

**Proceedings  
of the Russian-German  
Workshop “Future Vision II”**



**Deep-Sea Investigations  
in the Northwestern Pacific**

**Vladivostok, Russia, September 6-12, 2013**



Participants of the KuramBio expedition  
on board of the RV *Sonne*, summer of 2012



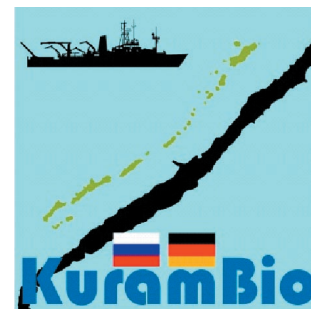
A.V. Zhirmunsky Institute of Marine Biology,  
Far Eastern Branch of the Russian Academy of Sciences

Zoological Institute and Museum of Hamburg University

*Proceedings of the Russian-German Workshop  
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Vladivostok  
Dalnauka



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**Proceedings of the Russian-German Workshop “Future Vision II” – *Deep-Sea Investigations in the Northwestern Pacific*, Vladivostok, Russia, September 6–12, 2013. Vladivostok: Dalnauka. 92 pp.**

The Proceedings of the Russian-German Workshop “Future Vision II” – *Deep-Sea Investigations in the Northwestern Pacific* held in the A.V. Zhirmunsky Institute of Marine Biology FEB RAS and Marine Biological Station “Vostok”, Russia, on September 6–12, 2013 contain extended abstracts and papers dealing with results of joint Russian-German studies on marine biodiversity of the deep-sea areas of the Northwestern Pacific in 2010 (SoJaBio – Sea of Japan Biodiversity Study) and in 2012 (KuramBio – Kurile-Kamchatka Biodiversity Study) and proposals and prospects for future research in the deep-sea basin of the Sea of Okhotsk and in the hadal of the Kuril-Kamchatka Trench. The workshop is the second one jointly organized by the IMB FEB RAS and the Zoological Institute and Museum of Hamburg University.

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by the FEB RAS grant 12-I-P30-07 and the DAAD grant (PKZ) A13/00417

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## **Russian-German workshop Future Visions II: Deep-Sea investigations in the Northwestern Pacific**

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In September of 2007 the bilateral workshop “Future Visions I” was held at the A.V. Zhirmunsky Institute for Marine Biology (IMB) in Vladivostok. During this workshop a memorandum of understanding has been established and signed which included the exchange of material, of scientists as well as the planning and realization of joint expeditions. Since then the Russian-German collaboration has been intensified and two deep-sea expeditions were performed jointly, the Russian-German SoJaBio (Sea of Japan Biodiversity Study) expedition in summer 2010 on board of RV *A.M. Lavrentjev* and the German-Russian KuramBio (Kurile Kamchatka Biodiversity Study) expedition to the abyssal plain adjacent to the Kuril-Kamchatka Trench on board of RV *Sonne* in summer 2012. These expeditions were rather successful, yielded a high amount of new scientific material of benthic animals of all size classes and enhanced our understanding of the biodiversity of the northwest Pacific area in the region studied. However, from these interesting results novel questions arouse which we would like to solve during two subsequent new expeditions, the SokhoBio (Sea of Okhotsk Biodiversity Study) and KuramBio II (Kurile Kamchatka Biodiversity Study II). The plans of the expeditions need to be elaborated jointly with Russian and German scientists during the bilateral workshop “Future Visions II” which should also be used to negotiate the sampling design necessary for the test of the working hypotheses

### **Scientific Master Plan and Aims**

In the recent past we have studied two rather different abyssal environments. The semi-enclosed Sea of Japan (an early successional stage of a deep-sea basin due to a recent anoxic phase until to about 8000 years ago) is about 3700 m deep and isolated by the adjacent deep-sea basins by a shallow sill of less than 150 m depth. The open, non-isolated geologically old abyssal northwest Pacific has also been investigated including some deeper slope sites (5800 m) in the Kuril-Kamchatka Trench. As expected, the biodiversity at the deepest stations of the Sea of Japan was much lower than on the Kurile Kamchatka abyssal plain. However, the SoJaBio expedition has extended the number of known species six times to more than 620, one third of these

are new to science and one third was being recorded for the first time in the northwest Pacific. In the open Kurile Kamchatka area (including the Kurile's bathyal and the hadal depths of the Kuril-Kamchatka Trench) 660 species were known from the RV *Vityaz* expeditions (after 40 years of intensive research). Only during five weeks of sorting on board of RV *Sonne* a small fraction of the KuramBio samples we already identified more than 700 benthic species from the depths between 4830 and 5780 m. Interestingly, the richest and most speciose samples were taken at the deepest stations of the expeditions, the slope of the Kuril-Kamchatka Trench in 5780 m depth. Our video images at this depth already documented a high density of large megabenthic animals and a high amount of aggregates (marine snow) in the near bottom layer. We therefore wonder, whether the v-shaped topography of the Kuril-Kamchatka Trench might enhance food availability and lead to an even higher biodiversity at larger depths. As the Kuril-Kamchatka Trench is situated between the Sea of Okhotsk and the open Pacific, it will be interesting to study the benthic community patterns including biogeography and endemism of species being isolated at hadal depths from the adjacent abyssal plains. Compared to these two environments, the Sea of Okhotsk has somewhat intermediate characteristics. Its basin has a similar depth (3372 m) like the Sea of Japan, but it is less isolated, as it has deep-sea straits to the northwest Pacific, the Bussol Strait (2318 m) and the Krusenstern Strait (1920 m).

Based on the results of the SoJaBio and KuramBio expeditions we want to design two further expeditions. One expedition shall focus on the deep basin of the Sea of Okhotsk (SokhoBio – Sea of Okhotsk Biodiversity Study) another expedition shall be performed in the hadal of the Kuril-Kamchatka Trench (KuramBio II – Biodiversity Study of the Kuril-Kamchatka Trench II). We want to test the following hypotheses:

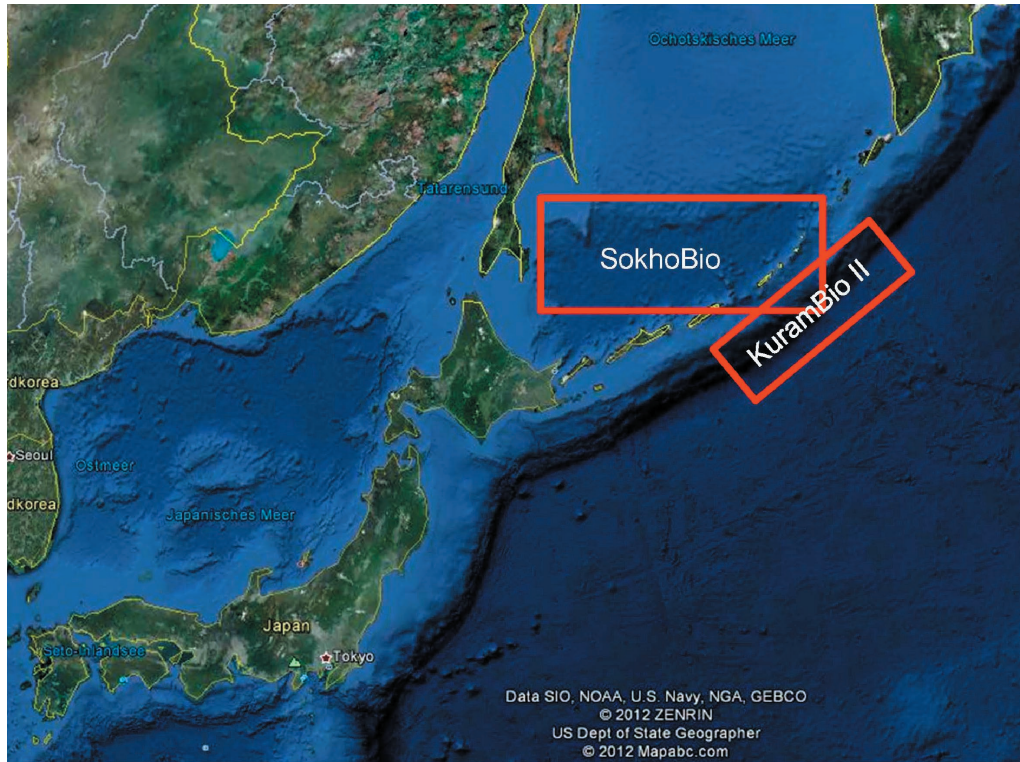
**Hypothesis 1: The Sea of Okhotsk is characterized by a higher number of species than the Sea of Japan, but lower species richness than the abyssal northwest Pacific.**

**Hypothesis 2: The hadal depths of the Kuril-Kamchatka Trench will isolate species of the Sea of Okhotsk from species of the abyssal northwest Pacific.**

**Hypothesis 3: The number of endemic species will increase with increasing hadal depth in the Kuril-Kamchatka Trench.**

The above outlined scientific hypotheses are just a framework for our Future Visions II workshop. During this workshop we plan to discuss scientific questions in more detail and to discuss the potential sampling and station design of the SokhoBio and KuramBio II expeditions necessary for the test of these three hypotheses (see Fig.). We also plan to inform the public with a public lecture and a podiums discussion on our recent results from the SoJaBio and KuramBio expeditions as well as the future visions of our collaboration. We will invite journalists (press and TV) for a report on





Work area of Future Visions II joint expeditions.

our joint Russian-German deep-sea efforts, which built on the Russian deep-sea biology expertise initiated by Prof. Zenkevitch during the RV *Vityaz* expeditions between 1950 and 1970. Since then no biological deep-sea investigations were done in the Kurile Kamchatka area.

Organization of the workshop was supported by the FEB RAS grant 12-I-P30-07 and DAAD grant A13/00417.

**The German-Russian deep-sea expedition KuramBio  
(Kurile Kamchatka Biodiversity Studies)  
to the Kuril-Kamchatka Trench  
and abyssal plain on board of the RV *Sonne***

***Angelika Brandt<sup>1</sup> and Marina Malyutina<sup>2</sup>***

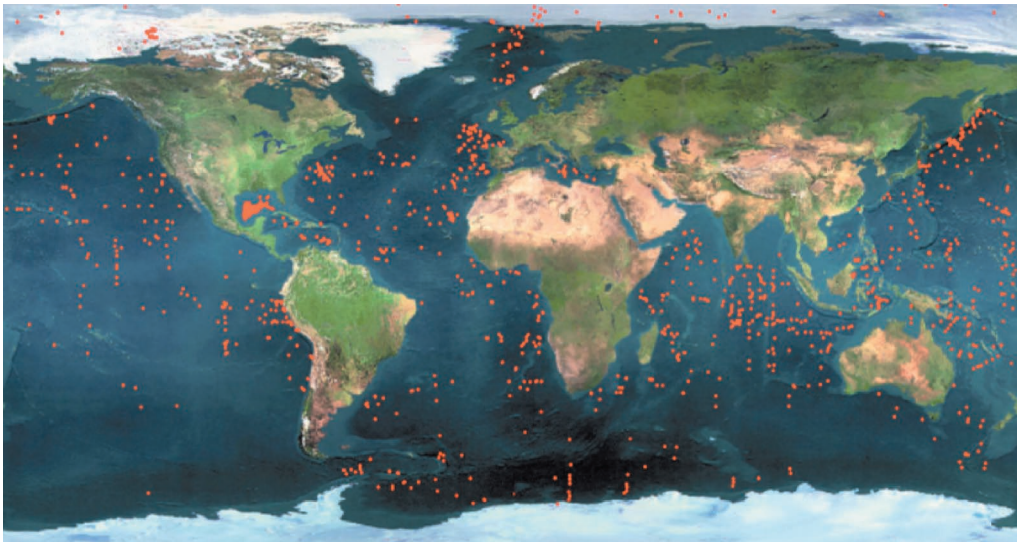
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The joint German-Russian expedition KuramBio (Kurile Kamchatka Biodiversity Study) onboard of the RV *Sonne* (SO 223) to the Kuril-Kamchatka Trench and adjacent abyssal plain was carried out from July 21<sup>th</sup> to September 7<sup>th</sup>, 2012. The project KuramBio is implemented within the frameworks of the Special Russian Federal Program “World Ocean”, the programs of the Presidium of the Far Eastern Branch of the Russian Academy of Sciences (FEB RAS) “Biodiversity changes in some areas of the World Ocean with space and time”, “Marine Biota Response to the Changes of Environment and Climate”, “Technologies of Investigation and Monitoring of Biodiversity of the Deep-Sea Regions of the Far Eastern Seas” and international projects and programs: “Census of the Diversity of Abyssal Marine Life” (CeDAMar) (Fig 1) and “Circulation



**Fig. 1.** Abyssal stations sampled in the abyss including the area of the Kuril-Kamchatka Trench (changed after Stuart et al., 2008).

Research in East Asian Marginal Seas” (CREAMS) within the North Pacific Marine Science Organization (PICES). A Memorandum of Understanding (MoU) was signed in Vladivostok in September 2007 by representatives of the A.V. Zhirmunsky Institute of Marine Biology (IMB), Zoological Institute and Museum (ZIM) of the University of Hamburg, and the Senckenberg am Meer, German Centre for Biodiversity Research (SAM), Wilhelmshaven. The MoU included exchange of material and scientists as well as the establishment of joint expeditions and projects. The KuramBio project is a follow-up project of the joint Russian-German project SoJaBio (Sea of Japan Biodiversity Study) with the expedition on the RV *A.M. Lavrentjev* performed in summer 2010. First data of this expedition are published in a special volume in Deep-Sea Research II (Guest editors: M.V. Malyutina and A. Brandt).

The boreal Pacific fauna is influenced in its origin by the fauna of the Kurile Islands region (Kussakin, 1979; Scarlato, 1981; Tyler, 2002). The species of this region can migrate into the Sea of Okhotsk and the Sea of Japan. Despite the limited data some faunistic similarities between these deep-sea areas were reported. For example, in the Sea of Japan isopod species from genera which were also known from the deep sea of the Kurile Kamchatka area were sample (deep-sea genera of the Asellota like *Eurycope*, *Ilyarachna*, *Mirabilicoxa* or some Arcturoidea) (Gurjanova, 1936; Golovan, Malyutina, 2006; Golovan, 2007). Until now, about 100 species of Isopoda were known from the Kurile Kamchatka area, for the abyssal depth of the Sea of Japan, on the contrary, only one species, *Eurycope spinifrons* Gurjanova, 1933 was known. The Russian-German expedition SoJaBio 2010 confirmed this low biodiversity for Isopoda, however, this species is the most abundant species in the benthic fauna, what is characteristic for an evolutionarily young or early successional stage of an ecosystem (Elsner et al., 2013; Malyutina et al., 2013; Malyutina, Brandt, 2013) (Fig. 2).

Aims of the RV *Sonne* expedition to the Kuril-Kamchatka Trench (KKT) area were the investigations of the biodiversity and community patterns of the meio-, macro- and mega-fauna for testing the following

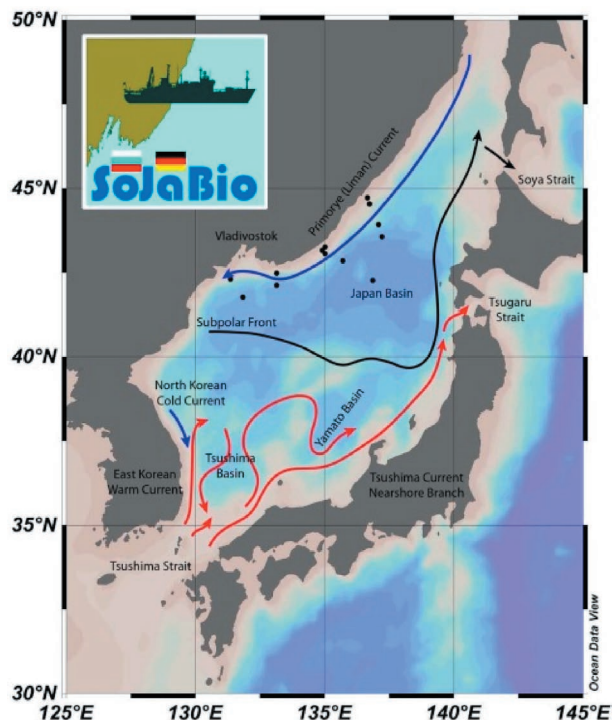


Fig. 2. Stations of the SoJaBio expedition.

hypotheses: 1. Communities of the Kurile Kamtschatka stations (and transects) differ in terms of species composition and richness. 2. The non-isolated abyssal plain of the KKT area causes an increase of the abyssal biodiversity in comparison to the geographically “relatively” isolated Sea of Japan. 3. In the KKT and adjacent abyssal plain we will sample around 50% of new species in the different taxa. 4. The standardised sampling techniques will increase the faunistic knowledge about that region. 5. Enhanced productivity leads to an increase in biodiversity (species richness) (Fig. 3).

The Kuril-Kamtschatka Trench (KKT) and the adjacent abyssal area has already been investigated in the last century during expeditions onboard the RV *Vityaz* in 1949, 1953 and 1966 (Zenkevich et al., 1955; Zenkevich, 1963; Belyaev, 1983, 1989; Belyaev, Vilenkin, 1983). The fauna found in this area has been described in many publications, for example data on 660 species were published into two volumes of the *Transactions P.P. Shirshov Institute of Oceanology* (1970, 1971). Isopoda was one of the dominant taxa in species richness (about 100 species) in the deep-sea macrobenthos (Birstein, 1963, 1970, 1971; Kussakin, 1971; Kussakin, Vasina, 1990). Nevertheless, Birstein (1971) noticed that that major fractions of the fauna were probably not sampled due to inappropriate sampling gear and methods used for sieving and washing; and thus the true deep-sea biodiversity was only partly studied. Biological expeditions with standardized and comparable sampling design, however, were not performed in that area until KuramBio and since the *Vityaz* expeditions the area was not revisited. We therefore think

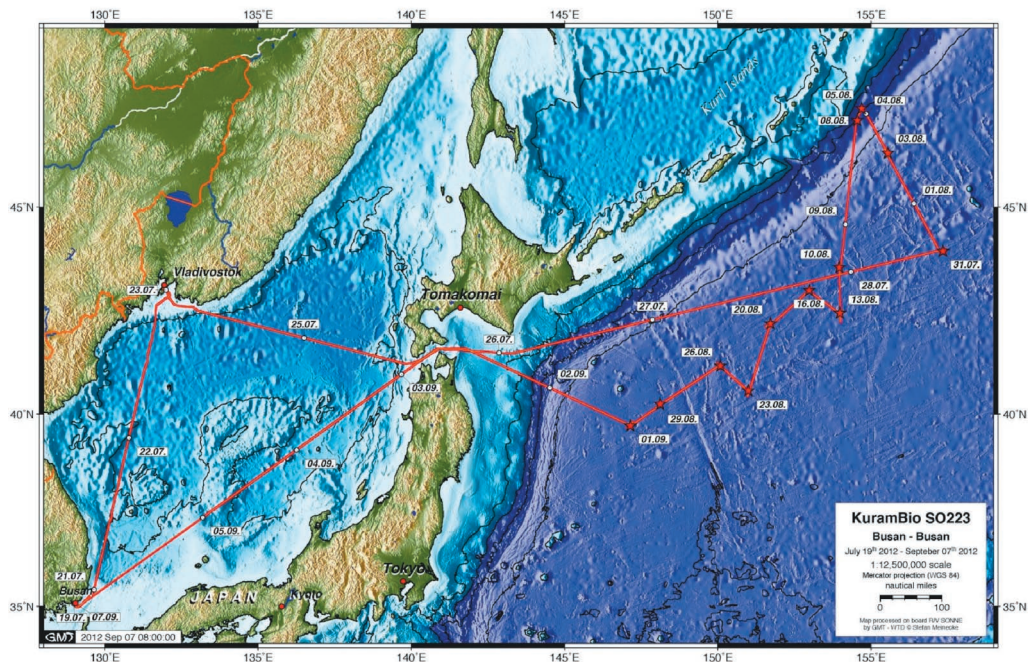


Fig. 3. Cruise track of the KuramBio expedition.

that new methods of sample treatment and more effective gears, which were already deployed successfully during previous expeditions (CeDAMar), will help to discover a higher biodiversity and collect more species than known at present. Previous deep-sea expeditions in the framework of the international CeDAMar project revealed a high patchiness (e.g., Brandt et al., 2007a–c; Kaiser, Barnes, 2008; Kaiser et al., 2009) leading to the anticipation that we will find a high number of different and new species in the KKT and adjacent abyssal plain.

On this background we can already state that during the KuramBio expedition on board of the RV *Sonne* in 2012 already more than 700 species were sorted and identified during the expedition (compared to 40 years of research on the *Vityaz* material). Further preliminary results will be presented and discussed during the workshop and future joint research will be derived from our joint KuramBio results.

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**Deep-Sea investigations  
of the A.V. Zhirmunsky Institute of Marine Biology,  
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In the course of implementation of the comprehensive target program “Biological Safety of the Far Eastern Seas of Russia” (2007–2012) launched by the Far Eastern Branch of the Russian Academy of Sciences (FEB RAS), the A.V. Zhirmunsky Institute of Marine Biology (IMB) has initiated a series of deep-sea expeditions to the Far-eastern seas of Russia. The main objectives of the expeditions were to study the biological diversity of the deep-sea and to examine the unique ecosystems of the northwestern Pacific Ocean using the most up-to-date underwater robotics and deep-sea sampling techniques. At present, deep-sea investigations in the Russia Far-Eastern seas and the adjacent areas of the northern Pacific constitute a separate research program of the IMB.

In 2009, the first deep-sea transect research on the continental slope at 200 to 1000 m depth in the eastern part of Peter the Great Bay (the Sea of Japan) offshore the Bay of Nakhodka has been made using a remotely operated underwater vehicle from board the RV *Vladimir Kasyanov* (owned by the IMB). A variety of bottom landscapes in this bathyal area, as well as high richness of macrobenthic forms with high population density indices were revealed for the first time. The use of the underwater unmanned vehicle allowed us to determine previously unknown peculiarities of the biology of deep-sea organisms and distribution patterns of certain commercially valuable invertebrates. Thus, unknown specific features of the feeding behavior were described in the squid *Berryteuthis magister*, which is able to anchor in areas of mass aggregations of mysids and shrimp on soft bottoms.

In 2010, the study of the biodiversity along deep-water transects (from 500 to 3660 m) in the deepest northwestern part of the Sea of Japan has been performed within the framework of joint Russian-German expedition SoJaBio (Sea of Japan Biodiversity Study) aboard the RV *Akademik Lavrentyev*. Sampled with the same most up-to-date gears and a standardised sampling methodology using in all expeditions of the international programme CeDAMar (Census of the Diversity of Abyssal Marine Life) unique samples of marine biota were collected and high biological diversity (earlier unanticipated) on the continental slope and the abyssal plain of the basin was revealed. A total of 621 species of invertebrates were collected; of these, 201 species are new to science, and 105 species are new records for the Sea of Japan. Previously, only about 100 species of

invertebrates were described from these depths in the deep sector of the Sea of Japan. As a result of merely one expedition, the number of species known for the deep-water part of the Sea of Japan has increased 6 times with the use of modern equipment. Detailed reports of the results of this expedition have been published in a special volume of the “Deep-Sea Research. Part II” (V. 86–87, 2013).

