

China - Russia Bilateral Symposium

PROCEEDINGS OF CHINA - RUSSIA BILATERAL
SYMPOSIUM ON“COMPARISON ON MARINE
BIODIVERSITY IN THE NORTHWEST PACIFIC OCEAN”



Institute of Oceanology, Chinese Academy of Sciences

A.V. Zhirmunsky Institute of Marine Biology,

Far East Branch of the Russian Academy of Sciences

10-11 October 2010 Qingdao, China

Conference Conveners



Institute of Oceanology, Chinese Academy of Sciences

Professor Song Sun
Professor Ruiyu Liu



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

Professor Andrey Adrianov
Professor Konstantin Lutaenko

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Asian-Pacific Network for Global Change Research

Secretary

Dr. Xiaoxia Sun

Tel: +86 532 82898599 Fax: +86 532 82868008

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

Dr. Mengtan Liu

Tel: +86 532 82898925

E-mail: liumengt@163.com

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Preface

The United Nations declared 2010 to be the International Year of Biodiversity. It is a celebration of life on earth and of the value of biodiversity for our lives. The world is invited to take action in 2010 to safeguard the variety of life on earth: biodiversity (see: <http://www.cbd.int/2010/about/>). Biological diversity - or biodiversity - is the term given to the variety of life on Earth and the natural patterns it forms. This diversity is often understood in terms of the wide variety of plants, animals and microorganisms. About 1.75 million species have been identified; scientists reckon that there are actually about 13 million species, though estimates range from three to 100 million (<http://www.cbd.int/2010/biodiversity/>). Both Institute of Oceanology, Chinese Academy of Sciences and A.V. Zhirmunsky Institute of Marine Biology, Far East Branch of the Russian Academy of Sciences played an important role in the study of marine biodiversity in the Northwest Pacific Ocean. The collaboration between the two Institutes is more and more important to reveal the changes on marine biodiversity and resources under the pressure of the global change in the Northwest Pacific Ocean.

With the support of the External Cooperation Program from Chinese Academy of Sciences (GJHZ200808) and the APN project, a series of research on marine ecology and biodiversity in the Northwest Pacific Ocean were conducted in both Institutes in recent years. In order to mark the progress in the last two years, we decided to hold a bilateral workshop on “Comparison of Marine Biodiversity in Northwest Pacific Ocean”. We held similar joint workshop in 2007. The proceedings were published: K.A. Lutaenko (Ed.). Biodiversity of the Marginal Seas of the Northwestern Pacific Ocean: Proceedings of the Workshop, Institute of Oceanology CAS, Qingdao, China, November 21-23, 2007. Qingdao: IOCAS, 2007. 105 pp. This time, the workshop will focus on comparison research between benthos communities along the Northwest Pacific coast, and the relationship between plankton distribution and climate change. Based on this, the effect of global change on coastal biodiversity, and the effect of biodiversity change on marine biological resource will be understood further. More than 30 scientists will participate in the workshop, and we would like to share important research findings among two countries. The output of this workshop is expected to provide scientific support for the development and management of the Northwest Pacific coastal ecosystems.

Conveners,
October, 2010

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BIVALVE MOLLUSCAN BIOGEOGRAPHY OF THE JAPAN SEA: AN OVERVIEW

Konstantin A. Lutaenko

A.V. Zhirmunsky Institute of Marine Biology, Far East Branch of the Russian
Academy of Sciences, Vladivostok 690041, Russia

E-mail: lutaenko@mail.primorye.ru

The Japan Sea – a marginal, deep basin enclosed by an island arc which separates it from the Pacific Ocean. The sea is directly connected with the Sea of Okhotsk by the Tatarsky (Mamiya) Strait, with the East China Sea by the Tsushima and Korea Straits (between Korea and Kyushu Island). Tsugaru (between Honshu and Hokkaido) and La Perouse (or Soya; between Sakhalin and Hokkaido) Straits connect the sea with the Pacific Ocean. The sea is rather isolated as the straits mentioned are shallow; the maximum depth of Korea Strait is 150 m, and Tsugaru Strait, 200 m; Nevelskogoko Strait (northernmost Tatarsky Strait) has a sill depth of 5 m, La Perouse Strait, 53 m. This suggests that the deep basin of the East/Japan sea has no exchange with deep Pacific waters (the maximum depth of the sea is 3695 or 3670 m in its eastern part). The East/Japan Sea is unique among the enclosed seas of the northwestern Pacific in having strong ocean currents in the form of powerful streams. The sea is divided by frontal zone (or “polar front”) into two distinct areas: the southeastern warm-water area washed by the Tsushima Current with three branches, and the northwestern area dominated by the cold Liman(ian), Primorskoye and North Korean Currents. This division is clearly reflected in the biota and biological production of the sea.

Biogeographically, the Japan Sea belongs to two regions (geographical zones/subzones): boreal (=temperate) and subtropical. We still do not know how many species of bivalve mollusks inhabit the sea – it is perhaps at the level of 300-500 based on indirect estimates. According to literature data, species richness of bivalve molluscan faunas in large bays and other localities of the Japan Sea varies from 88 (Vostok Bay, Russian sector) to 211 (Sado Island, Japan) (Table 1). Kafanov (1991) calculations show that there is a latitudinal gradient in bivalve distribution in Japan: in its southern part (36 °38' N) more than 250 species are found, while in the northern part (46 °47' N) less than 50 species are known (Fig. 1). Crame (2000) estimated that about 256 living species exist in the Far Eastern Russia (Sea of

Okhotsk, Kamchatka, Sakhalin, northern Sea of Japan, and part of the Bering Sea, i.e., between 43° and 66°N); Scarlato (1981) in his comprehensive monograph on the bivalves of temperate latitudes of the NW Pacific listed 279 species and subspecies. Kafanov (1991) stated that more than 540 species and subspecies of the Bivalvia live in the “Japanese-Manchurian Subregion of the North-Pacific Region” which includes most of the East/Japan Sea (except for its southern part), Pacific side of northern Honshu, Hokkaido, and southern Sakhalin.

Table 1 Species richness of bivalve molluscan faunas in bays and some other localities in the East/Japan Sea

Locality	Species richness	Reference
Wakasa Bay (Honshu)	207	Ito, 1990
Tsukumo Bay (Noto Peninsula, Honshu)	104	Habe, 1973
Ichikawa Prefecture (around Noto Peninsula)	119	Ito et al., 1986
Sado Island	211	Kuroda, 1957; Honma, Kitami, 1978, 1979, 1995
Mano Bay (Sado Island)	103	Ito, 1978
Yeongil Bay (Korea)	98	Lutaenko et al., 2003, 2006
Possjet Bay (Russia)	97	Golikov, Scarlato, 1967; Scarlato, 1981
Vostok Bay (Russia)	88	Evseev, 1981
Amursky Bay (Russia)	119	Lutaenko, 2002, 2003
Ussuriysky Bay (Russia)	124	Lutaenko, 2005, 2006

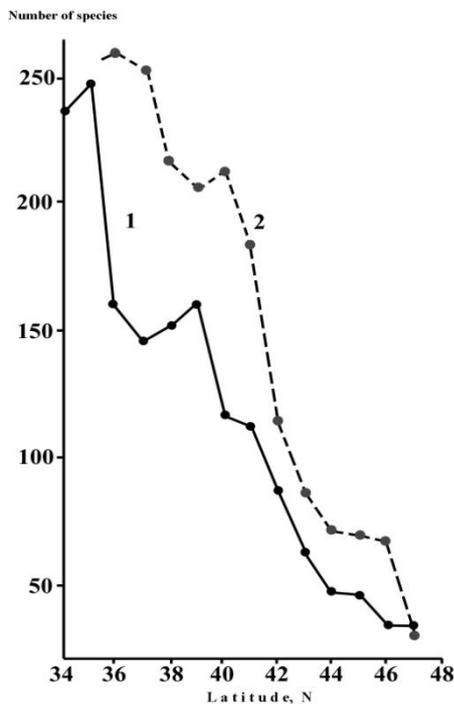


Fig. 1. Latitudinal changes of the bivalve species richness along the Pacific (1) and East/Japan Sea (2) sides of Japan (after Kafanov, 1991).

For comparison, 1176 species are believed to exist in the “East China Sea region” (between 22° and 41°N: East China Sea itself, Yellow Sea, southern Honshu, Taiwan and Hong Kong) (Crame, 2000), 1048 species are known for China seas (Xu, 1997), 1472 – in Japan (Higo et al., 1999), and 449 – in Korea (Lee, Min, 2002). Northern part of the East/Japan Sea belongs to the **Pacific Boreal Region** and southern – to the **Indo-Pacific Tropical Region** (and its subtropical subregion = outer tropical zone of Hall (1964)). According to Hall (1964) along the eastern coast of Japan, there are **cold temperate** (northern range 43° N), **mild temperate** (northern range 41° N), **warm**

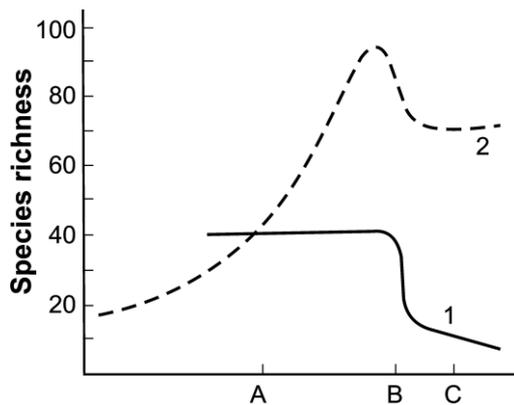


Fig. 2. Species richness of tropical-subtropical and subtropical (1) and boreal (2) mollusks along the continental coast of the East/Japan Sea; **A** – East Korean Bay, North Korea, **B** – Cape Povorotny, Russia, **C** – Vladimir Bay, Russia (after Scarlato, 1981).

temperate (northern range 38°N) and **outer tropical** (northern range 35°N) “marine climates” corresponding to Hokkaidan (cold temperate), Japonian (mild and warm temperate, with two subprovinces: Sendaian and Choshian, respectively), Osakan and Kyushuan (outer tropical) and Ryukyuan (inner tropical) molluscan provinces. It is not clear if there are corresponding provinces in the East/Japan Sea side of Japan. The boundary between boreal and subtropical parts

of the sea was roughly set by Scarlato (1981) between East Korean Bay and around Sado Island based on the fact that in these points subtropical species of bivalve mollusks begin to prevail over boreal ones (Fig. 2). However, biogeographical boundaries are not frontier lines but transitional zones between different faunas and it is rather difficult to determine them precisely. It seems that northern boundary of the subtropical subregion may lie further north, at around southern Hokkaido as many warm-water species penetrate to the north along the island coast of the Japan due to above-mentioned influence of Tsushima Current. If we look at the distribution of number of species in bivalve families, it becomes evident that species richness of warm-water families is higher in Wakasa and Mutsu bays (e.g., Arcidae, Limidae, Chamidae, Lucinidae, Lasaeidae, Veneridae) as compared to Yeongil and Peter the Great Bay. Thus, there is a pronounced asymmetrical pattern in the distribution and degree of penetration of warm-water mollusks to the north along the continental and island coasts of the sea.

Another interesting feature of the bivalve molluscan biogeography in the Japan Sea is a presence of so-called embaymental faunas. Embaymental faunas are characterized by some unique characteristics: they can be an example of refugium of some species distributed widely in adjacent areas in the past, they may have special patterns of local distribution, abundance patterns, etc. To illustrate embaymental zoogeography of local faunas, let us consider the zonal-geographical structure of the bivalve molluscan fauna in bays of the northwestern East/Japan Sea, i.e., Possjet Bay (Scarlato, 1981) and Amursky Bay (Lutaenko, 2003). These bays are characterized by strong

summer/winter contrasts: in summer, sea surface temperature in semi-enclosed bays can reach 28-30 °C (Biryulin et al., 1970; Grigoryeva, 2000), while in winter it can fall as low as -1.9 °C and coastal areas are covered by ice during 4-4.5 months in the year. Thus, nearly arctic conditions occur in coastal waters in winter and subtropical, in summer. Among 97 species of bivalve mollusks found in Possjet Bay, 37 species are subtropical and subtropical-lowboreal (36.2 %), 32 lowboreal (33 %) and 28 widely distributed boreal and boreal-arctic (28.8 %). In Amursky Bay, the biogeographical structure of the molluscan fauna is similar to that of Possjet Bay: the proportion of subtropical and subtropical-boreal mollusks is 33 % (38 species), while lowboreal (26 species, or 23 %) and widely distributed boreal and circumboreal (24, or 21 %) are dominant and make up altogether 44 % of the molluscan fauna. In Yeongil Bay, warm-water mollusks predominate over boreal ones, amounting up to 82 %, while in bays of the northwestern East Sea boreal species hold a dominant position (44-50 %) with a significant presence of cold-water (boreal-arctic) species, 11-20 %. This allows us to characterize the Yeongil Bay molluscan fauna as subtropical. However, in its taxonomic composition, the fauna is significantly impoverished due to the unfavourable oceanographic regime of the coastal waters and the narrow shelf adjacent to Yeongil Bay. Additional evidence in support of the conclusion about the subtropical character of the Yeongil Bay molluscan fauna is the presence in this bay of five truly thermophilous families not found in the northwestern East Sea – Parallelodontidae, Chamidae, Crassatellidae, Petricolidae and Myochamidae. All these families are present in Wakasa Bay (Ito, 1990) but disappear in Hokkaido (e.g., Akkeshi Bay – Habe, 1955b). However, they are recorded for northern Honshu (Mutsu Bay; except for Crassatellidae).

Biogeographical patterns can be understood partly from historical viewpoint. Molluscan fossils are good indicators of warming/cooling epochs and sea level changes in the Holocene (last 10000-11000 years). Migrations of mollusks to the north were the most important biotic events at that time and it was connected not only with general water warming, but also with shifts of currents (Taira, Lutaenko, 1993). The Tsushima Current's inflow in the East/Japan Sea started after 9000-9500 y BP, but the influx of the current on a full scale might occur approximately 8000 y BP. In the northeastern Hokkaido, the oyster (*Crassostrea gigas*) settlements were widely developed at the level of 5000 - 6000 y BP (Ohshima et al., 1972; Matsushima, 1982a, 1982b). Several warm-water subtropical bivalve mollusks at this time invaded the

area of Kushiro Bay (eastern Hokkaido) and Nemuro (north-eastern Hokkaido), but they do not live in these areas at present (Matsushima, 1984). The hydroclimatic conditions under which the so-called thermally-anomalous molluscan assemblages (TAMAs) existed on the northern and eastern coasts of Hokkaido in the mid-Holocene can be compared with those of the present-day Mutsu Bay (northern Honshu) (Matsushima, Yamashiro, 1992). It was found that the species - indicators of the climatic optimum first appeared on the East/Japan Sea side of Hokkaido at about 8000 (or 7500) y BP and contemporaneously they reached Cape Soya; they appeared about 6800 y BP on the Sea of Okhotsk side of Hokkaido and invaded the Pacific coast (Cape Erimo and Uchiura Bay) of the island at about 6000 y BP (Akamatsu, Kitagawa, 1983; Takagi et al., 1990; Akamatsu et al., 1995). An important feature of the mid-Holocene palaeoceanography was a difference in the rate of penetration of warm currents along the island and continental coasts of the sea, as was demonstrated by using molluscan assemblages (Taira, Lutaenko, 1993). In the Early Holocene, coasts of North Korea and Primorye were washed by intensified cold currents of Liman (Schrenck), Primorskoye and North Korean Currents, and thereby their cold waters acted as a barrier to any northward flow of warm waters. This seems to be supported by the lack of subtropical bivalve mollusks in the Early Holocene deposits along the Primorye (Evseev, 1981). We suggested that about 7000 - 6000 y BP, the East Korean Current, a branch of the Tsushima, moved northward at about 40° N, and subtropical bivalve mollusks reached Peter the Great Bay (northwestern East/Japan Sea) (Taira, Lutaenko, 1993). The meandering stream of the Tsushima Current, T-3 offshore stream (= East Korean Current), is known to be strongest (Nishimura, 1983). The intensification of the East Korean Current in the mid-Holocene led to the appearance not only of subtropical, but also of tropical-subtropical bivalve mollusks (whose geographical ranges are extended southward to the Philippines, Vietnam, and Indonesia) in the northwestern East/Japan Sea formed stable populations with annual reproduction - *Anadara inaequalvis*, *T. liratum*, *Dosinia penicillata* (Lutaenko, 1993). They settled in bays with an intense summer warming-up which is necessary for successful reproduction (winter cooling in itself does not prevent warm-water fauna from living in temperate latitudes). Thus, a combination of such factors as the considerable indentation of the coast (ria type of bays with shallow-water semi-enclosed areas in their tops) and penetration of the warm Tsushima waters to the

northwestern Sea of Japan which intensified the effect of local warming had resulted in the formation of subtropical-type molluscan fauna in this area during the Middle Holocene. The example of Peter the Great Bay mid-Holocene TAMA shows that three species of warm-water bivalves became extinct in the course of the Late Holocene coolings, while embaymental environments are still existing. This means that the climatic changes, not only coastal, are responsible for local extinctions of warm-water species.

