles, to assess fish food safety comprehensively. MPs (particles > 20 μm in size) were detected in 36.28% of gills and 39.63% of guts, but were not found in muscle tissues. Fish from upper layers had higher MP abundances and smaller average sizes compared to those from deeper waters. A significant negative correlation was observed between the MP abundance in fish and their length and weight. The global per capita MP consumption from captured fish, including all tissues and muscles, is approximately 5.60×10^4 items/year. To minimize MP exposure, humans should prioritize consuming only fish muscle and selecting fish from deeper waters and larger sizes whenever possible. Optimizing fish consumption patterns could reduce human exposure to MPs and associated health risks.

REPRODUCTION OF RHIZOCEPHALA: NEW DATA ON RECEPTACLE DEVELOPMENT

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Parasitic barnacles of the infraclass Rhizocephala parasitize mainly on decapods, including commercially valuable species. The adult rhizocephalan is a female organism consisting of a root system within the host's body (interna) that provides the parasite with food and the parasite's reproductive body (externa). In rhizocephalans with the kentrogonid type of development, the externa contains a visceral sac with developing ovary and receptacles, specialized organs that host cryptic dwarf males reduced to spermatogenic tissue. Dwarf males are implanted into receptacles by trichogon-larvae. Spermatogenic cells are nourished by surrounding female tissue and cyclically produce spermatozoa in synchrony with oviposition. Ultrastructural analysis of receptacles will help to clarify the cellular mechanisms of interaction between female and male organisms. Among sacculinids, there are species with both tubular receptacles located inside the visceral sac and globular ones arranged outside the visceral sac. To date, morphogenesis and the initial stages of the transformation of the trichogon in *Sacculina carcini* (Sacculinidae) with tubular receptacles have been studied, whereas no ultrastructural data for the organization of globular receptacles are available.

The complete cycle of receptacle development in the barnacle *Parasacculina pilosella* (Rhizocephala: Polyascidae) parasitizing on the spider crab *Scyra* aff. *ferox* from Peter the Great Bay (Sea of Japan) was studied by light and electron microscopy. This rhizocephalan has two globular receptacles located outside the visceral sac. Two variants of receptacle development from the same externa were observed: (1) with two fertile receptacles and (2) with one fertile (usually the larger one) and the other sterile. The presence of the second fertile receptacle probably extends the breeding season in *P. pilosella*. The following stages in the development of the fertile receptacle were identified: trichogon-free, trichogon-containing, early, middle, late, and degenerating. The sterile receptacle that had not received a trichogon continued to develop and, after reaching the middle stage, atrophied. The cell types composing the receptacle wall (accessory, large female, polygonal, small-sized, and sheath cells) and the meshwork formed by the intercellular matrix were examined in detail. The accessory cells that separated spermatogenic and large female cells were probably derived from the trichogon which implanted cells of both germ and somatic lines. Globular and tubular receptacles are organized differently. Both receptacle types lacked morphological structures separating female and male organisms. Further studies, involving a larger number of other rhizocephalan species, are needed to clarify whether the receptacle ultrastructure can be useful in resolving taxonomic issues.

All microscopic studies were carried out at the Far Eastern Center of Electron Microscopy, A.V. Zhirmunsky National Scientific Center of Marine Biology FEB RAS, Vladivostok, Russia.

DEEP-SEA FAUNA DISTRIBUTION AND EVOLUTIONARY MECHANISMS ON WESTERN PACIFIC SEAMOUNTS

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The deep sea remains largely unexplored yet plays a vital role in sustaining ocean ecosystems. Over the last decade, we have undertaken several deep-sea surveys on seamounts in the central West Pacific Ocean, and cooperated with the National Institute of Water and Atmospheric Research (NIWA), culminating in a joint dataset of seafloor video imagery and specimen collections from seamounts. This study comprehensively investigates the distribution patterns and evolutionary mechanisms of deep-sea fauna on seamounts in the western Pacific Ocean. By integrating historical data, establishing a database of deep-sea biological resources, analyzing international research trends, and conducting biodiversity and systematic studies, the project identifies over 300 species of macrobenthos, including cnidarians, molluscs, and echinoderms. These findings highlight the high heterogeneity and uniqueness of seamount ecosystems, strongly supporting the "biodiversity hotspot" and "island" hypotheses. Furthermore, by exploring dispersal pathways and evolutionary histories among seamounts, the study provides a novel theoretical framework for understanding the origin, dispersal, and evolution of deep-sea taxa. Analyses of seafloor imagery show that dominant taxonomic groups varied by seamount and differences between