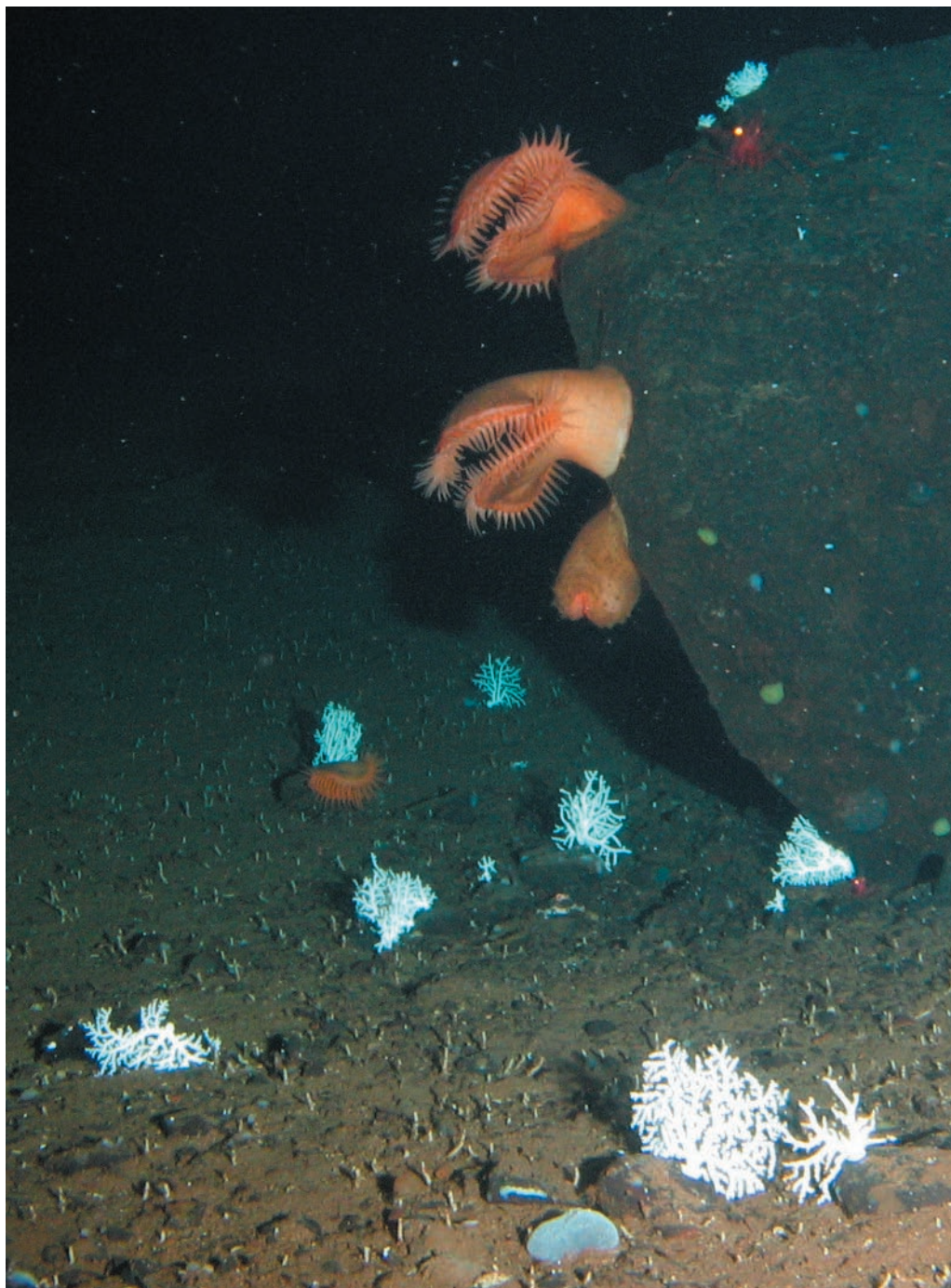
In 2011 and 2013, two expeditions aboard the RV *Akademik Lavrentyev* (owned by FEB RAS) to the Sea of Okhotsk have been organized together with the Far Eastern Aquarium, FEB RAS. For the first time, complex investigations of the deep-sea ecosystems of the Derjugin Basin (1700 m) in the deepest zone of the sea were performed using underwater robotics, among them a ROV, which is capable of sampling bottom substrates and certain marine invertebrates. Biological diversity was examined in active gas emission zones with high methane concentrations and in heavy-hydrocarbon seep areas. The so-called Barite Mountains (massive barite “smokers”), which provide the substrate for numerous benthic invertebrates, were examined with the use of remotely operated robotics for the first time. The peculiarities of the bottom landscapes of the Derjugin Basin were for the first time described in detail with the use of high resolution video equipment (Figs. 1–4). Unique bottom communities with high densities and biomass of sea organisms that are supported by bacterial chemosynthesis and methanotrophy were described. About 200 species of deep-sea organisms were recorded, which is indicative of the high biological diversity of these deep-water communities. Mass assemblages of Okhotsk Sea endemic mollusks that are maintained due to chemoautotrophic symbiotic bacteria were discovered. Aggregations of pogonophore worms that are also nourished by symbiotic bacteria were discovered. Remarkably, the most active zones marked by molluscan assemblages are characterized by the seeping of heavy hydrocarbons resembling petroleum or bitumen. A similar phenomenon is known for the low-temperature seep area in the California Bight, where the thermal solution passing through the thick sediment layer causes the heavy-hydrocarbon enrichment of the sediment.

These results may be useful for the development of methods of biological indication of hydrocarbon-bearing areas using indicator species that are nourished by chemoautotrophic bacteria characteristic of gas vent and petroleum hydrocarbon seep areas. In future, these methods may replace the expensive geological techniques for petroleum exploration, which are harmful to unique deep-sea ecosystems.

Mass aggregations of hydrocorals with high densities, the so-called coral gardens, were found in the Sea of Okhotsk for the first time. This research testifies to the importance of giving a strict protection status not only to coastal and marine areas, but also to unique deep-sea ecosystems (with a longer period of recover) that are threatened by anthropogenic influences.

In 2012, a German-Russian expedition aboard the German RV *Sonne* has been carried out with the aim to examine deep-sea benthic communities at 5000–6000 m depths in the area of the Kuril-Kamchatka Trench. Deep-sea investigations on twelve stations revealed high biological diversity on the trench slope and the adjacent abyssal





**Fig. 1.** Sea anemones *Phelliactis callicyclus* and hydrocorals *Stylaster eximius minor*, Sea of Okhotsk, Derjugin Basin, depth 1550 m.

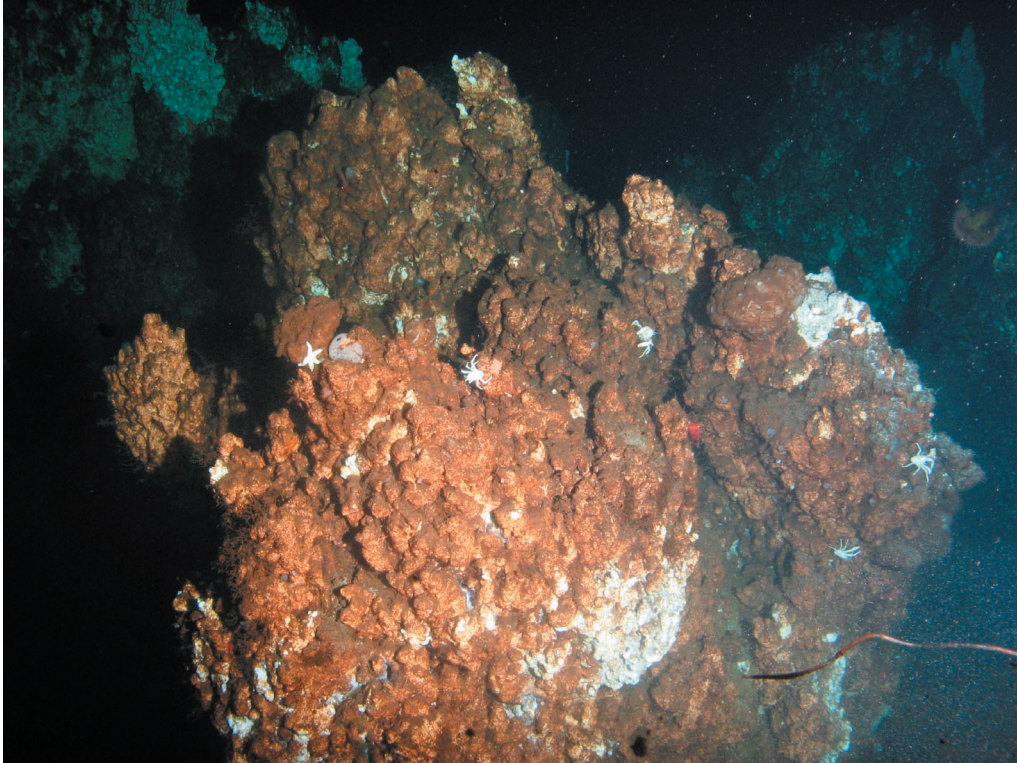


Fig. 2. Barite mountains in Derjugin Basin, Sea of Okhotsk, depth 1550 m.

plain. The number of benthic organisms collected using the most up-to-date equipment in the course of this expedition (more than 700 species) already exceeds the total number of species of deep-sea biota previously collected by the traditional deep-water trawling method during the entire period of research in this area (about 660). Particularly great abundance and species richness was observed on the western slope of the trench, which makes further studies of the biodiversity of the hadal depths of the Kuril-Kamchatka Trench and adjacent deep-sea areas of the Russia Far-eastern seas very promising and necessary. These joint investigations with our German colleagues will be undoubtedly continued in the near future.

In 2012, deep-sea transect investigations with the use of ROV have been carried out from board the RV *Vladimir Kasyanov* (owned by the IMB) along the bed of the Great Gamov Canyon (200 to 2500 m depth) in the southwestern part of Peter the Great Bay. Due to a combination of climatic and hydrological factors, large-scale slope convection, and great inclination of the continental slope, large amounts of organic matter are transferred to the canyon bed, thus supporting the richest bottom fauna with high population density and biomass. Investigations of this unique ecosystem will be continued in the near future.



**Fig. 3.** Starfishes *Hymenodiscus ochotensis*, Sea of Okhotsk, Derjugin Basin, depth 1550 m.

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

The study of deep-sea biota is very important not only from the viewpoint of expansion of biological resources for solving food security problems, but also for obtaining new types of biologically active compounds with the aim of developing new medicines. Deep sea species are the most promising for creating new antitumor medicines and new antibiotics.



Fig. 4. Grenadier fish *Coryphaenoides acrolepis*, Sea of Okhotsk, Derjugin Basin, depth 1550 m.

Within the IMB's deep-sea research program, which is supported by the Presidium of the FEB RAS, new interesting expeditions to the northern Pacific Ocean are planned to be conducted during the period of 2014–2015. In particular, these are an expedition of FEB RAS that will conduct investigations with the use of underwater robotics in the area of a deep-sea volcano in the Bering Sea and a joint expedition with German colleagues to the deep-sea basin of the southern Sea of Okhotsk in 2015 onboard of a Russian ship. In addition, investigations of the hadal depths of the Kurile-Kamchatka Trench will be continued in a joint German-Russian expedition onboard of the new RV *Sonne* in 2016. We will make all efforts for the projected expeditions to be realized and hope that they will give new unique findings and new evidence about wonderful biological diversity of oceanic depths.

This study was supported by the FEB RAS grant 12-I-P30-07.

**Analysis of Polychaeta fauna  
sampled in the KuramBio expedition  
by the epibenthic sledge and the Agassiz trawl**

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The present work is based on the samples taken during the joint German-Russian expedition KuramBio (Kurile Kamchatka Biodiversity Study) onboard of the RV *Sonne* (SO 223) to the Kurile Kamchatka Trench and adjacent abyssal plain in July–August 2012.

Investigations of the deep-sea polychaete fauna the Kurile-Kamtschatka Trench were begun with the expeditions of 1949 on board the RV *Vityaz* when more than 200 deep-sea stations including 33 stations in the Pacific Trenches were taken (Levenstein, 1962, 1969; Belyaev, 1983). Some publications concerning the abyssal polychaete species of several families and its distribution have been published. Ten new species, one new genus of phyllodocid Polychaeta and some worms from the family Polynoidae were described by Uschakov (1958, 1972, 1982). Among the families Fauveliopsidae and Opheliidae new and rare species were found by Levenstein (1962, 1967a, b). She also made a review of data on deep-water polychaete fauna of the Pacific Ocean (Levenstein, 1969). According her data, about 13 species of Polychaeta inhabiting abyssal depths greater than 2000 m in the Kurile-Kamtschatka Trench were recorded. The information on the deep-sea polychaete fauna of the Pacific Ocean is scarce although they belong to one of the most abundant and most diverse invertebrate groups in marine environments worldwide and form an important food base for many other animals.

To date, more than 36 different families, 85 genera and about 97 species of Polychaeta were identified from the Kurile-Kamtschatka Trench and the adjacent abyssal area sampled with an Agassiz trawl (AGT) and an epibenthic sledge (EBS) at depths from 4830 to 5780 m. In this work, the preliminary data are presented for this region as only part of the polychaete samples has been treated. The second part of polychaete samples is still being processed.

The results from different types of gear are more or less similar in family-level diversity, although some of them are represented with lower abundances or different diversity. The Agassiz trawl, with a mesh size of 1 cm, seems to be the least effective gear to capture abyssal polychaetes, because only about 20 families, 34 genera and about 36 species have been registered from AGT-samples (see Table). However, some of these taxa were only collected with this equipment, for example large specimens of *Nothria* sp., *Paradiopatra* sp. (Onuphidae) or *Rhodine* sp. (Maldanidae). The most

**KuramBio polychaete family composition**

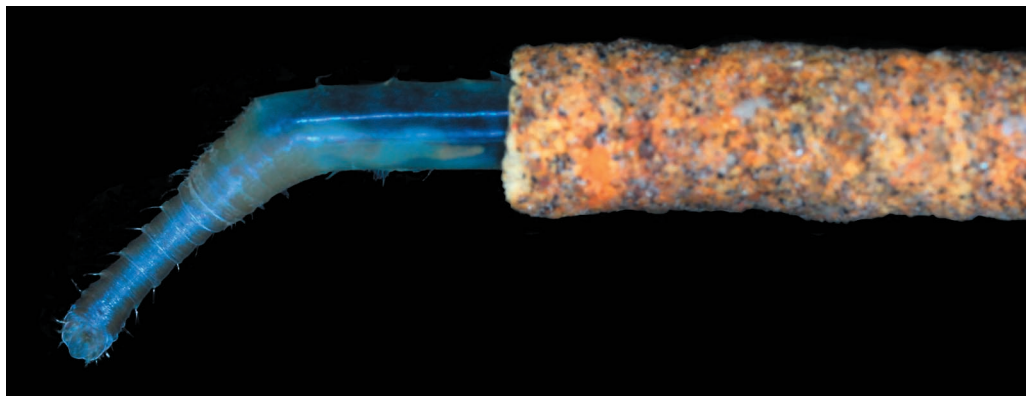
	Family	EBS – samples		AGT – samples	
		Individual (total)	Species (genera)	Individual (total)	Species (genera)
1	Fauveliopsidae	727	2 (2)	55	1 (1)
2	Spionidae	150	4 (4)		
3	Opheliidae	140	3 (3)	19	5 (3)
4	Ampharetidae	113	10 (7)	76	5 (5)
5	Acrocirridae	75	3 (3)		
6	Spaerodoridae	60	8 (5)		
7	Flabelligeridae	57	7 (5)	1	1 (1)
8	Polynoidae	54	2 (2)	2	1 (1)
9	Sabellidae	50	4 (4)	28	3 (3)
10	Syllidae	47	2 (2)		
11	Capitellidae	36	1 (1)	11	1 (1)
12	Scalibregmatidae	36	2 (2)		
13	Sigalionidae	32	1 (1)		
14	Orbiniidae	31	2 (2)	2	1 (1)
15	Paraonidae	30	5 (3)		
16	Cirratulidae	24	1 (1)	9	1 (1)
17	Maldanidae	22	6 (6)	44	4 (4)
18	Serpulidae	22	2 (2)	4	1 (1)
19	Chrysopetalidae	20	2 (2)		
20	Lumbrineridae	17	2 (2)	9	1 (1)
21	Glyceridae	16	1 (1)	4	1 (1)
22	Hesionidae	14	1 (1)		
23	Cossuridae	10	1 (1)		
24	Oweniidae	10	2 (2)	156	1 (1)
25	Onuphidae	6	1 (1)	94	3 (3)
26	Phyllodocidae	6	2 (2)	1	1 (1)
27	Terebellidae	6	2 (2)	6	2 (2)
28	Nereidae	4	1 (1)		
29	Chaetopteridae	3	1 (1)	9	1 (1)
30	Goniadidae	2	1 (1)	1	1 (1)
31	Lacydoniidae	2	1 (1)		
32	Aphroditidae	1	1 (1)	2	1 (1)
33	Dorvilleidae	1	2 (2)		
34	Polychaeta fam. gen. sp. 1	2	1 (1)		
35	Polychaeta fam. gen. sp. 2	11	1 (1)		
36	Polychaeta fam. gen. sp. 3	1	1 (1)		
	<b>Total</b>	<b>1838</b>	<b>90 (80)</b>	<b>533</b>	<b>36 (34)</b>

abundant species from AGT-samples were tubes' buildings worms from families the Oweniidae and Onuphidae which are colony-forming. The most speciose family was the Ampharetidae, Opheliidae and Maldanidae.

Much more diverse and abundant polychaete material was present in epibenthic-sledge samples (see Table). This gear designed for sampling small epifauna individuals or especially meiofauna organisms ranged in length between 1mm and 1 cm at any depth and on any substrate was used. Overall from suprabenthic EBS – samples 1838 individuals representing 36 families, about 80 genera and 90 species have been found until now. The most abundant families were the Fauveliopsidae (727 individuals), Spi-onidae (150 ind.), Opheliidae (140 ind.) and Ampharetidae (113 ind.). The most speciose family is the Ampharetidae with 10 species followed by the Sphaerodoridae and Flabelligeridae with 8 and 7 species, respectively, Maldanidae and Paraonidae with 6 and 5 species each. The remaining families are represented by 1–3 species. Many of these species appear to be undescribed. Some of them have unusual morphological features. For example, a member of the family Sphaerodoridae – *Sphaerephesia* sp. nov. differs from all other members of the genus in that it has sessile dorsal macrotubercles with 2 paired short terminal papillae.

This polychaete composition is similar to investigations reported from deep Pacific Ocean waters where about 33–37 families and 73–142 species have been found from benthic-sledge stations located in depths to 3000 m (Fauchald, Hanckock, 1981; Méndez, 2006). It was noted the family Maldanidae, Paraonidae, Ampharetidae, Cirratulidae and some others were the most species-rich. Presented results show that the composition of Polychaeta in the deep waters of the Kurile-Kamtschatka Trench and the adjacent abyssal area does not seem to differ at higher taxonomic level from that of other deep-sea regions world-wide.

Among the collected Polychaeta the most interesting species belonging to genera *Macellicephalo* and *Macellicephaloides* (Polynoidae), *Laubieriopsis* and *Fauveliopsis* (Fauveliopsidae) (see Fig.), *Anguillosyllis* (Syllidae), *Kesun* (Opheliidae) are described



*Fauveliopsis challengeriae* McIntosh, 1922 inhabiting the sand-agglutinating foraminiferan tube (photo by A. Maiorova).

mainly from bathyal and abyssal depths of the world's oceans. Little is known about these small carnivorous and detritus-feeding species. Most fauveliopsids are less than 2 cm long. They are free-living or inhabit the empty shells of scaphopod or gastropod molluscs, or the tubes of sand-agglutinating foraminiferans genus *Bathysiphon* (see Fig.).

### Acknowledgements

I would like to thank the participants of the KuramBio expedition for collecting the deep-sea material, initial sorting of macrobenthic samples and making the studied polychaete species available. This work was supported by the Government of the Russian Federation (Grant 11.G34.31.0010), KuramBio Project (Kurile Kamchatka Biodiversity Study (Grant OSL-13-13)) and FEB RAS (Grant 12-I-P30-07).

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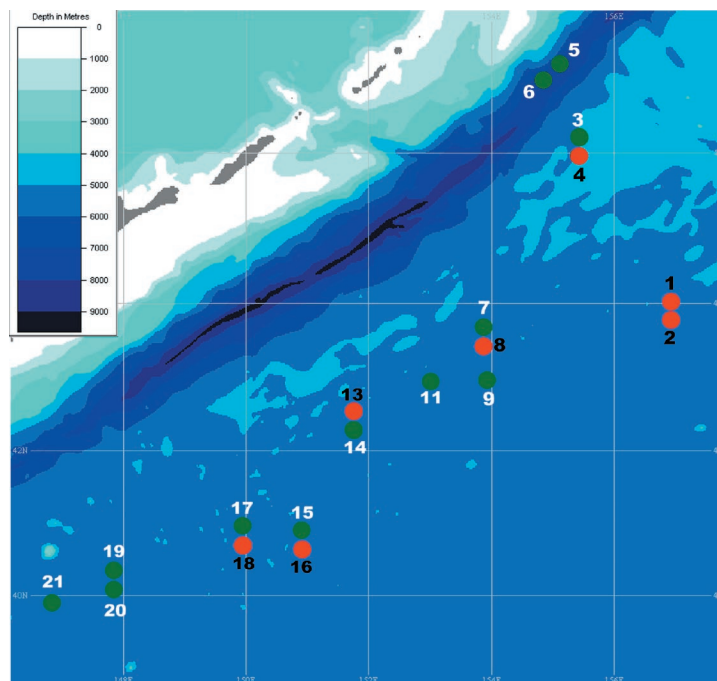
## Documentation of deep-sea fauna and environment using video-transects

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During the expedition KuramBio (RV *Sonne*, SO223) into the Kuril-Kamchatka region of the north-western Pacific, the deep-sea around the EBS transects was documented by camera. While the epibenthic sledge (Brenke, 2005) took the samples, the added digital underwater video camcorder and still camera (CliSap-Sledge: C-EBS; Brandt et al., 2013) recorded the seafloor during the deployments. The epibenthic sledge took samples on 21 transects. Pictures and video were taken on 19 transects (exception 10#6-12 and 12#7-10). Thereof eleven stations were successful, but in nine deployments the camera system had a malfunction (Fig. 1). In total the camera system took 11330 pictures and 1052 min (17.5 h) of video.

Fig. 1 shows that the video camcorder and still camera system of the C-EBS documented most parts of the research area. Except from stations one and two, we got pictures or video from the trench itself as well as from the abyssal plain in the north-western Pacific in front of the trench.



The observation of sediment surface with pictures and videos allows only a subjective interpretation of the viewed material. A sustainable analysis of digital information is only possible in comparison with the available samples. For a basic idea of

**Fig. 1.** The Video EBS stations in the Kuril-Kamchatka region of the Pacific. The numbers specify the EBS deployment; green symbols show stations with successful camera system results; red symbols indicate a camera or video failure.

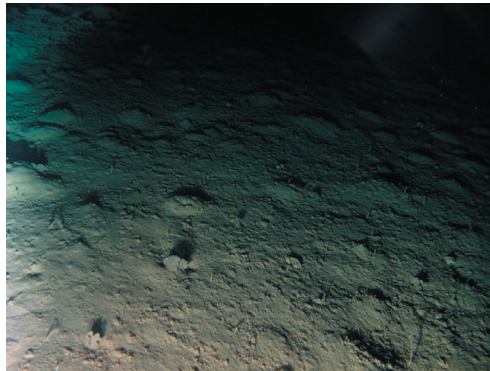
the deep sea floor in the Kuril-Kamchatka region see the following pictures of characteristic sediment structures (Figs. 2–8).

It is a well known fact that macrofauna animals are rare in the deep sea. Accordingly, images with clear identifiable organisms are rare. Only less than 200 pictures (1.17%) show organisms and the amount of identifiable species is frustrating small. Furthermore, the high amount of failures in the camera system (45%) makes it difficult to interpret the frequency and abundance of the animals in the Kuril-Kamchatka region.

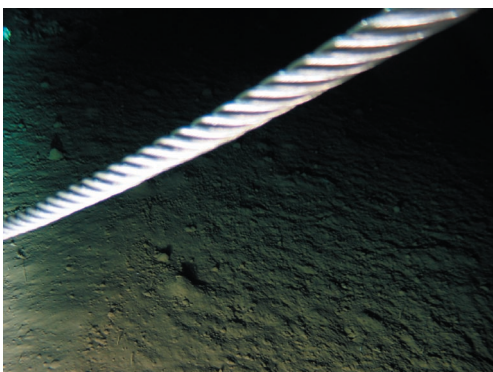
Nevertheless, based on the quantity of the animals on pictures or video we can indicate that holothurians (*Scotoplanes*, *Psychropotes*, *Benthodytes*) are the dominating group followed by fishes (mostly *Macrouridae*), polychaetes and sponges. Occasionally there are some decapod shrimps, medusae or different echinoids in the pictures.



**Fig. 2.** 3#2-9. Southern trench rim, 4830–4863 m, sediment: soft, no stones or shell detritus, current: strong, >1.5 m/sec. Traces of: holothurians; fauna: poor, only holothurians.



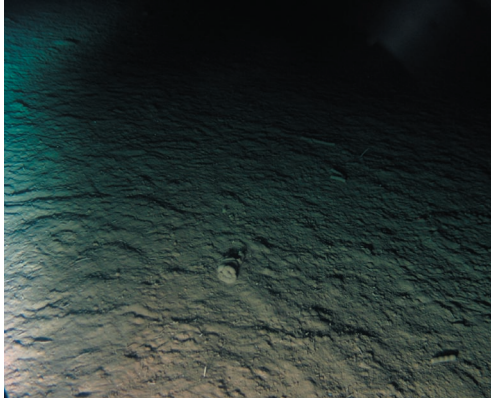
**Fig. 3.** 5#3-9. Kuril-Kamchatka trench, 4987–4991 m, sediment: coarse, current: fast, app. 1.0 m/sec. Traces of: foraminiferans, Polychaetes; fauna: bryozoans, most endobenthic, sponge.



