

Chinese Academy of Sciences
INSTITUTE OF OCEANOLOGY

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

**MARINE BIODIVERSITY AND ECOSYSTEMS
IN A CHANGING OCEAN:
TOWARD SUSTAINABLE DEVELOPMENT GOALS**

Proceedings of the China – Russia Bilateral Workshop

Edited by Sun Xiaoxia, Zhang Junlong, Zheng Shan

October 17–19, 2023, Qingdao, China

Proceedings of the China – Russia Bilateral Workshop

Marine Biodiversity and Ecosystems in a Changing Ocean: toward Sustainable Development Goals

October 17–19, 2023, Qingdao, China

Organizing Committee

CHINA: Prof. **Wang Fan**, Director of the Institute of Oceanology, Chinese Academy of Sciences (Chair), IEAS Academician, Prof. **Sun Song**, Prof. **Sun Xiaoxia** (Deputy Co-Chair), Prof. **Yu Rencheng**, Prof. **Xu Kuidong**, Prof. **Zhang Junlong**, Dr. **Li Yanwei**

RUSSIA: Dr. **Igor Yu. Dolmatov**, Director of the A.V. Zhirmunsky National Scientific Center of Marine Biology, Far Eastern Branch of the Russian Academy of Sciences (Co-Chair), RAS Academician, Prof. **Andrey V. Adrianov**, Dr. **Konstantin A. Lutaenko** (Deputy Co-Chair), Dr. **Tatiana Yu. Orlova**, Dr. **Olga G. Shevchenko**, Dr. **Tatiana N. Dautova**

CONTENTS

Deep-water Ecosystems in the North-West Pacific

A.V. Adrianov, V.V. Mordukhovich..... 1

Long-term changes in the phytoplankton community structure and their underlying drivers in the past decades in the southern Yellow Sea, China

Xiaoxia Sun, Shujin Guo..... 3

Environmental and climatic changes and their impact on mollusks in the Sea of Japan and adjacent areas: composition, abundance and distribution

Konstantin A. Lutaenko..... 4

Paralytic shellfish toxins produced by dinoflagellate *Gymnodinium catenatum* and their biokinetics in marine bivalves

Rencheng Yu, Zhuoru Lin 8

Subtropical brackish tintinnid community temporally organized by temperature preference and LOD class-size

*Jingyuan Li, Ping Du, Wuchang Zhang** 9

Primorsky Aquarium – Branch of the National Scientific Center of Marine Biology, Far Eastern Branch of the Russian Academy of Sciences (NSCMB FEB RAS)

Olga G. Shevchenko..... 11

Prediction and verification of hypoxia in central Bohai Sea in 2022

Jie Guo, Yanfang Li, Xiangyang Zheng, Diansheng Ji, Chawei Hou* 13

A comparison of the sensory and nervous systems in the larvae of the marine and freshwater bivalves

Elena M. Sayenko, Viktoria E. Nikishchenko, Vyacheclav A. Dyachuk, Igor A. Rodionov..... 14

Kinorhynch species show much wider distribution then previously thought <i>Andrey V. Adrianov, Anastassya S. Maiorova</i>	16
Degradation of plastics in marine habitats, studied using Raman microspectroscopy and atomic force microscopy (AFM) <i>Vyacheslav S. Odintsov, Alexander A. Karpenko, Maxim A. Karpenko</i>	18
Hidden diversity: discovery of an association of parasitic and hyperparasitic isopods (Crustacea: Isopoda: Epicaridea) from a king crab <i>Lithodes aequispinus</i> Benedict, 1895 in the Bering Sea, the North Pacific <i>Olga A. Golovan, Taras B. Morozov</i>	21
Algological studies of brackish waters (river estuaries, lagoon-type lakes) of the Russian Far East <i>Tatyana V. Nikulina, Irina V. Motylkova</i>	23
Global environmental changes and possible effects on microalgae communities with emphasis on toxic species on the Russian east coast <i>Tatiana Orlova</i>	25
Shell-boring worms – a problem in marine aquaculture <i>Vasily I. Radashevsky</i>	27
Sipunculans, the worms of every ocean <i>Anastassya S. Maiorova, Andrey V. Adrianov</i>	28
Molluscan remains in the Bohai archaeological sites (698–926 AD) in Primorye (south of the Russian Far East) as an indicator of regional climate and environmental changes <i>Konstantin A. Lutaenko, Elena M. Sayenko</i>	30
Basket stars Gorgonocephalidae (Echinodermata: Ophiuroidea) and their distribution on the Emperor Seamount Chain <i>Anastasia L. Volkova, Tatyana N. Dautova, Salim Sh. Dutov</i>	33

Activity of certain types of phagocytes of holothurians under the influence of damaging environmental factors

Ludmila S. Dolmatova 35

Biodiversity of the transboundary Razdolnaya River (Russia-China) and problems of its estuarian biota protection under climatic and anthropogenic impact

Tatyana S. Vshivkova, Tatyana V. Nikulina, Konstantin A. Lutaenko..... 37

Diversity and distribution of the order Cumacea in the Kuril—Kamchatka Trench area

Anna V. Lavrenteva..... 40

Trophic characteristics of Bivalvia from shallow-water Laptev Sea

*Alena V. Konoplina**, *Serguei I. Kiyashko, Konstantin A. Lutaenko, Tatiana N. Dautova*..... 42

Single-cell RNA-Seq Reveals Epithelial Cell Regulation of Intestine Regeneration Initiation in Sea Cucumber (*Apostichopus japonicus*)

*Fang Su, Lina Sun**, *Hongsheng Yang, Libin Zhang, Chenggang Lin* 44

Dynamics of glycerophospholipid molecular species during the embryonic development of the red king crab *Paralithodes camtschaticus*

*Ermolenko E.V.**, *Sikorskaya T.V., Rodkina S.A., Gevorgyan T.A., Maslennikov S.I.* 45

Corals as an indicator of the vulnerable marine ecosystems — state of knowledge and perspectives

Tatiana N. Dautova..... 47

Crabs of genus *Chaceon* Manning & Holthuis, 1989 (Decapoda: Brachyura: Geryonidae) in the deep-sea environment of Emperor Seamount Chain

Evgeniia L. Egorova 49

Investigations on the deep-sea Isopoda of the Northwest Pacific on base of recent expeditions

Olga A. Golovan, Marina V. Malyutina 50

Gastropods of the Kien Luong and Con Dao mangroves (Kien Giang Pr. and Ba Ria-Vung Tau Pr., Vietnam)

Prozorova Larisa A...... 52

On the systematic position of *Anadara kafanovi* Lutaenko, 1993 (Bivalvia, Arcidae) based on morphological and genetic analysis

Marina S. Ananeva, Ulyana V. Simakova, Galina A. Kolyuchkina, Philipp V.

Sapojnikov, Konstantin A. Lutaenko..... 54

Gastropods from the Pacific northernmost chemosynthetic ecosystems

Ivan O. Nekhaev, Yuri I. Kantor, Elena M. Chaban,

Elena I. Rybakova..... 56

Phylogenetic relationships of populations of chemosymbiotrophic bivalves *Calyptogena pacifica* (Vesicomidae: Pliocardiinae) from the Bering Sea and the eastern Pacific Ocean

Belov D.A., Kremenetskaya A.V., Krylova E.M...... 58

Macrobenthos functional feeding group and the ecosystem health assessment of the intertidal zone in the Yellow River Delta

Shaoyu Jiang, Chuanxin Zhang, Zirui Peng, Linlin Chen ,

*Quanchao Wang, Baoquan Li** 60

Macrobenthic diversity and eco-exergy evaluation of wetland restoration in the Yellow River Delta

Yanmei Ni, Chunyun Liu, Li Chen, Debin Sun, Zhiyuan Dong,

*Baoquan Li, Linlin Chen** 61

Benthic food web structure of Xiaoqing River Estuary revealed by carbon and nitrogen stable isotope analysis

Chuanxin Zhang, Jing Chen, Linlin Chen, Ronglian Xing, Baoquan Li** 63

Co-occurrence patterns of macrobenthic community in the intertidal zone and offshore areas of the Yellow River Delta, China

*Jiao Wang, Linlin Chen, Shaoyu Jiang, Baoquan Li** 65

Characteristics and temporal evolution of heat waves in Jiaozhou Bay	
<i>Jing Wang, Xiaoxia Sun, Yongfang Zhao</i>	67
Quantification of the vertical transport of microplastics by biodeposition of typical mariculture filter-feeding organisms	
<i>Liujiang Meng, Xiaoxia Sun*, Qingjie Li, Shan Zheng, Junhua Liang, Chenhao Zhao</i>	68
Scenario Simulations of marine ecosystem health on China’s coast	
<i>Ziyuan Hu</i>	70
Water column stratification governs picophytoplankton community structure in the oligotrophic eastern Indian ocean	
<i>Feng Wang, Shujin Guo, Junhua Liang</i>	71
Characteristics of microplastics in different matrices in Jiaozhou Bay, China	
<i>Shan Zheng, Kangning Zhang</i>	73
Long-term Ecological Dynamics of Phytoplankton Communities under Environmental Drivers in Jiaozhou Bay	
<i>Shimeng Yang</i>	74
Study on the spatiotemporal distribution of the sea star <i>Asterias amurensis</i> based on in-situ image in Jiaozhou Bay, China	
<i>Mingliang Zhu, Chenhao Zhao, Junhua Liang</i>	76
Occurrence, Characteristics, and Factors Influencing the Atmospheric Microplastics around Jiaozhou Bay, Yellow Sea	
<i>Chenhao Zhao, Junhua Liang, Mingliang Zhu, Shan Zheng, Yongfang Zhao</i>	77
Genetic diversity and population structure of <i>Acanthochitona rubrolineata</i> from China revealed by 2b-RAD	
<i>Shaobing Zong, Junlong Zhang*</i>	78

Cryptic diversity revealed by integrative taxonomy: common chitons (Polyplacophora, Mollusca) from the coastal areas of China	
<i>Huijie Liu, Junlong Zhang*</i>	80
Carbon biomass, carbon-to-chlorophyll a ratio and the growth rate of phytoplankton in Jiaozhou Bay, China	
<i>Shujin Guo</i>	82
Integrative taxonomy reveals a new razor clam (Bivalvia, Pharidae) from the South China Sea	
<i>Yanan Yu, Yingyi Jiao, Junlong Zhang*</i>	83
Seasonal dynamics of reserve lipids in symbiotic corals <i>Sinularia flexibilis</i> and <i>Millepora platyphylla</i> from the South China Sea	
<i>T.V. Sikorskaya, L.P.T. Dang</i>	84
Integrative taxonomy of four new octopods found in the northwestern Pacific Ocean	
<i>Yan Tang, Junlong Zhang*</i>	86

Deep-water Ecosystems in the North-West Pacific

A.V. Adrianov^{1,2}, V.V. Mordukhovich^{1,3}

¹*A.V. Zhirmunsky National Scientific Center of Marine Biology, Vladivostok 690041, Russia*

²*Lomonosov Moscow State University, Moscow 119991, Russia*

³*Far Eastern Federal University, Vladivostok, Russia*

The World Ocean occupies 71% of the surface of our planet, with an average depth of about 3700 m. It is a colossal volume of living space, two orders of magnitude greater than the volume of living space on land; life fills it from the surface to maximum depths. In recent years, thanks to the development of underwater robotics and bottom sampling technologies, deep-sea research of the World Ocean has been developing dynamically. High biodiversity has been found on continental slopes, abyssal plains, and in deep-sea trenches, and many hundreds of new species have been described from a variety of marine biota taxa originating from these zones.

The ideas about the resources of the World Ocean are also being revised. Biological, mineral and energy resources of the World Ocean are increasingly considered as a determining factor in the future sustainable development of our civilization. With their rational use, they can cover the needs of all mankind for hundreds of years to come, providing future generations with practically inexhaustible sources of energy, mineral resources for industrial development, high-quality food and medicines. However, the evaluation of the condition of deep-sea ecosystems, their stability, and the feasibility of rational nature management is substantially hampered by the lack of comprehensive data.

The Northwest Pacific is one of the most interesting regions of the world's oceans in terms of the diversity of landscapes, biotopes, and communities inhabiting them. It is also one of the most productive regions with the richest biological resources. Huge mineral deposits are concentrated there: gas hydrates, barites, ferromanganese crusts and nodules, cobalt-rich manganese crusts, and deep-sea polymetallic sulfides.

For many years, NSCMB FEB RAS has conducted integrated field studies of deep-sea ecosystems in the NW Pacific, including potentially ore-bearing seabed areas. Using modern technical tools (box corers, multicorers, automated sledges, remotely

operated (ROV) and autonomous (AUV) underwater vehicles) NSCMB FEB RAS studied unique ecosystems of deep-sea trenches, abyssal plains, and seamounts. Benthos of all size classes were collected for all types of biological studies.

A comprehensive study of biological diversity in deep waters has led to the most interesting discoveries, forcing us to significantly reconsider our ideas about the quantitative and qualitative composition of deep-sea biota. The data obtained indicate an extremely low degree of the knowledge of the deep-sea biota and, at the same time, its amazing diversity. A change in ideas about deep-sea biodiversity, including areas where mineral deposits are concentrated, has given rise to one of the urgent problems of modern deep-sea oceanology - the search for a scientifically based compromise between the extraction of valuable mineral and energy resources, the development of fisheries and the conservation of deep-sea ecosystems with their huge biological diversity.

Long-term changes in the phytoplankton community structure and their underlying drivers in the past decades in the southern Yellow Sea, China

Xiaoxia Sun^{1,2}, Shujin Guo^{1,2}

¹*Jiaozhou Bay Marine Ecosystem Research Station, Institute of Oceanology, Chinese Academy of Sciences, Qingdao 266071, PR China*

²*Laboratory for Marine Ecology and Environmental Science, Pilot National Laboratory for Marine Science and Technology (Qingdao), Qingdao, 266237, PR China*

E-mail: xsun@qdio.ac.cn

The phytoplankton community in the southern Yellow Sea (SYS) is experiencing significant physical and chemical stresses due to human-driven and climate-induced changes. We collected historical data on phytoplankton communities and various environmental factors spanning from 1959 to 2023 to investigate how the phytoplankton community responds to long-term environmental changes in the SYS. During this period, the SYS consistently witnessed warming trends, with a surface layer warming rate of 0.61 °C/decade observed from 1959 to 2023. Nitrogen (N) concentrations and N/P ratios increased due to eutrophication and the growth of the mariculture industry, while silicon (Si) levels remained relatively constant. These changes resulted in a substantial rise in phytoplankton biomass (cell abundance and chlorophyll a), accompanied by a decline in the diatom-dinoflagellate ratio within the SYS. In the past, dominant net-collected species were primarily chain-forming diatoms. However, more recently, larger dinoflagellates species have shown an increasing dominance in the SYS. Additionally, the ecological characteristics of phytoplankton have undergone transformation, with warm-water phytoplankton species becoming more frequent. Furthermore, the dominant species have shifted from temperate-eurythermal to temperate-subtropical taxa as the waters have warmed due to global warming and hydrographic changes. Our study suggests that the notable shift in phytoplankton communities in the past decades are closely associated with increased anthropogenic activities and climate change in the SYS.

Environmental and climatic changes and their impact on mollusks in the Sea of Japan and adjacent areas: composition, abundance and distribution

Konstantin A. Lutaenko

*A.V. Zhirmunsky National Scientific Center of Marine Biology FEB RAS, Vladivostok
690041, Russia*

E-mail: lutaenko@mail.ru

Mollusks play an important role as diversity-rich and abundant, often dominant organisms in coastal, estuarine and deep-sea communities and ecosystems. They are major ecological engineers in temperate and tropical-subtropical latitudes forming oyster banks and mussel beds, dense infaunal settlements and providing a substrate for many encrusting and fouling animals and plants, even their empty shells serve as a home for numerous bioeroding organisms. Mollusk' fishery and aquaculture are crucial in economies of many coastal countries. However, modern global environmental changes lead to deterioration of habitats and impact on biodiversity, distribution and abundance of mollusks and we summarize herein data on current changes in one of the molluscan biodiversity hotspot, the Sea of Japan and adjacent areas.

Driving forces of molluscan communities and biodiversity changes/modifications may include climate change impacts, pollution, hypoxia, impact of fisheries (and aquaculture) and poaching (illegal fishing), habitat transformation (coastal changes, urbanization, construction, etc.), invasive species impact, ocean acidification, impact of tourist industry. These factors are same for the overall biodiversity changes. However, a scale of changes and impacts in the Sea of Japan are not well-known.

In many areas of Peter the Great Bay, no substantial changes in benthic communities were detected despite earlier observations in the 1950s–1970s indicated a decrease of bivalve populations. For instance, Klimova (1975) suggested a decline of population density of the abundant infaunal boreal-arctic bivalve *Liocyma fluctuosum* (Veneridae) and even its complete disappearance at depths down to 70 m due to siltation. Data of Moshchenko and Belan (2008) about an “ecocatastrophe” confirmed at least by depressed state of bivalves fauna in the end of the 1980s the northern part of the

Amursky Bay are in contradiction to the faunal analysis of bivalves in Amursky Bay (Lutaenko, 2003) and the quantitative data of Galysheva and Nadtochy (2008): bivalves were most dominant by biomass in the inner part of Amursky Bay, contributing 74% of the total biomass; the composition of dominant species in the latter work was very different studies and included many large species while only smaller bivalves were indicated by Belan et al. (l.c.); excellent development of oyster reefs and their wide distribution, along with accompanied bivalves (Sokolenko, Kalinina, 2018), shows that previous information about their depressed state was incorrect and largely based on unreliable observation, without large-scale collecting and mapping of bottom communities. The most recent comprehensive study (Nadtochy, Kolpakov, 2017) showed that the average total biomass of the macrobenthos in 2011 was 241.8 ± 21.1 g/m², which is almost the same as in 2003 (265.4 ± 25.1 g/m²), the major taxonomic groups of macrobenthos by biomass were bivalves (34.0%) and polychaetes (23.0%).