regions aligned with the larger spatial scale analyses done for the physical specimens. In addition, while it is likely there is a gradation between regions, individual seamount community differences were very strong indicating the importance of understanding spatial scale in interpretation of regional biodiversity trends. The findings have significant implications for global ocean conservation efforts, including contributions to the UN Ocean Decade initiative and habitat suitability models for Vulnerable Marine Ecosystems (VMEs). These results enhance our understanding of deep-sea biodiversity and inform regional and international management strategies for sustainable marine resource use.

The study was supported by the National Key Research and Development Program of China (grant no. 2021YFE0193700).

PHYSIOLOGICAL AND BEHAVIORAL CHARACTERISTICS OF SEA CUCUMBERS: COGNITION AND APPLICATIONS

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The sea cucumber, *Apostichopus japonicus*, is abundantly found along the coastal areas of the Northwest Pacific Ocean. In China, *A. japonicus* holds a prominent position in the aquaculture industry, covering an expansive area of 250,400 hectares, which accounts for 12.07% of the nation's total marine aquaculture area, making it one of the most economically valuable species. Moreover, sea cucumbers (phylum Echinodermata) represent a critical transitional group in animal evolution between non-chordates and chordates, having evolved unique physiological and behavioral adaptations including aestivation, regeneration, reproductive strategies, and locomotor rhythms through long-term environmental selection. Our research team has made seminal contributions by establishing the first chromosome-level genome assembly for sea cucumbers, which has enabled groundbreaking insights into the molecular mechanisms governing their environmental adaptability and behavioral plasticity under climate change scenarios. To address pressing conservation challenges such as declining wild populations and germplasm deficiencies, we have pioneered innovative approaches including the development of germplasm preservation protocols, precision breeding systems incorporating molecular markers, and ecologically sustainable seedling production technologies. Furthermore, by elucidating the species' ecological functions, we have engineered novel habitat restoration devices and resource management solutions that synergistically enhance both sustainable aquaculture production and critical ecosystem services, demonstrating the translational potential of fundamental research in marine organism biology.

CHROMOSOME-LEVEL GENOME ASSEMBLY OF THE DEEP-SEA CHITON *GRANDIDENSICHITON CHINENSIS* PROVIDES INSIGHTS INTO THE ADAPTATION TO THE COLD SEEP HABITAT

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Cold seeps, characterized by methane, hydrogen sulfide, and other hydrocarbon chemicals, support one of the most widespread chemosynthetic ecosystems in the deep sea, which are densely populated by specialized benthos. However, the adaptive mechanisms of organisms to these extreme marine ecosystems remain poorly understood. In this study, we present a high-quality 2.01 Gb chromosome-level genome of a deep-sea chiton, *Grandidensichiton chinensis* n. sp., anchored to 11 pseudo-chromosomes. The genome assembly features with a contig N50 of 12.95 Mb and a scaffold N50 of 241.03 Mb, covering 95.7% of metazoan BUSCOs. Its large genome size, surpassing most reported chiton genomes, is likely attributed to the high proportion of transposable elements (TEs). Comparisons of the genomes between *G. chinensis* and the shallow-sea species *Acanthochitona rubrolineata* revealed that TE transposition may trigger chromosomal changes, including inter-chromosomal fusions and intra-chromosomal activities such as inversions, rearrangements and fusions. We predicted 24,550 genes for *G. chinensis*, with 93.79% having functional annotations. Divergence time estimation indicates that the ancestor of Mollusca emerged around 571.48 mya, and the ancestor of Polyplacophora around 348.49 mya. In the *G. chinensis* genome, 1,416 gene families expanded and 896 contracted. GO and KEGG enrichment analysis shows that the expanded gene family and positive selection genes are associated with various functions, including cell membrane, microtubule, cytoskeleton, DNA repair, immune response, ABC transporters, unsaturated fatty acid synthesis, hypoxia-inducing factors, circadian rhythm, and more. The expansion of the ABC transporter gene family may aid in detoxification, while the duplication of genes related to endocytosis, immunity, apoptosis, and anti-apoptotic domains may help *G. chinensis* combat microbial pathogens. Comparative analysis also identified positive selection signals in numerous genes, including the hypoxia up-regulated protein 1, a chaperone that may facilitate *G. chinensis* adaptation to hypoxic deep-sea conditions. These findings suggest that *G. chinensis* has adapted to extreme deep-sea environments, such as high hydrostatic pressure, darkness, hypoxia, and heavy metal ions, through gene expansion and positive selection. The high-quality assembly and in-depth characterization make the *G. chinensis* genome a vital resource for understanding the origin and adaptation of life in cold seeps.