**Fig. 4.** 6#4-3. Kuril-Kamchatka trench, 5681–5780 m, sediment: coarse, small stones, fauna: poor, only some sponges.



**Fig. 5.** 7#5-9. Abyssal plain, 5376–5380 m, sediment: soft, no stones or shell detritus, current: fast, <0.5 m/sec. Traces of: holothurians; fauna: poor, polychaetes, decapods, fishes and isopods.

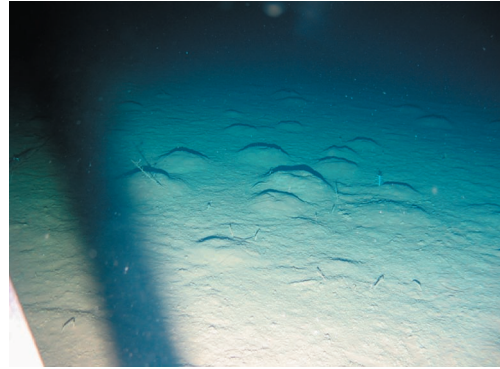


In the majority of cases we have only a small number of pictures for any taxon. So, statements about the patchiness are highly speculative. Only in the case of the holothurians it might be that the *Scotoplanes* cf. *globosa* (Fig. 7) are more frequently in the south-western part of the Kuril-Kamchatka region.

**Fig. 6.** 11#7-9. Abyssal plain, 5222–5223 m, sediment: soft, no stones or shell detritus, current: fast, <0.5 m/sec. Traces of: holothurians; fauna: holothurians.



**Fig. 7.** 15#9-9. Abyssal plain, 5399–5421 m, sediment: coarse, no stones, current: slow, <0.1 m/sec. Traces of: holothurians; fauna: *Scotoplanes* and fishes.



**Fig. 8.** 17#10-9. Abyssal plain, 5264–5266 m, sediment: soft, no stones, current: slow, <0.1 m/sec. Traces of: polychaetes, foraminiferans, holothurians and sea urchins; fauna: *Scotoplanes*, fishes, sponges.

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## Preliminary data on the nemertean worms from the KuramBio expedition

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About 1280 species of the phylum Nemertea are known in the World Ocean, but only three species of benthic nemerteans were collected from depths exceeding 3000 m: *Parborlasia corrugata* (Antarctic and Subantarctic waters, up to 3590 m), *Micrura bathyalis* and *Cephalothrix iwatai* (both in the Sea of Japan, up to 3334–3347 m). During Russian deep-sea expeditions in the Pacific and Atlantic oceans the fragments of unidentified nemerteans were detected at seven stations at depths of 6000–7239 m (Belyaev, 1989).

No less than 110 nemertean specimens were obtained during the German-Russian KuramBio (Kuril-Kamchatka Biodiversity Study) deep-sea expedition to the abyssal plain adjacent to the Kuril-Kamchatka Trench on board of RV *Sonne*: 102 specimens collected by an EBS (epibenthic sledge, supranet samples), five specimens by an Agassiz trawl (hereafter AGT), and three specimens by a Multiple Corer (MUC). Nemertean worms were found in all EBS supranet samples (see Table); this material includes

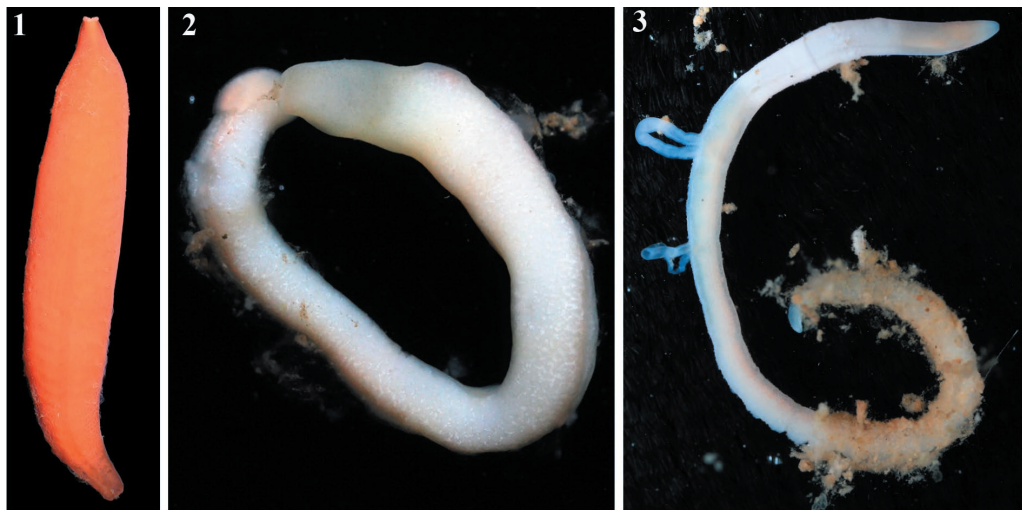
### Specimens of four nemertean taxa retrieved from the EBS supranet samples

EBS station (supranet samples)	Depths (m)	Higher nemertean taxa			
		Tubulaniformes	Archinemertea	Heteronemertea	Hoploneurertea
SO223-01-10	5423–5429	5	1	1	4
SO223-02-9	4830–4863	3	–	–	1
SO223-03-9	4987–4991	9	–	1	12
SO223-04-9	5681–5780	3	–	1	8
SO223-05-9	5376–5380	12	–	–	4
SO223-06-11	5305–5305	–	–	–	2
SO223-07-9	5222–5223	–	–	–	4
SO223-08-9	5125–5126	4	–	–	8
SO223-09-9	5399–5421	–	–	–	7
SO223-10-9	5264–5266	3	–	–	6
SO223-11-9	5263–5362	5	1	–	8

mainly small specimens (2–6 mm in body length), but a few nemerteans are 10–25 mm in length. Comparison of materials collected by the KuramBio expedition with those gathered by the SoJaBio voyage showed that 1) deep-sea samples from the Sea of Japan contained mainly archinemerteans and hoplonemertean, though heteronemerteans were not uncommon (Chernyshev, 2013); both archi- and heteronemerteans are very rare, while tubulanid palaeonemerteans and hoplonemerteans predominate in the KuramBio EBS samples; 2) nemerteans from the KuramBio samples are more fragmented and damaged than the SoJaBio material; 3) number of species collected by the KuramBio exceeds such number from the SoJaBio samples from depths below 1000 m. However, the reliable estimation of the actual species diversity can be achieved primarily using the molecular-genetic analysis.

Three heteronemertean and two hoplonemertean species were obtained in the AGT samples. Except one specimen of bathypelagic nemertean (*Protopelagonemertes* sp. (Fig. 1) possible captured by the AGT by chance), the other four species are new for science. The finding of the first abyssal symbiotic nemertean from the genus *Gononemertes* is especially interesting. A single female about 3.5–4 cm long (Fig. 2) with very short and reduced proboscis system was taken out from the peribranchial cavity of the stalked ascidian *Culeolus* cf. *murrayi* (AGT-station SO223-08-10, depths 5124–5125 m). Previously an unknown *Gononemertes* sp. was found in the peribranchial cavity of the bathyal ascidian *Culeolus nadejdae* in the Sea of Okhotsk at depths of 1040–1050 m (Sanamyan, 1992), but this deep-sea species possesses a longer proboscis.

Well preserved and unfragmented specimen of *Tubulanus* sp. n. (Fig. 3) was obtained from the MUC-sample (station 7-5 GKG, depth 5225 m). Up to now *Carinina grata* collected in depths of 2267–2450 m, has been the deepest finding of tubulanid



**Figs. 1–3.** Three nemerteans from the KuramBio samples: 1 – *Protopelagonemertes* (?) sp.; 2 – *Gononemertes* sp.; 3 – *Tubulanus* sp. (photographs courtesy of Dr. A. Maiorova).

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palaeonemerteans (Hubrecht, 1887). I examined the muscular and nervous systems of this species and of all specimens from AGT-samples using confocal laser scanning microscopy (CLSM) with phalloidin and antibody labeling. These data are the first experience of the morphology investigations of deep-sea nemerteans by the CLSM methods.

### **Acknowledgments**

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**Preliminary results of the macrofauna study  
with a special focus on the Isopoda  
from the Kuril- Kamchatka deep-sea area  
sampled by the means of an epibenthic sledge**

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**Introduction**

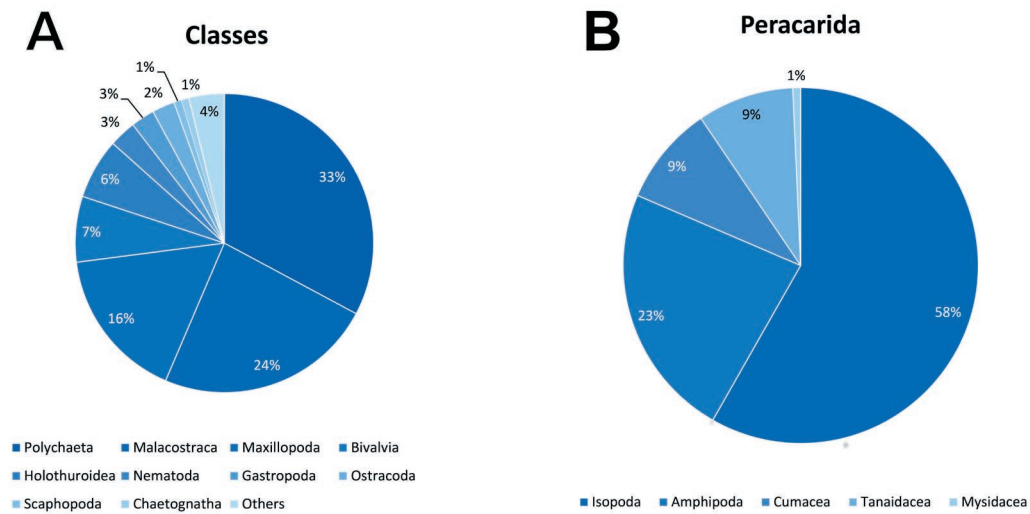
The Northwest Pacific is an interesting study area regarding biodiversity. Several marginal seas border the open Pacific towards the northwest. These marginal seas, including the Sea of Okhotsk and the Sea of Japan, are connected to the open Pacific through straits varying in depth (Zenkevitch, 1963). Supposedly, the depth of these straits limits the faunal exchange between these regions, especially regarding groups lacking larval dispersal like the widely distributed Isopoda. In the 1950s, the Russian RV *Vityaz* took samples in the area of the Kuril-Kamchatka Trench (Belyaev, 1983). Isopoda as one of the most diverse taxon was determined to species level from various stations and about 100 species were described and recorded (Birstein, 1963, 1970, 1971). This background provides the opportunity for an assessment about changes over the past 60 years and a detailed comparison between the KuramBio expedition and previous expeditions by using standardized gear with small mesh sizes. However, the preliminary results of this study merely allow an estimation of diversity at this point.

**Material and Methods**

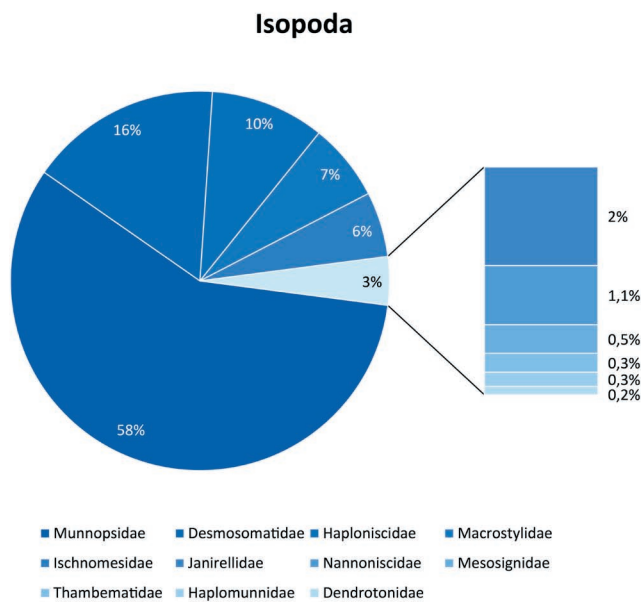
During the KuramBio expedition with the German RV *Sonne* to the Kuril-Kamchatka Trench and the adjacent abyssal plain in summer 2012, we sampled macrofauna at 12 stations in 4830–5780 m depths by the means of a camera epibenthic sledge (C-EBS) (Brandt et al., 2013). At each station (except st. 3, 4 and 12) the C-EBS was deployed twice. Each deployment brought two samples at two different heights: 25–60 cm (epi fraction) and 77–112 cm (supra fraction) above the sea floor. The samples were sieved on board using 300 µm mesh size and fixed in 96% precooled (–20°C) ethanol (first deployment) and in 4% formaldehyde (second deployment). The ethanol samples from the supra-net catches of 11 stations have been sorted on board to high level taxa (class/order) after 48 hours of fixing in a freezer; Isopoda were determined to family level. The supra-net sample of station 12 was sorted in Hamburg. Only the results of the supra fractions are included in this study.

## Results and Discussion

So far, 33,203 individuals belonging to 32 classes and 17 phyla were sorted from the supra fraction of the 12 stations. Polychaeta are the dominant class with 33% (Fig. 1A), followed by the crustacean classes Malacostraca (24%) and Maxillopoda (16%). Within the Peracarida, Isopoda is the dominant order with 58% (Fig. 1B), followed by the



**Fig. 1.** Percentage of the ten most abundant classes (A) and the Peracarida (B) sorted from the supra fraction of the ethanol C-EBS samples.



Amphipoda (23%) and the Cumacea and Tanaidacea with 9% each. Within the Isopoda, almost all sampled specimens besides several specimens of the suborder Valvifera and the parasitic suborder Epicaridea belonged to the suborder Asellota, represented by 11 deep-sea families. Munnopsidae are the dominant family with 58% (Fig. 2), followed by the Desmosomatidae (16%) and Haplonscidae (10%).

**Fig. 2.** Percentage of isopod families sorted from the supra fraction of the ethanol C-EBS samples.



Polychaeta, Bivalvia and Isopoda are known to be dominant taxa in deep-sea samples (Hessler, Jumars, 1974). Isopoda are the dominant group within the Peracarida and the Munnopsidae are the dominant group within the Isopoda which is in accordance with other deep-sea studies (Brandt et al., 2007; Malyutina, Brandt, 2007).

Regarding diversity of Isopoda, Birstein (1963, 1970, 1971) found impressive species richness (around 100 species) for the open Pacific including the Kuril-Kamchatka Trench. For the deep Sea of Japan, low diversity was found (Elsner et al., 2013; Golovan et al., 2013; Malyutina et al., 2013). Our preliminary results based only on the analysis of the part of the collected samples are in accordance with the literature data and indicate high diversity of the macrobenthos and high species richness of the Isopoda in the studied area of the deep-sea open Northwest Pacific.

### Acknowledgements

Tanja Springer is thanked for sample sorting. This study was supported by the Federal Ministry of Education and Research (BMBF), Project Management Jülich (PTJ) with the project SO 223 – KuramBio (Kuril-Kamchatka Deep-Sea Biodiversity Studies), study grant 03G0223A, grant OSL-13-13, RFBR grants (11-04-98586 and 13-04-02144) and FEB RAS grant 12-I-P30-07.

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**Preliminary data on the composition of the macrobenthic infauna from the Kurile-Kamchatka deep-sea area collected with a box corer, with a special focus on the Polychaeta (Annelida)**

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The region of the Kuril-Kamchatka Trench and its abyssal plains is located in the NW Pacific Ocean. It lies off the southeast coast of Kamchatka, parallels the Kuril Island chain and ends in the Japan Trench east of Hokkaido. Because of its proximity to the Kuriles this region is influenced by high summer productivity. The studied area has already been sampled by Russian scientists around 50 years ago. During the KuramBio-expedition in 2012 the area was resampled with standardized gears. For the investigation of the macrobenthic infauna a box corer was used. Here we give a preliminary overview of the macrobenthic infaunal composition and of the composition of the polychaetes.

**Material and Methods**

The joint German-Russian expedition KuramBio to the Kurile Kamchatka Trench and its adjacent abyssal plains on board of the RV *Sonne* took place between July 21<sup>st</sup> and September 07<sup>th</sup> 2012.

During this expedition a box corer with a sampling area of 0.25 m<sup>2</sup> was used to sample the macrobenthic infauna of this region. Altogether 23 deployments at 12 stations were sampled in water depths between 4870–5768m. The surface water of the samples was sieved through a 300 µm mesh. The sample was divided into two subsamples (0–2 cm and 2–20 cm sediment-depth). The upper layer was carefully washed in cooled sea-water and sieved through sieves of 1000, 500 and 300 µm mesh sizes. The sediment of the second layer was sieved in big buckets with seawater through sieves of the same mesh size. The separated animals from both layers and the 1000 µm fractions were immediately sorted in cooled seawater under stereomicroscopes to higher taxon level, while the other fractions were fixed for later studies. At each station, two box corers were deployed. The first one was fixed in 4% formaldehyde and after 48 hours transferred to 70% ethanol. The samples of the second deployment were fixed in 96% ethanol and kept in a cooling room at 4°C in order to preserve the material for later genetic analysis. At station 12 only one box corer was deployed and fixed in 96% ethanol.

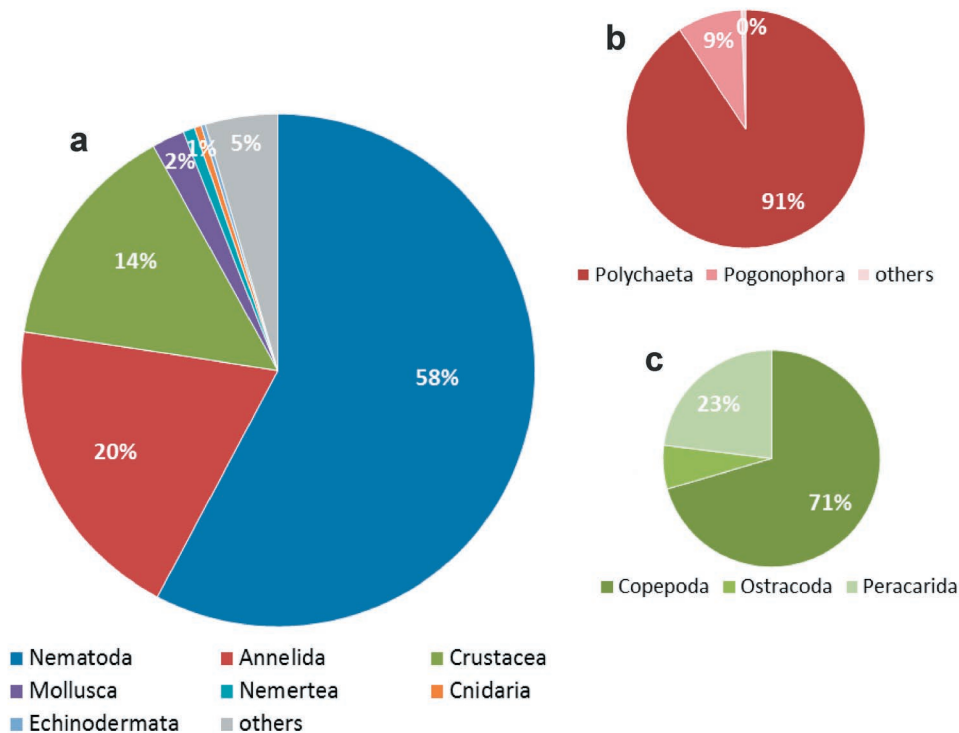
Some of the samples were sorted on board but most of the material was sorted in the laboratory in Hamburg. Polychaetes are now sorted to family level. All taxa will be worked up by specialists.

### Results and Discussion

To date, 23510 individuals belonging to 37 different supraspezific taxa could be identified from the box corer samples. Over 60% of these individuals populated the upper layer (0–2 cm) with the highest numbers in the 500 and 300 µm fractions. The collected infauna is clearly dominated by nematodes (58%), annelids (20%) and crustaceans (15%). The polychaetes clearly predominate among the annelida (91%) whereas the crustaceans are mainly represented by copepods (71%) (Fig. 1a–c). If the nematodes, which are often completely counted as meiofauna, are disregarded, annelids are dominating the macrofaunal community by almost 50%, followed by crustaceans with 34% and molluscs with 5%.

To date, 4479 polychaetes belonging to 31 families could be identified. The most dominant families in the sampled area are Spionidae (19%) and Cirratulidae (11%) followed by Ampharetidae, Capitellidae and Maldanidae (each 7%) (Fig. 2). The composition of the polychaetes communities varies among the stations.

The present results show that the macrofaunal community composition from abyssal depths of the Kurile-Kamchatka-area is comparable to other regions on higher taxon level. Meiofaunal taxa are prevalent in the GKG samples, although they are only partially retained by the 300 µm limit. Nematoda are most abundant as usual for the



**Fig. 1.** Composition of the dominant taxa of the macrofaunal community (a), supraspecific taxa within annelids (b) and same for crustaceans (c); all results according to the current state of the sorting.

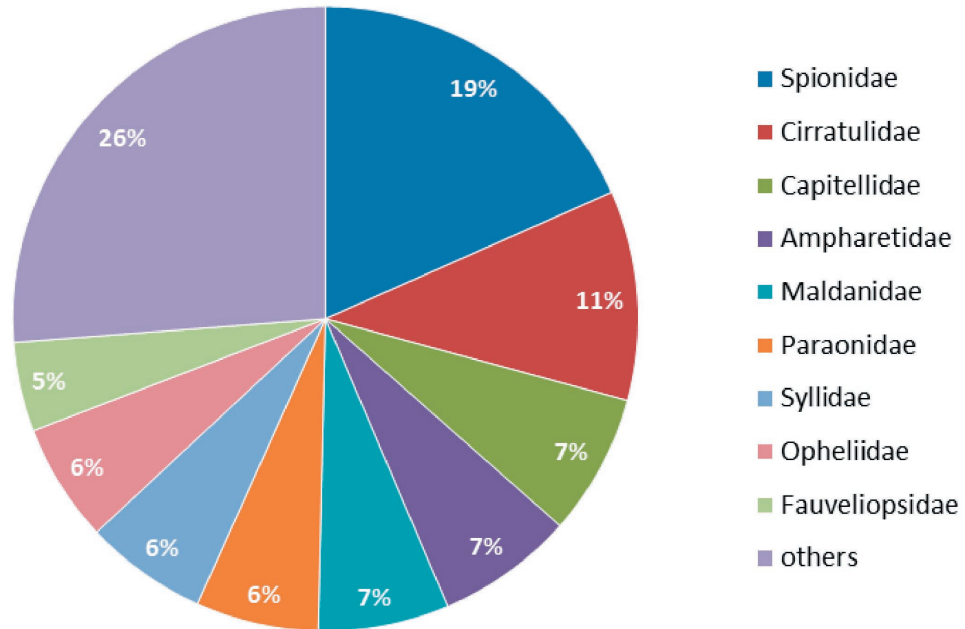


Fig. 2. Composition of the polychaete community of the Kurile-Kamchatka area (preliminary data).

deep sea, followed by Copepoda (Hessler, Jumars, 1974). Within the macrofaunal taxa Polychaeta are dominating the community as usual (e.g., Hessler, Jumars, 1974; Knox, 1977; Fauchald, Jumars, 1979) followed by Crustacea and Mollusca (Knox, 1977). As expected from other studies most of the animals are to be found in the upper 0–2 cm of the sediment (Snider et al., 1984).

### Acknowledgements

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**Desmosomatidae (Isopoda, Asellota)  
of the Kuril-Kamchatka region  
collected during the joint KuramBio expedition:  
new data on the diversity**

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Desmosomatidae is second family after Munnopsidae in abundance and species richness of the primarily deep-sea asellots, which plays an important role in deep-sea macrobenthic communities (Kussakin, 1999; Brandt et al., 2004, 2005; Brix, 2006). They have almost worldwide distribution, occurring at depths from 4 to 6134 m (Kussakin, 1999; Kensley et al., 2004), with maximal number of species at the bathyal and abyssal depths, as well as in the cold waters where some species have secondarily occupied the shelf zone. By now, about 140 desmosomatid species have been described (see Kensley et al., 2004), and according to preliminary estimations an even greater number of new species were collected and should be described (Brix, 2006).