However, abundance of selected, mostly large edible commercial species (and thus their role communities) have decreased after WWII due to overfishing and poaching (*Anadara broughtonii*, *Mizuhopecten yessoensis*, *Spisula sachalinensis*, *Crenomytilus grayanus*) and partly due to general degradation of habitats. In Ussuriysky Bay, the population density of the blood cockle *Anadara broughtonii* reached 13 ind./m² in the 1930s but decreased to 4.7 ind./m² in the 1990s; in some areas, the mean abundance of the giant mussel *C. grayanus* decreased from 27.4 ind./m² (1959) to 3.4 ind./m² (1970) (a review: Lutaenko, 2006). Active Japanese scallop fishing (*M. yessoensis*) in Peter the Great Bay was carried out from the 1920s to 1930s, and from 1933 to 1937 its catch reached 900 tons, and the average density was 0.3 ind./m² and up to ≥ 7 ind./m² in some areas; the total stock was estimated at approximately 10,000 tons (Sedova et al., 2007). Due to overfishing, the scallop fishery has been banned since the 1950s. In the 1970s, the Japanese scallop density ranged from 0.2 to 2.4 ind./m², and the total stock was approximately 1,700 tons; from 2000 to 2005, the abundance varied between 0.010 and 0.466 ind./m², and in some areas its stock decreased by 35 times due to poaching (Sedova et al., 2007). Abundance and biomass have decreased for the infaunal mactrid clam *S. sachalinensis* (Sokolenko, Sedova, 2008), a large shallow-water gastropod, the rapa whelk *Rapana venosa* (Rakov, 1998), deep-water buccinid dogwhelks (Repina, 2006), due to overfishing and poaching. Inevitably, benthic communities where these species were previously dominant or subdominant have also been modified.

The most drastic changes occurred in benthic populations in major port areas degraded to a degree of total lack of a majority of macro-invertebrates (e.g., Zolotoy Rog Bay, Vladivostok Port) and dominance of smaller organisms (nematodes and small polychaetes) (Fadeev, Fadeeva, 2007). Mollusk are found in port areas as a fouling component of ship hulls, piers, etc. Dredging operations in ports are additional impact factor in modifications of molluscan communities.

Thus, only local changes in composition and abundance of bivalve mollusks in Peter the Great Bay are obvious; the rest of areas along the Russian coast north of the bay do not experience major negative human impacts and mostly unpopulated, with a little pressure of mollusk fishing.

Global and regional warming of coastal waters in the Sea of Japan is well documented now, and their impacts are well known in changes of species composition and abundance of fish fauna whereas other biotic variations due to climate are little known. One of the consequences of the warming is introduction and/or improved acclimatization and survival and further spreading of distributional ranges of alien species of mollusks. Arrival and regional spreading of marine invasive species are related to ship traffic, treatment of ballast waters, warming and macroplastic pollution (Lutaenko et al., 2013). No cases of intentional introductions of mollusks are documented in the Russian waters so far. Among invasive species, we have detected six species of bivalves at different stages of acclimatization (if any): *Mytilus galloprovincialis*, *Macridiscus multifarius*, *Modiolus nipponicus*, *Musculus* sp., *Septifer* sp. and an ostreid (data on latter three species are unpublished as yet). Part of them are found on plastic debris and are potential invasive species. Several species of gastropods are found as invasive organisms in Peter the Great Bay.

Habitat degradation and landscape (seascape) changes lead to changes in both species composition (faunal changes) and abundance changes, not always in the way of decrease of mollusk abundance but in highly eutrophic areas, mollusks may thrive under the organic pollution or spread of new hard surfaces leads to denser settlements of oysters and mussels (concrete seawalls, piers, buoys, etc.).

The impact of hypoxia and ocean acidification on mollusks in Russian waters of the Sea of Japan are largely unstudied. Tourist impairment of coastal habitats are important factor, and we have observed an obvious faunal decline including lower abundance in areas of recreation activity and summer hotels/camps. However, it is connected with a range of factors: local (but strong) contamination by waste-waters

(many tourists summer camps/towns do not have any water treatment leading to organic pollution), harvesting shellfish including poaching, perhaps, collecting shells for decorations, etc.

Some mollusks in Primorye are rare and endangered and living at the northern edge of their distributional ranges (*Trapezium liratum*, *Maetra quadrangularis*, *Dosinia penicillata*, *Rapana venosa*, *Macoma contabulata*). We believe that protection measures should be taken on some vulnerable habitats such as estuaries of Razdolnaya and Artyomovka rivers, semi-enclosed bays (Expeditcii, Novgorodskaya, Sukhodol, inner part of Vostok Bay). Other declining species (*C. grayanus*, *M. yessoensis*) are living in open areas and are under protection in the Far Eastern Marine Biosphere Reserve. Monitoring of invasive species is of high necessity.

Paralytic shellfish toxins produced by dinoflagellate *Gymnodinium catenatum* and their biokinetics in marine bivalves

Rencheng Yu, Zhuoru Lin

Institute of Oceanology, Chinese Academy of Sciences Qingdao 266237, China

Paralytic shellfish toxins (PSTs) produced by toxic marine dinoflagellates can cause severe human intoxication through vectors like bivalves, and toxin biokinetics in bivalves strongly affect their toxicity and potential threats to seafood consumers. In toxic dinoflagellate *Gymnodinium catenatum*, a novel group of hydroxybenzoate PSTs named GC toxins have been detected using LC-MS/MS, but their biokinetics in bivalves were not carefully examined. In this study, we analyzed PSTs in bay scallops *Argopecten irradians* exposed to *G. catenatum* (strain MEL11) to determine their accumulation, elimination, anatomical distribution and biotransformation. Interestingly, we found up to 30% of the PSTs were accumulated in the adductor muscle of scallops at the end of the experiment, and the toxicity of adductor muscle exceeded the regulatory limit of 800 µg STXeq/kg in 6 days. High concentration of toxins in the adductor muscle is likely linked to the rapid transfer of GC toxins from viscera to other tissues. Moreover, most GC toxins in scallops were transformed rapidly to decarbamoyl toxins through enzyme-mediated hydrolysis, which was further supported by in vitro incubation experiments. Our study, for the first time, demonstrated that GC toxins actively participated toxin distribution and transformation in scallops, which may increase the risk of food poisoning associated with the consumption of scallop adductor muscle.

Subtropical brackish tintinnid community temporally organized by temperature preference and LOD class-size

Jingyuan Li^{1,3,4}, Ping Du², Wuchang Zhang^{1,3,4*}

¹*CAS Key Laboratory of Marine Ecology and Environmental Sciences, Institute of Oceanology, Chinese Academy of Sciences, Qingdao 266071, China*

²*Key Laboratory of Marine Ecosystem Dynamics, Second Institute of Oceanography, Ministry of Natural Resources, Hangzhou 310012, China*

³*Laboratory for Marine Ecology and Environmental Science, Qingdao National Laboratory for Marine Science and Technology, Qingdao 266237, China*

⁴*University of Chinese Academy of Sciences, Beijing 10049, China*

*E-mail: wuchangzhang@qdio.ac.cn

Tintinnids, planktonic ciliates with durable lorica, are ubiquitous in fresh water, brackish water, coastal and ocean water with different salinity. They are important feeders of phytoplankton, model organisms in plankton ecology study and environmental bioindicators. Annual variation of estuarine tintinnid community is mainly caused by the moving of water masses and seasonal variation of local species. Allochthonous tintinnid species are brought into the estuarine environment through the input of fresh water and tides. Local tintinnid community also show distinct patterns of species occurrence over time. In previous studies on annual changes of estuarine tintinnid community, the seasonal variation of brackish tintinnids was difficult to observe due to the complex hydrological environment and the influence of offshore water masses. Xiangshan Bay is an elongated subtropical estuary adjacent to the East China Sea. Tie Harbor, the innermost part of Xiangshan Bay, is isolated from the East China Sea with low water-residence times, which lead the little impact on the invasion of allochthonous species. In our study, samples were collected monthly in surface brackish water in Tie Harbor from January 2022 to January 2023. The results showed that brackish tintinnid community in Xiangshan Bay can be divided into three seasonal subgroups (winter, summer, autumn and spring-autumn species) under different temperature preferences. Total abundance distribution of tintinnids showed bimodal

annual distribution formed by seasonal tintinnid subgroups. Within each seasonal subgroup, the lorica oral diameter (LOD) of each species mostly scattered in different size-class, which avoided the competition of feeding between species and showed obvious niche differentiation. For species with the same LOD size-class in one subgroup, their peak abundance showed staggered temporal distribution, which also a strategy to avoid interspecific competition. Our study revealed the seasonal variation mechanism of the subtropical brackish tintinnid community, which is also valuable for the study of other protists with the same life history.

Keywords: tintinnid, ciliate, plankton, Bay, East China Sea

Primorsky Aquarium – Branch of the National Scientific Center of Marine Biology, Far Eastern Branch of the Russian Academy of Sciences (NSCMB FEB RAS)

Olga G. Shevchenko

The Primorsky Aquarium – Branch of the NSCMB FEB RAS is the first aquarium in Russia to have become a part of the Russian Academy of Sciences. Its construction began in 2010 and in September 2016 the Primorsky Aquarium was open to the public. The President of Russia Vladimir Putin and top-level officials from different countries participated in the Grand opening.

The Primorsky Aquarium exhibits represent marine and freshwater life from all climatic regions of the world. Evolution of Ocean Life exhibit tells the visitors about the key events in the evolutionary history from its very beginning till the Cenozoic. Microworld exhibit shows models of microscopic plants and animals, electron micrographs and some live microscopic aquatic dwellers. The group of exhibits representing Aquatic Regions of Russia begins with the freshwater Rivers and Lakes exhibit showcasing animals and plants of the Amur River basin and the Lake Baikal. The Polar World recreates the atmosphere of the Arctic and Antarctica. The Bering Sea, the Sea of Okhotsk and the Sea of Japan exhibits demonstrate the rich biodiversity of these Russian Far East water areas. Visitors of the Tropical Rain Forest exhibit enjoy colorful vegetation, tropical amphibians, reptiles and arthropods, as well as freshwater fish. The Tropical Seas and Ocean Abyss with its 70-m underwater tunnel showcase the richness of coral reef ecosystems and the life in the open ocean. Dolphinarium invites guests to performances twice a day. Artists include bottlenose dolphins, beluga whales, fur seals and a walrus.

The Primorsky Aquarium is home to 418 animal species, including 318 species of fish and over 8700 specimens of aquatic organisms. There are more than 8,6 thousand cubic meters of water in 105 tanks of the main exhibits and 14 thousand cubic meters of water in the Dolphinarium.

An important part of the Aquarium is the Shared Equipment Facility. It has several laboratory spaces with a range of lab equipment able to provide a variety of services for the Aquarium specialists and for partnering organizations. Among the most important and widely used equipment of the SEF are flow cytometers, scanning electron microscopes and light microscopes. Popular services include histological studies and isolation, as well as purification and propagation of microalgal cultures. The most significant services for the Primorsky Aquarium include regular marine mammal health checks and determination of the sex of penguins by genetic molecular testing.

Main areas of the Primorsky Aquarium activities include:

- supporting the exhibits and developing new ones
- improving and developing new husbandry and veterinary methods to provide the best possible welfare conditions of our animals
- conducting scientific research for the benefit of marine life
- entertaining and educating children and adults
- taking care of the 14,5-hectare walking area with koi ponds and other water features, and 56 species of trees, shrubs and grasses.

Finally, the Primorsky Aquarium has always been open to partnership, especially in science and environmental education, and is eager to expand it further.

Prediction and verification of hypoxia in central Bohai Sea in 2022

Jie Guo^{1,2*}, Yanfang Li^{1,2}, Xiangyang Zheng^{1,2},

Diansheng Ji³, Chawei Hou³

¹*Yantai Institute of Coastal Zone Research, Chinese Academy of Sciences (CAS),
Yantai 264003, China*

²*CAS Key Laboratory of Coastal Environmental Processes and Ecological
Remediation, Yantai China Shandong Key Laboratory of Coastal Environmental
Processes, Yantai, China*

³*Yantai Marine Environment Monitoring Central Station, State Oceanic
Administration (SOA), Yantai 264006, China*

The frequency of hypoxia in the central Bohai Sea (CBS) has gradually increased in recent years, threatening the ecology of the area. Seasonal variations in parameters such as sea temperature, salinity, dissolved oxygen (DO), and pH were analyzed using the data acquired from different depths three stations situated in the CBS, which had experienced frequent hypoxia during the previous eight years. The characteristics and eigenvalues of sensitive factors (CESF) that showed difference between upper and bottom layers were examined using the data acquired in June during all years in which hypoxia was determined to have taken place. The CESF were applied to survey data from 29 stations in the CBS collected at the end of May 2022, and it was predicted that 19 stations would likely suffer hypoxia during the summer. Based on the survey data of the same stations in summer, hypoxia was observed to have occurred in 14 stations and the prediction was verified for 12 stations, thus demonstrating a forecast accuracy of 63%. An area of severe oxygen depletion occurred during the summer of 2022 in the CBS, and the range of hypoxia values varied from 2.92 to 3.93 mg/L.

This research was supported by the National Natural Science Foundation of China (U2106211,42076197), Shandong Joint Key Fund (U1906217) and project from Chinese Academy of Sciences “The Impact of Climate Abnormal on Droughts and Floods from the Bohai Rim and Siberia to Russia and the Early Warning Research of Sensitive Factors.” This work is supported by the Data Center, Yantai Institute of Coastal Zone Research, Chinese Academy of Sciences.

A comparison of the sensory and nervous systems in the larvae of the marine and freshwater bivalves

**Elena M. Sayenko¹, Viktoria E. Nikishchenko²,
Vyacheclav A. Dyachuk², Igor A. Rodionov¹**

¹*Federal Scientific Center of the East Asia Terrestrial Biodiversity, Far Eastern Branch, Russian Academy of Sciences (FSCEATB FEB RAS), Vladivostok 690022, Russia*

²*National Science Center of Marine Biology Far Eastern Branch, Russian Academy of Sciences (NSCMB FEB RAS), Vladivostok, Russia*

In mollusks, the nervous system and its neurotransmitters are of great importance in feeding, digestion, reproduction and such various physiological processes as regulation of locomotor activity, contraction of muscles including the heart, regulation of metabolism, osmoregulation, and larval development. Marine bivalves have a few stages of development from free-swimming trochophores larvae, that later develop into veliger larvae which settle on the seabed and undergo metamorphosis into adults. Unlike marine mollusks, most freshwater bivalves have an unusual life cycle with glochidia larvae that for metamorphosis requires a parasitic period on fish. The appearance of glochidia is an important episode in bivalve evolution, which led to the colonization of freshwater environments by an ancestral unionoid species during the Triassic period, and glochidia played a special role in the process.

Here we review comparative data on the larvae sensory and nervous systems of the marine scallop *Azumapecten farreri* (Pectinidae) and freshwater mussel *Nodularia douglasiae* (Unionidae) possessed by different mode of development and strategies.

In the scallop larvae the first detection of the sensory elements included three 5-HT-lir cells with neurites between two FMRFamide-lir cells in the early veliger stage as a part of the developing so-called apical organ – non-paired sensory (ciliated) larval organ. At the mid-veliger stage, the number of 5-HT-lir cells increased and the morphology of some cells is changed. At the late scallop veliger in addition to the epidermal apical organ, subepidermal anlage of the cerebral ganglia appear. Additionally, FMRFamide-lir neurons emerged on the dorsal part of larva and their neurites were directed via apical organ to the ventral part of larva, where they connected

with other paired FMRFamide-lir cells. During the larva development the number of neuronal elements increased, as a result pediveliger larvae possessed a well-organized nervous system consisting of three ganglia (cerebral, pleural, and visceral) connected by connectives forming paired visceral nerve cords.

As to freshwater bivalves, the glochidia sensory system included four pairs of tubulin-lir multicilia hair cells connected with non-ciliated tubulin/FMRFamide-lir cells, which, in turn, communicate with other neurons via neurites. Non-ciliar tubulin-lir cells synthesize the neuropeptide FMRFamide and are identified as afferent neurons collecting information from peripheral tubulin-lir hair sensory cells to nervous regulators. In summary, the glochidial nervous system is represented by two 5-HT-lir cells and processes, and four paired FMRFamide-lir neurons connected by neurites, forming a complex system regulating the larva's behavioral patterns. The FMRFamide-lir system is more complicated than 5-HT and consists of several neuronal centers comprising neuronal bodies and their neurites in different areas of the larva. The FMRFamide-lir neurons are closely associated with sensory hair cells, and others, together with 5-HT-lir neurons, may be involved in the anlagen of adult ganglia.

Thus, we can summarize, that in scallop *A. farreri* larva before the apical organ emerges, peripheral sensory neurons differentiate utilizing various transmitters; the first expressing neurotransmitter cells are 5-HT-lir cells and flask-shaped FMRFamide-lir cells as a part of the apical organ. The nervous system of *N. douglasiae* glochidia is drastically different from the scallop and other marine mollusks because of 1) the absence of an apical organ and 2) different location and composition of FMRFamide and 5-HT cells where the 5-HT-lir glochidial system is arranged most simply innervating the single glochidial adductor.