АО «Восточный порт»

Экологическая безопасность, забота об окружающей среде и жителях – приоритет №1 в работе АО «Восточный Порт».

От выпуска миллионов мальков рыб до проведения масштабных экологических мероприятий – компания вносит большой вклад для сохранения природы Приморья. Недаром наш ежегодный «Экомарафон» уже 10 лет вдохновляет местных жителей на заботу о планете.

Среди многочисленных экопрограмм стивидорной компании особое место занимает поддержка проектов Национального научного центра морской биологии имени Алексея Викторовича Жирмунского Дальневосточного отделения Российской академии наук.

С 2021 года, в рамках двустороннего соглашения, предприятие оказывает поддержку проектам приморских учёных, направленным на изучение и сохранение среды обитания прибрежной флоры и фауны и создание условий для стабильного существования морских экосистем в заливе Петра Великого Японского моря.

За это время портовики приобрели самые современные камеры для наблюдения за ларгами в их естественной среде обитания на острове Кентавр в морском заповеднике, подарили океанариуму зимний карантинный модуль со всем необходимым оснащением для обследования животных, закупили новое эндоскопическое оборудование для осмотра и биопсии внутренних органов морских млекопитающих.

«Восточники» регулярно финансируют научные экспедиций, организацию круглых столов и научных конференций, посвященных изучению и защите морских млекопитающих.

Помощь АО «Восточный Порт» стала большим подспорьем для ученых в деле изучения биологического разнообразия Японского моря и сохранения популяции уникального пятнистого тюленя-ларги.

ВОСТОЧНЫЙ ПОРТ
АКЦИОНЕРНОЕ ОБЩЕСТВО

ООО «Группа компаний Лабконцепт» — официальный дистрибьютор ведущих мировых и российских производителей аналитического, испытательного, общелабораторного оборудования, мебели и расходных материалов. Собственные производственные площадки расположены в Санкт-Петербурге, на одной из них производится узловая сборка высокоэффективных жидкостных хроматографов под торговой маркой LicArt 62, на другой – полный цикл сборки лабораторной весоизмерительной техники, а также оборудования для пробоподготовки.

Преимущества компании:

- Аналитическая лаборатория, оснащенная современным оборудованием, позволяющая проводить полное тестирование приборов, оперативно работать с собственными и клиентскими методиками
- Собственное сборочное производство хроматографического оборудования и производство полного цикла высокоточного весоизмерительного оборудования, а также оборудования для пробоподготовки.
- Обучение персонала лабораторий заказчиков: начальное, углубленное, по индивидуальным программам, теоретическое и практическое.
- Возможности по доработке и адаптации приборов, в том числе сторонних производителей под специализированные задачи заказчиков.

Лабконцепт

Russia–China Bilateral Workshop *Marine Biology and Biodiversity Science in the 21st Century*, September 23–24, 2025, Vladivostok, Russia

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Лабконцепт