About two-third of the named species are known from the North Atlantic and Arctic, fewer number – from the South Atlantic, Antarctic, Australia, North and South Pacific (Brix, 2006; Kensley et al., 2004). However, this rather reflects an unequal state of knowledge on the desmosomatid fauna of different regions of the World Ocean than real distributional patterns and can partially be explained by irregular samplings and also the fact that these small and fragile animals often cannot be collected with traditional rough trawls and bottom grab samplers.

Thus, for example, until 2010 in North Pacific 18 species and 8 genera of Desmosomatidae were known, among them 11 species and 5 genera were recorded in its western part (Birstein, 1963, 1970, 1971; Kussakin, 1999; Golovan and Malyutina, 2010; Golovan et al., 2013; Kensley et al., 2004) (Table 1). The same number (11) of desmosomatid species (including 8 species apparently new to science) was found during the expedition SoJaBio (2010) only in the isolated deep-sea basin of the Sea of Japan, whose fauna was previously considered as poor (Golovan et al., 2013). In the SoJaBio macrobenthos was sampled using a camera-epibenthic sledge C-EBS (Brandt et al., 2013).

The open areas of the oceanic abyssal of the North Pacific are known as the much richer region with much higher diversity (e.g., Zenkevich, 1963; Birstein, 1963). The Kurile-Kamtschatka Trench (KKT) and the adjacent abyssal plain was previously investigated during the expeditions onboard the RV *Vityaz* in 1949, 1953 and 1966, where the Sigsbee trawl and bottom grab samplers (such as the “Ocean” grab sampler) were used (Zenkevich, 1963; Birstein, 1963). Only 3 desmosomatid species represented by single or few specimens were collected (Birstein, 1963, 1970, 1971).

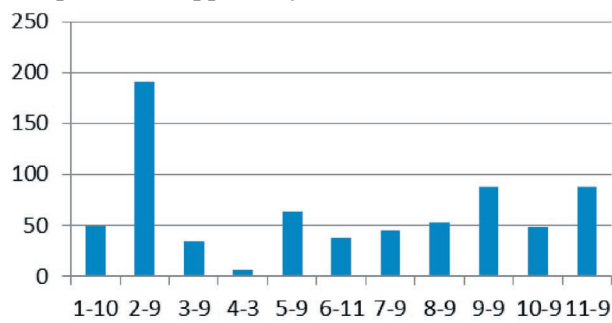
TABLE 1. List of Desmosomatida of the Northern Pacific according to published data

Species	Depth, m	Distribution
<i>Chelibranchus canaliculatus</i> Mezhov, 1986	1190	Gulf of Alaska, USA: 57°52' N, 149°02' W
<i>Desmosoma lobipes</i> Kussakin, 1965	220–3420	WKS and NW SoJ
<i>D. ochotense</i> Kussakin, 1965	220	WKS
<i>Desmosoma</i> sp. 1 Golovan et al., 2013	455–528	NW SoJ
<i>Desmosoma</i> sp. 2 Golovan et al., 2013	455–528	NW SoJ
<i>Eugerdella elegans</i> Kussakin, 1965	105	WKS
<i>E. fragilis</i> (Kussakin, 1965)	177–1900	WKS and NW SoJ
<i>E. kamshatica</i> Kussakin, 1965	68–220	WKS
<i>Eugerdella</i> (?) sp. 1 Golovan et al., 2013	455–528	NW SoJ
<i>Eugerdella</i> (?) sp. 2 Golovan et al., 2013	470–528	NW SoJ
<i>Eugerdella minutula</i> Mezhov, 1986	3240–3300	Gulf of Alaska, USA: 57°36' N, 148°36' W
<i>E. ordinaria</i> Mezhov, 1986	1550	Gulf of Alaska, USA: 53°43' N, 163°38' W
<i>Mirabilicoxa coxalis</i> (Birstein, 1963)	5005–5495	PO off the northern Honshu, KKT: 44°48' N 156°33' E
<i>M. kussakini</i> Golovan, 2007	455–578	NW SoJ
<i>M. magnispina</i> (Menzies, 1962)	1800–1906	Bay of Panama
<i>M. richardsoni</i> Mezhov, 1986	3240–3300	Gulf of Alaska, USA: 57°36' N, 148°36' W
<i>M. tenuipes</i> (Birstein, 1970)	6675–6710	KKT: 45°32' N 153°46' E
<i>Mirabilicoxa</i> sp. Golovan et al., 2013	470–1525	NW SoJ
<i>Momedossa symmetrica</i> (Schultz, 1966)	469	S. California, USA
<i>Paradesmosoma conforme</i> Kussakin, 1965	15–237	WKS
<i>P. orientale</i> Kussakin, 1965	66–111	NW SoJ; the Sea of Okhotsk: WKS and at the entrance to the bay Penzhinsky
<i>Prochelator kussakini</i> Mezhov, 1986	290	Gulf of Alaska, USA: 59°18' N, 141°58' W
<i>Prochelator</i> sp. Golovan et al., 2013	470–528	NW SoJ
<i>Pseudomesus similis</i> Birstein, 1963	5441	PO off the northern Hokkaido: 43°45.7' N 156°34' E
Desmosomatidae gen. sp. 18 Golovan et al., 2013	455–528	NW SoJ
Desmosomatidae gen. sp. 8 Golovan et al., 2013	470–528	NW SoJ

Note: WKS – Western Kamchatka shelf (the Sea of Okhotsk), NW SoJ – north-west part of the Sea of Japan, PO – Pacific ocean.

In 2012 the oceanic abyssal plain adjacent to the KKT was studied during the joint German/Russian expedition KuramBio (Kurile Kamchatka Biodiversity Study). Benthic material was collected with the same set of the gears as in the SoJaBio (Malyutina and Brandt, 2013). Twelve stations were sampled at the depth 4830–5780 m.

Even at the preliminary stage of the material processing it became clear that desmosomatid fauna of the open abyssal of the Northwest Pacific is actually much richer and more abundant than it was previously estimated (see Fig.). At stations 1–11, Desmosomatidae constituted from 2 to 37% (16% in general) of all isopod specimens in the C-EBS supranets. The highest number of desmosomatids (191 in the supranet) was recorded at the st. 2–9 (46°14,78'–46°14,94' N 155°32,65'–155°32,56' E, 4863–4862 m). By now the materials from this station have been sorted on the species level. Eleven species and 5 genera of Desmosomatidae (the same number as it was previously reported for the whole Northwest Pacific) were found (Table 2). *Mirabilicoxa coxalis* (Birstein, 1963) was known from the Pacific Ocean off the northern Honshu and KKT. The other 10 species are apparently new to science.



The number of the desmosomatid specimens in supranets per 11 KuramBio C-EBS stations.

**TABLE 2. List of Desmosomatida from the supranet of the KuramBio C-EBS station 2-9**

<i>Chelator</i>	sp. 1
<i>Chelator</i>	sp. 2
<i>Chelator</i>	sp. 3
<i>Eugerdella</i>	sp. 1
<i>Eugerdella</i>	sp. 2
<i>Mirabilicoxa</i>	aff. <i>richardsoni</i>
<i>Mirabilicoxa</i>	cf. <i>coxalis</i> (Birstein, 1963)
<i>Mirabilicoxa</i>	spp. 1
<i>Mirabilicoxa</i>	sp. 2
<i>Eugerdella</i>	sp. 1
<i>Pseudomesus</i>	sp. 1

The genus *Chelator* was previously known by 8 species from the North Atlantic, Arctic and Antarctic (Brix, 2006; Kensley et al., 2004), and is firstly recorded for the North Pacific. *Eugerdella* (16 species) and *Mirabilicoxa* (19 species) have a similar distribution (the North Atlantic, Polar Regions and the North Pacific). The members of *Eugerdella* are reported for the North Pacific for the first time. Five known species of *Pseudomesus* occur in the North and South Atlantic, Australia and the North Pacific. *Eugerdella* distributed in the Northern Hemisphere: in the North Atlantic, the Arctic and the North Pacific. *Mirabilicoxa* is relatively the deep-sea genus, inhabiting bathyal and abyssal from 455 to 5495 m. Other genera occur at the large range of depths from the shelf to the abyssal zone (5000 m and deeper).



The obtained in the first stage data suggest that in the abyssal of the Northwest Pacific is inhabited by the diverse desmosomatid fauna with a high proportion of endemic species.

### Acknowledgments

The work was supported by the Council of the President of the Russian Federation (Project MK-2599.2013.4), the Russian Foundation of Basis Research (Project 13-04-02144), Presidium of the Far East Branch of RAS (Project 13-III-B-06-082) and FEB RAS (Grant 12-I-P30-07).

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**A new species of *Triticella* (Bryozoa: Ctenostomatida)  
from the abyssal plain adjacent  
to the Kuril-Kamchatka Trench**

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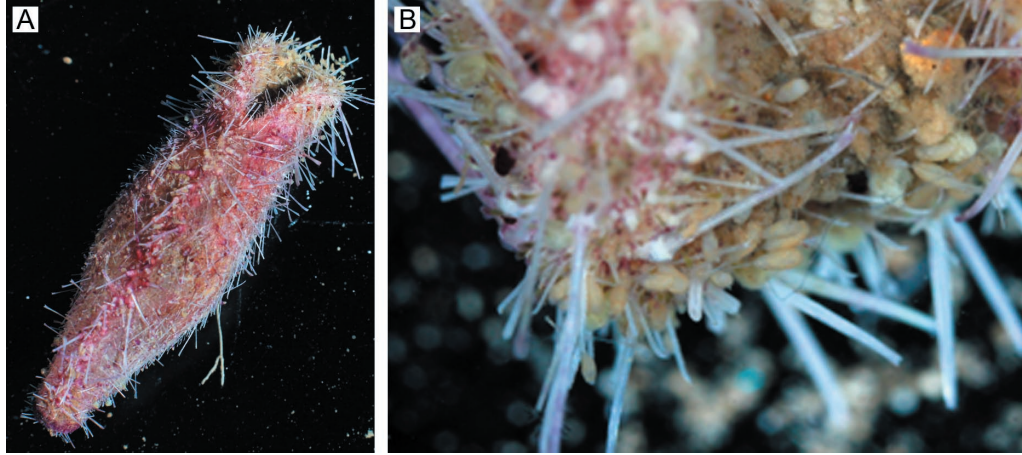
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Information on the abyssal bryozoan fauna of the northwestern Pacific remains extremely limited, with only two papers published reporting four deep-sea species. Kluge (1953) described *Kinetoskias beringi* from 3814 m depth in the southwestern part of the Bering Sea, and also recorded *K. beringi* together with *K. mitsukuri* Yanagi and Okada, 1918 from 3400 m depth from the southern basin of the Sea of Okhotsk. D'Hondt and Mawatari (1987) later described two new species in the ctenostomatid genus *Arachnoidea* (*A. brevicaudata* and *A. ophiidiomorpha*) from an abyssal station at 3835 m depth (33°38.3' N, 137°32.2' E) southeast of Honshu Island.

Examination of material recently collected by the German-Russian KuramBio (Kuril-Kamchatka Biodiversity Study) deep-sea expedition to the abyssal plain adjacent to the Kuril-Kamchatka Trench on board of RV *Sonne*, conducted in summer 2012, has revealed a low occurrence of Bryozoa, with only two taxa collected at two of 12 deep-sea stations: a single juvenile colony of the cheilostomatid *Kinetoskias* sp., and several colonies belonging to a new species in the ctenostomatid genus *Triticella*. The latter were gathered from a depth range of 5263–5362 m (40°12.49' N, 148°05.40' E – 40°12.37' N, 148°05.43' E), some 450 km southeast of Hokkaido, in association with the spines of the irregular sea urchin *Echinostigma* (*Echinogutta*) *amphora* (see Fig.).

Colonies of species in *Triticella* have creeping stolons bearing elongate, pedicellate, membranous zooids attached by flexible kenozooids. Zooids of some species can be clustered. The ten previously described species in *Triticella* are distributed predominantly in the Northern Hemisphere. Seven *Triticella* species commonly occur at shelf and slope depths, and are commensals on various crustaceans, hydroids, mollusks, and other bryozoans. The other three species (*T. calveti* d'Hondt et Hayward, 1981; *T. fusiformis* d'Hondt et Hayward, 1981; *T. gracilis* d'Hondt et Hayward, 1981) were reported from several abyssal stations in the northeastern Atlantic, with *T. gracilis* living in association with deep-water sipunculids (d'Hondt, Hayward, 1981; d'Hondt, 1983).



(A) Irregular sea urchin *Echinostira* (*Echinogutta*) *amphora* with numerous colonies of a new *Triticella* species attached to its spines. (B) Same, close up; (photographs courtesy of Dr. A. Maiorova).

Our new species clearly differs from congeners by having a strongly reduced discoidal stolon, with the bases of the pedicels clustered and closely appressed. We examined some details of the morphology and anatomy (muscular system) of this species using light microscopy (LM), scanning electron microscopy (SEM), and confocal laser scanning microscopy with phalloidin labeling (CLSM).

The deep-sea bryozoan fauna remains very poorly known at both global and regional scales (Silén, 1951; Menzies, 1963; Schopf, 1969; Hayward, 1981; Gordon, 1987). Roughly half of all deep-sea investigations have been conducted in the north-eastern Atlantic, and 75% were within the depth range of 200–1000 m (Hayward, 1981), i.e., mainly in the bathyal zone.

A series of Russian deep-sea expeditions in the northwestern Pacific on RV *Vityaz* in the 1950s and 1960s obtained the first reliable data indicating the occurrence of bryozoans at abyssal and extreme hadal depths. Colony fragments, preliminarily identified as *Kinetoskias*, were detected at five stations along the Kuril-Kamchatka Trench at depths of 6090–8400 m (Belyaev, 1989). Curiously, there were no records from the extensive adjacent abyssal plain. Discovery of the new species of *Triticella*, the deepest reported among members of the genus, provides the first precise taxonomic data on the bryozoan fauna in this deep-water basin in the northwestern Pacific.

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**Preliminary results of comparative analysis of the bivalve fauna  
of the deep-sea basins of the Sea of Japan and the Bering Sea  
and the Northwestern Pacific abyssal plain**

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All the Far-eastern seas of Russia (the Sea of Japan, the Sea of Okhotsk, and the Bering Sea) have deep-water basins with maximum depths more than 3500 m and communicate with the Pacific Ocean via straits of different depth. The most isolated from the Pacific is the Sea of Japan, which is connected with the ocean by straits no more than 130 m deep (Tada, 1994; Kitamura et al., 2011). The Bering Sea is the least isolated from the ocean; maximum depth of straits is up to 4420 m. The Sea of Okhotsk, like the Bering Sea, is connected with the Pacific Ocean by numerous and mostly deep-water straits. However, in contrast to the other Russia's Far-eastern seas, the Sea of Okhotsk is characterized by many extensive areas of gasohydrothermal vents and methane seep on the sea bottom and on the slopes of deep-water basins (Kuznetsov et al., 1989; Obzhirov, 1993; Kamenev et al., 2001). Thus, the different degree of communication of the Russia's Pacific seas with the Pacific Ocean and the presence of deep-water seepage and gasohydrothermal vent areas in some of the seas exert a significant influence on the formation and composition of the deep-water fauna of these seas.

During the period from 1949 to 1990, studies of deep-water macrobenthos of Russia's Pacific seas and the northwestern Pacific have been carried out by a large number of Russian hydrobiological expeditions. Nevertheless, extensive materials collected by these expeditions have not yet been entirely processed. Therefore, to-date very fragmentary data are available on the composition and distribution of the bottom fauna in the bathyal and abyssal zones of the Sea of Japan, the Sea of Okhotsk, and the Bering Sea, as well on the degree of similarity of this fauna with the specific abyssal fauna of the Pacific Ocean. The most recent joint expeditions conducted by Russian and German researchers have focused on the study of the biota of the deep-sea basin in the Sea of Japan (SojaBio, 2010) and the abyssal plain adjacent to the Kurile-Kamchatka Trench (KuramBio, 2012) and have significantly supplemented hydrobiological materials that were collected by previous Russian expeditions.

Bivalve mollusks occur from the intertidal zone to the greatest depth of the World Ocean (Knudsen, 1970; Filatova, 1971; Scarlato, 1981; Coan et al., 2000). Along with polychaetes and echinoderms, they are the most common and widely distributed animals in the abyssal zone of the World Ocean (Filatova, 1971, 1976, 1982). Therefore,

bivalves provide a convenient object for the study of the faunal relationships between the different deep-water regions of the northwestern Pacific. This work presents the preliminary results of comparative analysis of the species composition of bivalves found in the abyssal plan of the northwestern Pacific and the bathyal and abyssal zones of the Sea of Japan and the Bering Sea, respectively the most and the least isolated from the Pacific Ocean.

In the Sea of Japan, bivalve materials from the deep-water basin (465–3435 m) were collected by 4 expeditions of the P.P. Shirshov Institute of Oceanology of the Russian Academy of Sciences (IO RAS) (RV “Vityaz”, 1972, 1976, 1985; RV “Professor Khromov”, 2005) and the SoJaBio Russian-German expedition (RV “Akademik Lavrentyev”, 2010); in the deep-sea basin of the Bering Sea (440–4294 m), by 6 expeditions of IO RAS (RV “Vityaz”, 1950, 1951, 1952; RV “Zhemchug”, 1963; RV “Akademik Shirshov”, 1981; RV “Akademik Mstislav Keldysh”, 1990); and on the abyssal plain (4830–5786 m) adjacent to the Kurile-Kamchatka Trench, by the KuramBio German-Russian expedition (RV “Sonne”, 2012).

The study of the bivalves from the deep-water basin of the Sea of Japan revealed 26 species, of which only 5 species are endemic to the Sea of Japan (Kamenev, 2013). Three species out of the 5 endemics may be new to science. Generally, the deep-water bivalve fauna of the Sea of Japan is characterized by an impoverished shelf fauna and consists of widely-distributed and eurybathic species that are able to live in the bathyal and abyssal zones of the Sea of Japan. Three vertical depth ranges (200–1600, 1700–3000, and 3000–3500 m), were distinguished based on the species composition similarity; their faunas differed because of the gradual disappearance of subtidal-bathyal species rather than the appearance of endemic bathyal and abyssal species. In the abyssal of the Sea of Japan (below 3000 m), only 3 species were recorded (*Dacrydium vitreum*, *Delectopecten vancouverensis*, and *Thyasira (Parathyasira) sp.*), which are not dominant at these depths. Abyssal species characteristic of the Pacific abyssal plain were not found in the deep-water basin of the Sea of Japan.

In the deep-water basin of the Bering Sea, 51 species of bivalves were found, of which 23 species are new records for the fauna of Russia, and 5 species may be new to science. Most species are typical representatives of bathyal and abyssal faunas and have been previously recorded only in the northeastern Pacific (Coan et al., 2000). In the abyssal zone (below 3000 m), no less than 15 species were recorded; in contrast to the Sea of Japan, the greater part of these are endemic abyssal species characteristic of the North Pacific abyssal depths.

As a result of the KuramBio expedition, an extensive and unique material of bivalves was sampled from 12 hydrobiological stations that were worked in the abyssal zone of the Pacific Ocean at latitudes from the Sangar Strait (Japan) to the northern Kurile Islands. This expedition collected many small species, which were absent in the collections of the previous expeditions because of the different technical facilities in studying abyssal bottom fauna. According to our preliminary results, at least 40 species

of bivalves, of which about a half are new to science and to the northwestern Pacific fauna. The most common six species were characteristic of the abyssal of the Bering Sea, too. However, among the bivalves collected by the KuramBio, no one species was shared with the deep-water fauna of the Sea of Japan.

Thus, the abyssal bivalve fauna of the Sea of Japan is much more poor than in the Bering Sea and has no characteristic Pacific abyssal species. The poorness of the abyssal fauna and the lack of typical abyssal species of bivalves in the deep Sea of Japan are probably connected with the isolation of this body of water from the Pacific abyssal depths (Tyler, 2002). The relative richness and significant similarity of the abyssal fauna of the Bering Sea and the Pacific Ocean can be explained by the presence of deep and broad straits connecting this sea with the ocean and can also be related to the history of formation and the main migration routes of the northern Pacific faunas (Scarlato, 1981; Coan et al., 2000).

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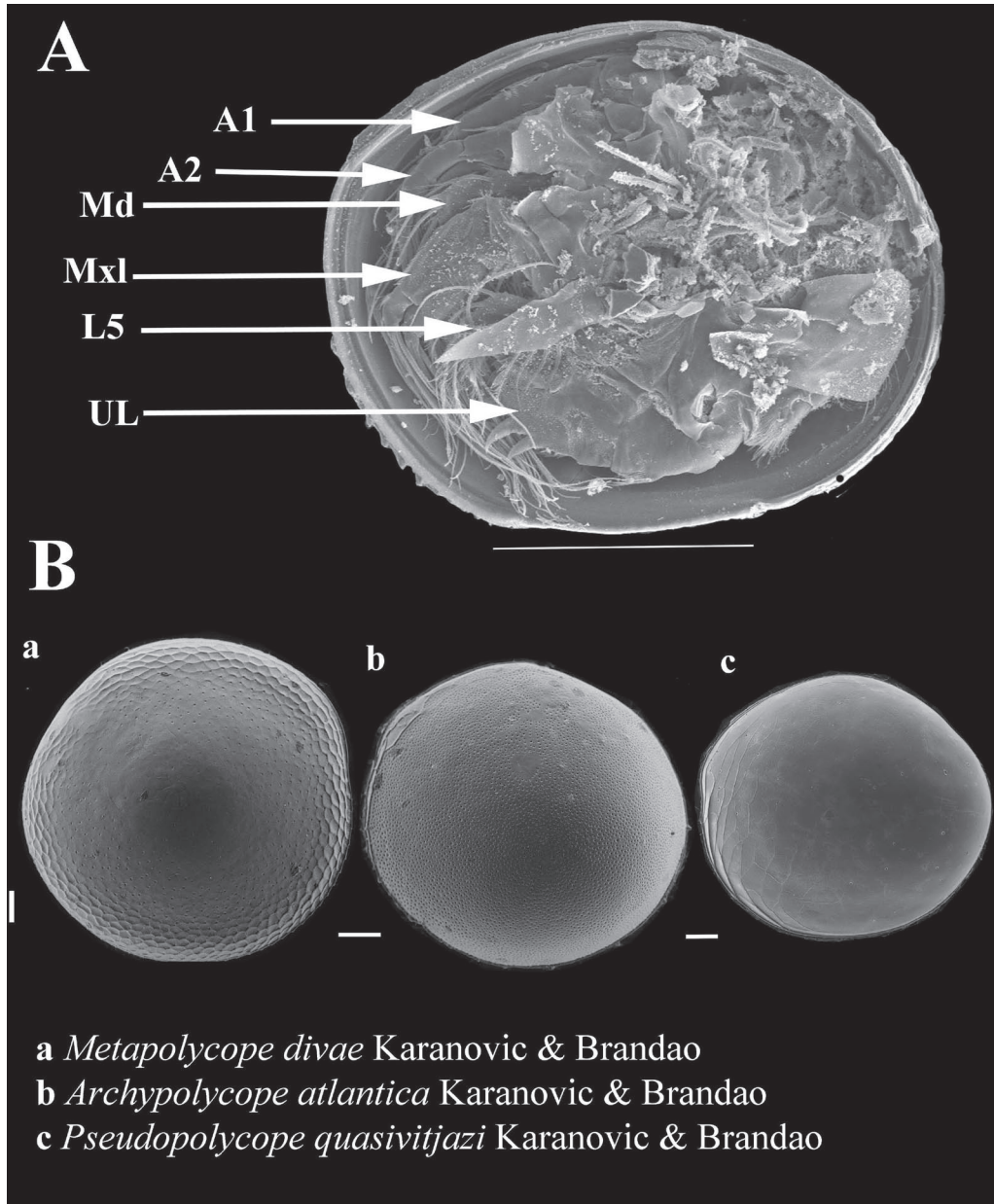
## **Diversity and importance of Polycopidae ostracods (Crustacea, Myodocopa, Cladocopina) in the deep sea**

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Ostracoda is a large group of small bivalve crustaceans with a rich fossil record, high diversity and ecological plasticity. During more than 500 million years of evolution, the class went through numerous reductions in the number of body limbs, and the suborder Cladocopina (order Halocyprida, subclass Myodocopa) is an extreme example. They have only five body appendages: antennula, antenna, mandibula, maxillula, and the fifth limb. The soft body terminates with paired uropodal lamellae. Although much reduced, the representatives of Cladocopina also have many “primitive” characters, such as a remnant of the trunk segmentation, biramous maxillula and the biramous fifth limb (Cohen et al., 1998) (Fig. 1A). The shell is in majority of species sub-circular in lateral view (Fig. 1B), often well-ornamented with pits, ridges, thorn-like structures, etc., and most usually lacking the anterior rostral elongation, typical for many myodocopids. The fossil record indicates that the oldest Cladocopina are from the Carboniferous (Moore, 1961). The suborder Cladocopina contains only one superfamily, Polycopoidea Sars, 1866 and only one family, Polycopidae Sars, 1866. Chavtur (1983) divided Polycopidae into two subfamilies, Polycopisinae Chavtur, 1981 and Polycopinae Sars, 1966. The former has only two genera together amounting to fewer than 20 Recent species. Polycopinae is also much more diverse, and has 15 genera, about 100 Recent and 55 fossil species (Tanaka et al., 2010). The family Polycopidae has a global distribution, with species recorded from all the oceans of the world. The greatest number of records of Recent species comes from the Kuril-Kamchatka region, due to the intensive taxonomic work by Chavtur (1977, 1979, 1981, 1983). It is interesting to note that only three species have so far been recorded from the Indian Ocean (Hartmann, 1974), which also probably reflects the taxonomic effort. Polycopids can be found at many different water depths, from sandy beaches, through continental shelves and slopes, to abyssal environments of more than 5000 m depth (Chavtur, 1981, 1983). Fossil and subfossil, deep-sea, benthic ostracods are quite well known from the Arctic, Atlantic and Pacific, but with the study of soft parts along with the shell structures, the cosmopolitan distribution of some deep sea species became doubtful (Schornikov, 2005; Jellinek et al., 2006; Brandão, 2008). Moreover, recent molecular data indicate that the biodiversity of the Southern Ocean benthos and of deep-sea ostracods is most probably underestimated, and what was previously considered as one circum-antarctic species holds a number of different species (Brandão, 2010; Brandão et al., 2010).