STUDY ON THE BIVALVE FAUNAL COMPOSITION OF THE YELLOW SEA AND BOHAI SEA

Fengshan Xu¹, Junlong Zhang^{1,2}

¹Institute of Oceanology, Chinese Academy of Sciences, Qingdao 266071, China

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

The Yellow Sea and Bohai Sea are semi-closed shallow seas located between mainland China and the Korean Peninsula. The Bohai Sea is very shallow, with the average depth of 18 m. And the seasonal change of temperature is severe. In summer, it can be above 25°C, while in winter the shore area can be frozen. The Yellow Sea is on average 44 m deep, and in the central part below the depth of 40-50m exists the Cold Water Mass. As the action of storm in winter, the surface water is well exchanged and mixed vertically with the bottom, which keeps low temperature of the bottom water. Even in the high temperature summer, the surface water temperature reaches to 25-28°C, as the existence of the thermocline, the bottom temperature is still low with 6-8°C in the north, and 8-10°C in the south. This forms the Yellow Sea Cold Water Mass, which is the most important hydrographic feature. It makes a lot of high latitude existed cold water species increase and develop in the mid-latitude Yellow Sea, some species even with great abundance. Some subtropical species present at the southeastern Yellow Sea, as the Yellow Sea Warm Current changes the local low temperature environment, which is another factor influencing the distribution of benthos. The eurythermal warm water species inhabit the shallow water area below 40-50m in Yellow Sea and the whole Bohai Sea, where is influenced by the continental climate, and the temperature and salinity change greatly. Though the area of the Yellow Sea is not very large, it has various hydrographic environment affecting the distribution of benthos and leading to the diversified composition of bivalve fauna, where there are cold water species, subtropical species and eurythermal warm water species.

A. There are 107 warm water bivalves in Yellow Sea and Bohai Sea, accounting for 59.1%. The faunal elements consist of:

1. Indo-West Pacific Species, 21 species, accounting for 19.6% of the warm water species. Such as,

Arca avellana Lamarck, 1819
Atrina pectinata (Linnaeus, 1767)
Anomia chinensis Philippi, 1849
Modiolus metcalfei (Hanley, 1844)
Trapezium liratum (Reeve, 1843)
Gastrochaena cymbium Spengler, 1783
Laternula anatina (Linnaeus, 1758) and so on.

2. West Pacific Species, 14 species, accounting for 13.1%. Such as,

Modiolus elongata (Swainson, 1821)
Maetrinula dolabrata (Reeve, 1854)
Raetellops pulchella (Adams et Reeve, 1850)
Solecurtus divaricatus (Lischke, 1869)
Solen dunkeriana Clessin, 1888
Dosinia corrugata (Reeve, 1850)
Laternula boschasina (Reeve, 1863)

3. Southeast Asia - China Seas Species, 12 species, accounting for 11.2%. Such as,

Arcopsis symmetrica (Reeve, 1844)
Cycladicama cumingii (Hanley, 1844)
Coelomactra antiquata (Spengler, 1802)
Nitidotellina iridella (Mastensi, 1868)
Solen grandis Dunker, 1861
Cyclina sinensis (Gmelin, 1791)
Potamocorbula ustulata (Reeve, 1865)

The above species mainly inhabit the intertidal zone and near shore shallow water area.

4. China Seas - Japan – Russian Far Eastern Seas Species, 5 species, accounting for 4.6%. Such as,

Arca boucardi Jousseume, 1894
Musculus senhousia (Benson, 1842)
Macra chinensis (Philippi, 1846)
Macra veneriformis Reeve, 1854
Potamocorbula amurensis (Schrenck, 1867)

5. Yellow Sea - Japan Species, 29 species, accounting for 27.1%. Such as,

- Yoldia similis* Kuroda et Habe, 1922
Musculus cupreus (Gould, 1861)
Xenostrobus atrata (Lischke, 1871)
Raeta pellicula (Reeve, 1853)
Dosinia biscocta (Reeve, 1850)
Sinonovicula constricta (Lamarck, 1818)
6. Yellow Sea and East China Sea - Japan Species, 11 species, accounting for 10.3%.
- Saccella gordonis* (Yokoyama, 1920)
Arcopsis interplicata (Grabau et King, 1928)
Pecten albicans Schröder, 1802
Moerella jodoensis (Lischke, 1872)
Leptomya minuata Habe, 1960
7. China Seas Endemic Species, 6 species, accounting for 5.6%.
- Nucula (Leionucosla) faba* Xu, 1999
Solen arcuatus Tchang et Huang, 1965
Meretrix petechialis (Lamarck, 1810)
Potamocorbula laevis (Hinds, 1843)
Barnea davidi (Deshayes, 1874)
Trigonothracia jinxiangae Xu, 1980
8. Yellow Sea - East China Sea Endemic Species, 1 species, accounting for 0.9%.
- Avella sinica* (Wang et Qi, 1984)
9. Yellow Sea Endemic Species, 6 species, accounting for 5.6%.
- Talonostrea talonata* Li et Qi, 1994
Angulus compressissima (Reeve, 1869)
Glaucanome primeana Crosse et Debeaux, 1863
Tugonia huanghaiensis Xu, 1987
Penitella dolichothyra Tchang, Tsi et Li, 1960
Sinolyonsia sinica Xu, 1992
10. Pacific and Atlantic Species, 1 species, accounting for 0.9%.
- Barnea fragilis* (Sowerby, 1844)
11. Cosmopolitan Species, 1 species, accounting for 0.9%.
- Teredo navalis* Linnaeus, 1758

There are 107 warm water bivalves, accounting for 59.1% of total (181) bivalves of this area. Among them, 29 are the Yellow Sea - Japan, Species, accounting for 27.1% of the total warm water species. The Indo–West Pacific Species are secondly, with 21 species, accounting for 19.6%. The thirdly are West Pacific Species, with 14 species, accounting for 13.1%. Southeast Asia - China Seas Species and Yellow Sea and East China Sea - Japan Species both have 12 species, accounting for 11.2%. According to the above, these warm water species have close relationship with Japanese species.

Most of the warm water species inhabit intertidal zone and subtidal shallow water area in Yellow Sea and Bohai Sea. Some of them are subtropic elements, but most are eurythermal warm water species, originating from subtropics. *Pecten albican* and *Avella sinica* can also distribute to the East China Sea. Their two distribution areas are isolated and discrete. *Paphia papilionacea* inhabit the sandy bottom area at the margin of the warm current.

B. There are 74 cold water bivalves in the Yellow Sea and Bohai Sea, accounting for 40.9%. Their faunal element composition is as follows,

1. North Hemisphere Boreal Species, 3 species, accounting for 4.1% of the cold water species.

Nucula (Leionucosla) tenuis (Montagu, 1808)

Musculus nigra (Gray, 1824)

Clinocardium ciliatum (Fabricius, 1780)

2. Amphi - Boreal Species, 2 species, accounting for 2.7%.

Modiolus modiolus (Linnaeus, 1758)

Mya arenaria Linnaeus, 1758

3. North Pacific Boreal Species, 1 species, accounting for 1.3%.

Clinocardium californiense (Deshayes, 1857)

4. Amphi - Pacific Boreal Species, 1 species, accounting for 1.3%.

Lucinoma acutilineatum (Conrad, 1849)

5. Russian Far Eastern Seas - Japan - Yellow Sea Boreal Species, 21 species, accounting for 28.4%.

Acila mirabilis (Adams et Reeve, 1850)

Scapharca broughtonii (Schrenck, 1867)

Porterius dalli (Smith, 1885)

Glycymeris yessoensis (Sowerby, 1889)

Mytilus coruscus Gould, 1861

Crassostrea gigas (Thunberg, 1793)

Solen krusonsterni Schreuck, 1867

The above type of species are boreal species. Their south distribution limit is the Yellow Sea. Only few species can get across the estuary of the Yangtze River and reach to Zhejiang and Fujian province.

6. Northern Atlantic and Northern Pacific Warm Temperate Species, 1 species, accounting for 1.3%.

Mytilus galloprovincialis Lamarck, 1819

7. Yellow Sea - Japan Warm Temperate Species, 42 species, accounting for 56.8%.

N. (N.) tokyoensis Yokoyama, 1920

N. (Thestyleda) yokoyamai Kuroda, 1934

Yoldia notabilis Yokoyama, 1922

Portlandia japonica (Adams et Reeve, 1850)

Solamen spectabilis (Adams, 1862)

Chlamys farreri (Jones et Preston, 1904)

Thyasira tokunagai Kuroda et Habe, 1951

Clinocardium buellowi (Rolle, 1896)

Trigonothracia pusilla (Gould, 1861)

8. Yellow Sea Endemic Species, 3 species, accounting for 4.9%.

Asthenothaerus huaughaensis Xu, 1989

Crassithracia ovata (Xu, 1989)

Liocyma chinensis Zhang, Xu et Leng

Among the above three endemic species, the first two are found in the deep part of the Yellow Sea, where the Yellow Sea Cold Water Mass is located. So they can be taken as cold water species. While the *Liocyma* is a cold water genus, and *Liocyma chinensis* found in Bohai Sea can also be taken as cold water element.

There are 41 Yellow Sea - Japan Warm Temperate Species, which are most among the 74 cold water bivalves, accounting for 55.4% of the Yellow Sea cold water species. Secondly is the Far Eastern Seas - Japan - Yellow Sea Boreal Species, with 22 species, accounting for 29.7%. According to the above data, the Yellow Sea cold water bivalves have the closest relationship with Japan, and the similarity with Russian Far Eastern Seas is also very high.

It can be seen from the above data, the faunal composition of the Yellow Sea and Bohai Sea bivalve is very complicated. This is the result of combined action of various local hydrographic environments. The bivalves inhabiting the Yellow Sea Cold Water Mass area are dominated by cold water species, amounting for 72 species and accounting for 97.6%. Only *Arca boucardi* and *Raetellops pulchella* are warm water species. In the Yellow Sea Warm Current controlled area in the South Yellow Sea, inhabit the typical subtropic species *Pecten albicans* and *Avella sinica*. At the vast nearshore shallow water area, most of the inhabitants are eurythermal warm water species. Nevertheless, there are also some cold water species, such as *Saxidomus purpurata*, *Macoma incongrua* and so on.

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DISTRIBUTION OF PEANUT WORMS (SIPUNCULA) IN THE WEST PACIFIC

Anastassya Maiorova and Andrey Adrianov

Institute of Marine Biology, Far East Branch of Russian academy of Sciences,
690041, Vladivostok

Far East State University, 690000, Vladivostok

Sipunculans, or peanut worms, constitute a well distinguished monophyletic group of exclusively marine non-segmented coelomate worms which are currently considered as a separate phylum Sipuncula. They are worldwide in distribution and live in a wide variety of marine habitats from intertidal waters to abyssal depths and from polar to equatorial seas. After a series of taxonomic revisions, about 150 valid species have been calculated currently (see Cutler, 1994).

The body is subdivided into two main regions: barrel-like trunk and long eversible introvert. The anteriormost introvert, termed head, bears a terminal tentacular apparatus, the ciliary tentacles of which function in gas exchange and in feeding.

The size of sipunculans varies considerably with trunk of mature specimens (with retracted introvert) from 2-3 mm long in meiobenthic *Phascolion psammophilum* (see Rice, 1993) and 3 mm in *Onchnesoma steenstrupii* to 500 mm in *Siphonosoma ingens*, 550 in *Sipunculus indicus* (see Stephen, Edmonds, 1972), and even 600 mm in *Sipunculus nudus* (see Murina, 1977).

Most sipunculans are deposit feeders, although a few are filter feeders, or sestonophages, with elaborate tentacular crown (species of *Thysanocardia* and *Themiste*). Sipunculans consume detritus and fecal material as well as bacteria, algae, protozoans and small invertebrates. In turn, they are eaten by fish, gastropods and cephalopods, carnivorous worms, crabs, starfishes, anemones, and other predators, including men, and also used as a popular ‘fishbait’.

Sipunculans may attain large densities as great as 700 specimens per m² in reef limestone, and up to about 8000/m² in some soft sediments (Williams, Margolis, 1974; Rice et al., 1983; Murina, 1984; own data).

In soft sediments, some species live just a few centimeters below the surface but some large species of *Sipunculus* burrow down a meter in coarse or silty sands, making a nearly vertical tunnels. Many species live in sand-filled cracks, crevices, or pockets in

the rocks and may also be found in seagrass roots, algal holdfasts and rhizoids, within sponges and under algal mats, in byssal threads of mussels. Some species inhabit empty mollusk shells, polychaete tubes, foraminiferan tests. Several species can bore into coral, rocks and in decaying whale skulls (*Aspidosiphon*, *Cloeosiphon*, *Lithacrosiphon*). Together with polychaetes, sipunculans are designated to be the most important bioeroders in many recent and fossil reefs. One species, *Phascolosoma turnerae*, was found in association with submerged wood, occupying burrows in the wood (see Rice, 1985). Some small sipunculans (e. g. *Phascolion psammophilum*) are interstitial in coarse sand and shell hash.

One species, *Phascolosoma saprophagicum*, is found only living on the flesh of a decomposing whale skull at about 900 m (see Gibbs, 1987).

Almost all sipunculans are dioecious and lack sexual dimorphism. Fertilization always occurs externally and mature gametes leave the coelom through the nephridiopores.

One hermaphroditic species, *Nephasoma minutum*, has been known. Two species (*Aspidosiphon elegans* and *Siphonosoma cumanense*) are capable of reproducing asexually by unequal transverse fission, or budding (see Rice, 1970; Cutler, 1994).

Four developmental patterns have been designated: (1) direct lecithotrophic development with no pelagic stage; (2) indirect development with one pelagic stage - lecithotrophic (non-feeding) trochophore; (3) indirect development with two pelagic stages - lecithotrophic trochophore and short-lived (2-14 days) lecithotrophic pelagosphere; (4) indirect development with two pelagic stages - lecithotrophic trochophore and planktotrophic (feeding) long-lived (1-7 months) pelagosphere .

Ranging in size from 0.2 to 5 mm, the long-lived oceanic pelagospheras are teleplanic and usually found in transoceanic currents. These larvae were classified in about 10 morphotypes which can be distinguished by size, head morphology, color, ciliation pattern, texture of body surface (see Hall, Sheltema, 1975) but only one was identified to species.

An evaluation of the significance of the oceanic larvae in the widespread geographic distribution of sipunculans has been impeded by the uncertainty of the adult affinities of the pelagic stages. Currently, three main approaches are used to identify larvae to known species described only based on the adult morphology: (1) comparison of fine morphology (characteristic papillae and epidermal sensory structures); (2) cultivation of sipunculans in labs; and (3) larval sequences and sequences from adults for the same genetic markers.

At the end of their planktonic life, pelagosphaera larvae undergo settlement and enter the benthos.