Kinorhynch species show much wider distribution then previously thought

Andrey V. Adrianov^{1,2}, Anastassya S. Maiorova¹

¹*A.V. Zhirmunsky National Scientific Center of Marine Biology, Far Eastern Branch
of Russian Academy of Sciences, Vladivostok 690041, Russia*

²*Lomonosov Moscow State University, GSP-1, Leninskie Gory, Moscow 119991,
Russia*

Meiofauna constitutes an essential component of marine benthos. Meiofaunal communities are mainly dominated by nematodes, annelids, harpacticoids, and other less common meiofauna that may also be found with low abundance, including kinorhyncha (Higgins, Thiel, 1988). Kinorhynchs may rich high density in some areas (muddy intertidal flats, coral sands, mangroves, cold seeps, abyss and ultraabyss plains), being among the top of dominant groups with values up to 100 ind./10 cm².

The diversity of Kinorhyncha increased dramatically in the past decades, reaching the number up to 384 valid species (Neuhaus, 2023). Until recently, specimens of every newly sampled location were bringing a description of new species (Adrianov, Maiorova 2016, 2018, 2019, 2020). Recently some species, especially from the intertidal and deep-sea locations started to repeat (Yamasaki et al. 2014; Adrianov, Maiorova, 2022). Several morphologically similar species, including *Echinoderes beringiensis* from the Bering Sea and species described off California, were found in the vicinity of New Zealand (Grzelak, Sørensen, 2022). Nonetheless, some species with a high level of morphological similarity that occur at the same locality have recently been established from the Gulf of Mexico and supported by barcoding methods (Anguas-Escalante et al., 2023). Another step in updating Kinorhyncha taxonomy happened when certain morphological patterns started to be recognized within the genus, and putative monophyletic species groups were defined. The first good-supported putative group within *Echinoderes* was the *E.coulli*-group (Sørensen, 2014; Randsø et al., 2019). The selection of closely related species within a genus may be a preliminary step before designing a new taxon within a species-rich genus. The progress in Kinorhyncha taxonomy is currently limited by old descriptions that lack many

characteristics, while some of the type specimens are lost or in poor condition. The minute size of kinorhynchs makes it difficult to use barcoding methods efficiently. Further accurate sampling and description processes, together with ecological and quantitative data, would help enhance the knowledge of Kinorhyncha and marine benthos in general.

Degradation of plastics in marine habitats, studied using Raman microspectroscopy and atomic force microscopy (AFM)

**Vyacheslav S. Odintsov, Alexander A. Karpenko,
Maxim A. Karpenko**

*A.V. Zhirmunsky National Scientific Center of Marine Biology, FEB RAS, Ul.
Palchevskogo 17, Vladivostok 690041, Russia*

The widespread use and intensive manufacture of plastics has led to the global pollution of oceans with polymer wastes. It is assumed that a serious threat to the living system comes from micro- and nanoplastics (MPs and NPs), the number of which in the ocean is constantly increasing due to the transformation of large fragments and plastic products. If the assessment of the prevalence of MPs is quite successfully solved, then the difficulty to identify MPs and NPs leads to an underestimation of the distribution of the waste. Very important is an estimation of the natural properties of an ecosystem to neutralize a plastic impact and the search alternative materials for minimizes the impact of plastics on the environment in case of release into the environment.

The aim of our study was selection of models for experimental studies, and transformation of plastic in biological systems: degradation as a result of exposure to microorganisms in bottom sediments and in the digestive system of aquatic organisms.

Micro- and nano-sized particles of PTFE (polytetrafluoroethylene) and acrylic fluorinated copolymer (Protacryl-M), widely applied in medicine for prosthetics in dentistry and orthopedics, are proposed to be used as model (reference) particles to study biological effects on plastic causing its degradation (biodegradation). Since the PTFE molecule contains fluorine, considered an "atomic label" that sharply distinguishes this compound from other common plastics, and micro/nanoparticles have a specific crystallinity, these are well identified by polarized light microscopy methods and Raman microspectroscopy. Due to their shape, Protacryl-M microspheres are also clearly distinguishable both in the water and in animal waste products by light

microscopy methods. Cellophane in microparticles and films as material close to natural polymer was used as a model for study biodegradation in digestive tract using marine gastropods of the genus *Littorina* (in particular, the periwinkle *L. brevicula*) as a model organism widely distributed in the marine intertidal zone. Also, degradation of some wide spread plastics as polyethylene terephthalate (PET) and polyvinyl chloride (PVC) from the Laptev Sea, cellophane fragments from the Weddell Sea, and polyethylene (PE) from the Amur Bay (Peter the Great Bay, East Sea) was investigated.

The Raman spectra were recorded on an inVia Reflex Raman microscope spectrometer (Renishaw, United Kingdom) coupled with a Leica DM2500M incident light microscope (Leica Microsystems, Germany). To identify the micromechanical characteristics of plastics, a BioScope Catalyst atomic force microscope (Bruker, United States) was used in combination with an AxioVert 200 inverted microscope (Carl Zeiss, Germany). The image was obtained in the semi-contact Scan Asyst mode.

Our research has shown that MPs and NPs after entering the digestive system of animal, change their properties, which can be considered signs of degradation. Although not all changes can be described in detail, these are assumed to increase the effects of the abiotic environmental factors on plastic making them more destructive, and leading to its faster degradation. Moreover, the maximum degradation in the digestive tract of gastropods was shown by cellophane, which in some cases was eaten completely without the detection of cellophane particles in fecal pellets. The most likely cause of MP changes in the digestive system of gastropods may be their symbiotic microflora. The studying both plastics from the Laptev Sea and plastics aged in an aquarium show that the destruction of PET samples leads to a decrease in their crystallinity. Interestingly, changes in the plastics surface associated with changes in PET crystallinity under aquatic conditions have been observed at the ground-water horizon. Above the ground surface, no changes in the phase composition of the PET surface were recorded. As well, the surface of PET from the Laptev Sea, compared with the surface of the reference polyethylene terephthalate, has significant roughness. The result of the study of PVC, which showed the presence of polyenes in it, indicates the degradation of plastics found in the sea. Raman spectrum of polyethylene indicates a change in the phase composition of polyethylene compared to the reference plastics, that is a sign of degradation. The spectrum of the found fragment from the Weddell Sea most of all corresponds to the reference cellophane. One important task is the

identification of products of the MPs and NPs degradation, that may be more harmful than plastic itself.

The questions as to what is the active factor that destroys plastic in the bottom sediments and digestive system of gastropods still remains to be addressed. However, in general, it is important to understand that biological objects can counteract the MPs and NPs pollution. The ability of free-living and symbiotic microorganisms to decompose or recycle plastic gives hope that the biosphere has a potential to control its accumulation, spread, and harmful effects.

Hidden diversity: discovery of an association of parasitic and hyperparasitic isopods (Crustacea: Isopoda: Epicaridea) from a king crab *Lithodes aequispinus* Benedict, 1895 in the Bering Sea, the North Pacific

Olga A. Golovan¹, Taras B. Morozov²

¹*A.V. Zhirmunsky National Scientific Center of Marine Biology, FEB RAS, Palchevskogo Str. 17, Vladivostok 690041, Russia. E-mail: golovan_olga@mail.ru.*

²*Kamchatka branch of Federal Research Institute of Fisheries and Oceanography (KamchatNIRO), Naberejnaya Str., 18, Petropavlovsk-Kamchatsky 683000, Russia.*

The suborder Epicaridea combines parasitic isopods infesting crustaceans. It includes ~800 species, but the number of undescribed species is presumably much higher due to insufficient knowledge and the cryptic lifestyle of epicarids. About 80% of the known species belong to the superfamily Bopyroidea, namely to the family Bopyridae, which infest decapods. However, only two species belonging to the genus *Eremitione* Williams and Boyko, 2019 (Bopyridae: Pseudioninae) are known from lithodoidean hosts: *E. giardi* (Calman, 1898) from the NE Pacific was recorded on hermit crabs of the genus *Pagurus* (Paguridae), as well as on the wrinkled crab *Dermaturus mandtii* Brandt, 1850 (Lithodoidea: Hapalogastridae); *E. tuberculata* (Richardson, 1904) occurs near the southern tip of South America on three species of king crabs from the genera *Paralomis*, *Neolithodes*, and *Lithodes* (Lithodidae). This species was included in the genus *Eremitione* with special remarks, as it morphologically differs significantly from other congeners. Representatives of the second superfamily Cryptoniscoidea parasitize various crustacean taxa, including other isopods (family Cabiropidae). In the adult female stage they have a strongly reduced morphology; the group is very poorly studied. During two cruises of the Federal Research Institute of Fisheries and Oceanography (VNIRO) on board the RV *Professor Kaganovski* (2020) and FV *Valeriy Maslakov* (2021) in the western part of the Bering Sea, 37 juvenile specimens of the king crab *Lithodes aequispinus* Benedict, 1895 were

collected at seven trawl stations from depths ranging within 236–450 m. Twenty-five of them (68% of specimens), sampled on slopes of the Koryak and Karaginsky regions, had signs of infestation by branchial epicarids (the lateral bulge on the carapace). The real percentage of the infected specimens may be even higher, since the early stages of infestation may be overlooked during the visual inspection onboard. Nine infected juveniles were fixed for more detailed studies. All of them appeared to be infected by the undescribed bopyrid species *Eremitione* sp. nov. The new species morphologically most closely resembles *E. tuberculata*, but it also has features that bring it closer to other congeners which parasitize Paguroidea and Hapalogastridae (e.g. the curved female body vs. linear body in *E. tuberculata*). Presumably it occupies an intermediate position within the genus *Eremitione*. In all observed cases, the female of *Eremitione* sp. nov. was accompanied by a male, attached on the ventral side of the female pleon. A third of the examined infected crabs bore the parasite only in their left branchial chamber, the rest bore parasites on both sides. In the case of dual infestation, first a pair of parasites is localized in the left chamber, and only if the left chamber is occupied, the next pair is localized in the right chamber. In turn, four of the fifteen examined females of *Eremitione* sp. nov. were infected by the cabriropid hyperparasite *Bourdonia tridentata* Rybakov, 1990. This species was previously described from *Bopyroides hippolytes* (Kryer, 1838) (Bopyrinae) infesting the caridean shrimp *Pandalus borealis* Kryer, 1838 (Decapoda: Pandalidae) from the Sea of Okhotsk. This is the first record of this species from the pseudionin host. The females of *B. tridentata*, filled with eggs, were lying freely in the brood pouch of *Eremitione* sp. nov. among the host's own embryos, singly or accompanied by 2–3 cryptoniscus larvae of their species (functional male in Cryptoniscoidea, which then must turn into a female). In one case, two hyperparasite females (ovigerous and juvenile) simultaneously presented in the brood pouch of *Eremitione* sp. nov., completely occupying the space, accompanied with two cryptoniscus larvae. The observed infestation rate is quite high for epicarids in general, but is similar to that reported for *E. tuberculata*. Further studies are needed to find out if it is permanent for the Bering Sea king crab population.

Algological studies of brackish waters (river estuaries, lagoon-type lakes) of the Russian Far East

Tatyana V. Nikulina¹, Irina V. Motylkova²

¹*Federal Scientific Center of the East Asia Terrestrial Biodiversity, FEB RAS, Vladivostok 690022, Russia. E-mail: nikulinatv@mail.ru*

²*Sakhalin Branch of “Russian Federal Research Institute of Fisheries and Oceanography”, Yuzhno-Sakhalinsk 693023, Russia. E-mail: surirella@mail.ru*

The study of natural algal communities in the estuarine zone of rivers, which is a transitional habitat between marine and freshwater, as well as brackish lakes of the lagoon type, is necessary to obtain additional information about the biology and ecology of each species. Algal floristic studies of brackish waters (river estuaries, lagoon-type lakes) are topical for floristic comparisons and generalizations of data, for identify the extent of ecosystem changes under the impact of natural and anthropogenic disturbances.

Algological studies of the brackish waters of the Russian Far East are carried out locally and unsystematically, unfortunately. They are mainly devoted to the study of the species richness of cyanobacteria and algae, and occasionally to obtaining data on the quantitative characteristics of algal communities and assessing the level of anthropogenic pollution. Due to insufficient information about state of phytoplankton, phytobenthos and periphyton communities in estuary and brackish water ecosystems, it is necessary to continue obtaining primary data, to conduct systematic monitoring studies to study species richness, the structure of algal communities, their quantitative characteristics and patterns of spatial and temporal variability in watercourses and reservoirs located on the border between fresh and marine waters.

Data on the species richness and structure of algal communities are known for a low number of river’s estuaries and lagoon-type lakes located on the territory of the Russian Far East. Studies of brackish water bodies were carried out on the territory of Primorsky Krai, Khabarovsk Krai and Sakhalin Region (Sakhalin Island, Kuril Islands). Only a few water bodies with different morphological structure, hydrological regime and located in specific natural conditions have been surveyed in the most detail and over a sufficiently long period of time, which makes it possible to identify changes and their

trends in the composition of algal communities, occurring under the impact of environmental parameters.

The transboundary Razdolnaya River (China-Russia) flows through the territory of Primorsky Krai and enters into the Amur Bay of Peter the Great Bay, the Sea of Japan. Starting from 1996 several stages of estuary zone of the Razdolnaya River phytoplankton study are known; over the all study period, an enrichment of the species composition of the algal flora, a change of the dominant species composition, while saving the main dominant *Aulacoseira* sp. was revealed. Since 2005, potentially toxic species and spores of dinoflagellates, diatoms, and raphidophytes (*Alexandrium tamarense*, *A. cf. tamutum*, *Dinophysis acuminata*, *D. rotundata*, *Akashiwo cf. sanguinea*, *Karenia mikimotoi*, *Protoceratium reticulatum*; *Pseudo-nitzschia calliantha*, *P. pungens*, *P. multistriata* и *Heterosigma akashiwo*) have been identified in the phytoplankton and sediments of the mouth of the Razdolnaya River and the territory of the inner part of the Amur Bay (Nikulina, 2006; Stonik et al., 2009).

Busse Lagoon (Aniva Bay, Sea of Okhotsk) is located on the western coast of the Tonino-Aniva Peninsula of Sakhalin Island. Intensive study of the algal flora of the lagoon was carried out by Russian scientists in 1970–80, after a long break, it was continued in 2014. Comparison of data for these study periods showed that the average vegetation quantitative indicators remained at the same level, but the seasonal dynamics patterns of the species composition and the list of dominant species changed. In September 2014, the abundant development of the harmful dinoflagellate species *Prorocentrum micans* was recorded for the first time in Busse Lagoon. For the last twenty years, *P. micans* has been regularly recorded as part of the dominant phytoplankton complex in autumn period (Kalganova, 1995; Efanov and Tepaeva, 2014).

The research was carried out within the state assignment of Ministry of Science and Higher Education of the Russian Federation (theme No. 121031000147-6).

Global environmental changes and possible effects on microalgae communities with emphasis on toxic species on the Russian east coast

Tatiana Orlova

*A.V. Zhirmunsky National Scientific Center of Marine Biology, FEB RAS,
Palchevskogo Str. 17, Vladivostok 690041, Russia.*

There is a growing understanding of the relationships between key phytoplankton groups and their role in biogeochemical cycles; however, data on the temporal scales of phytoplankton variability are scarce and insufficient. A long-term data set (1969-2023) of phytoplankton is used to investigate the temporal variability of the phytoplankton community in the Amursky Bay near Vladivostok (north-west part of the Sea of Japan). Phytoplankton was represented by 1211 taxa, including 43 potentially toxic species, which were ascribed to the following groups: diatoms, dinoflagellates, chlorophytes, chrysophytes, raphidophytes, cryptophytes, dictyochophytes, euglenophytes, prasinophytes, prymnesiophytes, undetermined small phytoflagellates, as well as cyanobacteria. The main features of the seasonal succession of phytoplankton in the Amur Bay are the most intense summer blooms caused by diatoms and dinoflagellates, cryptophytes as well as raphidophytes. Regular winter blooms of diatoms are observed under the ice during the freeze-up period. Blooming of small flagellates and prasinophytes occurred in late winter-spring during the period of ice melting and in late summer-early autumn during the period of the greatest warming of waters and increased continental runoff. Since the 70s of the last century, the following trends in the phytoplankton community structure have been traced: 1 - gradual change in the composition of blooming species towards non-diatom plankton; 2 - an increase in the density and frequency of blooms of small eukaryotes (not belonging to the division of diatoms with a cell size of less than 10 microns) - pelagophytes, cyanobacteria, haptophytes, chlorophytes, raphidophytes, cryptophytes, prasinophytes, prymnesiophytes; 3 - increasing diversity and abundance of species known to produce phycotoxins (amnesic and diarrheal types), as well as producers of ROS (reactive oxygen species) and fish killers. The analyses showed a large spatial, seasonal and

interannual variability of phytoplankton due to the influence of multiple drivers. In particular, phytoplankton dynamics are influenced by physiological responses, changes in hydrological properties, and grazing pressure. Moreover, since the composition of a community and its temporal changes are the result of a synergy of multiple environmental conditions, they are useful indicators for determining the current state of the environment and forecasting.