**Fig. 1.** SEM images of Polycopidae. **A** – inside view with left valve removed; **B** – outline of Polycopidae shells.

The most abundant deep sea group in the palaeontological and palaeoecological studies is the family Polycopidae (in some assemblages polycopids constitute more than 50% of all ostracod taxa), but is rarely identified further than *Polycope* spp. The first

living deep sea polycopid species was described in the late 1970's and until recently only 13 species was known from the depths of more than 2500 m. Most of these species are, in fact know from the Kuril Kamchatka region (*Metapolycope echinata* Chavtur, 1981; *Polycopsis compacta* Chavtur, 1981; *Archypolycope bonaducei* Chavtur, 1981; *A. squalida* Chavtur, 1981; *Polycope bathyalis* Chavtur, 1981; *P. gublini* Chavtur, 1981; *P. major* Chavtur, 1981; *Pseudopolycope vitjazi* Chavtur, 1981; *P. cornea* (Chavtur, 1981); *P. rotunda* (Chavtur, 1981)). Karanovic and Brandao (2012, 2013) described another 10 new species from a small sector in South Atlantic (*Metapolycope divae* Karanovic et Brandao, 2012; *Archypolycope atlantica* Karanovic et Brandao, 2012; *A. brandtae* Karanovic et Brandao, 2012; *A. louisii* Karanovic et Brandao, 2012; *A. martinezi* Karanovic et Brandao, 2012; *Pseudopolycope chavturi* Karanovic et Brandao, 2012; *P. quasivitjazi* Karanovic et Brandao, 2012; *P. spio* Karanovic et Brandao, 2013; and *Hyphalocope dorsoithys* Karanovic et Brandao, 2012), and from the deep Southern Ocean (*Pseudopolycope andeep* Karanovic et Brandao, 2013), almost doubling the number of known species. Among other results, the authors reported an exclusively deep sea genus *Archipolycope* Chavtur, 1981, previously know only from Kuril Kamchatka trench; they also erected a new subgenus of widely distributed genus *Polycope* Sars, 1866, namely *Divacope* Karanovic and Brandao, 2012, which seems to include only deep sea species (Fig. 2). In the same paper, Karanovic and Brandao (2012) provide a phylogenetic analysis of the family Polycopidae which may indicate both that the deep sea species collected from the same or close areas are not the most closely related, but in fact are more closely related to their shallow water relatives and/or deep sea ostracods from far apart ocean masses, and this may support the hypothesis that polycopids colonized deep sea recently (Mesozoic or Early Cenozoic). However, some primitive genera, such as *Hyphalocope* (Fig. 3), discovered in the deep sea Atlantic, leans towards more ancient origin and prolonged isolation. This genus has a very primitive shell outline with a flat dorsal margin, and has many plesiomorphic characters of the subfamily. The phylogenetic analysis also indicates that many genera are polyphyletic and in need of revision. Polycopidae are excellent model organisms for studying zoogeography, because they tend to have a very restricted distribution, they have a rich fossil record, and they are also present in all other marine environments of the world. The latter fact is providing the possibility to study ways of the deep sea colonization of the group.

What can potentially be an answer for the success of this group in the deep sea is the structure and composition of their shell. Namely, because of the thin layer of organic epicuticle, which englobes the shell, some ostracod groups can survive below the carbonate compensation depth (CCD) (i.e., "corrosive deep water condition"). So far, there has not been any published record on the shell ultrastructure of the deep sea polycopids. On the first look the only difference between the shallow water polycopids and their deep sea relatives is that the deep sea species tend to be slightly larger, but the deep-sea gigantism (also known as abyssal gigantism), known for other crustacean groups, has not been noticed. Also, observations under the compound microscope do not show any

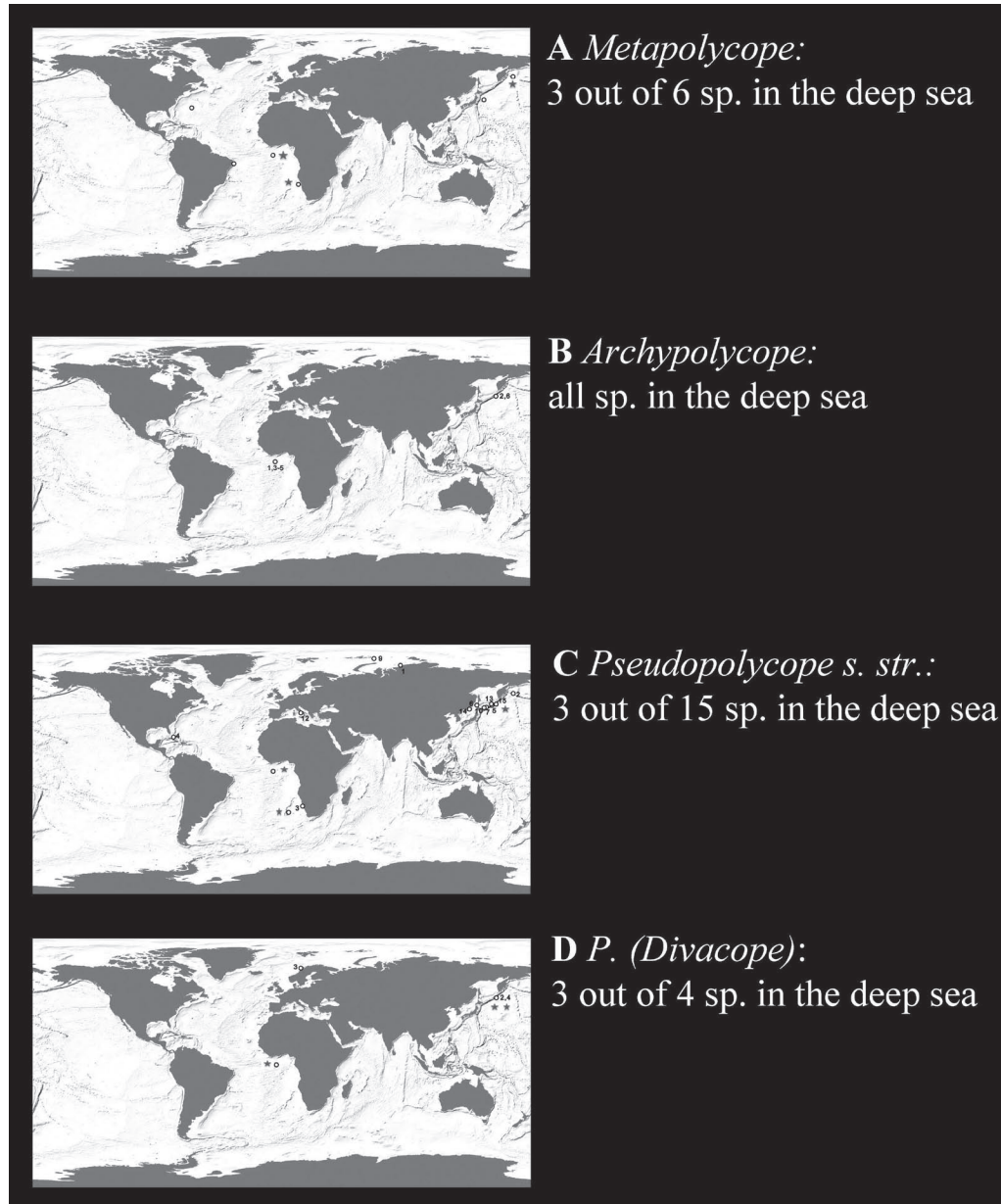
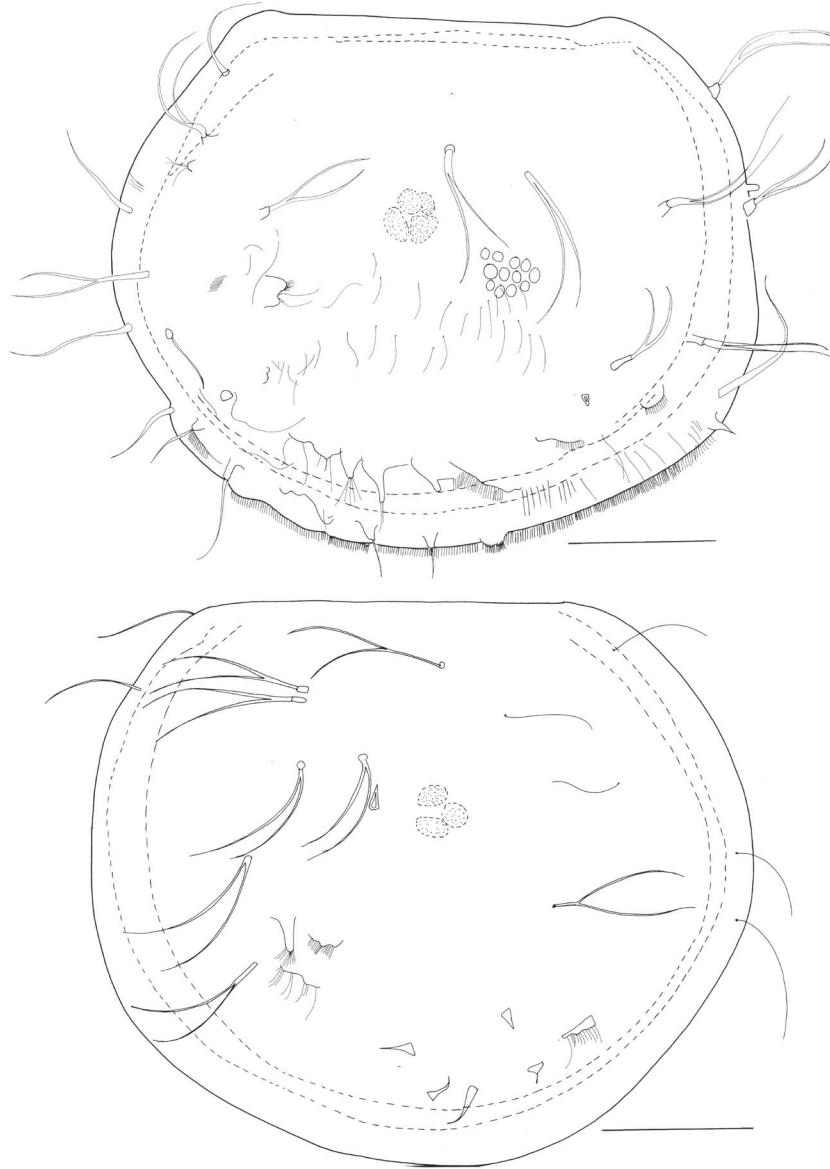


Fig. 2. Zoogeographical distribution of the deep sea Polycopidae genera.

kind of special adaptations to the deep sea, with the exception of complicated structures situated between claws of the uropodal ramus noticed by Karanovic and Brandao (2012), but these were also not studied in detail under scanning electron microscope (SEM), and their functional morphology is not known.



**Fig. 3.** *Hyphalocope* Karanovic et Brandao, the most primitive of all deep sea Polycopidae.

I strongly believe that the biological investigation of the deep sea should be based on the species level taxonomy, and not only assemblages, because only this can provide us with more accurate information relevant to the biodiversity, ecology, zoogeography, and adaptations. Unfortunately, the number of the taxonomy experts is in the constant decline over the years. On the other hand, specialist for numerous groups (including

ostracods) are still actively working and their expertise in the study of the deep sea environment can make a big difference when interpreting results and coming to the conclusions which may affect the way we protect and manage these ecosystems today.

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## **New and “rare” fatty acids of marine invertebrates from deep-sea areas of northwestern Pacific**

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The constant development of the methods for structural analysis of fatty acids resulted in the discovery of a significant concentration of rare acids in marine invertebrates. Typically, these findings occurred in the course of lipid analysis of marine invertebrates collected on the continental shelf. The study of bathyal and abyssal benthic fauna has allowed us to significantly expand the list of animals containing these rare acids and to discover new fatty acids.

### **Polyunsaturated Fatty Acids**

In the northwestern Pacific phytoplankton mainly consists of diatoms which are the main producers of organic matter. Phytoplankton synthesizes  $\omega$ -3 polyunsaturated fatty acids, and these polyunsaturated fatty acids predominate in the lipid composition of most marine invertebrates. Some abyssal invertebrates contain  $\omega$ -6 polyunsaturated fatty acids, mainly 20:4(n-6). Presumably, they get these fatty acids from the microbial food web. Until recently, all known long chain (C20 and more) polyunsaturated fatty acids were  $\omega$ -3 and  $\omega$ -6 fatty acids. The detailed analysis of the composition of polyunsaturated fatty acids in bivalves that inhabit cold-seep environments revealed unusual long chain  $\omega$ -1,  $\omega$ -4 and  $\omega$ -7 polyunsaturated fatty acids. Besides, in these bivalves no long chain  $\omega$ -3 and  $\omega$ -6 polyunsaturated fatty acids (20:5(n-3), 22:6(n-3) or 20:4(n-6)) were detected. These bivalves receive food from symbiotic chemosynthetic bacteria, and are to a large extent sustained by fatty acids synthesized by bacteria (Saito, Osako, 2007). We also obtained similar results in the study of three species of molluscs of the family Vesicomidae. Bivalves of the family Vesicomidae were collected near methane seeps during the expedition IBM FEB RAS onboard of the RV *Akademik Lavrentyev* in May 2013 to the Derugin Basin (the Sea of Okhotsk). Bivalves of the family Vesicomidae were collected using the remotely operated underwater vehicle “Comanche” (Fig. 1).

In the lipids of these bivalves containing chemosynthetic bacteria,  $\omega$ -3 and  $\omega$ -6 polyunsaturated fatty acids were not found. Among the polyunsaturated fatty acids in these bivalves the fatty acid 20:4(n-4) dominated with a content of more than 13%. The differences between the fatty acid composition of common species of abyssal bivalves and these deep sea bivalves with bacterial symbionts are clearly visible in Fig. 2.



**Fig. 1.** Photograph of *Akebiconcha soyoae ochotensis* with bacterial symbionts sampled at a methane seep using the remotely operated underwater vehicle “Comanche” (Derugin Basin, Sea of Okhotsk, May 2013).

These three variants of the composition of fatty acids of deep-sea organisms reflect three feeding mechanisms: deposit feeding (*Nuculana* sp.), predation (*Cuspidaria* sp.) and bacterial symbiotrophy (vesicomyids).

Besides these fatty acids we found rare and new fatty acids in abyssal invertebrates reflecting their biosynthesis or feeding mode. Abyssal invertebrates were sampled by means of the Agassiz trawl during KuramBio (Kurile Kamchatka Biodiversity Study) in the Kurile-Kamchatka Trench and abyssal plain of the Kurile-Kamchatka region on board RV *Sonne* in August 2012.

**$\omega$ -5 polyunsaturated fatty acids.** To the best of our knowledge in marine invertebrates  $\omega$ -1,  $\omega$ -2,  $\omega$ -3,  $\omega$ -4,  $\omega$ -6 and  $\omega$ -7 polyunsaturated fatty acids have been described. In the foraminifera species *Reophax* sp. (Fig. 3), we have discovered  $\omega$ -5 polyunsaturated fatty acids new for marine invertebrates. In this foraminifera species, the fatty acids 22:5(n-5) were found at a concentration of 5.9%, 22:3(n-5) at a concentration of 1.2% and 20:3(n-5) at a concentration 0.5%. One of these acids 22:5(n-3) was also found in sea urchins at low concentrations (0.3–0.4%). The structure of these acids is represented in Fig. 4. The origin of these fatty acids is unknown, most likely are they synthesized by this foraminifera.

**The fatty acid 21:4(n-7).** Previously this fatty acid has been found in the lipids of some marine invertebrates (the bivalves *Bathymodiolus japonicus* and *Bathymodiolus platifrons*, the crab *Shinkaia crosnieri*, and the opisthobranch mollusc *Scaphander*

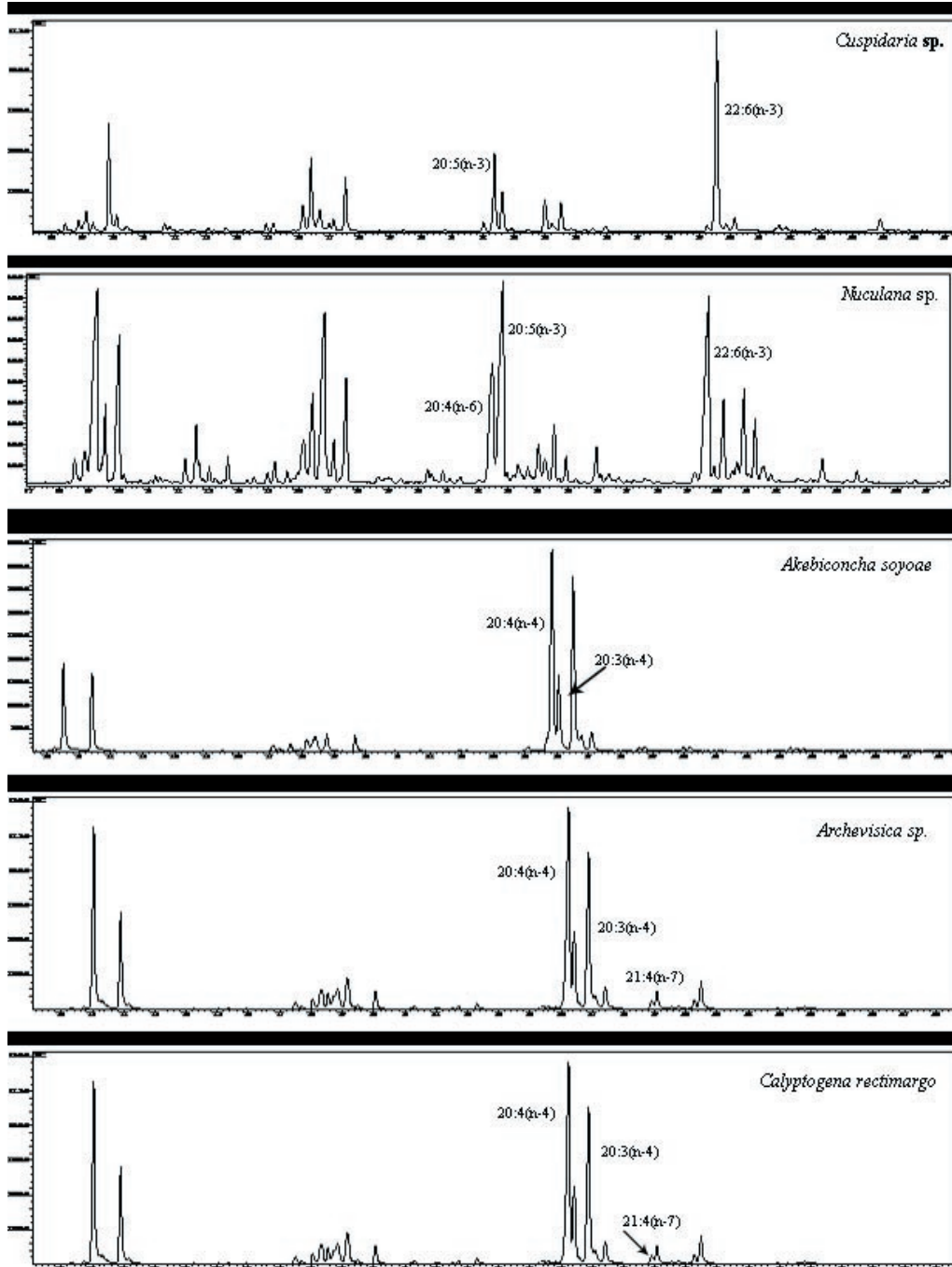
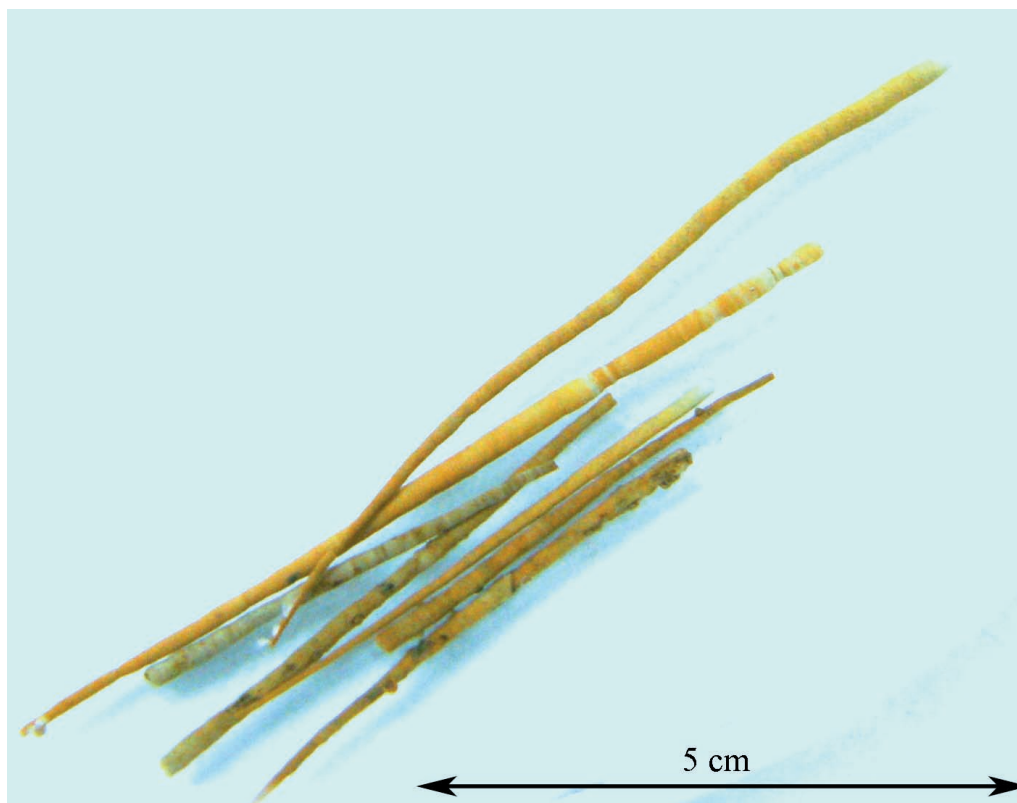


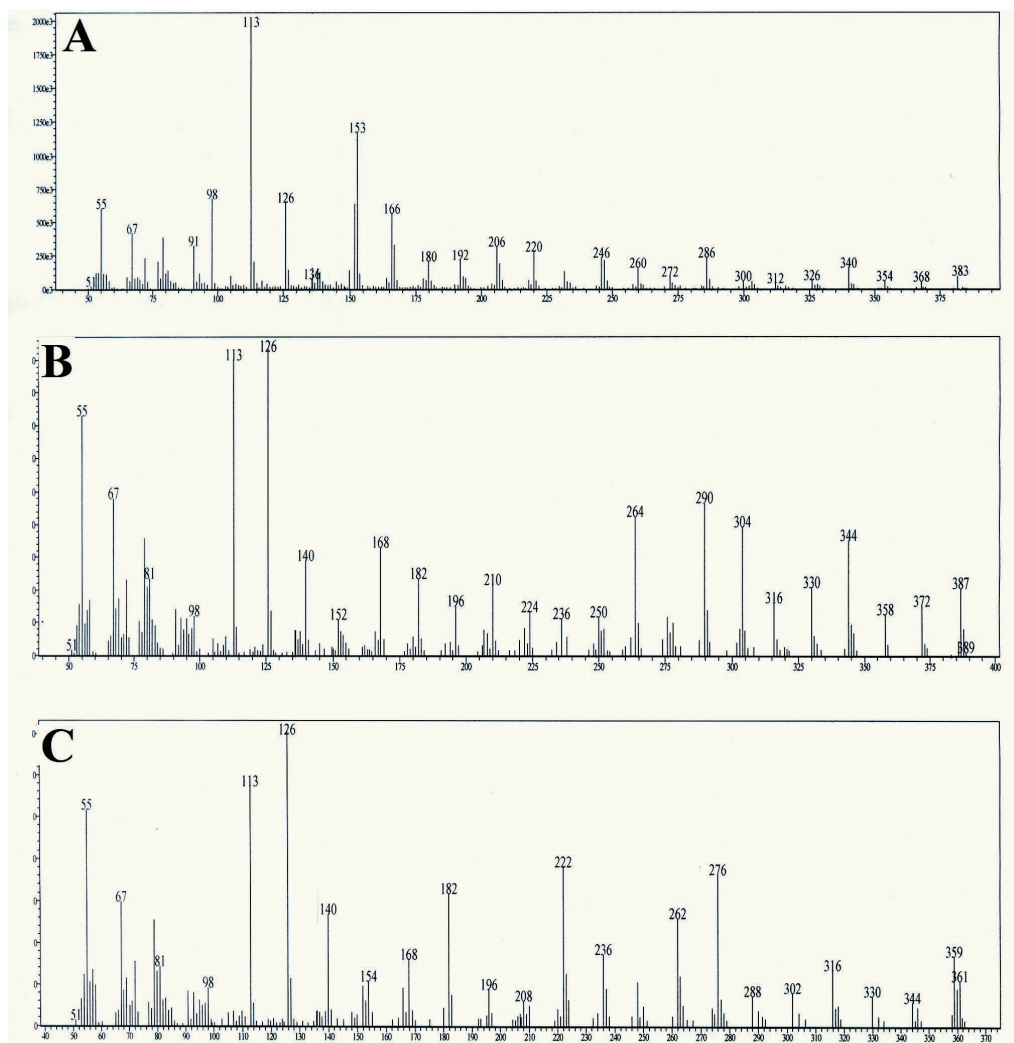
Fig. 2. Fatty acid chromatograms of five deep-sea bivalves.