About 30 species of sipunculans were found in the abyssal depth (below 3000 m). Some eurybathic species are found between 10 to 4000 m over a wide range of temperatures but some species are restricted to cold water deeper than 3000 m and never found above this isobath. At least 13 species are known from the depth below 5000 m: *Golfingia anderssoni* (Theel, 1911); *G. margaritacea* (Sars, 1851); *G. muricaudata* (Southern, 1913); *G. vulgaris* (de Blainville, 1827); *Nephasoma capilleforme* (Murina, 1973); *N. diaphanes diaphanes* (Gerould, 1913); *N. flagriferum* (Selenka, 1885); *N. minutum* (Keferstein, 1862); *N. schuettei* (Augener, 1903); *Phascolion lutense* Selenka, 1885; *P. pacificum* Murina, 1957; *Onchnesoma magnibatha* Cutler, 1969; *Apionsoma murinae* (Cutler, 1969) (see Cutler, 1994). Some species are common even at the ultraabyssal depth (more than 6000 m) (*Nephasoma minutum*, *Golfingia muricaudata*, *G. anderssoni*, *Phascolion lutense*, *P. pacificum*), but it should be emphasized that the ultraabyssal zone has no endemic species.

Contrary to shallow water species, nothing is still known about the development of abyssal sipunculans, their larval stages, life history and population biology. Because the absence of endemic abyssal species the deep sea fauna of sipunculans appears to be relatively young and is formed as a result of migration of some eurybathic species to a great depth. Probably, the dispersal of long-lived pelagosphaera larvae by ocean currents also allows sipunculans recolonize ocean depths as well as reach new geographical regions and maintain gene flow between widely separated populations.

About nothing is known about the fauna of sipunculans in the Bering Sea. In the Okhotsk Sea, we found four abundant species of peanut worms – *Golfingia vulgaris*, *G. margaritacea*, *Phascolion strombus* and *Phascolosoma agassizii*. Interestingly, that at the north coast of Sakhalin Island in the Okhotsk Sea, sipunculan *Golfingia margaritacea* (Sars, 1851) is an important component of the diet of grey whales, in some areas giving more than 50% of benthic biomass (own data). *P. agassizii* is a most common species in the Aniva Bay at the south-east coast of Sakhalin Island, the north frontier of the natural habit (areal) of this species.



Fig. 1. *Golfingia margaritacea margaritacea*, 1000 m, total view and head.

Currently, the fauna of the Sea of Japan is estimated as having about 29 species of peanut worms (Cutler et al., 1984; own data), most of them being found near the Japan Islands and Tsushima straight. In Russian waters of the Sea of Japan we found 7 species (*G. margaritacea*, *G. vulgaris*, *Nephasoma capilleforme*, *Phascolion strombus*, *Thysanocardia nigra*, *Themiste pyroides*, *Phascolosoma agassizii*). *P. agassizii*, *T. nigra* and *T. pyroides* inhabit the shallow water areas (0-50 m), while *G. margaritacea*, *G. vulgaris*, *Nephasoma capilleforme*, *P. strombus* are more deep water species, most common at the depth from 100 to 1000 m. The most deep point where we found *G. margaritacea* is the Bogorov elevation composed of lava stones covered with mud at the depth 1700 m.

At the Pacific coast of Japan, about 49 species have been noted (see Cutler et al., 1984).

During the cruise SoJabio 2010 we found three species in the deep area of the Sea of Japan - *Golfingia margaritacea*, *Nephasoma capilleforme*, *Phascolion strombus*. One more species from this area, *Golfingia vulgaris*, is known from the museum collection.



Fig. 2. *Phascolion strombus strombus*, 500 m depth.

The fauna of warm water species of sipunculans in the West Pacific is well studied in the East and South China Seas. Thus, around the Taiwan about 29 species has been calculated up-to-date (Hsueh & Kuo, 2009). In South China Sea, about 36 species are found, most of them being described from the Vietnam and China coast line (Zhou Hong & Li Fenglu, 1993; Pagola-Carte & Salinas, 1996). Thus, in the Nha Trang Bay (Vietnam) we found 20 species of sipunculans. Totally, the fauna of the Nha Trang Bay is estimated as having 24 species of peanut worms (Murina, 2003; own data).

According to our calculations, about 61 species can be accounted for the West Pacific Seas (except of the South Hemisphere). This number constitutes about 40 % of the known World fauna of peanut worms.

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THE SEAWEED AQUACULTURE IN CHINA

Guangce Wang

Institute of Oceanology, Chinese Academy of Sciences, Qingdao 266071, China

E-mail: gcwang@qdio.ac.cn

The aquaculture of seaweeds in China and the reduction of marine eutrophication with seaweed aquaculture was introduced in this paper. The history of seaweed cultivation in China was also included. The two types of the most important economic seaweeds, *Lamilaria japonica* and *Undaria pinnatifide*, both of which were introduced into China in 20 century, triggered both the seaweed aquaculture and the marine aquaculture in China, so the techniques for the two seaweeds were described in detail, which include 5 parts: spore collection and indoor cultivation of sporeling, sporeling transplantation, setting up cultivation raft in the field, cultivation management in the field, and harvesting. The second algal aquaculture industry which was developed in China was *Porphyra* cultivation. *Porphyra* is different from *Laminaria* since *Porphyra* has a very special character, being survived during desiccation. Thus, there 3 ways for *Porphyra* aquaculture, fixed pillars, semi floating method and fully floating. The third algal cultivation industry is the *Gracilaria* which has been appreciated as a food and feed for culturing marine animals. The most important use of *Gracilaria*, however, is the production of agar. It is known that the finfish aquaculture waste production include solid wastes (Uneaten Food, Feces) and dissolved metabolic wastes (CO_2 , NH_4 , PO_4), the heavy eutrophication will greatly decrease the production of marine animal such as finfish and scallop, so at present time the measures for the integrated cultivation of animal and seaweeds was strongly suggested.

Key Words: *Lamilaria japonica*, *Undaria pinnatifide*, *Porphyra*, *Gracilaria*, seaweed aquaculture

ZOOPLANKTON FUNCTIONAL GROUPS IN THE YELLOW SEA

Chaolun Li, Yuanzi Huo, Song Sun

Institute of Oceanology, Chinese Academy of Sciences

7 Nanhai Road, Qingdao, China

E-mail: lcl@qdio.ac.cn

Zooplankton plays a vital role in the marine ecosystems. The variations of zooplankton species composition, biomass and secondary production will change the structure and function of the ecosystems. How to describe this process and make it easier to be modeled in the Yellow Sea ecosystem is the main purpose of this paper. The biomass and secondary productivity are the basis of the food web in the marine ecosystem. Who are the main contributors in the biomass and secondary productivity of zooplankton? Which species take the roles to affect the structure and function of the ecosystem? It is very hard to describe in the temperate continental shelf area, such as in the Yellow Sea, where the species composition, biomass and secondary production changed seasonally. Therefore, when modeling the key process of ecosystem food production in the Yellow Sea, an approach which is both precise and easy must be applied. After adequately analyzing the structure of zooplankton community and features of physical oceanography, the zooplankton functional groups approach, which is considered to be a good method of linking the structure of food webs and the energy flow through ecosystems, is used in the Yellow Sea ecosystem modeling.

According to the size spectrum, feeding habits and trophic functionality, the zooplankton could be classified into 6 functional groups: giant crustacean (GC), large copepods (LC), small copepods (SC), chaetognaths, medusae and salps. The GC, LC and SC groups which are the main food resources of fish are defined based on the size spectrum. Medusae and chaetognaths are two gelatinous carnivorous groups, which compete with fish for food. The salps group, acting as passive filter-feeders, competes with other species feeding on phytoplankton, but their energy could not be efficiently transferred to higher trophic levels. From the viewpoint of biomass, the seasonal variations and geographical distributions of each zooplankton functional group, the ecoregions related to zooplankton functional groups, the secondary production of

zooplankton, the impact of chaetognaths group feeding on zooplankton and trophic ecology of *Calanus sinicus* were studied in this paper.

The mean zooplankton biomass was 2.1 g dry weight m^{-2} during spring, to which the GC, LC and SC contributed 19, 44 and 26%, respectively. High biomasses of the LC and SC were distributed at the coastal waters, while the GC was mainly located at offshore stations. In summer, the mean biomass was 3.1 g dry weight m^{-2} which was mostly contributed by the GC (73%), and high biomasses of the GC, LC and SC were all distributed in the central part of the Yellow Sea. During autumn, the mean biomass was 1.8 g dry weight m^{-2} which was similarly constituted by the GC, LC and SC (36, 33 and 23%, respectively) and high biomasses of the GC and LC were occurred in the central part of the Yellow Sea, while the SC was mainly located at offshore stations. The GC and LC dominated the zooplankton biomass (2.9 g dry weight m^{-2}) in winter, each contributing 57% and 27% and they as well as the SC were all mainly located in the central part of the Yellow Sea. The chaetognaths group was mainly located in the central and northern part of the Yellow Sea during all seasons, but contributed lower to the biomass compared with other groups. The small medusae and salps groups were distributed unevenly with sporadic dynamics, mainly along the coast line and at the northern part of the Yellow Sea. No more than 10 species belonging to the respective functional group dominated the zooplankton biomass and controlled the dynamics of the zooplankton community.

During spring, the Yellow Sea can be divided into 4 zooplankton ecoregions. The high biomass of zooplankton was mainly distributed at the coastal waters near the south shore of Shandong peninsula, which corresponded to the first ecoregion. The LC and SC were the dominated functional groups in the first ecoregion. In summer, autumn and winter, the Yellow Sea can be classified into 3, 4 and 3 zooplankton ecoregions, and the high biomass were all mainly distributed in the central part of the Yellow Sea, which all corresponded to the first ecoregion. The GC and LC were the dominated functional groups in the first ecoregion in these three seasons. The Yellow Sea Cold Bottom Water (YSCBW) plays a vital role in the distribution mode of GC, LC and SC. The geographical distribution mode of each zooplankton ecoregion in different season had important ecological meaning in the Yellow Sea ecosystem.

Key Words: Zooplankton, Function groups, Yellow Sea

**VARIOUS WAYS OF SPERM UTILIZATION IN THE POSTSPAWNING
TESTES OF MARINE ORGANISMS: A COMPARATIVE
MORPHOLOGICAL STUDY**

Yurchenko O.V., Kalachev A.V., Neznanova S.Yu, and Reunov A.A.

A.V. Zhirmunsky Institute of Marine Biology of the Far Eastern Branch of the
Russian Academy of Sciences, Vladivostok 690041, Russia

Mollusks, echinoderms and fishes being the subjects of the present study have an annular reproductive cycle and seasonal breeding. In such organisms gonad mass varies to total body mass within a year because of intensity of gametogenetic processes. The germinal epithelium of the testes in the studied organisms contains two interdependent populations of cells: somatic cells (also called accessory, auxiliary, nutritive, Sertoli cells, nutritive phagocytes) and germ cells - spermatogonia, spermatocytes, spermatids and spermatozoa. Annually, somatic cells vary their structure and function to produce a changing microenvironment for germ cells during gametogenesis and after spawning. Postspawning processes connected with utilization of the residual spermatozoa. Resorption of residual spermatozoa had been described in the various organisms repeatedly. In the various taxa in sperm degeneration the different somatic gonadial cell types can be involved, that was demonstrated in scanty reports concerned postspawning sperm resorption (Jørgensen & Lützen, 1997; Reunov et al., 2004; Walker et al., 2005, *etc*) or in those connected with morphological description of spermatogenesis and accompanied somatic cells (Pipe, 1987; Erkan & Sousa., 2002; Riesgo, 2010, *etc*). In our opinion, the study of the postspawning cells rearrangement in the testes of various hydrobionts taxa would be useful for understanding of interaction of cells population at inter-gametogenesis stage and wholeness of spermatogenesis in the organisms with seasonal reproduction. All hydrobionts were sampled in a month after spawning at Vostok Marine Biological Station (Peter the Great Bay, East Sea). The gonad tissues were treated in accordance with standard procedures of material preparation for ultrastructural and histochemistry study.

Echinoderms (sea urchin *Strongylocentrotus nudus* and sea star *Asterina pectinifera*).

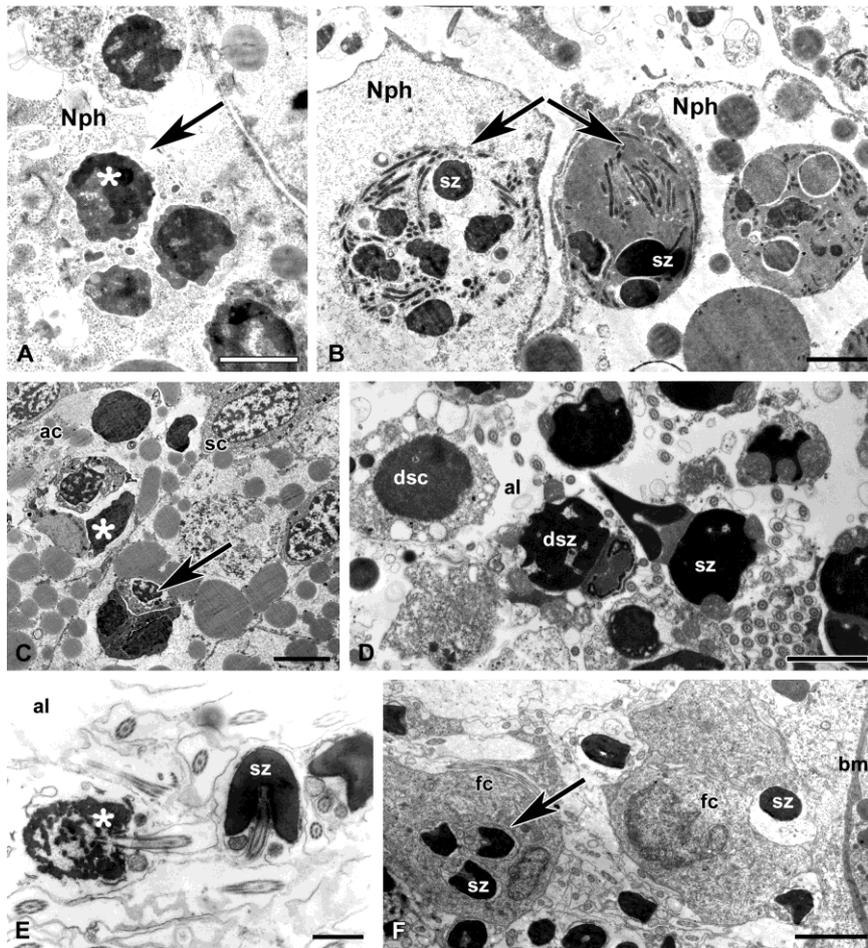


Fig. 1. Various ways of residual sperm utilization in sea urchin *Strongylocentrotus nudus* (A, B), horse mussel *Modiolus modiolus* (C, D), pinewood flounder *Cleisthenes herzensteini* (E, F) and flat-headed flounder *Hippoglossoides dubius* (G). **A.** Nutritive phagocyte with heterophagosome (arrow) containing early spermatogenic cells (asterisk). **B.** Nutritive phagocytes with heterophagosomes (arrows) containing spermatozoa. **C.** Accessory cells with heterophagosomes (arrow) containing early spermatogenic cells (asterisk). **D.** Acinus lumen with spermatogenic cells and spermatozoa. **E.** Intact spermatozoon and spermatozoon with fragmented chromatin (asterisk) in the acinus lumen. **F.** Follicular cell with heterophagosome (arrow) containing spermatozoa. Abbreviations: ac – accessory cell, al – acinus lumen, dsc – destructing spermatocyte, dsz – destructing spermatozoa, fc – follicular cell, Nph – nutritive phagocyte, sc – intact spermatocyte, sz – intact spermatozoa. Scale bars: A = 4 μ m, B, C = 5 μ m, D = 2 μ m, E = 1 μ m, F = 3 μ m.

In both species utilization of residual sperm cells by phagocytosis was found. In the studied species of echinoderms the complete destruction of spermatogenic cells in the acinus lumen was never observed. All spermatozoa in the acinus lumen had a usual

morphology, while individual early spermatogenic cells had initial features of cell death (electron-dense cytoplasm and condensed chromatin). Nutritive phagocytes in sea urchins had a large size and contained a numerous heterophagosomes with spermatogenic cells (Fig. 1A) and spermatozoa (Fig. 1B) and included granules with different electron density. Coelomocytes with spermatozoa could be found very seldom in the acinus lumen. In sea star *Asterina pectinifera* coelomocytes migrated from the hemal sinus into the acini were the only cell type that utilized sperm cells. Intra-gonadial accessory cells were small in size and did not participate in the sperm destruction (see Table 1).