This work was supported by grant FWFE-2023-0001 “Study of phycotoxins producers in Kamchatka coastal waters”

Shell-boring worms – a problem in marine aquaculture

Vasily I. Radashevsky

*A.V. Zhirmunsky National Scientific Center of Marine Biology, Far Eastern Branch of
the Russian Academy of Sciences, 17 Palchevsky Street, Vladivostok 690041, Russia*

E-mail: radashevsky@gmail.com

Cultivation of numerous organisms in high density in one place often leads in their diseases. Serious problems for the cultivation of marine molluscs: abalone, clams, mussels, oysters and scallops are often caused by perforation of shells by sea worms, polychaetes. Sever worm infestation damages the shells and often results in the formation of stinking mud blisters on the inner surface, which reduces the commercial value of the molluscs. Moreover, it reduces growth rate and meat yield, and in some cases leads to high mortality. With the globalization of the aquaculture industry, commercially important molluscs are constantly transported between countries, serving as vectors for unintentional introductions of various mollusc-associated organisms, including boring and non-boring worms. Among these worms, the most dangerous are species of the genera *Polydora*, *Dipolydora* and *Boccardia* from the family Spionidae (Annelida). Dozens of these species have been recorded in Asian coastal waters, including China, Japan, Korea, Vietnam and Russia. In my presentation, I provide a review of shell-boring worms and examples of the damage they cause to mollusc aquaculture in Asia. I also describe how these worms reproduce and their different types of larval development. Knowledge of the reproductive biology of shell-boring species is important for developing preventive measures or control of mollusc infestation. The specific identity of shell-borers and their native distribution are not always known and require further study.

Sipunculans, the worms of every ocean

Anastassya S. Maiorova^{1,2}, Andrey V. Adrianov^{1,2}

¹*A.V. Zhirmunsky National Scientific Center of Marine Biology, Far Eastern Branch of Russian Academy of Sciences, Vladivostok 690041, Russia*

²*Lomonosov Moscow State University, GSP-1, Leninskie Gory, Moscow 119991, Russia*

Sipuncula is an exclusively marine and benthic group of worms that can play a considerable role in benthic ecosystems. These abundant habitats inhabit all oceans, ranging from polar to equatorial waters and from the intertidal to the hadal zone. The phenomenon of bipolarity although known to several species (see Murina, 1961, 1971, 1973). The population density of this well-hidden benthic habitat may reach up to 8000 specimens per m², especially in soft, muddy sediments. The high-density population of sipunculans known both from the intertidal to abyssal depth, a high number specimen mix of *Phascolion* and *Nephasoma* species were sampled at depth 6500m at an abyssal plane near Kurile-Kamchka Trench in 1949 and in 2012 (Murina, 1971; Maiorova, Adrianov, 2016). Geologically, sipunculans may affect considerable geochemical alterations in the deposited strata by their deep-reaching burrowing, and the geochemical influence of sipunculans can vary between species. The high population density and capability of burrowing make these worms great bioturbators. The size of mature sipunculans varies from less than 1mm to 400 mm long. The greater size specimens are mostly dug out at intertidal depth, and in our day become rare. Specimens less than 1mm are often postlarvae or juveniles of larger species (Adrianov, Maiorova, 2009), but true meiofauna species although described.

Despite the occurrence of sipunculans in all oceans and a high number of samples, the description of each new species is a great event for this group. In the past decade, less than ten new species were described, but recent research has revealed multiple complexes of cryptic or pseudocryptic species, and the diversity of sipunculans is significantly higher than currently stated. A low number of valid species number of sipunculans may cause the highly cryptic nature of worms, their ancient origin, and a small number of good identification characters.

The knowledge of sipunculans from intertidal and shallow waters is better investigated than deep-sea due to easier sampling process and many samplings. Some recent investigations pointed to the most unexplored regions with a lack of knowledge about sipunculans in the Indian, Pacific, Southwest Atlantic Oceans (Kohlenbach et al., 2023). Further sampling efforts are needed to fill the gaps in data on sipunculan distribution and diversity.

Molluscan remains in the Bohai archaeological sites (698–926 AD) in Primorye (south of the Russian Far East) as an indicator of regional climate and environmental changes

Konstantin A. Lutaenko¹, Elena M. Sayenko²

¹*A.V. Zhirmunsky National Scientific Center of Marine Biology, Far Eastern Branch, Russian Academy of Sciences (NSCMB FEB RAS), Vladivostok 690041, Russia*
E-mail: lutaenko@mail.ru

²*Federal Scientific Center of the East Asia Terrestrial Biodiversity, Far Eastern Branch, Russian Academy of Sciences (FSCEATB FEB RAS), Vladivostok 690022, Russia*
E-mail: sayenko@biosoil.ru

Mollusks are one of the most reliable objects and indicators for climatic and environmental reconstructions. Molluscan shell remains can provide useful ecological information even in situations when no other invertebrates are abundantly preserved in the deposits. Marine mollusks as well as freshwater bivalves and gastropods represent a collected resource of considerable economic importance. Their remains provide evidence of food pattern in the past, in addition, tracking of intertidal shellfish resources by hunter-gatherers may have been a factor in early human dispersal. Marine shells can be useful indicators of the habitats exploited by food-gatherers, and thus, provide information on their past distributional ranges and the technology available to them. Remains of freshwater bivalves in the archeological sites reflect changes in the mollusks distribution as a result of climate change or human pressure. Findings of terrestrial mollusks, especially the tiny ones, are usually random in archaeological sites. However, data obtained on the species composition of the terrestrial malacofauna make it possible to clarify ancient landscapes, biotopes, and climatic conditions. Aiming to compare changes in the regional climate and environmental conditions in southern Primorye in the Bohai period (698–926 AD) and modern time, we used our own research results and published archeomalacological data on mollusks remains from the archeological sites.

Marine mollusks recovered at Bohai sites are mostly common shallow-water bivalves inhabiting Peter the Great Bay and adjacent areas of the Sea of Japan. Among them, two anadarine species (Arcidae) – *Anadara talmiensis* (= *A. “inaequivalvis”* aucct.) and *A. kagoshimensis* are locally extinct warm-water subtropical bivalves living now around southern Korea and Japan. This clearly indicates that climate at around 1000–1300 years BP was warmer than present-day one. Preliminary comparison of the species richness of marine mollusks found on the Bohai sites in Primorye suggests that the largest number of species, with 11 species of bivalves and 3 species of gastropods, is characteristic for the Kraskino settlement (an ancient Bohai port) in Khasan District located on the coast of the Possjet Bay; they were obviously used as food. Other sites have less species richness, e.g., Chernyatino-2 with 8 species of bivalves and 1 species of gastropods, Gorbatka with 8 species of bivalves and 4 species of gastropods. At other sites, 1–6 bivalve species and 1–2 gastropod species were collected. Low numerical abundance of shells and traces of grinding, drilling and polishing are indicative of predominant use of marine shells as ornaments, in rituals and funeral rites. Nearly all valves of *Glycymeris yessoensis* and *Anadara* have umbonal holes made by grinding. However, large mollusks, such as *Crenomytilus grayanus* and *Rapana venosa*, were a source of protein food.

Among freshwater bivalve mollusks, shells of the genus *Margaritifera* (= *Dahurinaia*) are common in archaeological excavations. In Primorye, shell fragments of *Margaritifera* were found in the following archeological sites of the Bohai period: Abrikosovsky-1, Chernyatino-2, Konstantinovka-1 (Razdolnaya River basin), Gorbatka, Nikolaevskoe I, Nikolaevskoe II (Khanka Lake basin), Maryanovskoe, Novogordecenskoye-2 (Ussury River basin). Nowadays, in Primorye freshwater mussels of the genus *Margaritifera* inhabit the Amur River and Khanka Lake basins, however, distribution within the range is very limited: *Margaritifera* occur only in the uppermost reaches of the Arsenievka river, between Smolnoye and Vinogradovka villages. The genus representatives are also known from Komarovka River (Razdolnaya River basin). Archeological findings show a much wider distribution of *Margaritifera* in historical time in Arsenyevka (from the upper reaches of Arsenyevka to its confluence into Ussuri) and in Razdolnaya rivers (mussels were common not only in a single river tributary, but also in the main riverbed). First record of terrestrial gastropod *Discus perspectivus* in archaeological site Chernyatino-2 testifies to a more favorable climatic situation in

Primorye in the early Middle Age because this recent species now occurs only in the mountain forests of Central Europe.

Of interest, no Bohai shell-middens are found in Primorye which is in contrast with wide distribution of shell mounds and heaps during the Neolithic and Iron Age along the coast of this province (e.g., more than 100 shell-middens are known for Yankovskaya culture of the Early Iron Age, 2300–3000 years BP). At the same time, Bohai people were actively gathering fresh-water mollusks. However, partly ancestral to Bohai State Mohe tribes (around 1300–1500 years BP) gathered marine mollusks in larger amounts and formed shell-middens on the coast of Russky Island (Novik-V site); in Zapovednoye 5 Mohe site (Kievka Bay), 23 species of marine mollusks were found. Thus, we suggest that later Bohai population mostly relied on other food sources through hunting (mammals and birds), fishing and plant and animal culturing while freshwater mollusks, unlike the marine ones, played an important role in their diet.

Basket stars Gorgonocephalidae (Echinodermata: Ophiuroidea) and their distribution on the Emperor Seamount Chain

Anastasia L. Volkova, Tatyana N. Dautova, Salim Sh. Dutov

A.V. Zhirmunsky National Scientific Center of Marine Biology FEB RAS, Vladivostok 690041, Russia

E-mail: al99volkova@gmail.com

So-called brittle and basket stars are of great significance in studies of benthic marine communities. The reason is they are found all over the world, make up a large part of the biomass, and have a major impact on the sea bottom fauna (Escolar, 2013; Schejter, 2016). Ophiuroids are frequently cited as a dominant component of vulnerable marine ecosystems and as one of the primary taxa that comprise habitats in terms of species composition (Baker, 1980; Venkataraman et al., 2012; Okanishi, 2020). They are also recognized as the large group within Echinodermata, exhibiting the highest abundance among all deep-sea megafauna taxa and contributing significantly to the community (Rodrigues et al., 2011; Okanishi, Fujita, 2018; Canessa, 2023). The studies of ophiuroids' diversity is a subject of great interest due to convincing factors such as the impact of increasing ocean acidification caused by climate change and the effects of trawling fisheries (Okanishi, 2020; Escolar, 2013).

With a current count of 34 genera, Gorgonocephalidae Ljungman, 1867 is the largest family within the Euryalida order (Okanishi, Fujita, 2018). Although they are ecologically important members of coral reef ecosystems, basket stars are not widely studied in most localities (Gondim 2012; Boissin, 2016; Stöhr, O'Hara, 2012). Most recently, other research has focused on taxonomic composition of benthic megafauna in the southern Emperor Seamounts region of the North Pacific Ocean. The findings indicate that the deep-sea benthic megafauna in the southern Emperor Seamounts area shows more similarities with those found near the Hawaiian Islands, than with those previously reported in the Aleutian, other Alaskan, Californian, and Japanese waters. Ophiuroidea occurred in more than 70% of all hauls (Miyamoto et al. 2017). The basket

star *Gorgonocephalus cf. eucnemis* were collected in July-August 2021 from the Koko guyot (Klimenko et al. 2023).

Continued collection and exploration of Gorgonocephalidae on the Emperor Seamounts chain would provide new knowledge about basket stars' distribution to the mountains of the chain as well as compare the species composition between them and identification of variances or lack thereof.

Activity of certain types of phagocytes of holothurians under the influence of damaging environmental factors

Ludmila S. Dolmatova

*Il'ichev Pacific Oceanological Institute, Far Eastern Branch, Russian Academy of
Sciences, Vladivostok, Russia*

E-mail: dolmatova@poi.dvo.ru

Phagocytes of invertebrates are involved in the active transport and detoxification of heavy metals (Homa, et al., 2005), and are also involved in protection against bacteria (Buchmann, 2022). In the sea cucumber (holothurian) *Eupentacta fraudatrix*, two types of phagocytes were obtained by centrifugation in a density gradient (Dolmatova et al., 2004), the role of which in protection against the damaging effect of the environment is unclear.

The work aims to analyse data on the activity of two types of phagocytes under the influence of lead and a thermostable lethal toxin of the bacterium *Yersinia pseudotuberculosis* (TcTYp), and to study the possibility of modulating this activity.

Recent studies (Dolmatova, Dolmatov, 2018) revealed that after 48 h exposure to $\text{Pb}(\text{NO}_3)_2$ (2 mg/L), the number of one type of phagocytes (P1) decreases and another type (P2 phagocytes) increases in the coelomic fluid, while the activity of the antioxidant enzyme protection is higher and apoptosis is lower in P1 compared to P2 phagocytes. This indicates the preferential recruitment of P1 phagocytes in the tissue and their greater resistance to lead damage. It can be concluded that P1 phagocytes play a leading role in protecting against the toxic effects of this heavy metal.

When studying the effect of TcTYp in vitro, Dolmatova et al. (2019) showed that toxin (0.2 and 0.5 $\mu\text{g}/\text{ml}$) did not decrease the viability of P1 phagocytes after 24 h of incubation, and even increased it at a concentration of 2–5 $\mu\text{g}/\text{ml}$. At the same time, the opposite concentration dependence of its effect on the viability of P2 phagocytes was noted. No direct correlation was found between chromatin condensation (a marker of apoptosis) and cell viability. Apparently, TcTYp is able to turn on other mechanisms of cell death in phagocytes, aimed at the preferential survival of P2 phagocytes. At an

earlier incubation period (1 h), TcTYp stimulated an increase in the level of reactive oxygen species mainly in P2 phagocytes, which, apparently, is associated with a bacterial strategy for suppressing the immune response as shown on M1 and M2 macrophages (Bi et al., 2012).

A comparative analysis of the available data indicates that maintenance of the activity of P1 phagocytes is important for protection against the damaging effects of both lead and TcTYp.

A study of the effect of an extract from holothurians with bacteriostatic and wound healing properties on the phenotype of the two types of phagocytes (in terms of lectin-binding ability) revealed the dependence of its efficacy on the ability to maintain the balance of P1 and P2 phagocytes. Further studies will focus on the effect of the extract on the activity of two types of phagocytes of sea cucumbers in aquaculture under pollution conditions.

This work was implemented under the state assignment of the Ministry of Science and Higher Education of the Russian Federation (№ 121021500052-9).

Biodiversity of the transboundary Razdolnaya River (Russia-China) and problems of its estuarian biota protection under climatic and anthropogenic impact

**Tatyana S. Vshivkova^{1,2,3,4}, Tatyana V. Nikulina^{1,4},
Konstantin A. Lutaenko⁵**

*¹Federal Scientific Center of the East Asia Terrestrial Biodiversity, Far Eastern Branch
of Russian Academy of Sciences, Vladivostok 690022, Russia*

*²Laboratory of Freshwater Ecology, International Institute of Environment and
Tourism, Vladivostok State University, Vladivostok, Russia*

*³UNESCO International Chair "Marine Ecology", World Ocean Institute, Far Eastern
Federal University, Vladivostok, Russia*

*⁴Department of Ecology, Biology and Geography, International Institute of
Environment and Tourism, Vladivostok State University, Vladivostok, Russia*

*⁵A.V. Zhirmunsky National Scientific Center of Marine Biology FEB RAS, Vladivostok
690041, Russia*

E-mail: vshivkova@biosoil.ru; lutaenko@mail.ru

The Razdolnaya (Suifen) River is the largest river of southern Primorye. Its origins are located in China, and the lower part is in Russia (Primorsky Territory). The upper part of the basin is located within the East Manchurian Highlands, then the river flows through the plain and flows into the Amursky Bay (part of Peter the Great Bay) of the Sea of Japan, 20 km northwest of Vladivostok. The total length of the river is 245 km (the length in the Russian part is 191 km). The catchment area is 16.830 km² (within Russia – 6.820 km²), the total fall of the river is 880 m, the average slope is 2.13 % (within Russia – 0.45%). The river on Chinese territory is a mountain watercourse and it keeps these features until the Novo-Georgievka Village (southwest Primorye); below the river takes on the appearance of a plain-type watercourse. Before flowing into the Amursky Bay, the Razdolnaya River branches into several tributaries and forms a delta, the so-called Tavrichansky Liman (wide estuary). The most striking feature of Razdolnaya River is a full-fledged "second" bottom (subsurface drain), stretching along the entire length of the main channel. It is so large that it can be called a full-fledged

river flowing under the upper solid layer. Due to the fact that the bottom of the "underwater" river consists of dense rock formation, the water in it is clean, suitable for drinking. This feature allows the river to self-clean and maintain relatively good water quality.

The Razdolnaya River belongs to the rivers of the highest category, it is a place of wintering and feeding of commercial fish, including salmon. In the Russian part of river channel, the main pollution of the Razdolnaya River is caused by tributaries – the Rakovka and Komarovka rivers, which flow into the main river near the City of Ussuriysk; they belong to the most polluted watercourses of Primorye. Recently (since 2010), the economically developing territories of China have begun to have an impact on the river water quality. Despite the fact that the Razdolnaya River is a very significant water and fisheries area, the study of its ecological health remains insufficient. Assessments of the ecological state of the river are complex, since hydrochemical indicators often conflict with microbiological and hydrobiological assessments (algae, zoobenthos), in order to overcome these contradictions, special studies are required to coordinate evaluation criteria and develop new methodological approaches that would adequately assess the quality of water in the river and estuary using various methods.