**Fig. 3.** Photograph of foraminifera *Reophax* sp. sampled at a depth of 5250 m on the abyssal plain of the Kurile-Kamchatka region (latitude 41°12' N and longitude 150°06' E) in August 2012.

*lignarius* (Vasskog et al., 2012)), as well as in several types of marine thraustochytrids (Saito, 2008; Chang et al., 2011; Saito, 2011). The role of this fatty acid is unknown, but 21:4(n-7) extracted from *Scaphander lignarius*, had much greater cytotoxic activity than  $\omega$ -3 and  $\omega$ -6 polyunsaturated fatty acids (Vasskog et al., 2012). In our view the list of marine invertebrates containing this acid is much longer, especially in respect to the poorly investigated abyssal invertebrates. This acid has been found by us in all the samples of sea cucumbers (0.5–4.3% of total fatty acids), scaphopods (1–3.3%), scleractinians (0.4–2.5%), actinians (1.7–2.3%) and sea stars (1.2–5.1%), as well as in some polychaetes (0.4–5.5% of total fatty acids) and sea urchins (2.9–3.9%). The origin of this fatty acid in abyssal invertebrates is unknown. It is unlikely that all of these species are able to synthesize this acid. Among the primary links of food webs this fatty acid is found in thraustochytrids in which concentration of 7.2% were found (Chang et al., 2012). The presence of significant concentrations of this fatty acid in marine invertebrates and thraustochytrids allows assuming that thraustochytrids may constitute a significant element of deep-sea ecosystems. Among the abyssal species, the maximum content of this



**Fig. 4.** **A** – MS peaks of a DMOX derivative of 22:5(n-5) are  $M^+$  383, 368, 354, 340, 326, 312, 300, 286, 272, 260, 246, 232, 220, 206, 192, 180, 166, 153, 140, 126 and 113 (base peak). 4 pairs of the peaks M312 and M300, M272 and M260, M232 and M220, M192 and M180, M153 and M136 are respectively reflected by five double bonds; **B** – MS peaks of a DMOX derivative of 22:3(n-5) are  $M^+$  387, 372, 358, 344, 330, 316, 304, 290, 276, 264, 250, 236, 224, 210, 196, 182, 168, 154, 140, 126 and 113 (base peak). 3 pairs of the peaks M316 and M304, M276 and 264, M236 and M224 are respectively reflected by three double bonds; **C** – MS peaks of a DMOX derivative of 20:3(n-5) are  $M^+$  359, 344, 330, 316, 302, 288, 276, 262, 250, 236, 222, 208, 196, 182, 168, 154, 140, 126 and 113 (base peak). 3 pairs of the peaks M288 and M276, M250 and 236, M208 and M196 are respectively reflected by three double bonds.

fatty acid (9.4%) was found in the opisthobranch mollusc *Paracteocina* sp. Furthermore, this mollusc contains the unknown fatty acid 23:4(n-7) at a concentration of 0.6%, which may be the elongation product of 21:4(n-7).

**The fatty acid 26:7(n-3).** In two brittle stars from the abyssal plain of the north-western Pacific Ocean the fatty acid 26:7(n-3) has been found. The concentration of this fatty acid in the one ophiurid was 12.4%. Formerly this fatty acid has been found in microalgae (Mansour et al., 2005a) and the roughscale sole *Clidoderma asperrimum* (Fukuda, Ando, 2009) at a concentration of no more than 1%.

### **Monounsaturated Fatty Acids**

**The fatty acid 20:1(n-13).** In invertebrates from the abyssal zone, we have regularly noted the presence of the fatty acid 20:1(n-13). This fatty acid has been found in all studied brittle stars, in which its concentration ranged between 3.5–13.0%, in many bivalves, some sea urchins, and almost in all sea stars. One species of brittle stars also contained the isomer 20:1(n-13), the content of which was 68.3% of the main isomer. We also found the fatty acid 18:1(n-13), which presumably is the precursor of 20:1(n-13) (Mansour et al., 2005b). The content of 18:1(n-13) in 4 species of brittle stars ranged between 3.6–5.0%, and between 2.0–2.3% in three species of sea urchins.

**The fatty acid 16:1(n-10).** Among the other monoenoic fatty acids widely represented among the studied invertebrate is 16:1 n-10. It has been found in sea cucumbers (1–2.9%), foraminifera (1.4–3.1%), many brittle stars (0.9–1.2%), sea stars (0.9–1.8%), some sea urchins (1.2–1.5%), anemones (1.5%) and bivalves (1.6%).

**The fatty acid 23:1(n-9).** Monoenoic fatty acid 23:1(n-9) at concentrations greater than 1% within marine ecosystems was previously found exclusively in sea cucumbers (Kaneniwa et al., 1986). In our study, this fatty acid has been found in brittle stars (0.3–1.7%), sea urchins (0.7–3.1%), and all scleractinians (1.6–2.8%).

**Minor components.** Among the minor components in all studied starfish the fatty acid 11-methyl-12 octadecenoic acid (19:1) was found. It is a fatty acid of bacterial origin and found in the toxic microalgae *Ostreopsis lenticularis* (Carballeira et al., 1998) at a concentration of 0.4%. Its content in the abyssal starfish was 0.3–0.8%. In addition, in these starfish the fatty acid 11-methyl-12 eicosanoic acid was found. The fatty acid 21:1(n-14) and its *iso*- and *anteiso*- derivatives was found at concentrations of 0.6–1.4% in starfish. The content of *anteiso*- 21:1(n-14) was up to 2.3%. The presence of these fatty acids also indicates the presence of bacterial symbionts.

### **Conclusion**

Usually, the description of new or rare fatty acids is limited to describing one or more (at low concentrations) fatty acids in one or several species. We found “rare” and new fatty acids in the large number of species from one ecosystem. The results obtained allow us to hope that the potential of fatty acids as markers of marine food webs has not been exhausted and the wide application of modern methods of analysis will allow to increase the number of marker fatty acids.

### Acknowledgments

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## Phylogeography of deep-sea demersal fishes inhabiting the Sea of Japan and neighboring areas

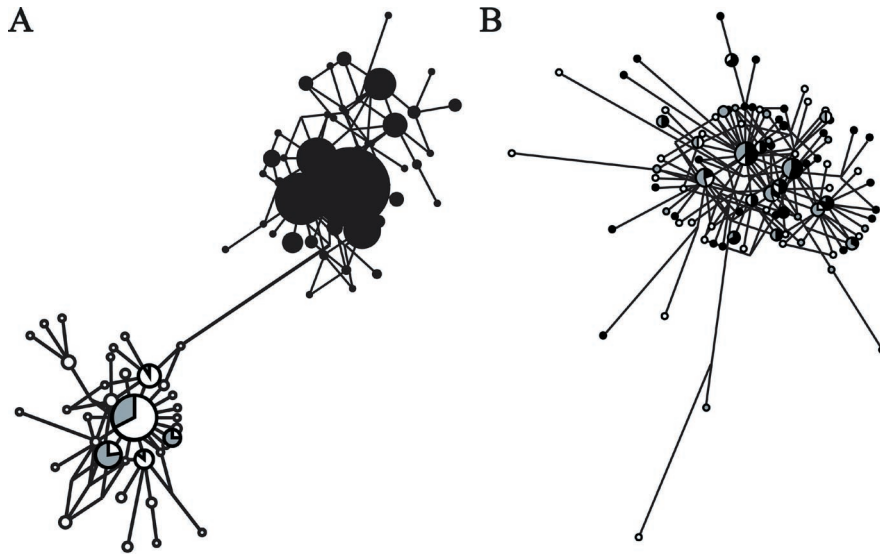
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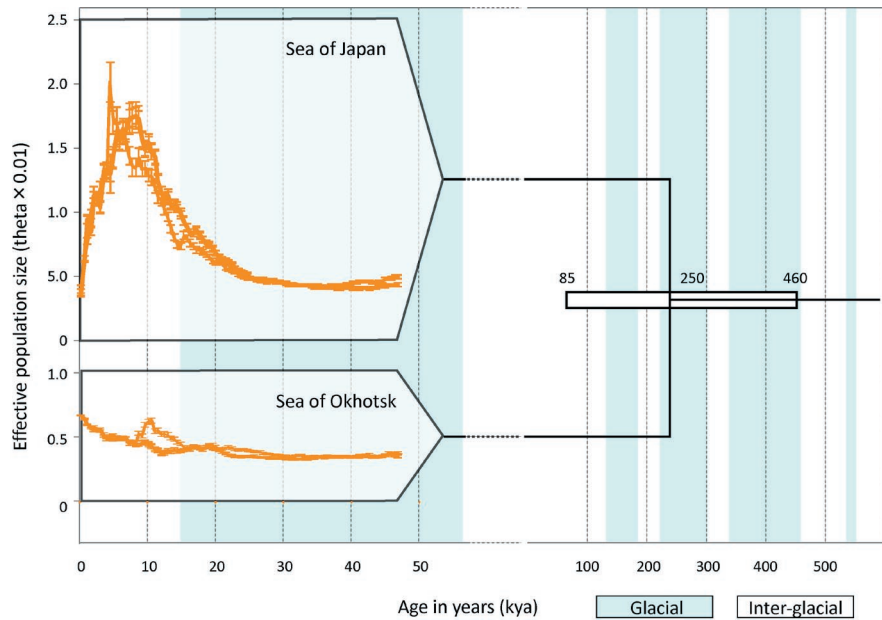
The Sea of Japan is a semi-closed marginal sea and only connected to neighboring sea areas by narrow and shallow straits. During the maximum period of the last glacial period (LGM), deep-sea areas of the Sea of Japan were thought to be completely anoxic due to a massive influx of freshwater from the Asian Continent and strong stratification (Tada et al., 1999). As a result, the deep-sea fauna became extinct and the present fauna was established by recolonization from outside habitats after the LGM (Oba et al., 1991). However, results of recent plaeoceanographic studies show that the oxic habitats were remained in restricted parts of the Sea of Japan during the LGM (Gorbarenko, Southon, 2000; Itaki et al., 2004).

For eight dominant deep-sea demersal fishes of the Sea of Japan, we compared genetic structures between this and neighboring sea areas. Three species or species complex with no ontogenetic vertical migration (*Bothrocara hollandi* (Fig. 1A), *Creproctus rastrinus* species complex, and *Lycodes nakamurai* species complex) showed complete genetic deviation between two areas (Kodama et al., 2008; Kodama, Kojima, 2009; Kojima et al., 2011; Hashiguchi et al., unpublished data; Sakuma et al., unpublished data), while two species with ontogenetic vertical migration (*Malacocottus zonurus* (Fig. 1B) and *Hippoglossoides dubius*) did not show such a deviation (Adachi et al., 2009; Kojima et al., submitted). Remaining three, which showed intermediate patterns, contained one species with ontogenetic vertical migration (*H. pinetorum*) and two without it (*L. tanakai* and *L. matsubara*). The structures of the latter might be attributed to the recent adult migration via the Soya Strait (Sakuma et al., submitted, unpublished data), while that of the former may be attributable to the secondary contact between two lineages that had been isolated in the Sea of Japan and neighboring sea areas, respectively, during the last glacial period (Kojima et al., submitted).

We confirmed ontogenetic vertical migration for *M. zonurus* and the absence of such migration for *B. hollandi* by elemental analyses (Sr/Ca ratio) of otoliths (Sakuma et al., unpublished data) and estimated the deviation age of a local population of *B. hollandi* in the Sea of Japan to be before the LGM (middle stages of the last glacial period; Kodama et al., 2008). In addition, we recently reconstructed population histories of *L. matsubara* in the Sea of Japan and the Okhotsk Sea by coalescence theory-based analyses, which suggested that the local populations in two sea areas were deviated from each other during the middle stages of the last glacial period, and the Sea of Japan population rapidly expanded after the last glacial period while the Sea of Okhotsk population



**Fig. 1.** Median-joining haplotype networks of two dominant deep-sea demersal fish of the Sea of Japan, *Bothrocara hollandi* (A) and *Malacocottus zonurus* (B) based on data in Kojima et al. (2011) and Adachi et al. (2009), respectively. The area of the circles is proportional to the frequency of occurrence of the haplotypes. The black and white sectors indicate the relative frequency of specimens from the Sea of Japan and those from neighboring sea areas, respectively.



**Fig. 2.** Evolution history of *Lycodes nakamurai* species complex estimated by coalescence theory-based analyses (Sakuma et al., unpublished data). A historical change of population size in each sea area is shown by the results of 4 replicate runs.

reduced (Sakuma et al., submitted). Similar results were also obtained for *L. tanakai* (Sakuma et al., unpublished data). *L. nakamurai* species complex was shown to have divided into populations of the Sea of Japan and the Okhotsk Sea before the last glacial period (Sakuma et al., unpublished data; Fig. 2).

In order to reveal the detailed formation process of deep-sea fauna in marginal seas in the northwestern Pacific, we desire to survey deep-sea faunas in the central parts of the Sea of Japan and the Okhotsk Sea.

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**First data on the Cumacea fauna  
based on materials collected  
during the Russian-German KuramBio expedition**

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In northwest part of the Pacific Ocean, cumaceans inhabit all depths from sublittoral to abyssal and is an obligatory element of bottom fauna of all this area. The wide-spread occurrence, ability to form aggregations, conjunction with a bottom sediments make Cumacea by convenient object of studying of vertical and geographical distribution.

Up to the present, despite undoubted importance of studying of deep-sea bottom fauna of northwest part of the Pacific Ocean, knowledge of abyssal Cumacea are very poor. The Kuril-Kamchatka Trench (KKT) and the adjacent abyssal area has already been investigated in the last century during the expeditions on board the RV *Vityaz* in 1949, 1953 and 1966 (e.g., Zenkevich et al., 1955; Zenkevich, 1963; Belyaev, 1983, 1989). The fauna was found in this area has been described in many publications, but the order Cumacea was studied slightly and only 2 species from the genus *Makrokyliindrus* were described from this area till now. The fauna of Cumacea of the adjacent Japan Trench was studied more detailed, with a number of articles of Gamo (1984, 1985, 1987, 1988a, b, 1989). There are described 14 species: *Paralamprops* (1 species), *Makrokyliindrus* (3 species), *Leptosylis* (2 species), *Paraleucon* (1 species), *Leucon* (1 species), *Bathycuma* (3 species), *Vemakylindrus* (2 species), *Hemilamprops* (1 species). Except *Paraleucon* and *Vemakylindrus* other six genera known for the Japan Trench were recorded in the KuramBio material. From 14 cumaceans species described from the Japan Trench 4 species were found in the KKT (*Leptostylis quadridentata* Gamo, 1985; *Bathycuma* aff *declinatum* Gamo, 1989; *Bathycuma* aff *granulatum* Gamo, 1989; *Makrokyliindrus* aff *micracanthus* Gamo, 1989). For related group Isopoda Birstein, (1971) pointed that the fauna of these neighboring trenches is very similar, and our preliminary results demonstrate similarity too.

The purpose of our work is to study the biodiversity and distribution of the key benthic taxa and Cumacea in particular in the Kuril-Kamchatka Trench and adjacent abyssal plain.

**Material and Methods**

The material for this study was collected in summer 2012 at the Kurile-Kamchatka Trench and adjacent abyssal plain during the Russian-German expedition KuramBio (Kurile-Kamchatka Biodiversity Study) on board of the RV *Sonne*. Macrofauna



was sampled using a newly modified camera epibenthic sledge (C-EBS). During the expedition 12 stations (21 deployments) using C-EBS were accomplished at depths ranging from 4830 to 5780 meters. All samples were sieved through of 300 µm mesh size sieve onboard immediately after hauling. Material from the first deployment at each station was fixed in pre-cooled 96% ethanol and from the second deployment (if it was accomplished) was primarily preserved in 4% formaldehyde for morphological studies, and after 48 hours washed with fresh water and re-fixated in 96% ethanol.

### Results and Discussion

In the studied samples 57 species Cumacea from 11 genera and 5 families were revealed. Dominating families collected at each station are (Fig. 1): the most specious family Nannastacidae (17 species, 127 specimens), the most numerous family Leuconidae (277 specimens, 11 species) and the family Diastylidae (13 species, 151 specimens). Defined below species had the greatest number of specimens: *Leucon* sp. 5 (103 specimens), *Leucon* aff. *spinulosus* (61 specimens), *Leptostylis* sp. 3 (41 specimens). It is interesting that *Leucon* sp. 5 was not a widespread species, and was found only twice – on station 3-9 placed at the western slope of the KKT (65 specimens) and at station 4-3 (38 specimens).

The family Bodotriidae (Fig. 2) is the smallest in terms of abundance (53) and by number of species of number of the found specimens (53), and by number of species – 7, 5 of which belong to the deep-sea genus *Bathycuma* (Fig. 3A–C). The *Cyclaspoides* sp. 1 (Fig. 3D) was the most abundant (presented by 18 specimens).

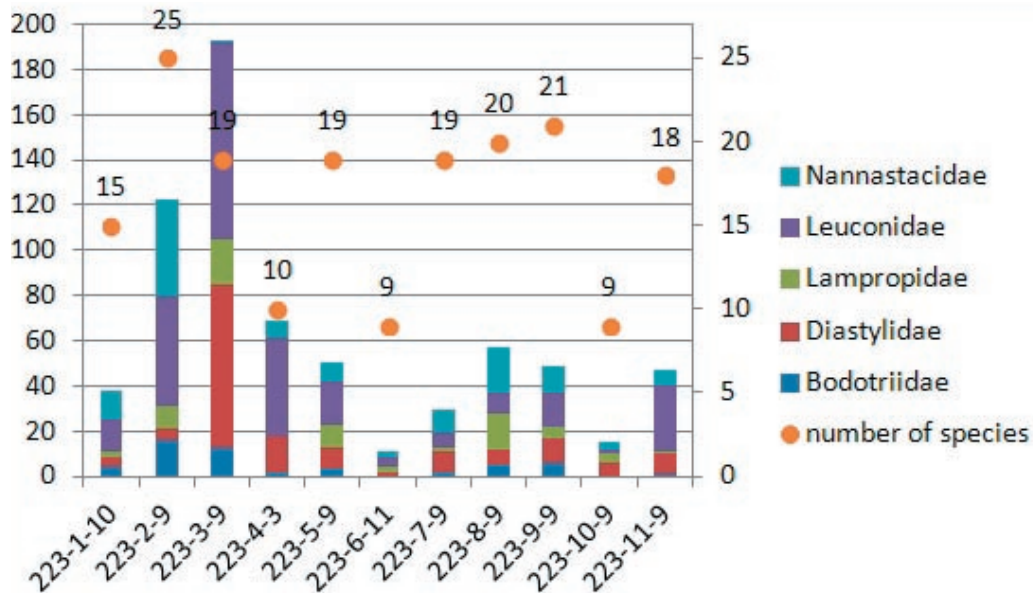


Fig. 1. The species diversity and abundance of cumaceans per stations of the KuramBio 2012 expedition.

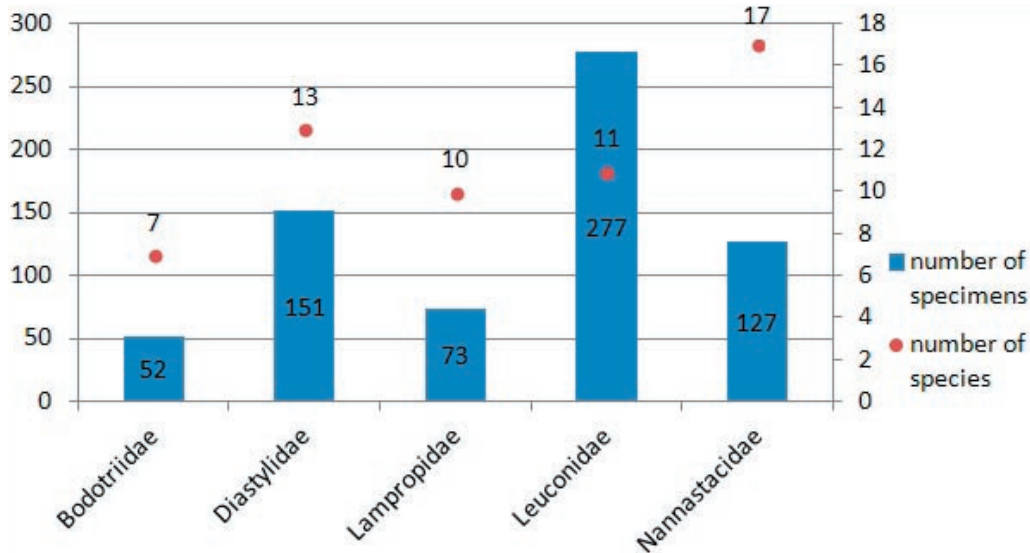


Fig. 2. The species diversity and abundance of cumacean families of the KuramBio 2012 expedition.