Table 1 Various patterns of residual sperm utilizations in the studied species (present study)

	Species	Pattern of residual sperm utilization			
		autolysis	accessory cells	coelomocytes	gonoduct
Mollusks	Horse mussel <i>Modiolus modiolus</i>	+++	++	+	+
	Pacific oyster <i>Crassostrea gigas</i>	+++	+	++	-:-
Echinoderms	Sea urchin <i>Strongylocentrotus nudus</i>	---	+++	+	-:-
	Sea star <i>Asterina pectinifera</i>	---	---	+++	-:-
Fish	Pinewood flounder <i>Cleisthenes herzensteini</i>	+++	---	---	-:-
	Flat-headed flounder <i>Hippoglossoides dubius</i>	+	+++	---	-:-

+++ - basic, ++ - less frequent, + - rare way of utilization, --- - not found, -:- - no data

Mollusks (horse mussel *Modiolus modiolus* and pacific oyster *Crassostrea gigas*).

According to our observations, in the postspawning testes acinal somatic cells were presented by attached accessory cells and movable coelomocytes. In the mollusks testes the accessory cells were smaller in size than that in the sea urchins. They contained heterophagosomes with early spermatogenic cells (Fig. 1C), while coelomocytes included spermatozoa only. It should be noticed that in both accessory cells and coelomocytes the heterophagosomes with sperm cells were not numerous. In

the intercellular space of the same acinus the residual spermatogenic and sperm cells with usual organization as well as those with feature of the cell death were found (Fig. 1D). Some of the degenerated cells underwent complete disorganization in the acinus lumen. Spermatogenic cells were also found in the gonoduct area. Among the acini that limited from the other by an acinal wall there were the structures looked like acini but lacking of the outer wall. The patterns of residual sperm cells utilization is summarized in Table 1. Usage of histochemistry staining (Apoptotic, Necrotic and Healthy Cells Quantification Kit, Biotium Inc.) and fluorescence microscopy let us suggest that spermatogenic cells generally underwent the necrotic cell death.

Fish (flounder species *Cleisthenes herzensteini* and *Hippoglossoides dubius*).

Despite both species from the same family Pleuronectidae two different ways of residual sperm utilization were found. In the testes of the pinewood flounder *Cleisthenes herzensteini* the cells-macrophages were absent as well as the phagocytic activity of the follicular cells was not noticed. Sperm cells destruction occurred probably by autolysis. Residual spermatozoa showed fragmentation of chromatin and following cell breakage (Fig. 1E). The major way of the residual sperm utilization in the *Hippoglossoides dubius* was phagocytosis by follicular cells but sperm cells with features of autolytic disorganization were rarely found (Fig. 1F, Table 1).

Utilization of the residual sperm cells is a preparatory phase before new spermatogenic cycle (Walker et al., 2005). Despite all studies species have primitive spermatozoa and sperm development is generally similar, the processes of postspawning sperm destruction show significant diversity. Our observations indicate the different intensity of sperm utilization by attached cells called nutritive phagocytes (in sea urchins), accessory (in mollusks), follicular cells (in fish). The phagocytic activity is likely to be connected with sizes of accessory cells. In species with large accessory cells (sea urchin and flat-headed flounder) phagocytosis of spermatozoa by accessory cells is the major way of sperm utilization. In the species with relatively small attached cells both accessory and coelomocytes take part in sperm destruction. Usually coelomocytes freely penetrate into the acinus at the postspawning stage and at the beginning of spermatogenesis they are absent. Thus, it is obvious that coelomocytes compensate poor activity of accessory cells. In sea star *Asterina pectinifera* coelomocytes are the only cells – macrophages, while accessory cells do not englobe any sperm cells, probably because of their very small sizes that were similar to spermatocytes sizes.

It may be suggested that large size of accessory cells in sea urchins and flat-headed flounder in postspawning testes may be considered as the consequence of the active resorption of sperm. But literature data (Walker et al., 2005; Harrington et al., 2007) as well as our seasonal observations (Kalachev et al., 2005) indicated that accessory cells in these species rather large during all year long, with the exception of prespawning stage.

As it was indicated by Nakanishi and Shiratsuchi (2004) in rates testes, the Sertoli cells recognize phosphatidyl-serine on the outer leaflet of the cell membrane in apoptotic spermatogenic cells as a signal for phagocytosis. Walker et al. (2005) suggested that such a mechanism may be active in sea urchins sperm utilization. But whether such a mechanism is attitude for coelomocyte phagocytic activity in sea stars and mollusks remains unclear.

The ways of sperm utilization, in our opinion, may also be defined by species-specific metabolic rate. In mollusks in some months after sperm release the gonad reduce to a narrow band of germinal epithelium, remain as scarce tubules. The germ cells present in the tubules are not sufficiently differentiated to allow sex identification (Franco et al., 2008). Accessory cells also reduce in their sizes dramatically. To shrink the acini for a short period of time the triple pattern of sperm utilization may be necessary.

The different ways of sperm utilization in fish may also be connected with difference in metabolic rate. However, the possibility of existence of species-specific features in the sperm degeneration process should not be ignored.

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THE MARINE BIODIVERSITY OF MACROBENTHOS FROM THE JIAOZHOU BAY, SHANDONG PENINSULA

Xinzheng Li

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

Ten stations, in which nine are normal research stations in the bay, one is control station out of the bay, were set up in Jiaozhou Bay, Shandong Peninsula for research macrobenthos. Based on the data mainly from these ten stations during past 30 years since 1980, the change of marine biodiversity of macrobenthos of Jiaozhou Bay was analyzed. The results show that the species numbers and mean abundances of macrobenthos from Jiaozhou Bay changed strongly before 1998, but they tend to be stable (changed little) since 1998. This may be because the stop of trawling in the bay since 1998, and the policy of Fishing Ban since 2001, there have not been strong disturb in the bottom. The mean biomass of macrobenthos from the bay fluctuated from 1980 to 2004, which was at lowest position during 1998 to 2000, increased from 2000 to 2004, then it tends to be stable. The Philippines clam, a very important biological resource in the bay and adjacent area, is the most important contributor to the macrobenthic biomass in the bay.

Key Words: macrobenthos, Jiaozhou Bay, biodiversity, abundance, biomass

STUDIES ON TOXIC ALGAE IN COASTAL WATERS OF CHINA

Rencheng Yu, Yunfeng Wang, Qingchun Zhang, Tian Yan, Mingjiang Zhou

Institute of Oceanology, Chinese Academy of Sciences,

Qingdao, 266071, China.

E-mail: rcyu@qdio.ac.cn

The rapid proliferation of some microalgae in the sea can lead to serious impacts, such as fish kill, seafood contamination, tourism impairment and ecosystem degradation, which we now call harmful algal blooms (HABs). The apparent global increase of HABs represents a significant and expanding threat to human health, fishery resources and marine ecosystems throughout the world (GEOHAB, 2001). Blooms of toxic algae are considered as a major group of HABs, leading to public health impacts due to the production of toxins. Examples of syndromes caused by toxic algal blooms include paralytic, diarrhetic, neurotoxic and amnesic shellfish poisoning (PSP, DSP, NSP and ASP) (FAO, 2004).

PSP incidents, which have caused human illness for centuries, are mainly caused by the blooms of toxic dinoflagellates in genus *Alexandrium*, *Gymnodinium* and *Pyrodinium*. Toxins corresponding for PSP include saxitoxin (STX) and over two dozen naturally-occurring derivatives of STX. DSP incidents are mainly resulted from the blooms of toxic dinoflagellates in genus *Dinophysis* and *Prorocentrum*. Okadaic acid (OA) and dinophysis toxins (DTXs) are major toxins corresponding for DSP incidents. ASP incidents are mainly caused by the blooms of toxic diatoms which can produce domoic acid (DA).

In China, PSP, DSP and ASP toxins are sometimes detected in shellfish products (Zhou et al., 1999). Studies have been carried out in the last two decades and knowledge on the potential toxic algae, as well as their toxicity and population dynamics, have been accumulated.

Toxic dinoflagellates and diatoms have been frequently found in coastal waters of China during the routine phytoplankton investigations. Three toxic species in genus *Alexandrium*, i.e. *A. tamarense*, *A. catenella*, and *A. minutum*, have been identified so far in China seas. In genus *Dinophysis*, toxic species like *D. acuminata*, *D. fortii*, *D. caudate* and *D. rotundata*, have been frequently reported. Potentially toxic diatom species in genus *Pseudonitzschia* are also quite popular.

During the last two decades, more and more toxic blooms were recorded in coastal waters of China. Blooms of *Alexandrium* spp. have been observed in Shandong province, Zhejiang province and Guangdong province. In sea areas adjacent to the estuary of the Changjiang River, blooms of *Alexandrium* cells were observed in spring of 2002, 2004, 2005 and 2006, during the cruises supported by the National Basic Research Priority Program (Zhou and Zhu, 2006). The cell density could reach 10^6 cells/L and the maximum affected area were over 1000 km² during the blooms. Although the cell density of *Dinophysis* is normally low in seawater, a large-scale bloom of co-occurring *Dinophysis fortii* and *Ceratium furca* was also recorded in the Bohai Sea (Liu et al., 1999).

Targeted on the toxins produced by the algae, analytical methods based on HPLC and LC-MS have been developed. Status of toxin production has been elucidated gradually for the toxic algae in coastal waters of China. For the PSP producing algae, it was found that most of the toxic strains of *A. tamarense* and *A. catenella* were characterized by the high proportion of low-toxicity C toxins. In a strain of *A. tamarense* isolated from Hongkong (ATHK), C1, C2, GTX1-6, NEO and STX were detected, with the total toxin content of 19.7 fmol/cell (Yu et al., 1998). In a strain of *A. catenella* isolated from the Changjiang River estuary, C1, C2, GTX1-4 and neoSTX were detected, with C toxins being the exclusively dominant components. For the *A. minutum* isolated from the China coastal waters, however, only GTX1, 2, 3 and 4 were detected. Due to the difficulties in culturing the DSP-producing *Dinophysis* spp., the hand-picked cells of *Dinophysis* were analyzed. OA, DTX1 and PTX2 have been detected in cells of *D. acuminata* collected from the Jiaozhou Bay of China. Although DA has been detected in some shellfish samples, no DA-producing diatoms were found in coastal waters of China. *Pseudonitzschia pungens*, a potential DA-producer and a popular red-tide causative species in China, was cultured in the laboratory to detect DA. However, no DA was found in the cultured cells (Li et al., 2005).

To effectively study and monitor the toxic algae, methods based on the molecular biological techniques have been established to identify and enumerate the toxic algal cells. For the toxic species of *Alexandrium* in China, the whole-length ribosomal RNA gene (rDNA), including the small subunit rDNA, the large subunit rDNA, the 5.8S rDNA and the internal transcribed spacers 1 and 2, were amplified and sequenced for the cultured strains of *Alexandrium* spp.. It was found that all the strains of *A.*

tamarense and *A. catenella* isolated from the coastal waters of China had the same sequence information and could be grouped into the Temperate Asian ribotype of “*tamarense* species complex”(Tang et al., 2006). The strain of *A. minutum* could be grouped into the New Zealand ribotype of *A. minutum*. Based on the sequence information, the species-specific probes were designed and the fluorescence *in situ* hybridization method was developed for the detection of toxic *Alexandrium* species (Yu et al., 2006, Tang et al., 2008).

In conclusion, more and the more toxic algal blooms were recorded in the coastal waters of China during the last two decades. Toxic species in Genus *Alexandrium* are the most popular toxic algae in China, which lead to blooms in many sea areas including the Changjiang River estuary. With the capabilities developed on toxin analysis and toxic algae identification, more detailed studies on the population dynamics could be carried on in the near future.

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SPECIES IDENTIFICATION OF THE BLACK PORGY, *ACANTHOPAGRUS SCHLEGELII* (BLEEKER, 1854), BASED ON MITOCHONDRIAL GENES

Jing Liu ^{1*}, Renxie Wu ², Jirong Fan ³, Yuanjun Zhao ³

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

2 College of Fisheries, Guangdong Ocean University, Zhanjiang 524088, China

3 Key Laboratory of Animal Biology, Chongqing Normal University, Chongqing 400047, China

*Corresponding author, E-mail: jliu@qdio.ac.cn

Fishes of the genus *Acanthopagrus* are coastal marine fishes that are important in commercial and recreational fisheries in tropical and temperate waters of the Indo-West Pacific Oceans. There are currently 13 recognized species (or subspecies) of *Acanthopagrus* worldwide, of which *Acanthopagrus schlegelii* is one of the most confused species in taxonomic status. *Acanthopagrus schlegelii* (Bleeker, 1854) was firstly described by Bleeker based on two syntypes with unicolored dark ash-grey body and a silver-white abdomen. Basilewsky (1855) described a new sparid species, *Sparus macrocephalus*, characterized by six to seven transverse broad dark stripes, which was reported by many Chinese authors. Berg (1914) reported another black porgy, *Sparus swinhonis czerskii* (= *A. schlegelii czerskii*) from the Tuman estuary, which had the same color patterns with *Sparus macrocephalus*. Accordingly, *A. schlegelii schlegelii* (unicolored specimens) and *A. schlegelii czerskii* (striped specimens) were recognized to be two different subspecies due to their different color patterns, and *Sparus macrocephalus* was synonymized with *A. schlegelii czerskii*. However, Dolganov et al., (2008) suggested that these two subspecies to be two valid species because both subspecies were recorded to occur in the Sea of Japan, Yellow Sea and East China Sea, which contradicts the criterion of a subspecies. Recently, Kharin and Markevich (2010) regarded that *S. swinhonis czerskii* (= *A. schlegelii czerskii*) was a junior subjective synonym of *A. schlegelii* after examining the morphological characters of the syntypes of these two species. Up to now, there have been no further molecular genetic studies to be reported.

To evaluate the taxonomic status of *A. schlegelii*, we sequenced two mitochondrial genes (COI and D-loop) in 16 individuals sampled from Chinese coastal waters. The

samples were divided into two groups for mtDNA identification according to their coloration type. In group WD, eight specimens with dark-colored sampled from fish markets of Qingdao, Xiamen and Zhanjiang are included; and in group YD, eight specimens with striped sampled from fish markets of Qingdao and Xiamen are included. Analysis of two mtDNA genes showed that the mean sequence divergence between group WD and group YD is 0.15% in COI data set and 0.45% in D-loop data set, respectively. The divergence values are much smaller than those between other closely related sparid species such as *Pagrus major* and *Evynnis cardinalis* (8.02% in COI data), *A. berda* and *A. latus* (11.63% in COI data), even lower than the those between populations in *P. major* (2.5% in D-loop data). Moreover, the neighbor-joining tree of genetic relationships among sequences did not show significant genealogical branches or geographic cluster. These results indicate that both dark-colored specimens and striped specimens belong to the same species. In conclusion, the three nominative species or subspecies, *Sparus macrocephalus*, *A. schlegelii schlegelii*, *A. schlegelii czerskii* were the junior synonyms of *A. schlegelii*.

Key Words: *Acanthopagrus schlegelii*; mitochondrial DNA; molecular phylogeny; taxonomy

MORPHOLOGY OF SPERMATOOZOA AS SPECIES-SPECIFIC FEATURE IN TELEOST

Neznanova S.Y., Reunov A.A.

A.V. Zhirmunsky Institute of Marine Biology of the Far Eastern Branch of the
Russian Academy of Sciences, Vladivostok 690041, Russia

In the present work, we studied the morphology of the spermatozoa of five flatfish (Pleuronectidae) and two cyprinid fishes (Cyprinidae). The aim of the present work was to reveal the species characters in spermatozoa structure (if they may be found). Ultrastructure of spermatozoa may be used for the decision of the taxonomic problems in teleost fish.

Ultrastructure of spermatozoa was investigated in the representatives of all taxa of modern fish. In the teleost fish was shown the most variety of spermatozoa structure, organization of which had been formed in coordination with the original evolution of reproductive characters (Jamieson, 1991; Mattei, 1991). Spermatozoa of teleost fish are organized very simply. Usually they have ovoid or spherical head; length of head in different species of fish varies from 1.5 to 5 μm , width – from 0.7 to 3 μm (Ginzburg, 1968). In the midpiece there is mitochondrion, encircling two centrioles. The flagellum is formed by the axoneme without any additional structures. Spermatozoa of teleost fish differ from the other vertebrates with one character – the absence of acrosome. Knowledge of species-specific sperm ultrastructure might not only be important in systematics and phylogeny, but might also have practical applications related to artificial fertilization and sperm preservation (Billard, 1978; Suquet et al., 1998; Fürböck et al., 2010).