In recent decades, the freshwater biota of the Razdolnaya River and its mouth have not been studied enough. Based on periodically obtained information about the appearance of thermophilic species in the lower reaches of rivers and estuaries, about changes in bottom communities, scientists tend to associate these data with climatic changes, but this information is fragmentary and not systematized. The same situation is observed when assessing the anthropogenic impact on the biota of the river and the estuary Tavrichansky Liman. It is required to carry out a revision of the available floral and faunal information, to conduct modern research on the algal flora, aquatic invertebrates and ichthyofauna with an emphasis to anthropogenic and climatic factors affecting the state of the biota.

Special attention should be paid to the study of the biota of specially protected natural areas, such as the "Liman of the Razdolnaya River", which is a natural heritage site of regional significance (established in 1974). The total area of the natural protected area is 2706.9 hectares. Protected areas are places of reproduction of valuable species of fish and invertebrates living in the estuary of the river. The Tavrichansky Estuary is permanently or temporarily inhabited by more than 100 species of fish from 37 families,

among them carp, bullhead, flounder, stichean and salmon, and other both marine and freshwater species. Of these, 57 species are objects of amateur and sport fishing, and 43 species are also objects of industrial fishing. For comparison, the species diversity of Primorye fish fauna as a whole is represented by 150 species of freshwater and estuarine fish, and in the Razdolnaya River (including the Tavrichansky Estuary), 75% of the total biodiversity of Primorye fish is recorded, which indicates the extremely high status of the natural protected area "Liman of the Razdolnaya River" as one of the valuable reserves of the ichthyofauna of the Sea of Japan basin. More than 200 species of birds are recorded within the boundaries of the natural monument, of which 55 species nest in this territory; 29 species of birds are included in the Red Book of the Russian Federation, 44 species in the Red Book of Primorsky Territory, and 23 species are included in the IUCN List. Several species of rare and endangered marine and brackish-water mollusks live in this area. In addition, this territory is included in the list of wetlands according to three criteria of the International Ramsar Convention.

It is necessary to raise the issue of attracting the international attention to the conservation of the protected natural area "Liman of the Razdolnaya River" and the Razdolnaya River as a whole. Of urgent necessity is arranging the international studies to assess the current state of the biota of the river and the estuarine zone and to make a serious decision at the international level on the conservation of freshwater and marine biota of this, still relatively well preserved, valuable natural international object – the transboundary Razdolnaya River.

Diversity and distribution of the order Cumacea in the Kuril—Kamchatka Trench area

Anna V. Lavrenteva

*A.V. Zhirmunsky National Scientific Center of Marine Biology, Far Eastern Branch,
Russian Academy of Sciences, Vladivostok 690041, Russia*

E-mail: avlavrenteva@yandex.ru

The Cumacea is a crustacean order from the superorder Peracarida, one of the dominating group of macrobenthic animals. Approximately 1900 cumacean species have been described worldwide, which are distributed across all oceans, from the intertidal zone to trenches (WoRMS, 2023).

Deep-sea cumaceans of the Kuril–Kamchatka Trench (KKT) and the adjacent area were first studied during the Soviet expeditions in the 1950s–1970s (Monin, 1983), but only two cumacean species were reported (Belyaev, 1989). Two complex expeditions using modern equipment for sampling small-sized, mobile, bottom-dwelling macrofauna were carried out in 2012 and 2016. Due to the intensive collaboration between German and Russian scientists, the Northwest (NW) Pacific is now one of the best investigated deep-sea areas in the world (Brandt et al., 2019).

During the German–Russian expedition KuramBio I (in 2012), 19 epibenthic sledges (EBS) were retrieved from 10 stations on the abyssal plain of the NW Pacific Basin and two stations on the western slope of the KKT at depths of 4830–5780 m. During the German–Russian expedition KuramBio II (2016), sampling was successfully performed at 11 stations with 17 EBS catches in the KKT at depths of 5120–9584 m. In both KuramBio expeditions, 26 EBS catches at depths shallower than 6000 m and 12 EBS catches deeper than 6000 m were obtained.

The examination of the materials collected by the KuramBio I expedition revealed a rich cumacean fauna belonging to 72 species, 24 genera, and five families. In the KuramBio II expedition samples, the Cumacea was represented by 33 species, 16 genera, and five families. In total, during both KuramBio expeditions, 81 species of Cumacea from 23 genera and five families were identified.

The deep-sea cumacean fauna collected during the KuramBio I and II expeditions was represented by 15 deep-sea and 8 eurybathic genera.

Classification (cluster) analyses employing group-average linking and ordination by nonmetric multidimensional scaling (nMDS) based on the Bray–Curtis similarity matrix were used to understand faunal similarity in the KKT area. Two clear groups could be distinguished: the first group included the samples from the abyssal zone, and the second from hadal depths. The tightest clustering was found among the abyssal plain stations.

At the hadal stations, the fauna of cumaceans consisted of 12 species from eight genera and five families. The species *Platycuma* sp.2 collected during the KuramBio II expedition at a depth of 8743 m was the deepest record of the order Cumacea. Two EBS stations were performed deeper than 9000 m but no cumacean specimens were found.

The faunal composition of cumaceans was different between abyssal and hadal depths even on the genera and family levels. The most diverse genera in the abyssal zone were *Campylaspis* (12 species) and *Bathycuma* (11 species). The most abundant genera were *Leucon* (15% of all cumaceans specimens), followed by *Campylaspis* (10%) and *Leptostylis* (10%). *Bathycuma* dominated in species richness in the hadal zone (three species). The *Bytholeucon* (30% of all cumaceans specimens) and *Platycuma* (36%) were the most abundant genera deeper than 6000 m.

The abundance of Leuconidae increased from 35% at abyssal stations to almost 50% at hadal stations. Leuconidae was also the most speciose family at hadal depths (five species). The most diverse family in the abyssal zone was the Nannastacidae (22 species). The latter was also the second most abundant family in both depth zones, but deeper than 6000 m it was represented by only one species, *Platycuma* sp.2. At abyssal depths, a significant part (22%) of the cumaceans consisted of family Diastylidae and was represented by 21 species, but no Diastylidae specimens were found deeper than 6200 m. The role of the families Bodotriidae and Lampropidae did not significantly change. A reduction in the number of genera and species with increasing depth was observed in each family.

Trophic characteristics of Bivalvia from shallow-water Laptev Sea

Alena V. Konoplina*, **Serguei I. Kiyashko**, **Konstantin A. Lutaenko**,
Tatiana N. Dautova

*A.V. Zhirmunsky National Scientific Center of Marine Biology, Far Eastern Branch,
Russian Academy of Sciences, Vladivostok 690041, Russia*

*E-mail: konoplina.av@bk.ru

Currently the Arctic region is one of the most interesting areas for studying the impact of climate change on benthic communities. In the context of global warming, it is here that changes in the temperature of the atmosphere and hydrosphere, weather conditions, the hydrological regime of rivers, the reduction of ice cover and the melting of permafrost are most pronounced, which has led to a significant increase in the rate of coastal erosion. The Laptev Sea is one of the Arctic regions most exposed to the effects of climate change. Abundant terrigenous runoff and the presence of methane seeps on the shelf have a great impact on the benthic communities of the Laptev Sea. In this regard, there is an increasing need for systematic monitoring of the state of benthic ecosystems in the Laptev Sea. One of the important aspects of the study of marine ecosystems is the research of trophic relationships in bottom biocenoses and the identification of sources of organic matter entering food chains. Bivalve mollusks (Bivalvia) are one of the main components of the Arctic ecosystems, however, their trophic ecology is poorly understood at the moment. In this work, we studied the trophic characteristics of some dominant species of Bivalvia collected during a multidisciplinary expedition aimed at studying the shelf of the Laptev Sea. The expedition was carried out onboard the R/V *Akademik Mstislav Keldysh* (expedition AMK-73) in September–October 2018. We found 7 species of bivalve mollusks at 15 bottom sediment collection stations. The determination of the main sources of food resources, as well as the trophic position of Bivalvia, was carried out using the analysis of stable isotopes of carbon and nitrogen. In the course of the study, we revealed significant variations in $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values in the muscle tissues of all Bivalvia: from -28.7 to -20.1‰, from 5.3 to 13.9‰, respectively. When analyzing the $\delta^{15}\text{N}$ values, 3 groups were identified, which, as we assumed, represented trophic guilds (detritivores,

filter feeders, and predators). Based on the results of the obtained $\delta^{13}\text{C}$ values in Bivalvia tissues, we determined a decrease in the inclusion of terrigenous organic carbon in the direction from the Lena River delta to the shelf slope. In addition, we determined the effect of methane seeps on the carbon isotope composition in the muscle tissues of the Bivalvia.

Single-cell RNA-Seq Reveals Epithelial Cell Regulation of Intestine Regeneration Initiation in Sea Cucumber (*Apostichopus japonicus*)

Fang Su, Lina Sun*, Hongsheng Yang, Libin Zhang, Chenggang Lin

*Institute of Oceanology, Chinese Academy of Sciences, 7 Nanhai Road, Qingdao
266071, Shandong, China*

*E-mail: sunlina@qdio.ac.cn

Intestine regeneration in sea cucumbers is a highly repetitive and consistent process of post-traumatic recovery that occurs after active evisceration under neural regulation. Sharing a common ancestor with chordates, sea cucumbers are an ideal choice for comparative analysis of vertebrate evolution, making them an emerging model species for regeneration. Ultrastructural and histological observations showed that epithelial cells underwent dedifferentiation and epithelial-mesenchymal transition (EMT) to initiate the formation of neonatal intestinal blastema. Here, we performed large-scale single-cell RNA sequencing (scRNA-seq) to classify cells throughout the early stage of intestine regeneration in *Apostichopus japonicus* and revealed that neuroendocrine cells during the regeneration period significantly expressed a neuropeptide named pigment-dispersing factor (PDF), which exhibited coordinated expression with a specific tandem-duplicated prostatic secretory protein of 94 amino acids (PSP94)-like gene family in epithelial cells, suggesting that PDF may be able to regulate the expression of PSP94-like genes. Overall, our analyses provide a foundation for future studies on the discovery of the key drivers for intestine regeneration.

Dynamics of glycerophospholipid molecular species during the embryonic development of the red king crab *Paralithodes camtschaticus*

**Ermolenko E.V.* , Sikorskaya T.V., Rodkina S.A.,
Gevorgyan T.A., Maslennikov S.I.**

*A.V. Zhirmunsky National Scientific Center of Marine Biology, Far Eastern Branch,
Russian Academy of Sciences, ul. Palchevskogo 17, Vladivostok 690041, Russia*

*E-mail: ecrre_711@mail.ru

The red king crab *Paralithodes camtschaticus* (Tilesius, 1815) is a valuable commercial object that is in great demand on the market. One of the areas of sustainable management of bioresources is the possibility of using artificial reproduction to smooth out unstable natural replenishment. A creation of an effective biotechnic for the cultivation of red king crab requires deep knowledge of the biochemistry of the crab embryonic development. Lipids are the main source of energy that fuel the developmental process of decapods. Glycerophospholipids (GPL), being the main component of biological membranes, are involved in such cellular functions as protein stabilization in the membrane and protein folding; they are cofactors in enzymatic reactions and precursors for biologically active mediators (eicosanoids, diacylglycerols, inositol phosphates). To increase knowledge about the biochemistry of embryogenesis the GPL molecular species composition was studied in eggs, larvae (zoea I-IV and decapodite stages) and juveniles of the red king crab.

Larvae were obtained from female eggs that were caught in December 2021 in the Ussuriysky Bay (the Peter the Great Bay, the Sea of Japan). The females were kept in tanks with flow sea water. Live food was used to feed the larvae. The water salinity in the tanks was $32.6 \pm 0.1\%$. The range of water temperature during the cultivation of crab larvae was 8-10 °C. Larvae (zoea I-IV and decapodite stages) were separated from seawater by filtration. Lipids were extracted from eggs, larvae, and juveniles of king crab. High-performance liquid chromatography with high-resolution mass spectrometry was used to analyze the main structural GPL glycerophosphoethanolamines (PE), glycerophosphocholines (PC),

glycerophosphoserines (PS), and glycerophosphoinositols (PI) in larvae at different stages of embryogenesis.

The minimal total content of detected GPL was noted in egg (15.56 ± 2.26 % of total lipids). The larval development of the red king crab was characterized by an increase in the content of GPL in total lipids compared to eggs, reaching maximum values at the zoea II stage (27.76 ± 2.40 % of total lipids) and in crab juvenile (31.93 ± 1.68 % of total lipids). At the same time, the GPL content decreased at the zoea III stage (20.50 ± 1.76 % of total lipids). At the zoea I stage, the content of PE, PI, and PS increased. At the other stages of crab embryogenesis, an increase in the content of all detected PL was observed.

In the lipids of eggs, larvae, and juveniles of the red king crab, the main molecular species of the studied GPL consisted of following fatty acids: C16:0, C18:0, C18:1, eicosapentaenoic acid (C20:5), arachidonic acid (C20:4), and docosahexaenoic acid (C22:6). Significant changes in the profile of molecular PL species were observed at the last stages of larval development (zoea III–IV and decapodite stages). There was a decrease in the content of the following groups of molecular species of GPL: PC containing odd fatty acids, C20:5 FA and C22:6, PE with C22:6 in the composition, PS with C20:4 and C22:6, as well as PI containing C20:4 and C22:6. At the same time, the content of PE and PC increased with acyl fragments (a total number of carbon atoms up to 37) and C20:4, PS with C20:5 and PI with odd acyl fragments and C20:5.

The dynamics of the total GPL content and the profile of its molecular species was associated with a sharp increase in the larvae mass, which occurred at the zoea III stage. Probably, the decrease in the content of GPL caused by their use as a source of energy and biologically active mediators during intensive larvae growth. In this case, the consumption of certain groups of GPL molecular species was observed. This study contributes to the development of lipidomics in marine invertebrates.

Corals as an indicator of the vulnerable marine ecosystems — state of knowledge and perspectives

Tatiana N. Dautova

*A.V. Zhirmunsky National Scientific Center of Marine Biology, Far Eastern Branch,
Russian Academy of Sciences, Vladivostok 690041, Russia*

E-mail: tndaut@mail.ru

Seamounts are areas with high biological productivity of benthic and pelagic communities, including industrially important accumulations of marine organisms that support commercial fishery. The reason for that high productivity – the concentration of the biogenic matter, larvae and plankton around the seamount. It is performing due to the so-called Taylor cone forming around the seamount summit which sometimes possess more food to filter-feeding animals like corals. Sea bottom elevations (seamounts, ridges) are, also, of interest to the scientific community because as areas of increased biodiversity being both reference points for the settlement of deep-sea fauna, refuges and faunistic centers and have a significant impact on the formation of the ocean fauna.

In high seas, where 90% of marine bioresources are located, several international fisheries management commissions operate in order to develop fishery quotas and restrictive measures of fishery near seamounts. These Commissions act basing on the Convention on the Preservation of Biological Resources of the High Seas, to which the countries fishing in this zone are parties. The Commission and Convention focus on deep-sea bottom VMEs (mainly coral gardens) on the seamounts as sources and indicators of high productivity of the region. The North Pacific Fishery Commission recognized the lack of information on the location and population status of *Octocorallia* populations in the region and the urgent need for their research in seamounts (March 2018, Yokohama, Japan). The deep-sea bottom ecosystems of the seamounts are classified as Vulnerable marine ecosystems (VMEs), since the recovery of the coral gardens after mechanical damage by bottom trawls proceeds extremely slowly.

There is the urgent need to discover the deep-sea areas for conservation for the future, referring to the development of deep-sea fishery and future mining increasing.

For it, the scientific community may be prospectively aimed to answer several global questions: 1) what is the ways for coral dispersal in the ocean? 2) how to enlarge our limited data on the Octocorallia fauna in the important areas of the Indo-Pacific and Pacific? Based on our findings, the Emperor Chain should be suggested as a series of “stepping stones” for deep-sea species dispersal in the North Pacific. There is an important challenge to study other significant seamount chains to fill gaps in our knowledge of biodiversity and the pathways of deep-sea inhabitants.

Crabs of genus *Chaceon* Manning & Holthuis, 1989 (Decapoda: Brachyura: Geryonidae) in the deep-sea environment of Emperor Seamount Chain

Evgeniia L. Egorova

*A.V. Zhirmunsky National Scientific Center of Marine Biology, Far Eastern Branch,
Russian Academy of Sciences, Vladivostok 690041, Russia*

E-mail: egorova.eug@gmail.com

The Emperor Seamount Chain, located in the Northwest Pacific, is a relatively underinvestigated region in regards to its biota, although it is well-known for its extensive fisheries. In the recent years, the Emperor Chain has attracted international attention as a region abundant with vulnerable marine ecosystems, requiring further research and observations against a backdrop of continuing trawling activities.

As active and mobile scavengers and predators, crabs play a significant role in seamount environments, maintaining the balance of the ecosystem by controlling the population of other species, recycling nutrients, and providing food source for larger animals, such as fish and cephalopod mollusks. Geryonid crabs, typically relatively large and robust animals, are commonly encountered deep-sea dwellers, represented in the Emperor Seamount chain mostly by the genus *Chaceon* Manning & Holthuis, 1989.