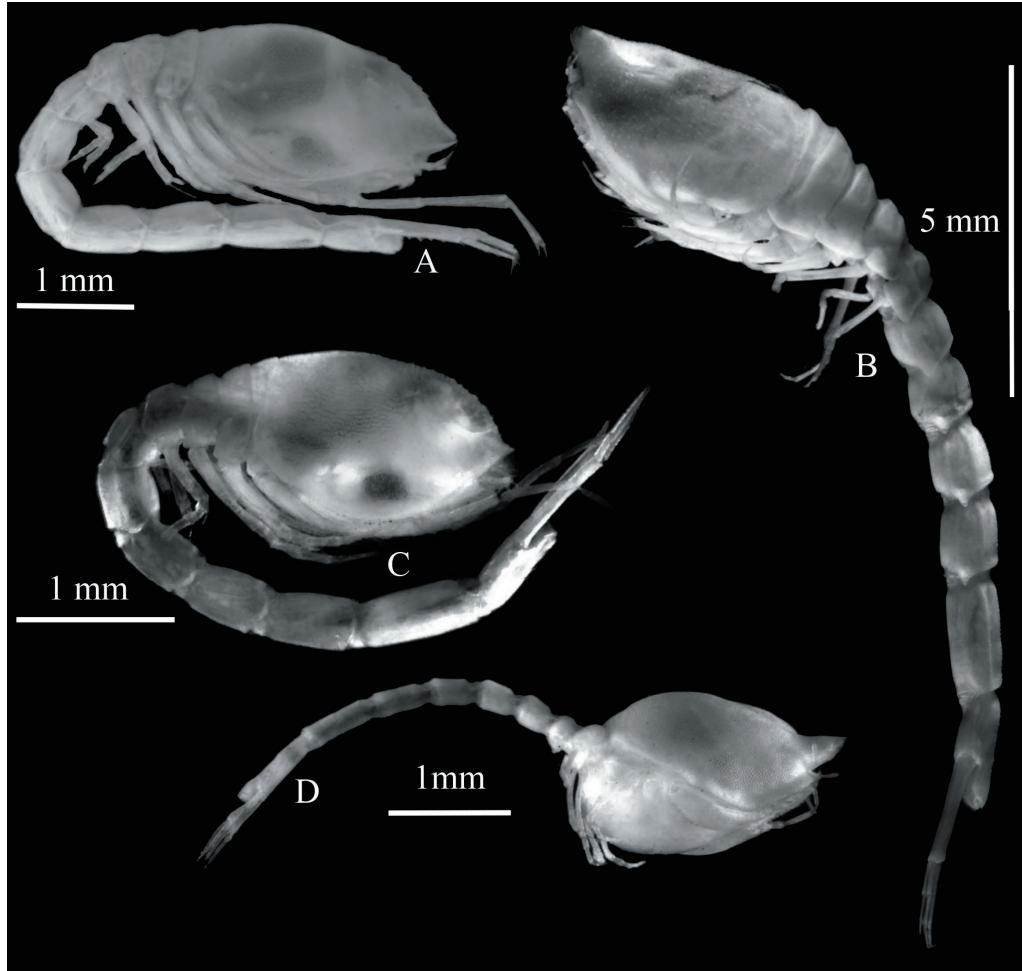
The family Diastylidae (Fig. 2) was presented by 13 species and 151 specimens. The members of the family Diastylidae are found throughout the world's oceans, and most of the described species come from depths greater than 1000 m (Jones 1969; Day 1980). Diastylidae from our material includes 9 species of the deep-sea genus *Makrokyllindrus* and 4 species from the genus *Leptostylis*. The *Leptostylis* sp. 3 was the most numerous in this family (41 specimens).

Family Lampropidae (Fig. 2) is presented most of all by singly found species (73 specimens of 10 species from the genera *Lamprops*, *Hemilamprops*, and *Paralamprops*) with the most numerous species in this family – *Paralamprops* sp. 1 (36 specimens). In this family, it is most of all singly found species.

The family Leuconidae (Fig. 2) the most numerous – 277 specimens from 11 species and 2 genera was found during the KuramBio: *Leucon* (10 species) and *Eudorella* (which possibly has been presented by a complex of species). The *Leucon* sp. 5 (103 specimens) and *Leucon* aff *spinulosus* (61 specimens) are the most numerous species.

Family Nannastacidae (Fig. 2) had the greatest number of species – 17 (127 specimens). 12 species belongs to the genus *Campylaspis* and 4 to genus *Cumella*.

Also one damaged specimen which is possibly will be identified as family Pseudocumatidae was found. Except for *Petalosarsia* and *Kerguelenica*, the cumacean family Pseudocumatidae is restricted to the Northeast Atlantic, Mediterranean, and the Ponto-Caspian region, including the Caspian Sea, Azov Sea, Black Sea and associated rivers (Bacescu, 1951, 1992; Ekman, 1953; Lomakina, 1958; Gerken, McCarthy, 2008; Jaume, Boxshall, 2008). In the north part of the Pacific Ocean only representatives of *Petalosarsia* were collected. Pseudocumatidae have been reported from shallow water, except for



**Fig. 3.** Cumacean family Bodotriidae collected during the KuramBio 2012 expedition: **A** – *Bathycuma* sp. 4; **B** – *Bathycuma* aff. *granulatum* Gamo, 1989; **C** – *Bathycuma* sp. 3; **D** – *Cyclaspoides* sp. 1.

a few species: *Monopseudocuma gilsoni* from the Northeast Atlantic is characterized by a wide depth range (Akiyama, Gerken, 2012); McCarthy et al. (2006) examined some specimens from 2200–2765 m depth in addition to specimens from 20–34 m depth, the two known species of *Kerguelenica* were collected from 195 and 1800 m depth (Gerken, McCarthy, 2008). Tadashi Akiyama and Sarah Gerken show that *Petalosarsia* was mostly deeper than 200 m (Akiyama, Gerken, 2012), but never found for the depth more than 3000 m. The authors consider that more detailed investigation of the Pacific is expected to reveal further undescribed deep-sea species of Pseudocumatidae (Akiyama, Gerken, 2012). But our finding family Pseudocumatidae from the KuramBio expedition need specification.

Preliminary results reveal that about 80% of species are new to science because of high level of an endemism. In contrast to the high species endemism, all genera and families are presented in other regions of the World Ocean. Although some specimens of these new species are immature or badly damaged because of pressure or fixation, their study will increase the knowledge of the deep-sea fauna. Among 57 species, 22 species were rare and met only at one station that can testify both on mosaic distribution, and on an insufficient covering the studied area by stations.

The analysis of distribution of Cumacea shows that the maximum number of specimens (193) were found at the station 3-9 (the western slope of the KKT), but the greatest species richness were at station 2-9 where number of specimens by one third lower (Fig. 1).

High number of specimens at station 3-9 was formed by families Leuconidae and Diastylidae and at the next station 2-9 by families Leuconidae, Nannastacidae and Bodotriidae. It indicates existence of spotty distribution with density increase almost in all families. The consistent pattern of increase in number of species with increase in quantity of the caught specimens isn't revealed (Fig. 1).

### Acknowledgements

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## **Distribution and diversity of sipunculans in the North-West Pacific**

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Sipuncula constitute a well distinguished small taxon of marine non-segmented worms with only a limited number of species that are reportedly widespread. The body of an adult sipunculan is divided into an unsegmented trunk and a retractable introvert. Commonly used externally visible taxonomic characters are the arrangement and number of the tentacles, the arrangement and structure of introvert hooks, and the distribution and shape of epidermal papillae. A relatively simple body plan that is conserved throughout the group limits number of taxonomically useful characters and gives sipunculans a bad reputation of the “difficult group” in terms of species identification.

Despite roughly 80 species (50%) of known sipunculans species were found in the Pacific Ocean, only a little number of species known from the North-West Pacific. Although, in some North-West Pacific shallow locations, sipunculans are dominant taxa both in terms of abundance and biomass (*Golfingia margaritacea* in Okhotsk Sea and *Phascolosoma agassizii* near Sakhalin). Sipunculans are also an important prey for many higher trophic species, including fish, grey whales and walruses (Cutler, 1994; Kedra, Grebmeier, 2012; Maiorova, Adrianov, 2013). They also play a significant role as bio-turbators of sediments and can transform suspension material from the water column, sediment interface, or sediment itself (Murina, 1984).

The main aim of this paper is to report on the current state of the sipunculan fauna in the North-West Pacific region and to attract attention to deep-sea species. A large number of benthic infaunal collections were made over the last years, allowing individual sipunculan species to be identified. After a number of revisions, 31 species became known from the Sea of Japan, 6 species from Bering and Chukchi Sea (Murina, Kholodov, 1985), 7 species from shallow waters of the Okhotsk Sea. On the contrary to well known shallow water sipunculans, in deep-sea areas of NWP in past years only 15 species were found. Some of the species recorded in deep-sea areas are well-known and widespread in the North Pacific trenches, abyssal flats and beyond, as had been reported in past publications, but only *Nephasoma confusum*, *Nephasoma vitjazi* and *Onchnesoma intermedium* had been previously cited from the single locations in the NWP.

New data were collected during KuramBio cruise in 2012 to abyssal floor near Kurile-Kamchatka Trench where five of the most widespread abyssal sipunculans were

found and *Golfingia muricaudata* was the most successful of them occurring at 8 out of 10 stations (Fig. 1). At two stations (#6 and #8), we collected five species (*G. muricaudata*, *Nephasoma minutum*, *N. diaphanes diaphanes*, *Phascolion lutense* and *P. pacificum*). *P. pacificum* was described originally from Kurile-Kamchatka Trench and known only at this area) (Fig. 2).



**Fig. 1.** *Golfingia muricaudata*, lateral view (with contracted introvert).



**Fig. 2.** *Phascolion pacificum*, lateral view (with contracted introvert).

However, at this moment the most unknown spot in sipunculan deep-sea diversity is deep area of the Okhotsk Sea and no any data are available. A new study of sipunculan diversity is necessary to reduce the knowledge gaps in the future as further data become available. To highlight potential geochemical importance of sipunculans as well as their role in sediment as bioturbators, there is a need to include sipunculan collecting in routine macrobenthic surveys. Despite their bad reputation of the “difficult group”, every effort should be made to increase the level of taxonomic expertise in this group in benthic studies.

### Acknowledgements

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**Preliminary analysis of the family Munnopsidae  
(Crustacea, Isopoda, Asellota)  
from the Kuril-Kamchatka Trench area**

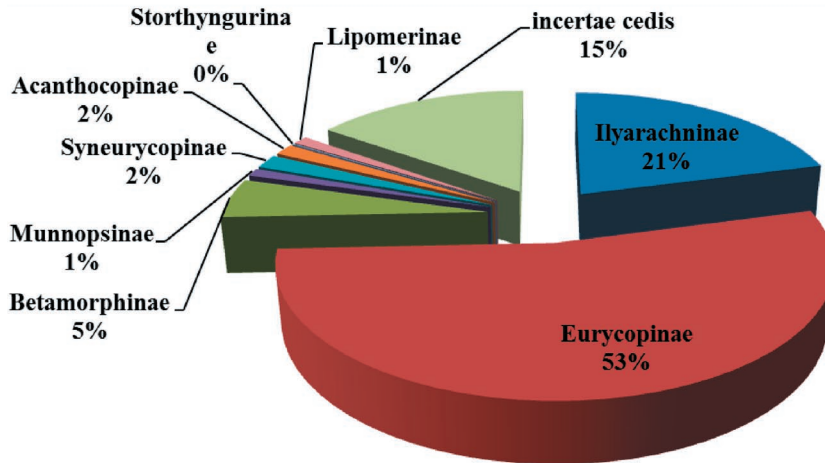
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The Kurile Kamchatka region, including the Kurile's bathyal, abyssal plain near the Kuril-Kamchatka Trench (KKT) and its hadal depths, was investigated by the RV *Vityaz* expeditions in the last century (Belyaev, 1983, 1989). As a result of the previous research 660 species of benthic organisms were discovered. Peracarida crustaceans of the order Isopoda were one of the most diverse taxon with about 100 species and 36 species, more than a third of the recorded isopods species for the area, belonged to the family Munnopsidae (Birstein, 1963, 1970, 1971). Munnopsidae was documented as a dominant family of deep-sea isopods faunas also in some other studied regions of the World Ocean (Wilson, Hessler, 1987; Wilson, 1989; Malyutina, Brandt, 2007).

One of the main goals and objectives of the joint German-Russian expedition KuramBio (Kurile Kamchatka Biodiversity Study) in summer 2012 to the KKT and the adjacent abyssal plain was investigation of biodiversity and distribution patterns of the deep-sea benthic fauna of the studied area. The epibenthic macrofauna collected by the camera-epibenthic sledge (C-EBS) was the most abundant and specious component of the sampled benthos. The C-EBS has been successfully deployed 21 times at 12 stations (2 deployments at each station) in 4830–5780 m depths. On board of RV *Sonne* the C-EBS samples were washed through 300 µm sieves and fixed in 96% precooled ethanol (first deployment) and in 4% formaldehyde (second deployment). The ethanol samples from the supranet catches of 11 stations have been sorted on board to high level taxa (class/order). Crustaceans superorder Peracarida was the second most abundant taxon after Polychaeta in the sorted supranet samples (23% of all individuals) The order Isopoda was the dominated within Peracarida (58% of all sampled peracarids). Almost all sampled isopods belonged to the suborder Asellota. The family Munnopsidae was the most abundant among 11 recorded deep-sea Asellota families at all sampled stations (58% of all isopod specimens).

Despite the fact, that just a quarter of all samples have been checked, the number of found species of the Munnopsidae is more than it was known before our expedition: 42 munnopsids species were identified from the sorted KuramBio materials and only 13 munnopsids species were known for this area in 5000–6000m depths interval. Therefore two thirds of the collected munnopsids species are considered as new for science. The most abundant subfamily in each station was Eurycopinae consisting a half of all munnopsids specimens (Fig. 1).



**Fig. 1.** Relative abundance of munnopsid subfamily from the sorted EBS supranet ethanol samples.

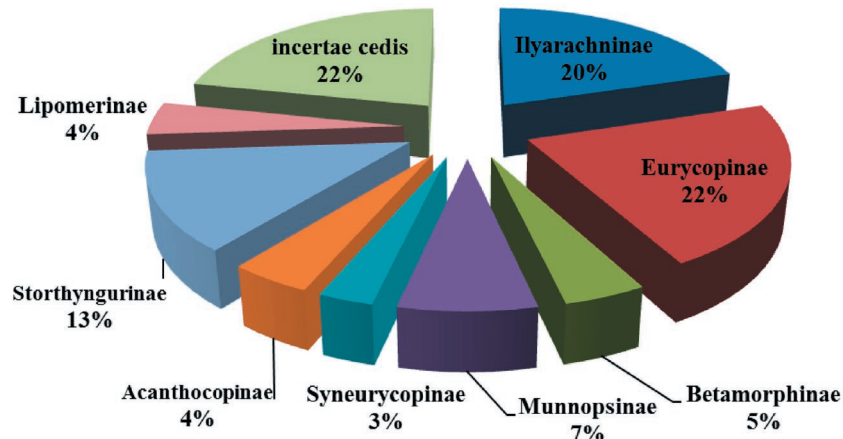
The preliminary analysis of the new and published data together revealed that the Munnopsidae fauna of the whole KKT area included not less than 67 species belonging to 8 subfamilies and 22 genera. The dominant munnopsids subfamilies are Eurycopinae with 15 species of the genera *Eurycope* (10 species), *Disconectes* sp. (3), *Belonectes* (1) and *Tytthocope*? (1) and Ilyarachninae with 14 species of *Ilyarachna* (6 species), *Echinozone* (5) and *Aspidarachna* (3) followed by Storthyngurinae (*Rectisura* (6), *Vanhoeffenura* (2), *Microprotus* (1)), Munnopsinae (*Munnopsis* (2), *Munnopsoides* (1), *Paramunnopsis* (1), *Acanthamunnopsis* (1)), Betamorphinae (*Betamorphia* (5)), Acanthocopinae (*Acanthocope* (3)), Syneurycopinae (*Syneurycope* (2)) and Lipomerinae (*Lipomera* (1 species), *Coperonus* (1) and *Mimocopelates* (1)). The *incertae sedis* genera: *Munneurycope* (7), *Munnopsurus* (3), *Microcope* (2) and *Munnicope* (2) are rather numerous group in the studied munnopsids fauna (Fig. 2).

Subfamily Lipomerinae, found in the Kurambio material, was recorded the first time for the North Pacific. It is an interesting fact, even it is a rare component of the fauna.

Some species with unclear position between genera and even subfamilies have been found: “strange *Eurycope*”, “strange *Munneurycope*”, *Munnopsurus–Tytthocope*, *Tytthocope–Mimocopelates*.

The preliminary work with the part of the collected material already revealed that the number of the collected species of Munnopsidae is more than it was known before the KuramBio expedition and most of the species of the sampled fauna are new for science. The similarity between the Munnopsidae fauna of the KKT area and the munnopsids from the Weddell Sea (Malyutina, Brandt, 2007; Malyutina, 2008) was observed. Not only the compositions of the subfamilies and genera are comparable, but also some morphologically very similar species were found like species *Microcope*, *Betamorphia*, some similar intermediate new genera.

*Analysis of the family Munnopsidae (Crustacea, Isopoda, Asellota)*



**Fig. 2.** Percentage of species richness of munnopsids subfamilies (KuramBio and published data together).

Since the most part of the material is still in a sorting process in the Zoological Museum in Hamburg and will be available for study in September–October 2013 most likely that the rest of the samples will contain more species, both known and new ones.

### Acknowledgements

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## **Decapod crustaceans (Arthropoda: Crustacea: Decapoda) of KuramBio 2012 expedition**

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Study of the diversity of decapod crustaceans (Arthropoda: Crustacea: Decapoda) from Russian Far-Eastern seas started at the first half of the 20<sup>th</sup> century. Deep water decapod crustaceans of Kuril-Kamchatka Trench and adjacent area was firstly studied during Russian expeditions at 50–70<sup>th</sup> years of the last century (e.g. Vinogradov, 1950; Birstein, Vinogradov, 1951, 1953; Marin, 2013). But since that time no additional freshly collected material has been collected that why material from German-Russian Expedition KuramBio 2012 is in great scientific interest. Sampling was accomplished by RV *Sonne* with the help of trawl (OST) at the depths of 4700–5500 m and the superior layer of the water when it goes up.

### **Preliminary Results**

Totally, 33 specimens of decapod crustaceans (Arthropoda: Crustacea: Decapoda) belonging to 8 species (preliminary identification) were collected at abyssal plain near Kuril-Kamchatka Trench. They are *Acanthephyra quadrispinosa* Kemp, 1939 (Acanthephyridae), *Hymenodora frontalis* Rathbun, 1902 (Acanthephyridae), *Hymenodora* cf. *gracilis* Smith, 1886 (Acanthephyridae), *Hymenodora gracilis* Smith, 1886 (Acanthephyridae), *Plesiopenaeus armatus* (Spence Bate, 1881) (Aristeidae), *Hemipenaeus spinidorsalis* Spence Bate, 1881 (Aristeidae), *Benthescymus* sp. (Benthescymidae), *Bentheogennema borealis* (Rathbun, 1902) (Benthescymidae), *Bentheogennema-Genadas* sp. (Benthescymidae). Most species are pelagic shrimps mostly living at the range of depths 500–3000 m and were caught during the ascent of the trawl, while 2 species, *Plesiopenaeus armatus* and *Hemipenaeus spinidorsalis*, are bathypelagic living close to the bottom (see Table and Fig.).

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*Decapod crustaceans (Arthropoda: Crustacea: Decapoda)*

**List of decapod crustaceans collected at abyssal plain near Kuril-Kamchatka Trench**

Station	Species name	Number of specimens and station trawl number
Station 1 (4 species, 10 specimens)	<i>Sergestidae</i> gen. sp.	1 highly damaged specimen (1-13)
	<i>Hymenodora gracilis</i>	3 specimens (1-12, 1-13)
	<i>Bentheogennema borealis</i>	4 specimens (1-12, 1-13)
	<i>Hymenodora glacialis</i>	2 specimens (1-12)
Station 3 (1 species, 1 specimen)	<i>Plesiopenaeus armatus</i>	1 male (3-10)
	<i>Hymenodora frontalis</i>	2 specimens (5-11)
Station 5 (2+ species, 6+ specimens)	<i>Hemipenaeus spinidorsalis</i>	4 specimens (1 spec, 2 females, 1 male) (5-11, 5-12)
	? <i>AcanthePHYra</i> sp.	1 carapace (5-11)
Station 6 (1 species, 1 specimens)	<i>AcanthePHYra quadrispinosa</i>	1 female (6-10)
Station 7 (1 species, 1 specimens)	<i>Hemipenaeus spinidorsalis</i>	1 male, 1 female (7-11)
Station 8 (1 species, 1 specimens)	<i>Hymenodora frontalis</i>	1 specimen (8-11)
	Megalopa of Lithodidae	1 specimen (8-11)
Station 9 (1 species, 1 specimens)	<i>Hemipenaeus spinidorsalis</i>	1 female (9-11)
Station 10 (5 species, 6+ specimens)	<i>Benthesicymus</i> sp.	1 female+1 damaged specimen (10-11)
	<i>AcanthePHYra quadrispinosa</i>	1 female (10-11)
	<i>Hymenodora frontalis</i>	1 specimen (10-11)
	<i>Hymenodora</i> cf. <i>gracilis</i>	1 specimen (10-11)
	<i>Bentheogennema-Gennadas</i> sp.	1 male, 1 female (10-10)
Station 11 (2 species, 2 specimens)	<i>Bentheogennema borealis</i>	1 specimen (11-10)
	<i>Hymenodora</i> cf. <i>gracilis</i>	1 specimen (11-10)
Station 12 (3+ species, 3+ specimens)	<i>Plesiopenaeus armatus</i>	1 female (12-5)
	? <i>Hemipenaeus spinidorsalis</i>	1 abdomen (12-5)
	<i>Hymenodora frontalis</i>	1 specimen (12-5)
	<i>AcanthePHYra quadrispinosa</i>	1 male (12-5)



Alive coloration of deep water shrimps collected during KuramBio 2012 Expedition: **1** – *Plesio-  
penaeus armatus* Bate, 1881, **2** – *Hemipenaeus spinidorsalis* Bate, 1881, **3** – *Bentheogennema borealis*  
(Rathbun, 1902), **4** – *Sergia* sp.

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**Preliminary report on deep-sea  
Holothuroidea, Asteroidea and Echinoidea  
collected in KuramBio expedition**

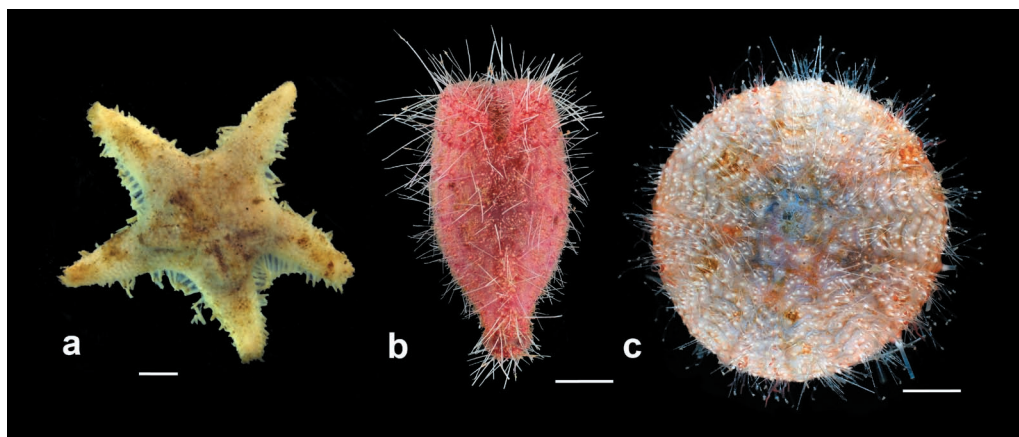
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Echinoderms are among the most common and abundant taxa of benthos at abyssal depths, especially among megafauna. Extensive collections of deep-sea echinoderms from the North-West Pacific, the Kuril-Kamchatka Trench and surrounding area were obtained in the 2<sup>nd</sup> half of the 20<sup>th</sup> century by series of expeditions of the P.P. Shirshov Institute of Oceanology on research vessels *Vityaz*, *Dmitry Mendeleev* and *Akademik Kurchatov*. Based on this material, numerous new species were described, several taxonomic revisions and reviews of a number of taxa of echinoderms were published (Belyaev, 1969, 1989; Mironov, 1971, 1976, 1995, 1997; Korovchinsky, 1976; Gebruk, 1983, 1990; Korovchinsky, Galkin, 1984; Belyaev, Moskalev, 1986a, b; Belyaev, Mironov, 1993; Golotsvan, 1998). Nevertheless, the abyssal fauna of this region remains far from being well known. Recent German-Russian expedition KuramBio to the Kuril-Kamchatka Trench area obtained new abyssal samples which are currently being analysed. Modern sampling gears such as epibenthic sledge equipped with cameras (Brenke, 2005) provided unique material which was hard to obtain with sampling methods of previous expeditions.