Materials and Methods

Individuals of the flatfish were collected in the Ussuriiskii Bay (Sea of Japan) in July 2002, while individuals of the *Tribolodon* were collected in the Vostok Bay (Sea of Japan) in May-June 2009 at Vostok Biological Station. To evaluate the reproductive state of the fish, a visual determination of the degree of gonad maturity was conducted in five males of each species. For electron microscopy analysis, pieces of the testes of all species of fish were taken. Small pieces of gonads were fixed for 2 h in 2.5% glutaraldehyde in 0.1 M cacodylate buffer (pH 7.4) with postfixation for 2 h in 2%

osmium tetroxide in the same buffer. Then, the material was dehydrated in the series of alcohols and acetones and embedded in Epon-Araldite (Sigma, United States). Ultrathin sections were prepared on a Reichert-E ultramicrotome (Germany). Sections stained with uranyl acetate for 20 min, then with lead citrate (for 2 min), and were examined and photographed using a JEOL 100S transmission electron microscope (Japan).

Results and Discussion

The spermatozoa of the investigated species of flatfishes: flat-headed flounder *Hippoglossoides dubius*, pinewood *Cleistenes herzensteini*, black flounder *Pseudopleuronectes obscura*, brown sole *P. herzensteini* и Far Eastern smooth flounder *Liopsetta pinnifasciata* (Pleuronectidae) have different structure and unlike sizes. The form of the head of spermatozoa at the *Hippoglossoides dubius*, *Pseudopleuronectes obscura*, *P. herzensteini* and *Liopsetta pinnifasciata* has bullet-like shape (Fig. 1A, 2A, 2B, 3A), that is very similar in structure with European plaice *Platichthys flesus* (Jones, Butler, 1988). The *Cleistenes herzensteini* have bell-like shape (Fig.1B) with a deep invagination extending up to the middle of a nucleus. In all investigated species in basal part of the nucleus there are fossae in which the centriolar apparatus consisting of two centrioles, arranged at an angle to each other is located: *Hippoglossoides dubius*, black *Pseudopleuronectes obscura*, *P. herzensteini*, *Liopsetta pinnifasciata* (Fig. 1A, 2A, 2B, 3A); in *Cleistenes herzensteini* proximal centriole is arranged on one axis with the basal body and also is oriented (Fig.1B). The distal centriole in all investigated specimens is the basal body of the flagellus, which has typical structure, composed of nine peripheral and two central pairs of microtubules covered with a cytoplasmic case. The diameter of flagellum is 0.2 μm . The centriolar apparatus of *Hippoglossoides dubius*, *Pseudopleuronectes obscura*, *P. herzensteini* is located symmetrically and is surrounded with a ring, consisting of eight (Fig. 1C, 2C, 2D), in *Liopsetta pinnifasciata* – of seven – eight (Fig. 3B), in *Cleistenes herzensteini* – of six mitochondria with irregular lamellar cristae (Fig. 1D), located in electron-lucent matrix.

From the received results, it is obvious, that the morphometric data confirm the specific individuality of spermatozoa. For each of the investigated species of flatfishes the shape of the head of a spermatozoa and of centriolar fossa, quantity of mitochondria in the mitochondrial ring (Tab. 1) and the angle of proximal centriole in relation to distal one are characteristic.

For the spermatozoa of the big-scaled redbfin *Tribolodon hakonensis* and Eastern redbfin *T. brandtii* (Cyprinidae) like for the other cyprinids are characterized by the spherical shape of head. The heads of spermatozoa in *T. hakonensis* and *T. brandtii* have sizes more similar to the head size in *Carassius aurata*, *Cyprinus carpio* (Kudo, 1980; Baccetti et al., 1984). In both species the head contains nucleus, consisting of electron-dense chromatin. Among the dense chromatin, lacunas with electron lucent matrix are occurred (Fig. 4A). In basal part of nucleus there is a shallow centriolar fossa with centriolar apparatus, located asymmetrically to central axis of head spermatozoa (Fig. 4A, B). Centrioles are arranged at an angle to each other. The proximal centriole lies within the centriolar fossa, whereas the distal is found outside the nuclear fossa (Fig. 4A, B). In big-scaled redbfin *Tribolodon hakonensis* midpiece contains from one to four mitochondria (Fig. 4C), in Eastern redbfin *T. brandtii* - one mitochondria (Fig. 4D). The cytoplasm of the midpiece of the both species contains vesicles (Fig. 4C, D). In spermatozoa of other cyprinids the number of mitochondria varies from one in Chinese bitterling *Rhodeus ocellatus* to ten in gold fish *Carassius aurata* (Baccetti et al., 1984; Emel'yanova, Makeeva, 1985).

The spermatozoa of both species accept the general characteristics of sperm cells of other cyprinids (Baccetti et al., 1984; ЕМЕЛЬЯНОВА, МАКЕЕВА, 1985; Jamieson, 1991; Hu et al., 2005; Rutaisire et al., 2006; Fűrböck et al., 2010), but they differentiate from the other species by larger sizes of heads. Heads of spermatozoa of *Tribolodon* are close in sizes between themselves, but differ in the number of mitochondria in the midpiece (Tab. 1), that on the opinion of Baccetti et al., (1984), can be good distinction for cyprinid in the construction of phylogenetic relations. As the same authors consider (Baccetti et al., 1984), the angle between the two centrioles is the differentiation character of phylogeny, but it is rather difficult to identify as the section can pass in different flats and the angle of gradient varies little.

Spermatozoa of majority of studied teleosts are characterized by typical spherical head with short middle part and lack an acrosome (Grier, 1981; Thiaw, Mattei, 1989; Lahnsteiner, et al., 1991; Jamieson, 1991; Munoz et al., 2002; Cruz-Landim et al., 2003; Lee et al., 2006; Chung, 2008; Neznanova, Reunov, 2009; Fűrböck et al., 2010), that is in agreement with primitive type of sperm organization (Jamieson, 1991; Mattei, 1991), with the differences in the shape of head, short middle part and location of flagellum.

Unlikenesses in the structure of spermatozoa of different groups of animals was marked long away and it is characteristic for Metazoa in general (Retzius, 1904). This concept was affirmed by different authors, who researched structure of spermatozoa of the great number of representatives of very diverse taxa Metazoa (Franzen, 1955; Baccetti, Afzelius, 1976; Jamieson, 1991).

Species specific of spermatozoa is accepted as additional phylogenetic character, on the base of which the status of some taxa has been reconstructed continually (Franzen, 1955; 1956; 1970; Popham, 1979; Hodgson, Bernard, 1988).

Table. 1. Dimensional characters of the sperm compartments in the fish (Pleuronectidae, Cyprinidae)

species	Total length head, μm	Nucleus: length/width μm	Proportion length/width μm	Midpiece: length/width μm	Length of centriolar fossa, μm	Number of mitochondria
PLEURONECTIDAE						
<i>Hippoglossoides dubius</i>	2.2	1.8/1.25	1.44	0.3	0.5	8
<i>Cleistenes herzensteini</i>	2.8	2.3/1.7	1.35	0.46	0.8	6
<i>Pseudopleuronectes obscura</i>	1.6	1.45/1.2	1.2	0.2	0.6	8
<i>Pseudopleuronectes herzensteini</i>	2.7	2.2/1.6	1.37	0.5	0.8	8
<i>Liopsetta pinifasciata</i>	2.2	1.8/1.5	1.2	0.4	0.6	7-8
CYPRINIDAE						
<i>Tribolodon hakonensis</i>	2.64	1.77/1.92	0.9	0.86		1-4
<i>T. brandtii</i>	2.51	2.21/1.98	1.11	0.6		1

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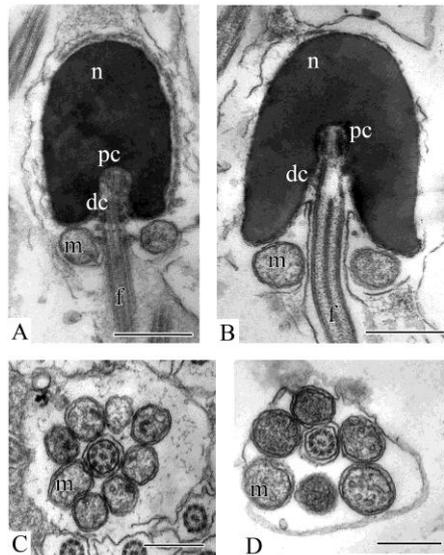


Fig. 1. The spermatozoa flat-headed flounder and pinewood: A – *Hippoglossoides dubius*, B – *Cleistenes herzensteini*, scale bar – 1 μm ; C – cross-section mitochondrial ring *Hippoglossoides dubius*, D – cross-section mitochondrial ring *Cleistenes herzensteini*, scale bar, 0.5 μm ; n – nucleus, m – mitochondrion, f – flagellum, pc – proximal, dc – distal centriole.

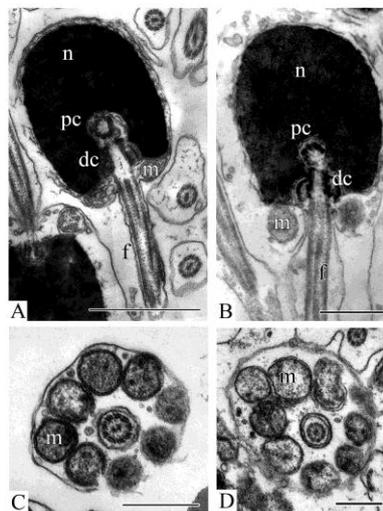


Fig. 2. The spermatozoa black flounder and brown sole: A – *Pseudopleuronectes obscura*, B – *Pseudopleuronectes herzensteini*, scale bar – 1 μm ; C – cross-section mitochondrial ring *Pseudopleuronectes obscura*, D – cross-section mitochondrial ring *Pseudopleuronectes herzensteini*, scale bar, 0.5 μm ; n – nucleus, m – mitochondrion, f – flagellum, pc – proximal, dc – distal centriole.

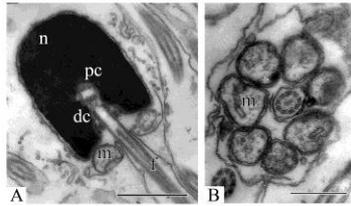


Fig. 3. The spermatozoa Far Eastern smooth flounder: A – *Liopsetta pinifasciata*, scale bar – 1 μm ; B – cross-section mitochondrial ring *Liopsetta pinifasciata*, scale bar, 0.5 μm ; n – nucleus, m – mitochondrion, f – flagellum, pc – proximal, dc – distal centriole.

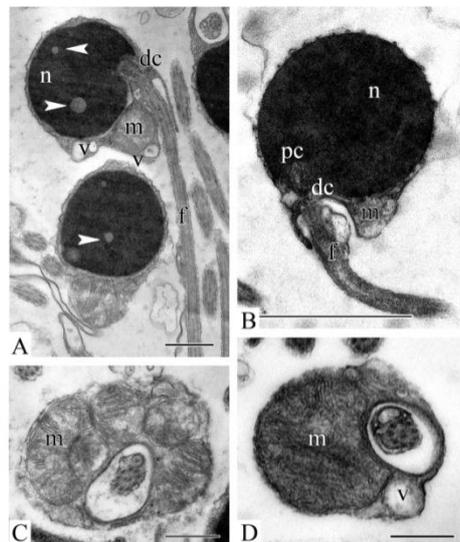


Fig. 4. The spermatozoa big – scaled redbfin and Eastern redbfin: A – *Tribolodon hakonensis*, scale bar – 1 μm ; B - *T. brandtii*, scale bar – 2 μm ; C – cross-section mitochondrial ring *Tribolodon hakonensis*, D - cross-section mitochondrial ring *T. brandtii*, scale bar, 0.5 μm ; n – nucleus, m – mitochondrion, f – flagellum, pc – proximal, dc – distal centriole, v – vesicles.

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SPECIES COMPOSITION AND FAUNAL CHARACTERISTICS OF FISHES OF THE YELLOW SEA

Jing Liu, Ping Ning

Laboratory of Marine Organism Taxonomy and Phylogeny, Institute of Oceanology,
Chinese Academy of Sciences, Qingdao, Shandong Province, 266071, P.R. China

E-mail: jliu@qdio.ac.cn(LJ); goodman123@vip.sina.com (NP)

Based on the collections in the Museum of Marine Biology, Institute of Oceanology, Chinese Academy of Sciences, and some literature sources, the authors analyzed the species composition and faunal characteristics of fishes of the Yellow Sea. The results show that 321 species are occurred in the Yellow Sea, belonging to 4 classes, 35 orders, 118 families, 220 genera. Among them, 138 species are warm-temperate type, 108 species are warm-water type, 70 species are cold-temperate type and only 5 species are cold-water. The Yellow Sea has the most species in common with the East China Sea and Japanese coastal waters, but it lacks some tropical or subtropical warm-water species. Some cold-temperate or cold-water species live in the Yellow Sea all the year round in common with the Far-East Sea, the Okhotsk Sea and the Bering Sea, such as *Liparis tanakae*, *Enchelyopus elongatus* and *Cleisthenes herzensteini*, which rarely appear in the East China Sea. The fish fauna of the Yellow Sea belongs to the sub-fauna of North Pacific Temperate Biotic Region.

There are 193 species belonging to demersal fishes, 29 species are benthopelagic fishes, 34 species are Pelagic-neritic fishes, 41 species are reef-associated fishes, 15 species are pelagic-oceanic fishes and 9 species are bathydemersal species. Several demersal species such as *Gadus macrocephalus* and *Cleisthenes herzensteini* which dominated the catches in the 1950s and 1960s were gradually depleted with a fully utilization by the 1970s and 1980s; Some small demersal fishes which are only by-catch 40-50 years ago such as *Enchelyopus elongatus* and *Ammodytes personatus* have an increasing fishing catch now. The Pelagic-neritic fishes such as *Engraulis japonicus*, *Scomberomorus niphonius*, *Scomber japonicus* and *Trachurus japonicus* are mainly warm-water or warm-temperate small species which are major fishing targets now, especially the *Engraulis japonicus* has become the absolutely dominant species. Some benthopelagic fishes, such as *Larimichthys polyactis*, *Trichiurus japonicus*, *Pampus argenteus* and *Pennahia argentatus*, have lost their dominant

status with a low CPUE now because of the overfishing. Nevertheless, the resources of several economic species, such as *L. polyactis*, increase obviously after some effective protection in recent years. The fishery resource of the Yellow Sea has been over- exploited. Therefore, it is important to exploit the resource reasonably. The effective management of fishery resource and ecological protection should be payed attention..

Key Words: fish fauna; species composition; biodiversity; the Yellow Sea.

**DIVERSITY AND DISTRIBUTION OF POLYCHAETES IN THE CHINESE
SEAS AND COMPARISON OF THE YELLOW SEA FAUNAL
CHARACTERS TO THE OTHER SEA AREAS**

Yanli Lei, Ruiping Sun, Zhiyuan Zhao, Wenlong Liu

(Institute of Oceanology, Chinese Academy of Sciences, Qingdao 266071, China.

E-mail: leiyali@qdio.ac.cn; Tel: 0086-532-82898795

Polychaetes are one of the most frequent and dominant groups among the marine macrobenthos. Thus, they often play an important role in marine benthic ecosystems. In this study we summarized the literature data on the taxonomy and biogeography of marine polychaetes recorded in the China seas and investigated polychaete specimens which were sampled during several cruises in recent years. The faunal characteristics and biogeographical patterns of the polychaetes from the Yellow Sea were compared with those from the other areas within or near the China seas. Shallow sea-floor harbored more polychaete species than intertidal flats, and silt-sandy sediments were their favorite habitat. More than 1000 species were recorded in Chinese sea areas: the East China Sea and the Yellow Sea recorded beyond 300 species each, and excess 600 species were recorded in the South China Sea. Recent polychaete fauna in the Yellow sea usually dominant by *Nereis longior* Chlebovitsch et Wu, *Ampharete acutifrons* (Grube) , and *Ninoe Palmata* Moore, *Nephtys oligobranchia* Southern. In addition, *Heteromastus filiformis* (Claparède) was also frequently occurred. The polychaete fauna in the Yellow Sea was rather different with that in the South China Sea, however, was more resembled to that in the Japanese seas compared to that in the East China Sea. Moreover, around one-third of the Yellow sea species were also recorded in the Russian Far Eastern Seas. Our study suggested that the Yellow Sea fauna are more closed to that of the temperate fauna common to northwest Pacific waters.