While true crabs of the genus *Chaceon* are targeted by commercial fisheries worldwide, there is not much information available for the status of this genus in the Emperor Seamount Chain. In this study, we report the number, depth, location and the substrate conditions of the *Chaceon* crabs observed during the 86th research cruise RV *Akademik M.A. Lavrentyev* in July-August 2019, which surveyed Koko, Jingu, Nintoku, Ojin and Suiko seamounts. The animals were observed and recorded with the cameras of ROV *Comanche 18*, and several specimens were taken to support preliminary genus and species identification with further morphological analysis. The *Chaceon* crabs were observed in a wide range of depths, from 360-380 to more than 1300 meters, most abundant in the 800-1200 meters bracket. The total number of recorded *Chaceon* crabs is 186, with the majority (117) belonging to the species *C. imperialis* Manning, 1992.

Investigations on the deep-sea Isopoda of the Northwest Pacific on base of recent expeditions

Olga A. Golovan, Marina V. Malyutina

*A.V. Zhirmunsky National Scientific Center of Marine Biology, FEB RAS,
Palchevskogo Str. 17, Vladivostok 690041, Russia. E-mail: golovan_olga@mail.ru.*

Crustaceans of the order Isopoda are a common component of the marine benthos. In the deep sea communities, they are one of the dominant taxa in terms of abundance and diversity. In the deep sea >95% of isopods are represented by the primarily deep-sea families of the suborder Asellota. These 20 families originated, diverged and spread widely in the abyssal of the World Ocean (WO). The share of Munnopsidae and Desmosomatidae is especially large (usually ~50 and 20% of isopods). The deep-sea fauna of the Northwest Pacific (NWP) was studied during four Russian-German expeditions in 2010–2016, SoJaBio, SokhoBio, KuramBio I and II, which explored the Sea of Japan (SJ), the Sea of Okhotsk (SO) and the area of the Kuril-Kamchatka Trench (KKT) using epibenthic sledges (EBS). In addition, reducing communities of the Bering Sea bathyal were studied during the expedition of the NSCMB FEB RAS in 2018 using ROV. The studied isopod fauna was represented by ~ 340 morphospecies from 79 genera and 21 families, making the NWP one of the richest areas of the WO in terms of isopod fauna. More than 80% of the collected species appeared to be new to science. Among the deep-sea NWP asellotes, families Munnopsidae (~50% %, 157 species) and Desmosomatidae (~30%, 82 species) dominated. A comparison of the isopod fauna from the four studied NWP areas showed its depletion from the open abyssal of the Pacific Ocean (PO) to the abyssal of the SO, which is connected with the PO by the deep-water straits (down to 2341 m depth), then to the hadal of the KKT and to the most isolated abyssal of the SJ with shallow straits (up to 73 m). The richest and most diverse fauna was observed in the open oceanic abyssal plain in the KKT area (245 species, 18 families). The main factor influencing the distribution of fauna here is the amount of food entering the system. In the hadal of the KKT the richness of the fauna drops sharply: e.g. 106 species of munnopsids were collected in the abyssal, 41 species below 6000 m, 31 below 7000 m, 19 below 8000 and only one species was found at max. depth of 9584m. The fauna of the Kuril Basin of the SO resembles the

depleted PO abyssal fauna. Munnopsidae (41%, 38 species) and Desmosomatidae (29%, 17 species) predominated, 37 morphological species of desmosomatids and munnopsids were common with the PO abyssal. In the SJ the fauna was the poorest – 22 species, 7 families, almost 100% of the abundance were Munnopsidae and Desmosomatidae (4 and 11 species, respectively). Species richness decreased with depth. At depths below 3000 m, the only endemic munnopsid species occurred, reaching a huge abundance (to 2029 specimens in a sample). Clarification of the isolating role of the KKT for the dispersal of abyssal taxa was one of the aims of the last hadal expedition. Its role as a barrier for many families of isopods was noted, but some of the Munnopsidae, Desmosomatidae, Haplomunnidae species were found on its both sides. Further studies using molecular methods are needed. Thus, molecular analysis revealed cryptic desmosomatid species within species complexes in the KKT area, including those separated by habitat depth. In the hydrothermal communities of the Piip underwater volcano (Bering Sea, 373–472 m), munnopsids dominated in number among the collected isopods. However, in order to characterize the deep sea fauna of the Bering Sea, comparable collections with EBS are required.

Gastropods of the Kien Luong and Con Dao mangroves (Kien Giang Pr. and Ba Ria-Vung Tau Pr., Vietnam)

Prozorova Larisa A.

*Federal Scientific Center of the East Asia Terrestrial Biodiversity, Far Eastern
Branch of the Russian Academy of Science, Stoletiya Prospekt 159, Vladivostok
690022, Russian Federation*

The country of Vietnam with a long coastline and with shallow maritime biodiversity which are highly threatened. In particular, mangrove forests which in South Vietnam mainly occur in the Mekong Delta, are being destroyed rapidly in spite of their importance to economics, coastal stability, and habitat for organisms.

In 2017– 2019 in the frame of the Russian-Vietnamese ecological study of the Mekong Delta (FEB RAS – ITB VAST 17-000) investigations of the mangrove malacofauna in the Kien Giang and Ba Ria-Vung Tau provinces were carried out.

The Kien Luong Protected Area is one of the 3 key areas of the Kien Giang Biosphere Reserve, recognized by UNESCO in 2006. That supports one of the last significant areas of the natural Vietnamese mangroves and is recognized as one of the highest priority sites for conservation in the Mekong delta.

In 2017 and 2018 molluscs were collected in Kien Luong mangrove forest alongside the estuaries and bays, from mud, trunks and roots of trees. Preliminary analysis revealed more than 40 species in Potamididae (*Cerithidea*, *Terebralia*, *Pirenella*, *Telescopium*), Littorinidae (*Littoraria*), Neritidae (*Nerita*, *Clithon*, *Neripteron*), Pachychilidae (*Sulcospira housei*), Nassariidae (*Nassarius* cf. *stolatus*), Assimineidae, Haminoeidae, Onchidiidae (*Onchidium*, *Melayonchis*), Ellobiidae (*Cassidula*, *Melampus*, *Ellobium*), Amphibolidae (*Naranjia*) and others. Most of species are new to the Mekong Delta, and some species and genus *Naranjia* are new to the country as well. These mudflat snails turned out to be the most interesting find and were studied by molecular genetics methods. Unlike rare amphibolides snails of the family Ellobiidae are very abundant in Kien Luong mangroves. All of 6 recorded ellobiid species, including the largest *Ellobium aurisjudae* are new for the Kien Giang

Province and the Mekong Delta. The new data add to the malacofauna of Vietnam's mangrove forests and mudflats, and support the view of the Kien Giang Biosphere Reserve as a biodiversity hot spot.

Con Dao Archipelago is located about 80 km from mainland Vietnam and includes 16 islands and islets with the total land area 76 km². Uninhabited islands and part of the Con Son Is. are under protection since 1984 as the Con Dao National Park, recognized as the 2203rd Ramsar site in the world by UNESCO in 2014.

In early March 2019 malacological survey was conducted on two largest islands Con Son and Bay Canh. Two places with unique “sandy” mangroves on the territory of the national park were examined as well. Mangrove forest of Bay Canh Is. occurs on white sandy beach formed by coral sand. This forest is assessed as more developed and dwelled by 23 gastropod species in genera *Littoraria*, *Cassidula*, *Terebraria*, *Monodonta*, *Clypeomorus*, *Nerita*, *Haminoea*. Under deadwood on sand with mud *Melampus* cf. *adansianus* and small *Neripteron* sp. were found. Smaller mangrove forest in Dam Tre Bay of Con Son Is. is dwelled mainly by *Clupeomorus pellucida* with sporadic *Littoraria*, *Monodonta*, *Tenguella*, *Nerita* and *Cellana* species.

The data obtained provide a basis for studying biodiversity, as well as for more effective protecting and monitoring of Vietnam's threatened mangrove ecosystems and their malacofauna with key ecological functions.

On the systematic position of *Anadara kafanovi* Lutaenko, 1993 (Bivalvia, Arcidae) based on morphological and genetic analysis

Marina S. Ananeva¹, Ulyana V. Simakova¹, Galina A. Kolyuchkina¹,

Philipp V. Sapojnikov¹, Konstantin A. Lutaenko²

¹*Shirshov Institute of Oceanology of the Russian Academy of Sciences, Moscow, Russia.*

²*A.V. Zhirmunsky National Scientific Center of Marine Biology, FEB RAS, Palchevskogo Str. 17, Vladivostok 690041, Russia.*

E-mail: ananeva_marya@mail.ru

The tropical-subtropical Pacific anadarine species *Anadara kafanovi* Lutaenko, 1993 (Mollusca, Arcidae) was first described from the South China Sea (Vietnam, Bien Shen Island). Later it was synonymized with *Anadara broughtonii* (Schrenck, 1867) by Huber (2010) based on a morphological analysis. This synonymization was criticized later based on clear differences in shell shape size and number of species between the species (Lutaenko, Volvenko 2013). Here we tested the hypothesis of *A. kafanovi* species validity using both molecular and morphological data. We compared morphological data and partial sequences of 5 genes (COI, H3, ITS, 18S и 28S) of *A. kafanovi* (3 specimens, South China Sea), *A. broughtonii* (13 specimens, Sea of Japan) and *Anadara kagoshimensis* (3 specimens, Black, Yellow, East China seas).

Morphological characteristics of the *A. kafanovi* specimens used for molecular analysis corresponded to the species original description (Lutaenko, 1993). These three specimens were clearly distinguished from *A. broughtonii* by a smaller size and fewer number of radial ribs (36–39 vs 39–50). The shells of *A. broughtonii* were much taller than that of *A. kafanovi*. The ratio of height to length was 0.75 and 0.60, respectively.

The sequences of nuclear ribosomal genes (partial 18S, 1191 bp and 28S, 333 bp) of all three *Anadara* species were quite similar (100% and >99,7% of similarity respectively). For ITS1-5,8S-ITS2 (1038 bp) gene similarities of *A. kafanovi* with 1) *A. kagoshimensis* (97,95–98.3%), and 2) *A. broughtonii* (97.95–98.59 %) were lower than within species (>99,7%). The latter two species were more close to each other (<99,4%).

The sequences of H3 histone gene (324 bp) were similar for all three species (>98,8%). Specimens of each species had character states (discrete nucleotide substitutions) in the sequences of ITS and H3 genes. Maximum likelihood phylogenetic reconstruction (FastTree 2.1) based on COI partial sequences (573 bp) showed that all three species formed distinct clades. The similarity within each clade varied from 99,9% to 100% and between – 85,5% to 89,7%. This difference corresponds to clear barcoding gap. Also *A. kagoshimensis* and *A. broughtonii* were closer to each than to *A. kafanovi*.

The presence of clear barcoding gap in mitochondrial gene (COI), character states in nuclear (ITS and H3) genes and morphological distinctness supports the existence of *Anadara kafanovi* as a separate distinct valid species.

Gastropods from the Pacific northernmost chemosynthetic ecosystems

**Ivan O. Nekhaev¹, Yuri I. Kantor², Elena M. Chaban³, Elena I.
Rybakova⁴**

¹*Saint Petersburg State University*

²*A.N. Severtsov Institute of Ecology and Evolution*

³*Zoological Institute, Russian Academy of Sciences*

⁴*P.P. Shirshov Institute of Oceanology, Russian Academy of Sciences*

The study is based on materials collected during the cruises of the RV Akademik M.A. Lavrentyev in 2016 and 2018 in two types of the reducing biotopes: hydrothermal fields on the underwater Piip Volcano and the methane seeps on the Koryak slope both localities are in the Bering Sea. The Piip Volcano (~ 368 – 495 m) is the northernmost (55°22' – 55°24' N) hydrothermal region in the Pacific. Methane seep fields of the Koryak slope found between 400 and 700 m depth are the northernmost chemosynthesis-based habitats known to date in the Pacific (60°49 – 61°10).

In total, 27 species of shell-bearing gastropods were identified from both areas. Three of them (*Provanna annae* Nekhaev, 2023, *Parvaplusgtrum wareni* Chaban, Schepetov, Ekimova, Nekhaev et Chernyshev, 2022, *Astyris axicostata* Kantor, Zvonareva et Krylova, 2023) have been described as new for science, and at least three more species are presumably new to science but not described yet. Also, five species were new to the fauna of the Bering Sea and adjacent areas of the Pacific Ocean.

Nine species were encountered at the Piip Volcano, including one, *Provanna annae*, previously only found in chemosynthesis-based communities, and another, *Parvaplustrim wareni*, potentially exclusive to such environments. The methane seeps on the Koryak slope revealed nineteen species; however, none were identified as specific to chemosynthesis-based communities. Gastropod populations displayed a more dispersed structure on the Koryak slope compared to the Piip Volcano, where four times as many specimens were collected. Generally, the distribution patterns of taxonomic and functional groups in the Koryak slope methane seep area appear to resemble those in background communities, while in the hydrothermal zone of the Piip Volcano, they align with other extreme community types.

Phylogenetic analysis has revealed that at least two of the newly discovered species (e.g. *Provanna annae* and *Astyris axicostata*) share their closest relatives with hydrothermal communities off the Japanese coast. Additionally, one species was found to be common to both the Piip Volcano and the American shore.

Phylogenetic relationships of populations of chemosymbiotrophic bivalves *Calyptogena pacifica* (Vesicomysidae: Pliocardiinae) from the Bering Sea and the eastern Pacific Ocean

Belov D.A., Kremenetskaya A.V., Krylova E.M.

*Shirshov Institute of Oceanology, Russian Academy of Sciences, 36, Nakimovskiy
prospect, Moscow 117997, Russia*

Bivalves of the subfamily Pliocardiinae (Vesicomysidae) live in symbiosis with sulphide-oxidizing chemoautotrophic bacteria contained in the molluscs' gills. These bacteria synthesize organic matter that is the primary source of nutrition for the molluscs. However, the bacteria require sulphides, which are available exceptionally in specific reducing habitats such as hydrothermal vents, cold methane seeps, and accumulations of decomposing organic matter. These habitats differ significantly from the surrounding environment and are separated from each other, resulting in fragmented distribution patterns of molluscs.

Calyptogena pacifica occurs in reducing habitats in the eastern Pacific Ocean on the continental slope from the Dickson-Entrance Strait in the north to the California Peninsula in the south, at depths ranging from 361 to 2423 m. In the western Pacific, *C. pacifica* has been found in the Bering Sea on the Piip Volcano (470-490 m) and on the Koryak Slope (400-695 m). Molecular data on *C. pacifica* from the Koryak Slope of the Bering Sea were not available. The aim of our study was to determine whether the population of *C. pacifica* from the Koryak slope differs genetically from spatially distant populations of this species from the eastern Pacific.

In 2018, during the 82nd cruise of the R/V "Akademik M.A. Lavrentyev" organized by the NSCMB FEB RAS (Vladivostok), molluscs were collected from areas of methane seeps at depths of 660-690 m using the manipulator of the ROV "Comanche-18". Fragments of adductor and foot tissue of 50 specimens of *C. pacifica* were fixed in 96% cold ethanol and stored at -20°C. Fragments of the cytochrome c-oxidase subunit 1 (*COI*) gene of 482 bp length were analyzed. Phylogenetic analysis was conducted using Bayesian statistics with MrBayes 3.2.7a, and a haplotype network

was constructed using the median linkage algorithm in POPART. Additionally, 31 *COI* sequences published in GenBank were used in the analysis.

Preliminary results show a quite high level of connectivity of populations from the Koryak slope and the eastern Pacific. Seven different haplotypes were identified on the Koryak Slope, four of which were unique, and three were shared with populations on the east coast of the United States. The highest genetic diversity was observed in clam populations from the Monterey Bay, where nine haplotypes were identified, three of which were shared with the *C. pacifica* population of the Koryak Slope, and six were unique. The high level of genetic diversity may be related to the greater diversity of *C. pacifica* habitats in Monterey Bay, recorded at depths ranging from 361 m to 959 m, and probably to the longer occupation of *C. pacifica* in this region. The significant similarity of the Koryak Slope population to populations of the eastern Pacific Ocean suggests the possibility of an intense gene flow. It is assumed that the gene flow can occur through hypothetical populations inhabiting the Bering Sea slopes to the north of the studied area.

Macrobenthos functional feeding group and the ecosystem health assessment of the intertidal zone in the Yellow River Delta

Shaoyu Jiang^{1,2}, Chuanxin Zhang¹, Zirui Peng¹, Linlin Chen^{1,3},
Quanchao Wang^{1,3}, Baoquan Li^{1,3*}

¹*CAS Key Laboratory of Coastal Environmental Processes and Ecological Remediation, Yantai Institute of Coastal Zone Research, Chinese Academy of Sciences, Yantai 264003, China*

²*University of Chinese Academy of Science, Beijing 10049, China*

³*Center for Ocean Mega-Science, Chinese Academy of Sciences, Qingdao 266071, China*

The Yellow River Delta (the YRD) is the youngest, broadest, and the most integrated wetland ecosystem in China, but it is suffering from threats by human activities and alien species invasion, resulting in the local habitats destruction and species depletion. To assess the ecosystem health status (EHS) of the intertidal zone in the YRD, we surveyed and analyzed the macrobenthic assemblages in spring, summer, and autumn in 2017, respectively. The results showed the species number, abundance, and biomass of macrobenthos functional feeding groups (FFGs) varied with seasons. In spring, the phytophages group (*Ph* group) and omnivores group (*O* group) were dominant; but the more carnivorous group (*C* group) appeared in summer and more planktivorous group (*Pl* group) in autumn. In addition, disturbance status and the EHS of the macrobenthos were different in different seasons. The macrobenthic community was less disturbed in summer, while the EHS was worse. The species number, abundance, and biomass of macrobenthos FFGs also were spatially different. The EHS was in a “good” to “moderate” condition in most stations, although some stations with “poor” or “bad” health. Possible factors responsible for the “poor” EHS are complex in the YRD. For instance, the combined effect of local industrial and sewage effluents, salinization and alkalization, over-exploitation, and exotic species invasion.