Preliminary results are based on processing 14 specimens of holothurians, 66 specimens of sea urchins and 18 specimens of sea stars, collected from 15 trawl samples, 2 grab samples and 6 epibenthic sledge samples. Examination of the asteroid specimens revealed 12 species. Of these species, four are new for the Kurile-Kamchatka region, and one seems to be a new to science. The most interesting finding is a specimen of *Pteraster ifurus* Golotsvan, 1998 (Fig. 1a), described originally from the Kurile-Kamchatka Trench based on only two specimens. Among holothurian specimens examined 8 species were found. At least two of them (*Peniagone* unknown sp. 1, *Peniagone* unknown sp. 2) are new to science and two belong to combined species requiring taxonomic revision (*Psychropotes longicauda* Théel, 1882 and *Peniagone purpurea* (Théel, 1882)) (Fig. 2). In the KuramBio samples echinoids are characterized by a lower number of species than asteroids and holothurians. Only 5 species of sea urchins are found. One of them, *Pourtalesia heptneri* Mironov, 1978 (Fig. 1b), is found in Kurile-Kamchatka Trench area for the first time. Previously this species was known only from Banda and Palau trenches (Mironov, 1995). Another species, *Kamptosoma* cf. *abyssale* Mironov, 1971 (Fig. 1c), requires taxonomic revision.





**Fig. 1.** Asteroids and echinoids from KuramBio samples: **a** – *Pteraster ifurus* Golotsvan, 1998, station SO223 3-10; **b** – *Pourtalesia heptneri* Mironov, 1978, station SO223 12-2; **c** – *Kamptosoma abyssale* Mironov, 1971, station SO223 12-5. Scale length is 5 mm. Figures 1b and 1c: © A. Maiorova, 2012/IMB FEB RAS.



**Fig. 2.** Holothurian *Psychropotes longicauda* Théel, 1882, on the seafloor of the Kurile-Kamchatka Trench area. © N. Brenke, 2012/UHH, funded by BMBF, Germany, project KuramBio.

Record of two trench species (sea star *Pteraster ifurus* and echinoid *Pourtalesia heptneri*) at the abyssal plain is of particular interest. Both species were previously known only from hadal depths. The work on KuramBio samples is being continued.

This study was supported by the FEB RAS grant 12-I-P30-07.

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## **The geochemical features of the deep-sea sediments from the Northwestern Pacific**

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The deep basins are of particular interest attracting the attention of researchers to their structure and geography. Such basins in the ocean are not numerous and most of them are located in the Pacific Ocean, mostly on its western margin.

The Kuril-Kamchatka Trench is one of the Pacific trenches, conjugated with the structures of the island arcs. It is a kind of area of deep-sea sediment formation, which has some features in common with the sedimentation in the marginal seas, and with the oceanic pelagic sedimentogenesis, but at the same time, characterized by a number of significant features. The conditions of sedimentation are determined by the morphological features, modern tectonic and volcanic processes and the hydrological regime and high biological productivity of waters. Earlier, the Kurile-Kamchatka Trench from its bathyal to maximum depths was investigated in cruises on RV “Vityaz” in 1949–1957 and 1966 (Bezrukov, 1955; Udintsev, 1955; et al.). The studies of the past years have provided the limited data on geochemistry of the sediments. The aim of this research was a detailed study of the deep-sea sediments sampled in the German-Russian expedition on RV “Sonne” (SO 223) near the Kurile-Kamchatka Trench.

The actual material is the deep-sea sediments, selected using 12 glasses of multicorer. These samples of the deep-sea sediments were pre-dried at 25–30°C and milled in an agate mortar to particle sizes less than 0.063 mm.

Analysis of the grain composition of samples was carried out on a laser particle size analyzer “ANALYSETTE 22” (FRITSCH, Germany) according to a proven technique (Botsul, 2002). The content of total organic carbon was determined on an analyzer “TOC-VCPN” with the attachment for the incineration of solid samples SSM-5000A. The relative standard deviation in the combustion of total carbon was 1.5% and inorganic carbon – 2.0%. Silica was determined by gravimetric method based on a precise measurement of the mass of poorly soluble siliceous compound. The matrix elements were determined by atomic emission spectrometry with inductively coupled plasma spectrometer “iCAP 6500Duo” (Thermo Electron Corporation, USA) with the addition of an internal standard solution of cadmium ( $10^{-4}\%$  concentration). The correct determination of the elements of the analysis is confirmed by the standard samples: OOPE 402 (siliceous ooze) OOPE 201 (mud volcano-clastic).

The general chemical composition of the surface layer (0–1 cm) of deep-sea sediments is presented in Table. The content of silica in the sediments ranges 56.70–68.12% that reflects the high biological productivity of surface waters. The high concentration

Location, depth and main chemical composition of the sediment samples (%)

Stations no.	Location		Sea depth (m)	Type of sediments	SiO <sub>2</sub>	Al	Fe	Mn	Ti	Mg	Ca	Na	K	P
	Lat. N	Long. E												
1(A1)	43°58,190'	157°19,796'	5412	Clayey silt	61.14	1.38	3.31	1.31	5.90	1.38	0.39	3.94	0.06	0.26
2(A2)	46°14,024'	155°33,100'	4869	Clayey silt	61.39	1.59	3.75	1.28	5.97	1.50	0.36	3.61	0.05	0.31
3(A3)	47°14,261'	154°42,319'	4976	Silt	60.63	1.83	3.60	1.09	5.38	1.58	0.15	3.98	0.06	0.30
4(B1)	46°58,001'	154°32,703'	5767	Clayey silt	58.48	3.06	4.94	1.07	6.91	1.88	0.19	3.29	0.07	0.42
5(B2)	43°34,990'	153°57,964'	5378	Clayey silt	61.74	1.56	3.12	1.25	5.84	1.24	0.30	4.14	0.05	0.25
6(C2)	42°29,002'	153°59,905'	5297	Clayey silt	59.33	1.65	3.15	1.40	6.38	1.28	0.32	4.49	0.05	0.27
7(C1)	43°02,217'	152°59,129'	5222	Silt	68.12	1.67	2.46	1.17	6.57	0.75	0.21	3.66	0.04	0.19
8(D3)	42°14,614'	151°43,506'	5127	Silt	64.72	1.94	2.64	1.21	6.41	0.89	0.28	3.94	0.04	0.22
9(D1)	40°35,012'	150°59,630'	5401	Clayey silt	57.95	0.97	3.36	1.63	5.95	1.39	0.95	3.77	0.07	0.27
10(D2)	41°11,985'	150°05,718'	5251	Silt	—	0.93	1.17	1.07	2.01	2.04	0.32	13.40	0.04	0.09
11(E1)	40°12,891'	148°06,042'	5349	Clayey silt	56.06	0.94	3.05	1.35	5.11	1.32	1.02	4.44	0.05	0.24
12(E2)	39°43,417'	147°10,014'	5229	Clayey silt	61.29	1.00	3.12	1.31	5.20	1.27	0.60	3.97	0.06	0.24

of total organic carbon is marked at several stations with a maximum (1.55%) at station 3(A3) (Fig. 1). The sediments from station 4(B1) are characterized by a maximum content of lithophile elements, probably coming with the products of erosion of submarine outcrops.

According to the composition of grains the sediment are silt and clayey silt, mainly diatom ooze. Together with geochemical methods in the surface sediments were determined a quantitative content of diatoms and their species composition (Fig. 2). In the result of diatom analysis was found that the basis of diatom complexes (up to 100%) make up the oceanic species. The main dominant group in the complexes of all stations was represented by the species *Neodenticula seminae*, *Thalassiosira latimarginata*, *Rhizosolenia hebetata* f. *hiemalis*, *Thalassiothrix longissima*, *Coscinodiscus marginatus*, *Actinocyclus curvatulus*.

Also in the diatom complexes at stations 3(A3), 9(D1), 10(D2), 11(E1), 12(E2) were met a neritic cold-water species *Thalassiosira antarctica* and *T. gravida*, represented mainly by spores. These species are indications of the low temperature of water, high salinity and habitat of sheet-ice for a long time (Cremer, 1998). They are common in early spring plankton of the Arctic and sub-Arctic waters (Makarova, 1988; Polyakova, 1997). It has been recorded in the sediments of some stations the spores *Chaetoceros*. In the northern regions of the Pacific Ocean the abundance of species of this genus is an indicator of high productivity of surface waters and unstable hydrological situation (Lopes et al, 2006).

In the sediments of 2 stations 11(E1), 12(E2) was marked a significant part of littoral species *Odontella aurita*. The finds of this species in the deep-sea sediments indicates a freshening of surface water or the effect of a strong onshore flow. Most likely it is connected with the inflow of water from the Far Eastern seas in the ocean through the Kamchatka Strait and the middle and southern Kuril straits.

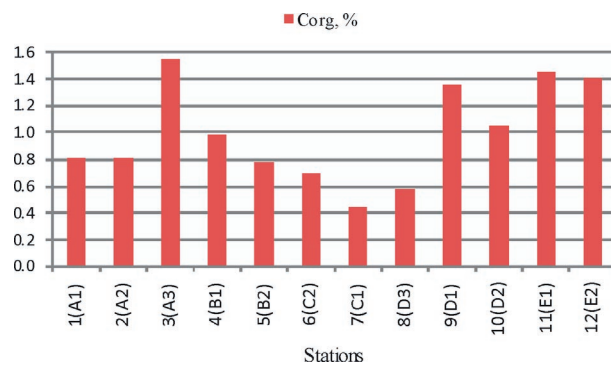


Fig. 1. The content of total organic carbon in sediments.

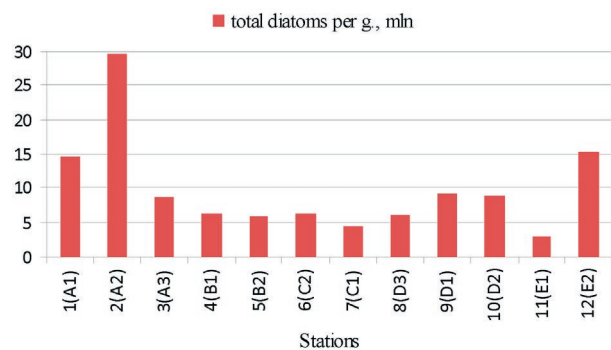


Fig. 2. The content of diatoms in 1 g of air-dried sediment.

### Acknowledgments

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## **Is the northern Pacific a radiation centre for the chitonophilid copepod – mollusc association?**

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### **Introduction**

Parasitism in marine invertebrates is mainly studied as side effect of systematic analyses of linked host taxa. One of the major taxa infesting marine invertebrates is the crustacean subclass Copepoda. The parasitic forms of this group show a broad variety of adaptations to their relevant host from the loss of appendages to complete hypermorphosed body shapes.

Within the copepods, the family Chitonophilidae comprises of nine recognized genera with a total of 19 described species, surprisingly all restricted to mollusc hosts, namely Gastropoda and Polyplacophora (Huys et al., 2002; Avdeev, Sirenko, 2005). Further ten taxa attend a throughout study; of these, most were recognized as copepods by a restudy of deep-sea limpets formerly thought to be brooding.

Chitonophilids are well-adapted copepods and show an extreme sexual dimorphism. Females are usually hypermorphosed without external segmentation, reduced to a well-developed rootlet system (endosoma) with a variable shaped trunk (ectosoma). In mesoparasitic forms they may be found in the host's pallial cavity or, in endoparasitic forms, entirely in the viscera of its host. Males are distinctly smaller than females, not segmented, with either antennae or maxillipeds as the only appendages. In mesoparasitic females eggs are usually connected to the genital openings by individual egg strings, while endoparasitic forms have eggs laying freely in cysts or tubes (Huys et al., 2002). Chitonophilids occur from the splash zone down to abyssal depths and show a world-wide distribution, but records from the Indian Ocean are to date missing (Avdeev, Sirenko, 2005). The majority of involved taxa are recognized from the Northern Pacific Ocean, whereupon polyplacophoran associated taxa dominate: besides a single specimen currently studied by the author, which was found in a deep-sea limpet during the SoJaBio expedition, and a yet undescribed species from a chemosynthetic environment in the NE Pacific deep-sea (Tunnicliffe et al., 2008), no further confirmed records of gastropod-infesting chitonophilids are known from the Northern Pacific. On the one hand, being one of only two records makes the SoJaBio specimen something of a rarity. Moreover, the scarcity of records describing gastropod-infesting chitonophilids also raises the question whether the NW Pacific region serves as a diversity centre of forms which exclusively infest polyplacophorans. However, as indicated above, gastropod-associated chitonophilids have in the past been misinterpreted as gastropod egg clusters. These facts make an interpretation of Pacific chitonophilid distribution and diversity insufficient and further thorough studies are required.

### Preliminary Results

The chitonophilid under study still needs a detailed SEM study for a final identification. External characteristics, however, clearly distinguish the copepod from the undescribed material mentioned by Tunnicliffe et al. (2008) from the NE Pacific Ocean. The latter was collected from the Explorer to Juan de Fuca Ridges infesting the afferent branchial vein of *Lepetodrilus fucensis* McLean, 1988 – a hot-vent species. Huys et al. (2002) demonstrated that brooding records in deep-sea limpets mainly refer to infections by chitonophilid copepods. That is why, the “brooding” records of *Bathyphytophilas diegensis* Haszprunar et McLean, 1996 (p. 37, fig. 1) from Mexico, Baja California, off Tijuana and of *Caymanabyssia vandoverae* McLean, 1991 (see Huys et al., 2002: 212) off Oregon could also be unconfirmed chitonophilid records from the NE Pacific.

### Chitonophilidae gen., sp.

**Locality:** Sea of Japan, B7-8, 43°13.5215' N, 135°04.3071' E – 43°13.6778' N, 135°04.4447' E; 532 m depth, 25.08.2010, trawl.

**Host:** *Lepeta caeca* (Müller, 1776) (Lepetellidae) (see Fig.).

**Position in host:** Mesoparasitic in the cephalic region of the mantle cavity of the host. Penetration between the host's tentacles in the neck.

**Remarks to station:** A remarkable feature in faunal composition was the high density of scaphopods at the shallow station B7-8 (532 m), where 59 individuals were found. This station was characterized by sediment which was made up of a high amount of soft material mixed with stones.

Brandt et al. (2013, fig. 5) provide a seafloor image from the nearest EBS Station, check their also for species composition. A-biotic factors obtained by Aandera SEA-GUARDS (for details see Brandt et al., 2013) are as follows: temperature 0.6°C, max press. 6324, 24 kPa, oxygene about 263.5 µMol. The latter value might be influenced by the steel frame of the gear.

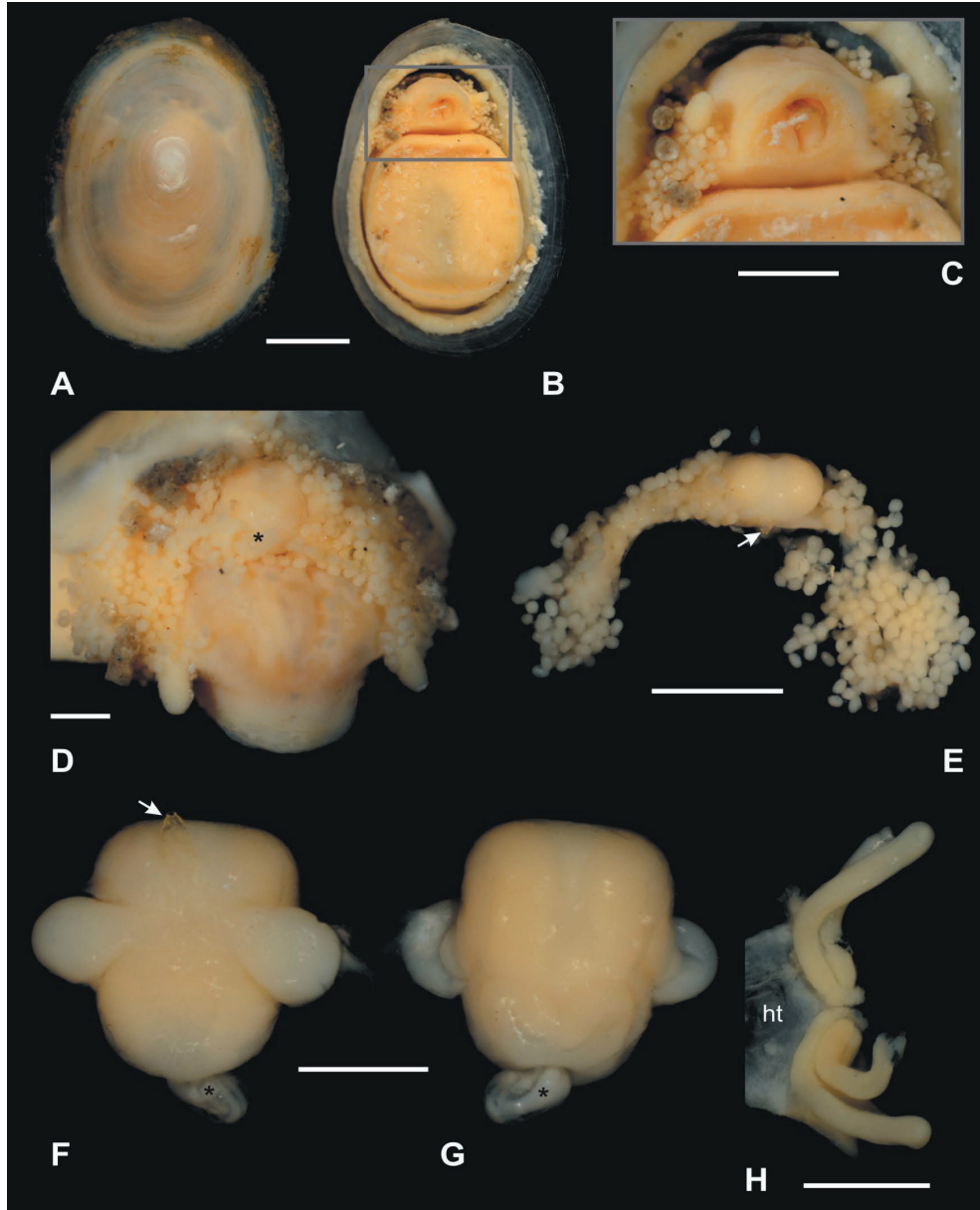
### Short description

A single female was found attached to the neck of the gastropod. Ectosoma squarish with globular lateral lobes, with ventro-lateral genital openings. Branching rootlets (6) short and tubular. Neck sharp-pointed, conical. One male posteriorly attached (not yet examined), Eggs on individual strings, forming cluster that perfectly matches the shape of the host's neck.

Despite the lack of a thorough study of the material at hand, the morphology of the chitonophilid female distinguishes it from both described mesoparasitic forms infesting gastropods: the NZ species *Cocculinika myzorama* Jones et Marshall, 1986 and from the North Atlantic *Lepetellicola brescianii* Huys, López-González, Roldán et Luque, 2002. *L. brescianii* has a heart shaped ectosoma with elongated lateral lobes, with genital openings situated posteriorly. This species also has an elongated parallel sided neck.



*Is the northern Pacific a radiation centre for the chitonophilid copepod?*



**A, B**, the host species *Lepeta caeca* (Müller, 1776): **A**, dorsal view; **B**, ventral view, inlet indicates the host's cephalic region with the mesoparasitic chitonophilid; **C**, enlargement of fig. B (inlet) to show the egg cluster of the parasite; **D**, the host species in frontal view (shell removed), in the host's neck is the ovigerous female of the chitonophilid located, asterisk indicates the male; **E**, isolated female copepod with attached eggs, frontal view, arrow indicates the host penetrating neck; **F, G**, ectosoma of the female chitonophilid with removed eggs, **F**, ventral view, **G**, dorsal view, arrow indicates the neck, asterisks indicate the attached male; **H**, endosoma (rootlets) of the female parasite, ht – host tissue. Scale bars: A, B, 2 mm, C, E, H, 1 mm, D, F, G, 500  $\mu$ m.

### Work at Sea

Taken the above mentioned into account, the upcoming SokhoBio and KuramBio II expeditions provide a unique possibility to not only conduct a more detailed study of potential host taxa, but also to fix chitonophilids in a variety of solutions allowing detailed studies: genetic material might serve as source for a phylogenetic analysis and species separation and histological material may allow 3-D reconstructions for a better understanding of morphologic adaptations the parasites undergo to successfully infest their hosts. The material will be analysed in the sense of parasite-host intensity, as well as bathymetric and geographic distribution. Whenever possible, special attention will be paid to developmental stages of the parasite, preferably from eggs via various naupliar stages to the hypermorphosed adults. Especially data on nauplius larvae may also shed light on the systematic position of some of the involved taxa, of which often only the adults and eggs are known.

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## First morphological and molecular results of meiofauna biodiversity in the Kurile-Kamchatka region

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During the expedition SO225 (Kurile-Kamchatka deep sea region, Pacific Ocean) 12 stations were sampled using the multiple corer (MUC). 351 benthic samples for molecular and morphological meiofauna studies and 175 samples for sediment analysis were collected.

First, the benthic organisms were extracted from the sediment. For the quantitative detection of meiofauna taxa all organisms were stained with rose bengal and then counted under a stereo-zoom microscope. Adult copepods were sorted out from the samples and identified up to family level. However, it is aimed to determine genus or species level in the future. The families found in the present study have also been reported in the study of Kitahashi et al. (2012). Table shows an overview of copepods orders and families found in the KuramBio multiple corer samples. Biogeographically interesting is the fact, that two cyclopoid copepods, namely *Cyclopicina sirenkoi* and *Einslepinella mediana* were found in the present study, which have been originally described from the Laptev Sea (marginal sea of the Arctic Ocean). This demonstrates a faunal exchange between the Arctic and the Kurile region (station D3) (Martinez Arbizu 1997, 2006).

The taxa found in the MUC samples are mainly nematodes (92%). Among all stations copepods were found most dominant at station A3. Beside the typical taxa, also some free-living Tantulocarida could be identified. These parasites have an interesting life cycle and are still poor studied (Boxshall, Lincoln, 1987). One future aim is to make some pictures on confocal microscope. Other taxa found in the MUC samples were Kinorhyncha, Gastrotricha, Ostracoda, Tanaidacea, Priapulida, Bivalvia, Tardigrada, Loricifera and Isopoda.

Overview of Copepoda orders and families found in the KuramBio samples

Order	Families Overview
Calanoida	Not specified
Cyclopoida	Cyclopicinidae
Harpacticoida	Aegisthidae Ameridae Argestidae Canthocamptidae Cletodidae Ectinosomatidae Idantidae Pseudotachidiidae Zosimeidae

Organisms used for the molecular part of the study were not stained and counted. In these samples all adult copepods were initially picked. The sorted copepods were photographed and then extracted. Thereafter, the nuclear and mitochondrial gene 12S and 28S gene was amplified. In contrast to the mitochondrial DNA, nuclear DNA shows low sequence variability between species, which allowed an inter-specific comparison to investigate phylogenetic relationships. The amplicons were sequenced in the following by a company in the Netherlands, named Macrogen. After the sequences were processed using the software Geneious and compared with the Genebank using BLAST. The sequences were analyzed using MEGA and CD hit. A total of 500 extractions and amplifications have been performed and 84 usable sequences were previously evaluated. The preliminary results of the sequences show a very diverse fauna, but also meet the expectations. By using the 28S gene it could be shown that the same species was discovered at two different stations (station C2 and A1). The species is not described until now. Furthermore, the same genus (*Cerviniella*) was detected three times at the following stations: C2, A1, A2.

Moreover, at three copepods the food sources in the stomach was identified by using the 28S gene amplification. After comparing with the genebank, the diatom *Chaetoceros* sp. could be identified. The results of the sequences of the 12S gene segment show more diverse results as the 28S gene. All copepods are different species and genera in the studied samples so far. But there was a large Ectinosomatidae cluster which indicates that this family is the most abundant in the Kurile region. A first comparison with the paper by Kitahashi et al. (2012) supports this assumption. It has yet to prove whether this statement is to support.

Currently, sediment analyzes are performed to determine the particle sizes. These data for sediment texture in the Kurile region will provide some interesting results, as the Kurile region has not been adequately studied in this field. In addition, there are some interesting correlations between distribution patterns of animals and sediment texture. Kitahashi et al. (2012) postulated that the sediment properties even play a key role in the Kurile-Kamchatka-region. It is also planned to analyze pigments and C-/N-content of the sediment. This will give interesting insights to food availability for example. This study was supported by the grants FEB RAS 12-I-P30-07 and DAAD A13/00417.

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