COMPOSITION AND DISTRIBUTION OF ECHINODERMS IN THE YELLOW SEA

Ning Xiao^{1,2}, Yulin Liao¹

¹Institute of Oceanology, Chinese Academy of Sciences, Qingdao 266071, China

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

This paper deals with the composition and distribution of echinoderms in the Yellow Sea. The materials based upon were collected from the benthic investigations of the Yellow Sea conducted by the Institute of Oceanology, Chinese Academy of Sciences, Qingdao, over the past fifty years. A total of 59 species have been found in the Yellow Sea, belonging to 5 classes, 16 orders, 26 families, and 43 genera. These include 1 crinoid, 10 asteroids, 16 ophiuroids, 9 echinoids and 23 holothurians. In the species composition, the species of North temperate fauna share 52.5%, most coldwater species of which inhabit the Yellow Sea Cold Water Mass; the eurythermal warm-water species are widely distributing the shallow and coastal waters, sharing 40.7%; the stenothermal water-water species (tropical and subtropical species) are found from southernmost part of the Yellow Sea affected by the Taiwan Warm Current and Yellow Sea Warm Current, sharing 6.8%. Analysis shows that the echinoderm fauna of the Yellow Sea is dominantly temperate though it includes quite a few warm-water elements. Consequently, we suggest that the echinoderm fauna of the Yellow Sea should be considered as a constituent portion of the temperate fauna, being a subregion belonging to North Pacific Temperate Biotic Region. In addition, there is evidence that the structure and depth of Cold Water Mass are possible factors controlling patchy distribution and high dominance of coldwater species.

INTRASPECIFIC POLYMORPHISM OF *UNDARIA PINNATIFIDA* IN PETER THE GREAT BAY

Shibneva S. Yu., Skriptsova A. V.

Institute of Marine Biology Far-Eastern Branch of Russian Academy of Science

Palchevsky st., 17, Vladivostok, 690041, Russia

E-mail: askriptsova@mail.ru

Introduction

Undaria pinnatifida (Harvey) Suringar is endemic to Japan, Korea, and China. Lately *Undaria* is introduced to the France, New Zealand, Australia, and Argentina. In Russia, *Undaria pinnatifida* is distributed only in Peter the Great Bay (cited from Skriptsova et al., 2004).

Undaria pinnatifida, in similarity to other marine macrophytes, shows great intraspecific phenotypic variability. At present *U. pinnatifida* is divided into two recognized forms on the basis of morphology: f. *typical* and f. *distance*. *U. pinnatifida* f. *typica* has a short stipe, shallow pinnate division of the blade and sporophyll development is often confluent with the base of the blade. *U. pinnatifida* f. *distance* is characterized by an elongated stipe and deeply-divided blade, with large sporophyll development limited at the basal portion of the stipe (Okamura, 1915). A third form, f. *narutensis*, was described by Yendo (1911) as containing a short stipe, with less folded sporophylls which became confluent with the lamina and grew sterile ligules from the sporophyll margin. This form was subsequently recognized as an extreme expression of f. *typica* (Okamura, 1915).

Such intraspecific variability may be result of environmental factors, such as differences between or within habitat. The most important environmental factors affect variability of marine plant morphology are water movement, nutrient concentration, light intensity. On the other hand within-species morphological variability exhibited by different organisms may reflect different levels of genetic differences.

It was shown, that morphological variability depends on just local conditions of microhabitat (Stuart, 1999), but other researchers found that morphological distinct forms have genetic differences (Lee & Sohn, 1993). In this research different morphs, cultivated in the similar conditions, maintained distinctive morphological features.

However, later Japanese phycologists did not find any difference in genome of these morphs (with ITS и rbcL-markers) (Uwai, 2006).

The objective of the present study was to reveal the morphological variation in *Undaria pinnatifida* in Peter the Great Bay (Sea of Japan) and to find the correlation between thallus morphology and light exposure.

Materials and Methods

Sampling

Sampling was carried out during 2000, 2004, 2006, and in 2008 – 2010. Ten locations were selected within Peter the Great Bay (Fig. 1).

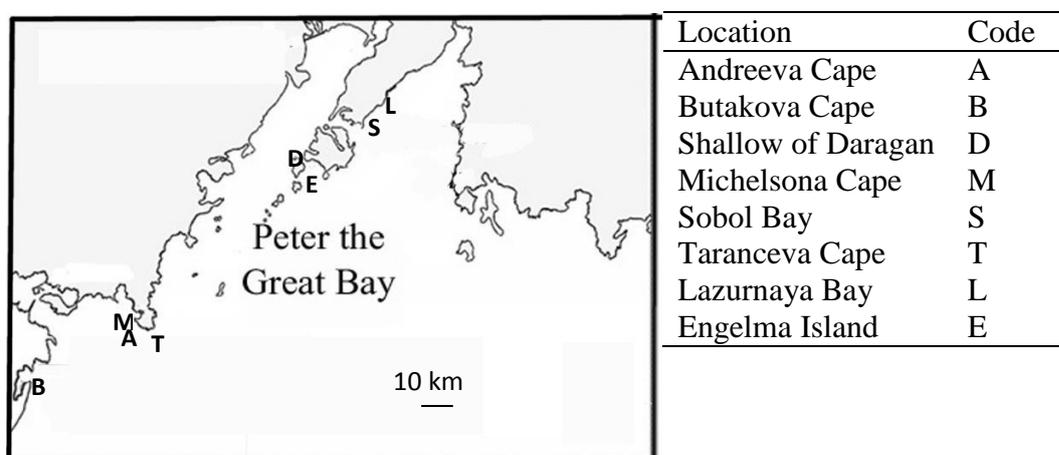


Fig. 1. Locations of sampling *Undaria pinnatifida* within Peter the Great Bay.

Within each location 6-10 adult individuals were randomly collected in mid of June at 1.5-2 m depth by SCUBA diving. In June algae have well developed fronds. In addition we analyzed plant morphology in relation to shaded and light ecotopes in four locations (Sobol Bay, Andreeva Cape, Butakova Cape and Lazurnaya Bay). Five morphological characteristics were chosen to cover most parts of the thallus. The morphological characters and procedure for measurement are given in Fig. 2. In addition we calculate the relations StL/TL , BL/BW and WW/BW based on measured morphological characteristics.

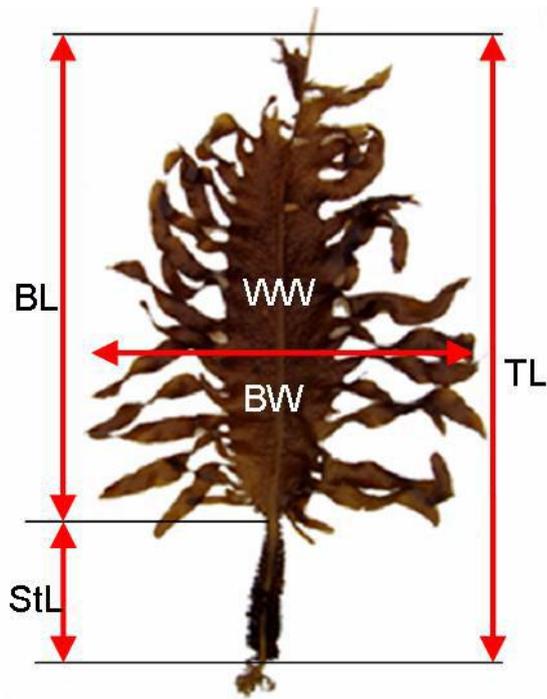


Fig. 2. Procedure of measurement of morphological parameters of *Undaria pinnatifida*. TL – frond length, BL – lamina length, StL – stipe length, BW – lamina width, WW – width of undivided part of the lamina.

Discriminant analysis was performed to determine the morphological characteristics contributed morphs separation that could be used to define morphs from each environment. Principal components analysis was performed on morphometric data to reduce morphometric variables into fewer scores of principal components. Interpretation of the loading matrix was facilitated by varimax rotation. The resulting principal components (factors) were analyzed using main-effect ANOVA to compare these characteristics between locations, light environment and individuals. Then the relative magnitude effect (CO^2) was calculated based on Sums of squares according to Plochinsky (1970). Before testing, the data set was checked for normality and homogeneity of variances (Levene's test). The software that was used is Statistica 6.0.

Results and Discussion

Spatial variability of *Undaria pinnatifida* morphology

Most morphological characteristics of *Undaria pinnatifida* showed considerable variation among locations (Table 1). For example, total frond length and stipe length differed by 3-fold between the individuals from Butakova Cape and Shallow of Daragan. Width of undivided part of the lamina of plants collected in Shallow of

Daragan was 2-times higher in comparison with plants from other locations. BW and BL were the less variable morphological characteristics between sites.

Table 1. Summary statistics of morphological characteristics of *Undaria pinnatifida* in Peter the Great Bay. Each location: data given are means \pm SE. Location codes are given in Table 1. Codes for morphological characters see in Fig. 2.

Area	TL	BL	StL	WW	BW	TL/StL	WB/WW	BL/BW
B	119.7 \pm 4.1	87.4 \pm 3.2	32.3 \pm 1.7	6.7 \pm 0.3	50.6 \pm 2.6	4.0 \pm 0.2	7.9 \pm 0.5	1.9 \pm 0.1
A	72.9 \pm 2.5	58.9 \pm 2.1	13.5 \pm 0.8	6.0 \pm 0.3	45.2 \pm 1.7	6.2 \pm 0.4	7.8 \pm 0.3	1.4 \pm 0.1
L	61.8 \pm 2.2	49.3 \pm 2.1	12.4 \pm 0.4	7.6 \pm 0.5	35.6 \pm 1.8	5.1 \pm 0.2	5.9 \pm 1.2	1.5 \pm 0.1
S	70.0 \pm 2.2	56.2 \pm 1.9	13.8 \pm 0.6	8.2 \pm 0.3	39.7 \pm 1.4	5.4 \pm 0.2	5.1 \pm 0.2	1.5 \pm 0.1
M	77.3 \pm 2.4	63.1 \pm 2.3	14.1 \pm 0.9	7.1 \pm 0.4	58.8 \pm 2.8	5.9 \pm 0.3	8.5 \pm 0.4	1.1 \pm 0.1
T	72.2 \pm 6.4	57.4 \pm 5.5	14.7 \pm 1.4	5.9 \pm 0.4	57.2 \pm 3.9	5.1 \pm 0.4	10.1 \pm 0.7	1.0 \pm 0.1
D	43.5 \pm 2.5	30.5 \pm 2.3	13.1 \pm 0.4	14.6 \pm 0.7	54.8 \pm 1.9	3.4 \pm 0.2	4.1 \pm 0.2	0.6 \pm 0.1
E	68.2 \pm 2.5	55.9 \pm 2.1	12.3 \pm 0.5	9.4 \pm 0.4	47.4 \pm 1.6	5.6 \pm 0.2	5.5 \pm 0.3	1.3 \pm 0.1

Discriminant analysis showed that stipe length and width of undivided part of lamina have a greatest contribution in *Undaria pinnatifida* polymorphism. These morphological characteristics are satisfactory for morph separation. The distribution of the plants according to co-effect of measured morphological characteristics on the two discriminant functions (Score 1 and 2) is shown in Fig. 3. The first axis (score 1) explained 65.7% and the second axes (score 2) 21.8% of the morphological variation. Width of undivided part of lamina gives a highest loading on the first axis, and stipe length yield the highest loading on the second axes (Table 2). Plants collected in the Shallow of Daragan and on the Butakova Cape form separate groups based on these two scores.

Thus, *Undaria pinnatifida* in Peter the Great Bay have three morphologically different forms.

Form B (Fig. 4A) inhabit in the Butakova cape. Plants are characterized by high frond length (119 \pm 4.1 cm) and long stipe (up to 30-50 cm), thalli have a marked transitional zone between sporophyll and lamina. This form is the most close to the *U. pinnatifida* f. *distance* described from Hokkaido (Okamura, 1915).

Fig. 4. Morphologically different forms of *Undaria pinnatifida* in Peter the Great Bay.

It should be pointed that groups of individuals, resulted from Canonical analysis, were not homogenous that suggested morphological differentiation of plants within location. So, we test morphological variability of *Undaria pinnatifida* morphology in depend on light exposure (shaded and open ecotopes) in four locations (Sobol Bay, Lazurnaya Bay, Butakova Cape and Andreeva Cape).

Variability of *Undaria pinnatifida* morphology with light.

Mean frond length, blade length and stipe length was significantly greater for all individuals (except algae collected in the Sobol Bay) from shaded ecotopes (depth more than 3 meters or canopy of *Costaria costata* and sargassaceous algae) compared with the light ecotopes (Fig. 5).

Principal component analysis performed on the suite of morphometric measurements revealed three morphological factors that explained 40.9, 24.4, and 17.9% of the variance, respectively (Table 3). Factor 1 was characterized by high positive loadings for stipe length and frond length. Factor 2 was associated with relation of BW/BL, which characterized lamina form. Factor 3 was characterized by high positive loadings for WW and negative loadings for BW/WW, variable combination associated with a frond division.

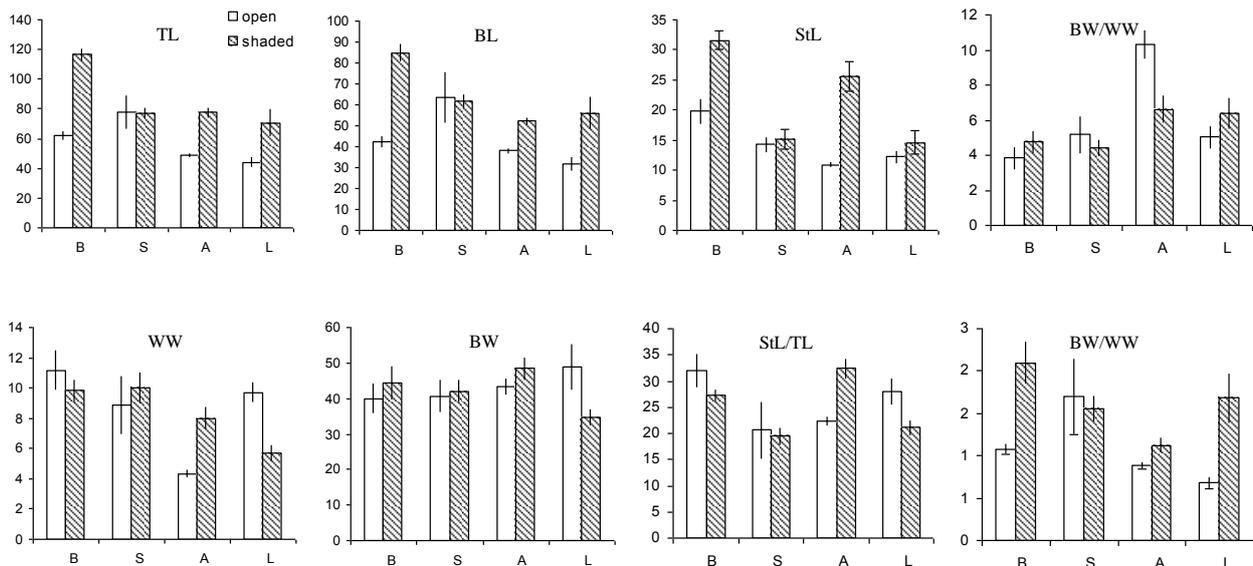


Fig. 5. Variation of morphological characteristics of *Undaria pinnatifida* between shaded and open ecotopes in four locations. Location codes are given in Fig. 1.

Factor loadings from individual thalli at each site were plotted on the first two orthogonal axes to visualize any separation of morphs from the different light environments (shaded and open ecotopes). Analysis revealed a separation by gross morphology defined by the first two components between thalli from shaded habitats and open ones, however this separation was not obvious, suggesting strong impact of inter-sites environmental variations in the morph separation (Fig. 6).