Keywords: macrobenthos functional feeding group, AMBI and M-AMBI index, functional group evenness index, ecosystem health status, the Yellow River Delta

Macrobenthic diversity and eco-exergy evaluation of wetland restoration in the Yellow River Delta

**Yanmei Ni¹, Chunyun Liu¹, Li Chen¹, Debin Sun¹, Zhiyuan Dong¹,
Baoquan Li^{1,2}, Linlin Chen^{1,2*}**

¹ *CAS Key Laboratory of Coastal Environmental Processes and Ecological Remediation, Yantai Institute of Coastal Zone Research, Chinese Academy of Sciences, Yantai 264003, China*

² *Center for Ocean Mega-Science, Chinese Academy of Sciences, Qingdao 266071, China*

In order to effectively curb the decline in wetland biodiversity, ecosystem degradation, and ecological service function, a series of freshwater replenishment projects of different scales has been carried out since 2002 in the Yellow River Delta, in which the international important wetland biodiversity conservation project of the Yellow River delta was started in 2019. To understand the restoration effects in the ecological restoration area after 3 years, samples of macrobenthos and environmental factors were investigated in May, August and October 2022. The community characteristics, biodiversity, and correlation with environmental factors of macrobenthos were analyzed using biodiversity index, Cluster clustering, MDS analysis and Spearman correlation analysis. The eco-exergy as one of the most effective methods in the evaluation of wetland restoration, the sustainability and self-organizational level of the wetland before and after restoration were evaluated using thermodynamic indices (eco-exergy and specific eco-exergy) in benthic macroinvertebrate communities. Results showed that a total of 16 macrobenthic species were collected, belonging to 5 phyla, 6 classes and 15 families. The number of macrobenthic species in the Yellow River Delta wetland restoration area showed an increasing trend during the survey period, with chironomid larvae, elliptical radish snails, and pointed mouth round flat snails becoming the dominant species in the area. The correlation analysis of community structure parameters with environmental factors indicated that the dominant species, Chironomidae, showed a significant positive correlation with DO, NO₃-N and PO₃-P, and a significant negative correlation with pH and SiO₂-Si (P <0.01). Compared with historical data, the Eco-exergy and Specific

Eco-exergy increase by 1.45-fold and 0.95-fold, respectively. The restoration area is developing towards a healthier and more orderly direction but is currently in a "sub healthy" state, and the restoration work still needs to be continued. Ecological succession is a long-term and slow process, so it is necessary to conduct long-term ecological monitoring, analyze the reconstruction process of the disturbed macrobenthic community structure in the Yellow River Delta ecological restoration area and explore the regular changes in ecological succession.

Key words: the Yellow River Delta; ecological restoration; Eco-exergy; macrobenthos; community structure

Benthic food web structure of Xiaoqing River Estuary revealed by carbon and nitrogen stable isotope analysis

**Chuanxin Zhang^{1,2}, Jing Chen¹, Linlin Chen^{1,3}, Ronglian Xing^{2*},
Baoquan Li^{1,3*}**

*¹CAS Key Laboratory of Coastal Environmental Processes and Ecological
Remediation, Yantai Institute of Coastal Zone Research, Chinese Academy of
Sciences, Yantai 264003, China*

²College of Life Sciences, Yantai University, Yantai 264005, China

*³Center for Ocean Mega-Science, Chinese Academy of Sciences, Qingdao 266071,
China*

Stable isotope analyses represent integrative records of food intake over long time scale and now has become a powerful tool for the study of food web structures in aquatic communities. The ratio of stable N isotopes ($\delta^{15}\text{N}$) is used to quantify the consumer's trophic level, while the ratio of stable C isotopes ($\delta^{13}\text{C}$) is used to determine the carbon sources of predators. This research examined the benthos food web structure in Xiaoqing River Estuary adjacent sea area by combining carbon and nitrogen stable isotope technique. Four potential food sources, including sediment organic matter (SOM), suspended particulate organic matter (POM), zooplankton and phytoplankton, and 35 aquatic organisms were collected in October 2020. Bayesian Mixing Model (MixSIAR) were used to analyze the food web structure and the trophic relationship of benthos. The results showed that the $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values of potential food sources varied from -25.56‰ to -17.91‰ and 2.43‰ to 10.33‰, respectively. Moreover, the $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values of benthos varied from -23.48‰ to -18.31‰ and 8.79‰ to 18.01‰, respectively. The trophic levels of the main consumers ranged from 1.43 (*Arcuatula senhousia*) to 4.54 (*Ctenotrypauchen chinensis*). Trophic relationship analysis showed that there were two main energy transfer pathways in the Xiaoqing River Estuary adjacent sea area. One was the planktonic food chain with plankton as the major energy source, in which bivalves (except *Solen brevissimus*), small shrimps, and polychaetes were the main primary consumers. The other was the benthic food

chain with SOM as the major energy source, in which *Solen brevis* and gastropods were the main primary consumers. On the whole, there was a certain degree of niche overlap and fierce competition among species in Xiaoqing River Estuary adjacent sea area.

Key words: Xiaoqing River Estuary; food web structure; trophic level; stable isotope; food source

Co-occurrence patterns of macrobenthic community in the intertidal zone and offshore areas of the Yellow River Delta, China

Jiao Wang^{1,3}, Linlin Chen^{1,3}, Shaoyu Jiang^{1,2}, Baoquan Li^{1,3*}

¹*CAS Key Laboratory of Coastal Environmental Processes and Ecological Remediation, Yantai Institute of Coastal Zone Research, Chinese Academy of Sciences, Yantai 264003, China*

²*University of Chinese Academy of Science, Beijing 10049, China*

³*Center for Ocean Mega-Science, Chinese Academy of Sciences, Qingdao 266071, China*

The exploration of species co-occurrence patterns remains a primary pursuit among ecologists, mainly due to the essential role species coexistence plays in assessing diverse theories, principles, and concepts. However, the species co-occurrence patterns of macrobenthos in intertidal zone are poorly understood in terms of spatio-temporal dynamics. In this study, we explored co-occurrence patterns of macrobenthos in the intertidal zone and offshore areas of the Yellow River Delta based on both the matrix level and the species-pair level methods. In this study, the intertidal zone displayed lower species diversity, primarily featuring mollusks, crustaceans, and polychaetes, while the offshore area consistently exhibited higher crustacean abundance, particularly shrimps and crabs, along with an increased fish species count across multiple months. Matrix-level results using a null model indicated that macrobenthic species with low mobility predominantly exhibited a random pattern across the intertidal zone, including the high-tide, mid-tide, and low-tide zones. On the other hand, macrobenthic species with high mobility showed a significant segregated pattern within offshore regions. The pairwise-level analysis showed that within the intertidal zone and its various subdivisions, there are notably fewer species pairs demonstrating significant aggregation and separation. Furthermore, species pairs displaying significant aggregation are more numerous than those showing separation among the overall pairs. These findings further support the notion that macrobenthic species within the intertidal

zone tend to lack a distinct structure, likely due to the diminished impact of interspecific competition in this environment.

Keywords: co-occurrence patterns, null model, macrobenthic community, intertidal zone, Yellow River Delta

Characteristics and temporal evolution of heat waves in Jiaozhou Bay

Jing Wang, Xiaoxia Sun, Yongfang Zhao

Jiaozhou Bay Marine Ecosystem Research Station, Institute of Oceanology, Chinese Academy of Sciences, Qingdao 266071, PR China

Extreme heat events come up frequently with global warming, and the frequency, intensity, duration and other parameters of heat waves have been previously found general growth trends. The emergence of heat waves will have pronounced impacts on organisms, ecosystems, human beings and society. The limitation of regional climatology hampers the unification of the definition and quantitative research criteria of heat waves. More regional basic research data is grounded in unbinding region boundaries. We analyzed several individual characteristics of 156 heat waves to study the temporal variation of heat waves, based on the temperature data obtained in Jiaozhou Bay during 1954-2022. We find that both HWN and HWD increase to five times of the original according to the fitted straight line. The frequency of heat waves increased by 81.99%. We discover a regular fluctuations with progressively shorter periods in heat wave intensity. The decrease of intensity fluctuation period is directly associated with the increase of heat wave frequency. We also catch the apparent seasonal variation of heat waves, peaking in summer. The results further confirm that future heat waves will be more frequent, longer lasting, and more intense. These results provide the foundation for the study of the spatio-temporal changes of heat waves, the changes of complex characteristics and the tracking of single heat wave events in the future.

Keywords: Heat wave, Characteristics, Variation

Quantification of the vertical transport of microplastics by biodeposition of typical mariculture filter-feeding organisms

Liujiang Meng^{1,3}, Xiaoxia Sun^{1,2,3*}, Qingjie Li¹, Shan Zheng^{1,2},
Junhua Liang¹, Chenhao Zhao^{1,3}

¹Jiaozhou Bay National Marine Ecosystem Research Station, Institute of Oceanology,
Chinese Academy of Sciences, Qingdao 266071, China

²Center for Ocean Mega-Science, Institute of Oceanology, Chinese Academy of
Sciences, Qingdao 266071, China

³University of Chinese Academy of Sciences, Beijing 100049, China

*E-mail: xsun@qdio.ac.cn

The tremendous loss of microplastics from the sea surface and the low density of microplastics found in the water column and sediments indicate that the oceans have mechanisms capable of transporting microplastics from the surface to the seafloor. These include physicochemical processes and biological influences from marine organisms that drive the vertical migration of microplastics. Little is known, however, about the biological processes involved in the deposition of plastics in the marine environment. A considerable number of mariculture filter-feeding organisms can consume substantial amounts of suspended substances in the water column, and these organisms are ideal candidates for depositing microplastics. In this study, we analyzed microplastic abundance in typical mariculture filter feeders, i.e., ascidians (*Halocynthia roretzi*), oysters (*Crassostrea gigas*), scallops (*Chlamys farreri*) and clams (*Ruditapes philippinarum*), quantified the number and characteristics of the microplastics they deposited in situ, and further compared microplastic biodeposition rates. Microplastics were present in feces and pseudofeces and sank to form biodeposits rather than accumulating to significant levels in organisms. Microplastics were found in significantly higher numbers in the biodeposits of mariculture organisms than in the control deposits ($p < 0.01$). The highest microplastic biodeposition rate was found in scallops (1.14 ± 0.07 items·ind⁻¹·d⁻¹ or 0.5 ± 0.03 items·g⁻¹·d⁻¹). The shape and color

of the microplastics in the sediments were not impacted by the presence of organisms ($p > 0.05$), but the deposition of $< 1000 \mu\text{m}$ and positive-buoyancy (less dense than seawater) microplastics was significantly increased in the biodeposits ($p < 0.05$). These results suggest that mariculture filter-feeding organisms have important biodepositional functions that influence the fate of microplastics through the transfer of microplastics from the surface to the seafloor. This study could contribute to a better understanding of the biological plastic pump mechanisms in oceans, assess the source-sink dynamics of microplastics under the effects of marine organisms to further clarify the fate of microplastics once they enter the ocean and guide remediation measures to eliminate microplastic pollution based on a nature-based solution.

Keywords: Microparticle, Vertical transport, Bivalve; Ascidian, Biodeposition rate

Scenario Simulations of marine ecosystem health on China's coast

Ziyuan Hu

Jiaozhou Bay Marine Ecosystem Research Station, Institute of Oceanology, Chinese Academy of Sciences, Qingdao 266071, China

Laboratory for Marine Ecology and Environmental Science, Pilot National

Laboratory for Marine Science and Technology (Qingdao), Qingdao, China

Center for Ocean Mega-Science, Chinese Academy of Sciences, Qingdao, China

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 using machine learning methods. Climate change and human activity impact scenarios were designed and individually applied and integrated to predict the possible responses of marine ecosystem health conditions.

Water column stratification governs picophytoplankton community structure in the oligotrophic eastern Indian ocean

Feng Wang^{1,2}, Shujin Guo^{1,3,4}, Junhua Liang^{1,3,4}

¹*Jiaozhou Bay National Marine Ecosystem Research Station, Institute of Oceanology, Chinese Academy of Sciences, 7 Nanhai Road, Qingdao, China*

²*University of Chinese Academy of Sciences, Beijing, China*

³*Laboratory for Marine Ecology and Environmental Science, Pilot National Laboratory for Marine Science and Technology (Qingdao), Qingdao, China*

⁴*Center for Ocean Mega-Science, Chinese Academy of Sciences, Qingdao, China*

Under the background of global warming, the area extent of the oligotrophic tropical oceans has growing due to increased water-column stratification over the past decades. Picophytoplankton is usually the most dominant phytoplankton group in oligotrophic tropical oceans and substantially contribute to carbon biomass and primary production there. Understanding how vertical stratification governs the community structure of picophytoplankton communities in oligotrophic tropical oceans is important for comprehensively understanding the plankton ecology and biogeochemical cycle in these areas. In this study, the distribution of the picophytoplankton communities in the eastern Indian Ocean (EIO) was investigated during a period of thermal stratification in the spring of 2021. *Prochlorococcus* contributed most (54.9%) to picophytoplankton carbon biomass, followed by picoeukaryotes (38.5%) and *Synechococcus* (6.6%). Vertically, the three picophytoplankton groups showed quite different distribution pattern: the abundance of *Synechococcus* was highest in the surface layer, while *Prochlorococcus* and picoeukaryotes were usually located between 50 m and 100 m. The relationship between the abundance of picophytoplankton and environmental factors was analyzed, and the results revealed that picophytoplankton distribution was strongly correlated with the degree of vertical stratification of the water column. The density of *Synechococcus* was higher in strongly stratified waters, while *Prochlorococcus* was more abundant in regions of weaker stratification. This is mainly attributed to variation

of physicochemical parameters such as nutrient structures and temperature resulted from water column stratification. Understanding the distribution patterns of these organisms and their relationship with stratification in the oligotrophic EIO is essential for comprehensive understanding on oligotrophic tropical ecosystem with increasing stratification in future.

Keywords: Phytoplankton, Biomass, Community composition, Stratification, Environmental impact, Eastern Indian Ocean

Characteristics of microplastics in different matrices in Jiaozhou Bay, China

Shan Zheng, Kangning Zhang

Jiaozhou Bay Marine Ecosystem Research Station, Institute of Oceanology, Chinese Academy of Sciences, Qingdao 266071, PR China

E-mail: zhengshan@qdio.ac.cn

In the current global environmental problems, marine plastic pollution, ozone depletion and ocean acidification are included. With the development of research on microplastics, we have obtained important understandings on the temporal variation of the spatial distribution characteristics and the spatial variation of the temporal distribution characteristics of microplastics in China's coastal waters. However, due to the complexity of microplastics features, the study of microplastic sources is in a relatively preliminary stage. Based on topographic features and chemical composition, an integrated index for microplastics complexity (MCI) was developed, and was applied in reflecting microplastics complexity in different media in Jiaozhou Bay. We compared the differences in microplastic complexity in wastewater treatment plants (WWTPs) and seawater, sediments and biota by in Jiaozhou Bay. MCI range from 0.35 to 57, with the average of 0.49 in wastewater in WWTPs. The MCI in zooplankton, which was 0.3 in average. The MCI in zooplankton is rather lower than that in the seawater, as zooplankton are so small as not to ingest large size particles of microplastics. The MCI of benthic shellfish was 0.46, which was higher than that in zooplankton, indicating that the complexity of microplastics in benthic shellfish were higher. The results of the study suggest that the value of MCI can be used for quantitative analysis of microplastic source apportionment. The MCI in wastewater in WWTPs, seawater, sediments, shellfish, and zooplankton showed the complexity of microplastic contamination in each phase and the connection between different media. Quantitative source apportionment is continuing to further promote the accomplishment of goal 14.1 in SDGs and decision support.

Long-term Ecological Dynamics of Phytoplankton Communities under Environmental Drivers in Jiaozhou Bay

Shimeng Yang

*Jiaozhou Bay National Marine Ecosystem Research Station, Institute of Oceanology,
Chinese Academy of Sciences, Qingdao 266071, China*

University of Chinese Academy of Sciences, Beijing 100049, China

Phytoplankton, with its profound impact on ecosystem structure and function, warrants comprehensive investigation to anticipate future changes and formulate effective conservation strategies. This study focuses on the factors influencing the structure of phytoplankton communities in Jiaozhou Bay, encompassing both environmental and anthropogenic stressors. Samples collected from 2003 to 2016 were analyzed using the FlowCAM method, resulting in the identification of 36 taxa. Diatoms emerged as the dominant group, comprising 25 taxa, followed by dinoflagellates (8 taxa) and other groups (3 taxa). The findings reveal significant shifts in nutrient inputs, with decreasing concentrations of NH_4 , P, and Si, suggesting potential changes in nutrient dynamics within the bay. Diatoms, particularly *Thalassiosira*, *Biddulphiaceae*, *Chaetoceros*, *Pseudonitzschia*, and *Coscinodiscus*, have successfully adapted to local conditions, affording them a competitive advantage in utilizing available nutrients. Long-term trends in the phytoplankton community exhibit variations in species diversity, evenness, biomass, abundance, and individual size. These declining trends indicate potential shifts in the overall structure and function of the community. Key environmental drivers, including NH_4 , NO_2 , nitrogen, phosphorus, salinity, and nutrient ratios, have been identified as influential factors impacting different aspects of the phytoplankton community. Furthermore, different phytoplankton groups display distinct response mechanisms to environmental factors, with *Dactyliosolen* demonstrating adaptability to varying conditions and *Ditylum* responding to changes in salinity and nutrient levels. Notably, nutrient ratios, particularly P/N and Si/N , play a significant role in driving community abundance and diatom dominance. This study enhances our understanding of the ecological dynamics

in Jiaozhou Bay, providing valuable insights for informed decision-making and sustainable management of coastal marine ecosystems.