Table 3. Factor loadings getting by Principal component analysis and Varimax rotation of morphological characters of *Undaria pinnatifida* from Peter the Great Bay.

Morphological character	Factor 1 (length)	Factor 2 (lamina form)	Factor 3 (lamina division)
TL	0,747214	-0,532747	0,131744
StL	0,974895	-0,087813	0,155647
WW	0,170850	0,091962	0,927237
BW	0,204648	0,688477	-0,109911
StL/TL	0,597043	0,493642	0,193604
BW/WW	-0,106398	0,305531	-0,917999
BL/BW	0,285760	-0,936221	0,141673
Expl.Var	2,029260	1,987529	1,813706
Prp.Totl	0,289894	0,283933	0,259101

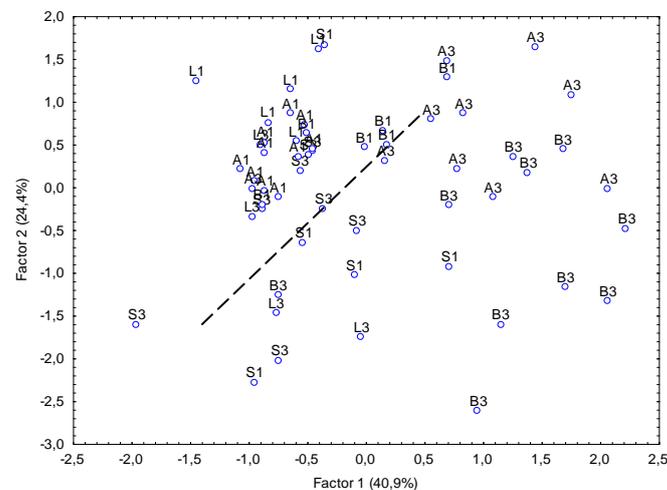


Fig. 6. Plot of Factor 1 (variables defining length of frond and its' parts) against Factor 2 (variables defining lamina form) for individuals collected from shaded and open ecotopes in four locations. Locations codes are given in Fig. 1. Line shows separation of individuals from shaded (additional code 3) and open ecotopes (additional code 1).

Results from main-effect ANOVA affirm that location was the dominant contributor to variance in all morphological factors. Variation among individuals within a site generally had a low (<15%), contribution towards the total variation. Light exposure influence length of frond and its' parts only (Table 4).

Table 4. *Undaria pinnatifida*. Results from ANOVA on individual morphological characters [df=1, 5 and 9 for depth, site and individuals within site]. No transformations were necessary to homogenize variances (Levene's-test of homogeneity of variance: $P > 0.05/4$ for all). ω^2 - magnitude of effect (%).

Morphological character	Levene test		SS	MS	F	p	ω^2
Factor 1 (Length)	0.36	Light exposure	11.0419	11.0419	18.9545	<0.0001	19.4
		Location	16.3440	5.4480	9.3520	<0.0001	28.7
		Individuals	4.2093	0.4677	0.8028	0.6157	7.4
Factor 2 (Lamina form)	0.04	Light exposure	3.1434	3.1433	3.7900	0.0579	5.5
		Location	7.5270	2.5090	3.0251	0.0394	13.2
		Individuals	6.9072	0.7674	0.9253	0.5127	12.1
Factor 3 (lamina division)	0.89	Light exposure	0.2492	0.2492	0.3273	0.5701	0.4
		Location	14.9803	4.9934	6.5584	0.0009	26.3
		Individuals	5.6654	0.6294	0.8267	0.5951	9.9

Our results demonstrated significant correlation between light environment and frond length. Similarly effect of different light intensity on thallus morphology was observed in other works (Cheshire & Hallam, 1989; Skriptsova & Yakovleva, 2002). The shade-induced elongation consistent with the concept of foraging for light. It is wellknown that an efficient orientation of photosynthetic structures to light flow is

one of the general biological reactions that coincides with an increase of light absorption with surface area of the organism.

Besides, as our research demonstrated (Table 4), thallus morphology depends on location more significantly than on light exposure. This fact may be explained with influence of other factors, such as water movement and nutrient concentration. Light factor can not explain morphology variety of *U. pinnatifida*, as thallus morphology is conditioned by complex of many environmental factors. Therefore, to estimate influence of environment most completely comprehensive approach should be applied for researching morphology adaptation depending on complex of environmental factors. In addition, variability in thallus morphology from different populations may be explained by genetic variety.

Conclusion

Thus, *Undaria pinnatifida* in Peter the Great Bay is morphologically polymorphic. It represented by at least three morphs different by frond length, stipe length, lamina division.

Light exposure influences length of frond and its parts, but this factor explained 19,4 % of morphological variance only. Environment differences between locations determined higher morphological variability. Influence of other factors (water movement, nutrient concentration and whole complex of factors) on the *U. pinnatifida* morphology and its genetic diversity will be a subject of further investigations.

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THE SPECIES DIVERSITY AND ITS FLORA OF ORDER ECTOCARPALES (PHAEOPHYTA) FROM CHINA COAST

Rixiao Luan^{1,2}, Lanping Ding^{1*} and Hongwei Wang³

¹ Institute of Oceanology, Chinese Academy of Sciences, Qingdao 266071,
China

² Dalian Museum of Natural History, Liaoning Province, Dalian 116023, China

³ Liaoning Normal University, Dalian 116029, China

Corresponding author: lpd2118@hotmail.com

Ectocarpales (Phaeophyta) is a very large order in the brown algae. Its thallus are composed of heterotrichous filament which can produce branches consisted of uniseriate cells, and live by attachment, floating or endogeny.

In the recent past years, lots of specimens belonging to this Order were collected while marine algal resources were investigated along the coasts of China. With such rich specimen material collected above, authors carried on its morphological taxonomy in more detail. By identification, this Order can be divided into 3 families, 13 genera and 62 species in China. Among them, family Ectocarpaceae includes 9 genera, vs. *Acinetospora*, *Ectocarpus*, *Feldmannia*, *Hincksia*, *Kuckuckia*, *Laminariocolax*, *Rotiramulus*, *Spongonema* and *Streblonema* with 57 species, family Pilayellaceae includes 3 genera, vs. *Bachelotia* and *Pilayella* with 3 species, and family Sorocarpaceae includes 2 genera, vs. *Botrytella* and *Polytretus* with 2 species, respectively, and of them, 4 new species, 2 new record, 6 new combinations, and 3 modified species. It is introduced to the species' characteristic, habitats and geographical distribution with a key referring to family, genus and species.

The coastal waters of China mainly are divided into three marine flora. The species distributes into three marine flora. There are 35 species in the flora of Yellow-Bo Sea, 3 in East China Sea and 17 in South China Sea respectively, with extra overlapping species 1 for Yellow-Bo Sea and East China Sea, 3 for East China Sea and South China Sea, and 3 for these three intact flora.

Key Words: species diversity, Ectocarpales, China coast, flora

**SPATIAL DISTRIBUTION AND COMPOSITION OF MICROBENTHOS
IN PARTICULAR CILIATES IN RELATION TO BENTHIC
ENVIRONMENTAL FACTORS IN THE YELLOW SEA**

Zhaocui Meng^{1,2}, Kuidong Xu^{1*}, Yanli Lei¹, Yingying He^{1,2}

¹Department of Marine Organism Taxonomy & Phylogeny, Institute of Oceanology,
Chinese Academy of Sciences, Qingdao 266071, China

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

E-mail: kxu@qdio.ac.cn

Using the epifluorescence microscopy and the quantitative protargol stain, we investigated the spatial distribution and composition of microbenthos in the surface sediments of 48 stations in the Yellow Sea. The abundance of bacteria in the surface 0-5 cm sediment ranged from 2.36×10^8 to 1.85×10^9 cells cm^{-3} and cyanobacteria from 2.31×10^4 to 2.31×10^6 cells cm^{-3} . The abundance of phototrophic (PNF) and heterotrophic nanoflagellates (HNF) were about three orders of magnitude lower than that of bacteria, but one order of magnitude higher than that of cyanobacteria, ranging from 6.43×10^5 to 8.8×10^6 cells cm^{-3} and from 5.78×10^4 to 5.91×10^6 cells cm^{-3} , respectively. The abundance of diatoms highly varied from 3 to 1.06×10^5 cells cm^{-3} in the surface 0-8 cm sediment, but distinctly higher than that of heterotrophic microflagellates (HMF, 1 to 182 cells cm^{-3}) and ciliates (1 to 221 cells cm^{-3}). The biomass partitioning indicated the primary importance of PNF (on average $40.73 \mu\text{g C cm}^{-3}$), followed by bacteria ($22.62 \mu\text{g C cm}^{-3}$), HNF ($19.34 \mu\text{g C cm}^{-3}$), and cyanobacteria ($8.84 \mu\text{g C cm}^{-3}$). By contrast, diatoms ($0.84 \mu\text{g C cm}^{-3}$), ciliates ($0.15 \mu\text{g C cm}^{-3}$) and HMF ($0.03 \mu\text{g C cm}^{-3}$) contributed only a very small fraction to the total microbial biomass. About 94% of diatoms, 77% of ciliate and 56% of HMF numerically distributed in the surface 0-2 cm sediment layer, while there were no distinct differences in vertical distribution of bacteria, cyanobacteria, PNF and HNF. Comparing with the pelagic environment in the Yellow Sea, the densities of individual microbenthos in the upper sediment layer were about three (2 to 4) orders of magnitude higher per unit volume compared to the abundance of corresponding planktonic assemblages. These findings, coupled with the high abundance of microbenthos, emphasize the potential for rapid primary and secondary production of

microorganisms and detrital utilization in the sediments of the Yellow Sea cold water mass.

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NITROGEN UPTAKE BY MACROALGAE IN SANYA BAY (HAINAN ISLAND, CHINA)

Eduard A. Titlyanov^{1*}, Serguei I. Kiyashko¹, Tamara V. Titlyanova¹, Irina M. Yakovleva¹, Li Xiu Bao², Huang Hui²

¹A.V. Zhirmunsky Institute of Marine Biology, Far Eastern Branch of the Russian Academy of Sciences, Palchevskogo 17, Vladivostok, 690041, Russia

²China South Sea Institute of Oceanology Chinese Academy of Science, No 164, Xingangxi Rd. 510301 Guangzhou, China

Composition of macroalgal and cyanobacterial communities was investigated at the Luhuiton coral reef in Sanya Bay (Hainan Island, China). It was shown that in the intertidal zone, mainly mono- and bi-dominant communities of crust algae and algal turf represent macroalgal communities. In the upper-subtidal zone, both communities of algal turf and those of frondose and fleshy algae (*Sargassum* spp., *Padina* spp., *Turbinaria ornata*, *Lobophora variegata* and etc.) were common. The algae, especially, in the upper-subtidal zone, were tightly overgrown by epiphytes. The invasive species and algal blossom were not recorded.

Nitrogen stable isotope ratios ($\delta^{15}\text{N}$) and molar C: N ratios were determined for 18 species of green, red and brown macroalgae and for 2 species of cyanobacteria collected at the Luhuiton coral reef. Concentrations of dissolved inorganic nitrogen (DIN) and orthophosphates in seawater at the Luhuiton and the Xiaodonghai reefs were measured during different seasons. High $\delta^{15}\text{N}$ values of macroalgae ($> 8\text{‰}$) confirmed that wastes from the marine animal farms and sewages were the main sources of dissolved inorganic nitrogen (DIN) in Sanya Bay. The main source of nitrogen for cyanobacteria was determined as molecular nitrogen dissolved in seawater. Concentrations of orthophosphates and DIN in seawater above the reefs averaged $0.15\ \mu\text{M}$ and $2.35\ \mu\text{M}$, respectively, exceeding the threshold concentrations (algal blooms) in 1.5 – 2.5-fold. However, at that level of pollution by DIN in Sanya Bay.

Analyses of the molar C: N ratio in the tissue of macroalgae inhabiting Luhuiton reef showed that they were N limited besides the high seawater DIN concentration, suggesting a limited ability of the algae to absorb dissolved inorganic nitrogen. This is theoretically in account with either some difficulty of nitrogen access to the attractive

centers or with the seawater deficiency in elements or substances contributing to nitrogen absorbance, or with the presence of nitrogen assimilation inhibitors in the polluted waters of Sanya Bay. We suggest that assimilation of seawater nutrients by macroalgae is prevented by low photosynthetic rates of the algae over the limitation in CO₂ and bicarbonate diffusion to chloroplasts under the thick layer of sediments covering the algal thalli and the dense overgrowth of thalli by epiphytes. However this hypothesis needs an accurate experimental verification both in the field and laboratory experiments.

DINOFLAGELLATES IN EPIPHYTIC ASSEMBLAGE OF PETER THE GREAT BAY, SEA OF JAPAN

M. S. Selina, T.V. Morozova, T. Yu. Orlova

A.V. Zhirmunsky Institute of Marine Biology FEB RAS, Vladivostok 690041

E-mail: marsel@imb.dvo.ru

Dinophytes or dinoflagellates are one of the most diverse and widely distributed groups of microalgae in the World's Oceans. Representatives of this group are found in the water column, surface sediments, and in fouling on natural and artificial substrates. At the end of the 1990s, 332 dinoflagellate species of 58 genera (Konovalova, 1998) were known from the plankton of the Far Eastern seas of Russia and the adjacent areas of the Pacific Ocean. There had been no information on dinoflagellates from other biotopes of this region until the beginning of the current century.

Recently started studies of benthic dinoflagellates in sands of the upper subtidal of Peter the Great Bay revealed a high diversity and uniqueness of these organisms, most of which were recorded in the seas of Russia for the first time (Selina, 2008).

Epiphytic dinoflagellates, like their planktonic counterparts, are able to produce toxins causing fish mortalities and various poisonings of warm-blooded animals and humans. Out of 80 species of toxin-producing dinoflagellates (Hallegraeff, 2002), about 20 are found in epiphytic and in benthic assemblages.

The aim of the present work was to study the species composition of dinoflagellates and to reveal potentially toxic species in fouling on macrophytes from Peter the Great Bay, Sea of Japan.

Samples of epiphytic microalgae were collected from macrophytes in a bight of Peter the Great Bay, Sea of Japan (43°04'N and 131°57'E). This bight is an open-type embayment, which is free of ice during the winter and is weakly protected from the action of waves and wind. Water temperature varies during the year from (-1.5) to 24 °C, salinity is 30-34 psu. Macrophytes were collected in August, September, and October 2006 at a depth of 0.5-3 m. The material consisted of one species of seagrass, 18 red, 13 brown, and 3 species of green algae, which constitute the bulk of the phytocenosis of the study area. Algae were thoroughly rinsed in sea water, washing off the epiphytes. The suspension was passed through fine gauze (mesh size of 150

µm) and concentrated by filtration through a 20 µm mesh size gauze. The concentrate was fixed with Lugol's solution and concentrated using the sedimentation technique to 5–7 ml.

The cell morphology was examined by light and scanning electron microscopy. We found 29 species of epiphytic dinoflagellates on macrophytes. Planktonic forms representing 54% of total dinoflagellate species diversity were predominant. These were mainly representatives of the genera *Dinophysis*, *Torodinium*, *Pyrocystis*, *Alexandrium*, *Gonyaulax*, *Protoperidinium* and *Dipllopsalis*, as well as *Prorocentrum* having both planktonic and benthic forms. Resting spores of the parasitic dinoflagellate *Dissodinium pseudolunula* Swift ex Elbrächter et Drebes were recorded.