Keywords: phytoplankton, community assemblage, FlowCAM, seasonal variations, environmental influence

Study on the spatiotemporal distribution of the sea star *Asterias amurensis* based on in-situ image in Jiaozhou Bay, China

Mingliang Zhu^{1,2}, Chenhao Zhao^{1,2}, Junhua Liang¹

¹Jiaozhou Bay Marine Ecosystem Research Station, Institute of Oceanology, Chinese Academy of Sciences, Qingdao 266071, China

²University of Chinese Academy of Sciences, Beijing 100049, China

Jiaozhou Bay has suffered from the dual impact of natural changes and human activities, and starfish outbreaks have occurred many times in recent years, causing huge losses to marine ecology and aquaculture economy. In this study, the observation method based on underwater in-situ image and biomass estimation method of *Asterias amurensis* were established. The spatiotemporal distribution characteristics of *Asterias amurensis* from December 2021 to July 2023 were revealed: the monthly abundance and biomass range of *Asterias amurensis* was 0.031 ~ 0.274 / m², 1.440 ~ 5.952 g/m², correspondingly. The maximum abundance and biomass of a single site was 1.964/m² and 41.220 g/m², correspondingly, both are in June. The distribution of *Asterias amurensis* was affected by water temperature and substrate environment, so the distribution in Jiaozhou Bay was very uneven, and the abundance and biomass of *Asterias amurensis* in the culture area were much higher than those in the non-culture area.

Keywords: Jiaozhou Bay, Starfish, *Asterias amurensis*, Image technology, Spatiotemporal distribution

Occurrence, Characteristics, and Factors Influencing the Atmospheric Microplastics around Jiaozhou Bay, Yellow Sea

Chenhao Zhao^{1,3}, Junhua Liang^{1,2}, Mingliang Zhu^{1,2}, Shan Zheng^{1,2},
Yongfang Zhao^{1,2}

¹*Jiaozhou Bay National Marine Ecosystem Research Station, Institute of Oceanology,
Chinese Academy of Sciences, Qingdao 266071, PR China*

²*Laboratory for Marine Ecology and Environmental Science, Laoshan Laboratory,
Qingdao 266237, PR China*

³*University of Chinese Academy of Sciences, Beijing 100049, PR China*

Atmospheric microplastics are attracting increasing attention as an emerging pollutant. However, research on its characteristics and influencing factors is insufficient. This study examines the characteristics and spatiotemporal distribution of atmospheric microplastics around Jiaozhou Bay, the Yellow Sea. The results showed that the dominant shapes of microplastic were fragments (61.9%) and fibers (25.6%), and the main types were polyethylene terephthalate (23.8%), polyethylene (31.6%) and cellulose (rayon, 34.9%). The deposition rate of microplastic varied from 8.395 to 80.114 items·m⁻²·d⁻¹, with a mean of 46.708 ± 21.316 items·m⁻²·d⁻¹. The deposition rate was higher in the dry season than in the rainy season, indicating the influence of weather condition. The annual mass of atmospheric microplastics entering the bay was estimated to be 7.612 ± 3.474 tons. For the first time, this study reveals that atmospheric microplastics in Jiaozhou Bay change spatiotemporally due to monsoons, which pose a potential threat to marine ecosystems.

Keywords: Atmospheric fallout, Air-sea interaction, Seasonal variation, Monsoons, Rainy season.

Genetic diversity and population structure of *Acanthochitona rubrolineata* from China revealed by 2b-RAD

Shaobing Zong¹, Junlong Zhang^{1,2*}

¹Laboratory of Marine Organism Taxonomy and Phylogeny, Qingdao Key
Laboratory of Marine Biodiversity and Conservation, Institute of Oceanology,
Chinese Academy of Sciences, Qingdao 266071, China

²Marine Biological Museum, Chinese Academy of Sciences, Qingdao 266071, China

*E-mail: zhangjl@qdio.ac.cn

Chitons (class Polyplacophora) are a group of marine mollusks, characterized by having eight articulating shell plates on their dorsal body surface. They represent suitable materials for studying the phylogeographic patterns and population structure against heterogeneous environments along China's coast. Here we performed population genetic analyses on the chiton *Acanthochitona rubrolineata* using Reduced-Representing Genome Sequencing from 260 individuals sampled from 13 populations from the coastal waters of China. Substantial and significant divergences were revealed between the Northern and Southern populations divided by the Yangtze River Estuary with pairwise F_{ST} . ADMIXTURE, PCA, DAPC and Neighbour-joining tree analyses all corroborated the results. TreeMix plots and larval dispersal modelling suggest the gene flow between the Northern and Southern populations was weak. The assumed limited dispersal ability of *A. rubrolineata*, coupled with coastal currents and Changjiang Diluted Water, might have contributed to the genetic differentiation between the two groups. Meanwhile, a high level of within-group genetic homogeneity was detected, indicating extensive coastal currents might facilitate gene flow among the populations within each group. DIYABC coalescence results demonstrated the divergence time between the Northern and Southern populations of *A. rubrolineata* was approximately 1,156,000 years ago when dramatic climatic changes occurred with the fluctuation of sea level, successive exposure of the shelf, and isolation between populations. Together, these results suggest that the present-day phylogeographic

patterns of *A. rubrolineata* are strongly affected by the interplay of historical and/or contemporary oceanography and species-specific life-history features.

Keywords: genetic diversity, population structure, phylogeography, population genomics, *Acanthochitona rubrolineata*

Cryptic diversity revealed by integrative taxonomy: common chitons (Polyplacophora, Mollusca) from the coastal areas of China

Huijie Liu¹, Junlong Zhang^{1,2*}

¹*Laboratory of Marine Organism Taxonomy and Phylogeny, Qingdao Key
Laboratory of Marine Biodiversity and Conservation, Institute of Oceanology,
Chinese Academy of Sciences, Qingdao 266071, China*

²*Marine Biological Museum, Chinese Academy of Sciences, Qingdao 266071, China*

*E-mail: zhangjl@qdio.ac.cn

Polyplacophora, also called chitons, is one of the primitive clades in the Mollusca phylum. They are believed to have diverged relatively early from other molluscan lineages and play essential roles in the evolution. However, because of the shortage of systematic studies on polyplacophorans, their species diversity has far from fully discovered in China seas. In this study, we studied common chitons from the coastal areas of China, synthetically using valves, radulae morphological characters and four gene sequences of COI, 16S rRNA, 12S rRNA, and 28S rRNA genes. Species were delimited based on the analyses of both genetic distances, Automatic Barcode Gap Discovery (ABGD), the Bayesian implementation of the Poisson tree processes (bPTP) and General mixed Yule-coalescent (GMYC). Phylogenetic relationships were conducted by Maximum Likelihood (ML) and Bayesian inference (BI) methods. Total of 20 species belonging to 4 families including two cryptic species, were revealed. Both *Acanthochitona rubrolineata* and *Ischnochiton comptus* should be taken as different species in the north and south China coast, respectively. Phylogenetic analysis reveals for the first time the present evolutionary patterns of chitons from the coastal areas of China. The cryptic species disclosed by integrative analysis of chitons suggesting the morphospecies may presence distinct taxonomic subdivisions due to the changes in geographical patterns. Based on the estimation of fossil calibrated molecular clock, we speculate that most species from the coastal areas of China appeared to radiate during the Pliocene to Miocene. In addition, expanding the sample range and using integrated

taxonomy methods are effective ways to uncover biodiversity and solve taxonomic issues regarding polyplacophorans.

Keywords: Polyplacophora, chiton, valves, radula, phylogeny

Carbon biomass, carbon-to-chlorophyll a ratio and the growth rate of phytoplankton in Jiaozhou Bay, China

Shujin Guo^{1,2}

¹*Jiaozhou Bay National Marine Ecosystem Research Station, Institute of Oceanology,
Chinese Academy of Sciences, Qingdao 266071, PR China*

²*Laboratory for Marine Ecology and Environmental Science, Pilot National
Laboratory for Marine Science and Technology (Qingdao), Qingdao 266237, PR
China*

E-mail: shujin135@qdio.ac.cn

Carbon biomass, carbon-to-chlorophyll a ratio (C: Chl a), and the growth rate of phytoplankton cells were studied during four seasonal cruises in 2017 and 2018 in Jiaozhou Bay, China. Water samples were collected from 12 stations, and phytoplankton carbon biomass (phyto-C) was estimated from microscope measured cell volumes. The phyto-C ranged from 5.05 to 78.52 $\mu\text{g C/L}$ in the bay, and it constituted a mean of 38.16% of the total particulate organic carbon in the bay. High phyto-C values appeared mostly in the northern or northeastern bay. Diatom carbon was predominant during all four cruises. Dinoflagellate carbon contributed much less (<30%) to the total phyto-C, and high values appeared often in the outer bay. The C: Chl a of phytoplankton cells varied from 11.50 to 61.45 (mean 31.66), and high values appeared in the outer bay during all four seasons. The phyto-C was also used to calculate the intrinsic growth rates of phytoplankton cells in the bay, and phytoplankton growth rates ranged from 0.56 to 1.96/d; the rate was highest in summer (mean 1.79/d), followed by that in fall (mean 1.24/d) and spring (mean 1.17/d), and the rate was lowest in winter (mean 0.77/d). Temperature and silicate concentration were found to be the determining factors of phytoplankton growth rates in the bay. This study reports the phytoplankton carbon biomass and C: Chl a based on water samples in Jiaozhou Bay, and it will provide useful information for studies on carbon-based food web calculations and carbon-based ecosystem models in the bay.

Integrative taxonomy reveals a new razor clam (*Bivalvia*, *Pharidae*) from the South China Sea

Yanan Yu¹, Yingyi Jiao¹, Junlong Zhang^{1,2*}

¹*Laboratory of Marine Organism Taxonomy and Phylogeny, Qingdao Key
Laboratory of Marine Biodiversity and Conservation, Institute of Oceanology,
Chinese Academy of Sciences, Qingdao 266071, China*

²*Marine Biological Museum, Chinese Academy of Sciences, Qingdao 266071, China*

*E-mail: zhangjl@qdio.ac.cn

The present study describes a new species of the genus *Cultellus* Schumacher, 1817 collected from the South China Sea. An integrative taxonomic approach incorporating morphological comparisons, geometric morphometrics and genetic analyses was used to identify and distinguish the new species. *Cultellus exilis* sp. nov. is distinguished from its congeners by its slender, fragile, and translucent valves, curved posteroventral margins, and relatively large protractor scars. The geometric morphometric analyses based on outlines data showed that samples of *Cultellus exilis* sp. nov. clustered together and were clearly separated from other species. Multiple species delimitation results based on COI support the separation of *Cultellus exilis* sp. nov. from its related congeners. Phylogenetic analyses of a nuclear (28S rRNA) and two mitochondrial (COI, 16S rRNA) genes using maximum likelihood and Bayesian inference methods reveal that the species belongs to the genus *Cultellus*. The superfamily Solenoidea Lamarck, 1809, which includes the families Solenidae Lamarck, 1809 and Pharidae H. Adams & A. Adams, 1856, is more closely related to the family Hiattellidae Gray, 1824 than to Solecurtidae d'Orbigny, 1846. Furthermore, we found that the genus *Siliqua* was clustered with the genera *Ensiculus* and *Phaxas* as a sister clade, which is inconsistent with the current taxonomy system of the subfamily in the family Pharidae. This work expands the number of currently known species of razor clams and highlights the usefulness of integrative taxonomy for species identification and phylogenetic research.

Seasonal dynamics of reserve lipids in symbiotic corals *Sinularia flexibilis* and *Millepora platyphylla* from the South China Sea

T.V. Sikorskaya, L.P.T. Dang

*A.V. Zhirmunsky National Scientific Center of Marine Biology, FEB RAS,
Palchevskogo Str. 17, Vladivostok 690041, Russia.*

E-mail: miss.tatyanna@yandex.ru

Most coral species are symbiotic organisms gastrodermal cells of which contain symbiotic Symbiodiniaceae dinoflagellates. This associations contributes to the formation of coral reef ecosystems. Stony corals are a key group that forms the habitat for many marine organisms in tropical regions. One of the most important representatives of stony corals are symbiotic corals from the Milleporidae family (Cnidaria: Hydrozoa: Anthoathecata: Milleporidae). Octocorals (Cnidaria: Anthozoa: Octocorallia: Alcyonacea: Alcyoniidae) are the second most common group of macrobenthic animals after stony corals on many Indo-Pacific reefs.

Lipids play an important role in the coral organism. Neutral lipids serve as the reserve and source of energy. They include wax esters, triacylglycerides (TG), and monoalkyldiacylglycerides (MADAG). Previously, seasonal changes in coral lipids caused by food availability, sexual reproduction, and oogenesis have been studied. These studies were based on integral lipid parameters (total lipids, fatty acid (FA) composition and the content of lipid classes). Lipids combine many individual lipid molecules, known as lipid molecular species. Compared to classical lipidology, the lipidomic approach provides more detailed information about the lipid composition and allows more accurate quantitative analysis. Studying the seasonal dynamics of lipid profiles can help to establish the range and possible causes of seasonal lipid fluctuations in corals, and be useful for future analysis of trophic relationships and symbiont-host interactions in symbiotic corals. In this work, we studied the seasonal fluctuations in the content of photosynthetic pigments (chlorophylls *a*, *b*, and *c*), the total content of TG and MADAG, and changes in the profile of their molecular species in two

cnidarians: *M. platyphylla* (Hydrozoa) and *S. flexibilis* (Anthozoa), collected in coastal waters of Vietnam (South China Sea) monthly for one year.

By supercritical fluid chromatography couple with mass spectrometry, 26 molecular species of TG and MADAG were identified in the lipid extract of the hydrocoral *M. platyphylla*, the main of which contain saturated FAs and a 22:6n-6 polyunsaturated FA (PUFA). In the lipid extract of the soft coral *S. flexibilis*, 15 molecular species of TG and MADAG were identified, the main of which contain saturated FAs and 16:2, 18:2 and 20:4n-3 PUFAs. It was shown that the seasonal dynamics of the reserve lipids in *M. platyphylla* differed greatly from their dynamics in *S. flexibilis*. The total content of reserve lipids in *M. platyphylla* correlates with seawater temperature, which may indicate a higher contribution of the heterotrophic type of nutrition to the overall energy balance of the coral. It was shown that with a decrease in the total content of reserve lipids, the content of TG with mono- and dienoic FAs in *S. flexibilis* decreased, like as, in *M. platyphylla*, the content of TG with 22:6n-6 PUFA. The source of these FAs for the coral host may be their symbiotic dinoflagellates. The seasonal dynamics of chlorophylls in *M. platyphylla* and *S. flexibilis* corals was studied. The hydrocoral *M. platyphylla* contained chlorophylls *a* and *c*. Chlorophyll *a*, *b*, and *c* were found in the soft coral *S. flexibilis*. It has been shown that a decrease in lipid content leads to an increase in the level of chlorophylls in *M. platyphylla*, indicating an increase in the density of symbiotic dinoflagellates or an increase in their photosynthetic activity. Probably, during the summer period, the coral received energy mainly due to heterotrophic feeding, and in the autumn, the type of feeding changed to autotrophic.

Integrative taxonomy of four new octopods found in the northwestern Pacific Ocean

Yan Tang¹, Junlong Zhang^{1,2*}

¹Laboratory of Marine Organism Taxonomy and Phylogeny, Qingdao Key
Laboratory of Marine Biodiversity and Conservation, Institute of Oceanology,
Chinese Academy of Sciences, Qingdao 266071, China

²Marine Biological Museum, Chinese Academy of Sciences, Qingdao 266071, China

*E-mail: zhangjl@qdio.ac.cn

This study discovered three new incirrate octopuses, *Callistoctopus paucilamella* sp. nov., *C. sparsus* sp. nov., *C. gracilis* sp. nov. They were placed in the genus *Callistoctopus* and added to the octopod fauna of China. In addition, we opportunisticly obtained a cirrate octopus (*Grimpoteuthis* sp.) using a remotely operated vehicle (ROV) during the exploration of Caroline Seamount. All of the four new species were analyzed using integrating approaches including standardized measurements of external features, molecular species delimitation, and phylogenetic analyses. The results indicated that all target species formed separate lineages with strong support values. The phylogenetic analyses confirmed the polyphyly of the *Callistoctopus* and *Octopus* and inferred the relationships of (((*C. sparsus* sp. nov.+*C. aspilosomatis*))+(*C. ornatus*+*C. macropus*))+((*C. paucilamella* sp. nov.+*C. gracilis* sp. nov.))+((*C. xiaohongxu*+*C. tenuipes*)+‘*O. minor*’)+*C. luteus*. Our study supported a close relationship between Opisthoteuthidae and Cirroctopodidae, then clustered together with other *Grimpoteuthis* species respectively, thus also providing evidence for the polyphyly of the genus *Grimpoteuthis*.

Keywords: new species, northwestern Pacific Ocean, COI gene, species delimitation, phylogenetic position