A significant proportion of dinoflagellates (33% of total species) were benthonic forms; benthic-planktonic forms were 13%. Benthic and benthic-planktonic forms of dinoflagellates were represented by 13 species of 8 genera (Table 2), among which species with autotrophic feeding were predominant (71% of all species). Heterotrophs made up 29% and were only represented by benthic species. *Prorocentrum fukuyoi* Murray et Nagahama, *Cabra matta* Murray, Patterson, *Ostreopsis* cf. *siamensis* Schmidt, and *O.* cf. *ovata* Fukuyo are first records for the seas of Russia. *Amphidinium carterae* Hulburt is the first record for the Far Eastern seas; *Pseudothecadinium campbellii* Hoppenrath et Selina is the first record for the Sea of Japan. The number of species of epiphytic dinoflagellates on a host macrophyte varied from 1 to 10 during the observation period. Only one species was recorded on *Phyllospadix iwatensis*, the largest number of species was observed on *Codium fragile*. The most widespread were *Ostreopsis* cf. *ovata*, *Ostreopsis* cf. *siamensis*, and *P. fukuyoi*. The former two species were found from August to October at a water temperature of 7–25°C on almost all investigated macrophytes, the latter species occurred in September. In October, *P. campbellii* was observed on most (69%) macrophytes. Among other dinoflagellates with a frequency of more than 20%, there were *C. matta* and *Prorocentrum lima* (Table).

Among dinoflagellates found on macrophytes in Peter the Great Bay, *A. carterae*, *A. operculatum* Claparede et Lachmann, *P. lima* (Ehrenberg) Dodge, *Ostreopsis* cf. *ovata*, and *Ostreopsis* cf. *siamensis* are known as potentially toxic species.

The species of the genus *Ostreopsis* are important components of epiphytic assemblages of subtropical and tropical regions and are thought to be potential progenitors of toxins responsible for ciguatera fish poisoning (Faust et al. 1996). However, some species of this genus were recently recorded in temperate regions such as the Mediterranean Sea and Tasmania. Our records of *O. cf. ovata* and *O. cf. siamensis* in a region characterized by extremely cold (below zero) winter temperatures suggest a high tolerance to a wide temperature range. This is the first record of the genus *Ostreopsis* in Russian seawaters, which are characterized by cold temperatures during the winter season.

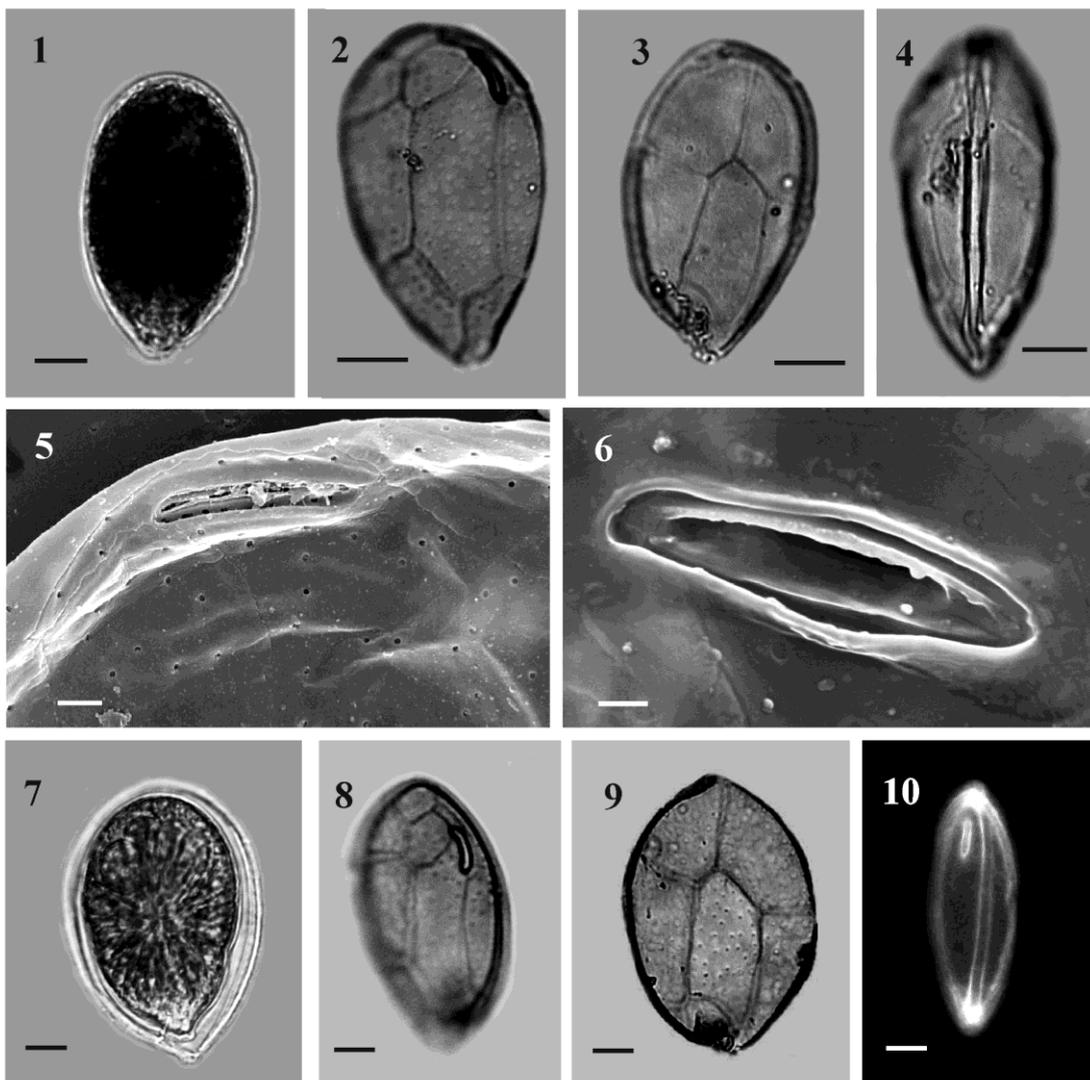
The two species (*O. cf. ovata* and *O. cf. siamensis*) differ from each other in cell size and the length of the Po plate. *O. cf. ovata* cells are smaller in length and width, with a dorsoventral diameter of 36–60 μm and a transdiameter of 24–45 μm (Figs 1-3), in comparison with *O. cf. siamensis* having corresponding measurements of 63–78 μm and 36-54 μm , respectively (Figs 7-9). Cells of *O. cf. siamensis* are slightly flattened in comparison with *O. cf. ovata* cells; dorsoventral diameter to anteroposterior diameter ratio is 1.9-2.7 for *O. cf. ovata* (Fig. 4) and 1.8– 3.5 for *O. cf. siamensis* (Fig. 10). The length of the pore plate in *O. cf. ovata* (6.3-8.3 μm) is shorter (Fig. 5) than in *O. cf. siamensis* (11-13 μm) (Fig. 6). The diameters of the thecal pores in *O. cf. ovata* and *O. cf. siamensis* markedly overlap (0.12–0.25 μm and 0.16–0.20 μm , respectively). Further studies of the *Ostreopsis* cultures are also needed to support our morphological identification and to determine the toxicity of these two species in Peter the Great Bay.

Other potentially toxic species, such as *P. lima* and *A. carterae* were recorded in the Sea of Japan during previous research. Most of epiphytic dinoflagellates did not show any significant preference for any algal group, although the highest abundance of *Ostreopsis* spp. occurred on the rhodophyte *Neorhodomela larix*. Due to the constant occurrence of new potentially toxic dinoflagellates during the summer–autumn period, monitoring of epiphytic assemblage is a necessity.

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Figures 1-10 *Ostreopsis* species from Peter the Great Bay, Russian Sea of Japan.

Figures 1–5 *Ostreopsis* cf. *ovata*. 1–general view of cell, 2– cell in epithelial view, 3– cell in hypothecal view, 4– cell in side view, 5– view of the apical region showing the pore plate.

Figures 6–10 *Ostreopsis* cf. *siamensis*. 6–view of apical pore, 7– general view of cell, 8– cell in epithelial view, 9– cell in hypothecal view, 10– cell in side view.

Figures 1–4, 7–9 : LM; scale bars= 10µm. Figure 10 : LM, epifluorescence ; scale bar = 10 µm. Figures 5 and 6 : SEM ; scale bars= 1 µm.

Table: Frequency of occurrence of benthic and benthic-planktonic species of dinoflagellates in epiphytic assemblage in Peter the Great Bay in August–October 2006

Species	Type of nutrition	Biotope	Frequency of occurrence, %		
			VII	IX	X
<i>Amphidinium operculatum</i>	A	B-P	12	20	31
<i>Ampidinium carterae</i>	A	B-P	-	-	15
<i>Cabra matta</i>	H	B	35	-	8
<i>Cabra sf. matta</i>	A	B?	6	-	15
cf. <i>Gymnodinium</i>	A	-	12	-	-
<i>Ostreopsis</i> cf. <i>siamensis</i>	A	B	24	100	46
<i>Ostreopsis</i> cf. <i>ovata</i>	A	B	94	100	31
<i>Prorocentrum fukuyoi</i>	A	B	6	80	100
<i>Prorocentrum</i> sp.	A	-	12	-	-
<i>Prorocentrum lima</i>	A	B-P	24	-	-
<i>Pseudothecadinium campbelii</i>	A	B-P	-	-	69
<i>Sinophysis stenosoma</i>	H	B	-	-	8
<i>Thecadinium kofoidii</i>	A	B	12	-	8

A – autotrophic, H – heterotrophic, B – benthic, B-P – benthic-planktonic species

THE DIVERSITY OF HABs CAUSATIVE ORGANISMS ON THE RUSSIAN PACIFIC COAST

Tatiana Yu. Orlova, I.V.Stonik, M.S. Selina
A.V. Zhirmunsky Institute of Marine Biology, Far East Branch, Russian Academy of
Sciences, Vladivostok, 690041, Russia.

E-mail: torlova06@mail.ru

Introduction

The term “harmful algal blooms” (HABs) covers a heterogeneous set of events that share two characteristics: they are caused by microalgae and they have a negative impact on human activities. HABs involve a wide diversity of organisms, bloom dynamics and mechanisms of impact. Of the approximately 5,000 known species of phytoplankton, only some 300 species form HABs that are deleterious to aquatic ecosystems in one way or another, and only about 80 of these species are known to be toxin producers. Some phytoplankton toxins can be accumulated and/or transported in food chains to higher trophic levels where they contaminate shellfish, making them unsuitable for human consumption, or poison upper-level consumers, including fish, seabirds, marine mammals, and humans. In terms of the harmful effects two types of causative organisms are considered: the high-biomass producers and the toxic producers. Toxic events can be produced by a very low concentration of the causative organism. The Russian Pacific coast is one of many areas affected by HABs. Toxic events and reports of poisoning and subsequent death are not common in these waters, however concern centers on the high diverse representation of these potentially toxic algae in these waters.

Results

Based on a broad phytoplankton/microphytobenthos/ephyphytes sampling program bloom-forming and potential toxin producing species have been identified to date on the Russian Pacific coast. Continuous studies of harmful algae have been made only in some localities include Peter the Great Bay in the Sea of Japan, coastal waters of Sakhalin Island and Avachinskaya Guba Inlet off the Pacific coast on Kamchatka. The collection of data covers the period 1969-2010. Improved methods of sampling, preservation of samples, quantitative-qualitative analysis, laboratory cultures, cyst survey and toxicity detection were used. These investigations have revealed 48

species causing blooms of water and 35 species which are known as toxic producers (Table 1). Among the toxic species the great majority are dinoflagellates and diatoms. Diatoms are the most common bloom-forming algae in the Far Eastern Seas of Russia. 26 species of diatoms cause water blooms in the study area. Among the species studied, 8 species (Table 1) are known as potential producers of domoic acid. Toxicity of a culture of *P. multiseriis* isolated from the northwestern Sea of Japan has been found (Orlova et al. 2008). Domoic acid has been detected in cultures of *P. calliantha* and *P. pungens* from Peter the Great Bay. A blooms of both *Pseudo-nitzschia multiseriis*/ *P. pungens* were recorded in Amurskii Bay near Vladivostok and in the coastal waters of Sakhalin Island (Orlova et al, 1996, Stonik et al., in press). In recent 20 years the appearance and massive development of new, uncommon for this region, potentially toxic raphidophytes has been observed. The short-term outbreaks of *H. akashiwo* were recorded in Amurskii Bay near Vladivostok and in the coastal waters of Sakhalin Island. The distribution of species of the genus *Chattonella* is restricted by the northern part of the Sea of Japan. An extensive red tide that was caused by *Chattonella* sp. and resulted in fish mortality was first recorded in Amurskii Bay (Simakova et al., 1990; Shumilin et al., 1994).

Table 1. Harmful algae in the Far Eastern Seas of Russia

*Toxins have been detected in cultures of microalgae and shellfish from Russian waters

Group	Toxic*/potentially toxic species	Bloom- forming/red tides species
Diatoms	<i>Amphora coffeaeformis</i> <i>Pseudo-nitzschia delicatissima</i> , <i>P. multiseriis</i> *, <i>P. multistriata</i> , <i>P. pungens</i> *, <i>P. calliantha</i> *, <i>P. fraudulenta</i> <i>P. seriata</i>	<i>Cerataulina dentata</i> , <i>Chaetoceros affinis</i> , <i>C. constrictus</i> , <i>C. concavicornis</i> , <i>C. convolutus</i> , <i>C. contortus</i> , <i>C. debilis</i> , <i>C. decipiens</i> , <i>C. salsugineus</i> , <i>C. socialis</i> , <i>Coscinodiscus wailesii</i> , <i>Cylindrotheca closterium</i> , <i>Ditylum brightwelli</i> , <i>Eucampia zodiacus</i> , <i>Proboscia alata</i> , <i>Pseudo-nitzschia americana</i> , <i>P. multiseriis</i> , <i>P. multistriata</i> , <i>P. pungens</i> , <i>P. calliantha</i> , <i>Skeletonema costatum</i> , <i>Rhizosolenia setigera</i> , <i>Thalassionema nitzschioides</i> , <i>Thalassiosira anguste lineata</i> , <i>T. mala</i> , <i>T. nordenskioldii</i>
Dinoflagellates	<i>Akashiwo sanguinea</i> , <i>Alexandrium acatenella</i> , <i>A. ostenfeldii</i> , <i>A. tamarense</i> *, <i>A. catenella</i> , <i>Amphidinium</i>	<i>Alexandrium tamarense</i> , <i>Cochlodinium polykrikoides</i> , <i>Heterocapsa rotundata</i> <i>Karenia mikimotoi</i> , <i>Noctiluca scintillans</i> ,

	<i>carterae</i> , <i>A. klebsii</i> , <i>Dinophysis acuminata</i> *, <i>D. acuta</i> , <i>D. fortii</i> *, <i>D. norvegica</i> , <i>D. rotundata</i> , <i>D. tripos</i> , <i>Gonyaulax</i> <i>spinifera</i> , <i>Gymnodinium</i> <i>catenatum</i> , <i>Karenia brevis</i> , <i>K. mikimotoi</i> , <i>Karlodinium</i> <i>veneficum</i> , <i>Ostreopsis</i> cf. <i>ovata</i> , <i>O. cf. siamensis</i> , <i>Prorocentrum lima</i> , <i>P. reticulatum</i> , <i>Protoperidinium crassipes</i>	<i>Prorocentrum minimum</i> , <i>P. triestinum</i> , <i>Oblea rotundata</i> <i>Oxyrrhis marina</i> , <i>Protoperidinium bipes</i> , <i>Scrippsiella trochoidea</i>
Raphidophytes	<i>Chattonella marina</i> <i>Heterosigma akashiwo</i> <i>Fibrocapsa japonica</i>	<i>Chattonella marina</i> , <i>Heterosigma akashiwo</i>
Euglenophytes		<i>Eutreptiella eupharyngea</i> , <i>E. gymnastica</i> , <i>E. pascheri</i> , <i>Eutreptia globulifera</i> , <i>E. lanowii</i>
Chlorophytes		<i>Pyramimonas</i> aff. <i>cordata</i>
Chrysophytes		<i>Dinobryon balticum</i>
Prymnesiophytes	<i>Phaeocystis pouchetii</i>	<i>Phaeocystis pouchetii</i> <i>Chrysochromulina</i> sp.
Ciliates		<i>Mesodinium rubrum</i>

In the past 20 years *Noctiluca scintillans* caused most of the visible red tides recorded the southern part of the Pacific coast of Russia (Vyshkvartsev et al., 1982; Zhirmunsky, Konovalova, 1982). 23 species of dinoflagellates in Far Eastern Seas of Russia are known as toxin producers. *Alexandrium* spp. known as potential producers of PSP (paralytic shellfish poisoning). *A. tamarense* is a more common species in the coastal waters of the Far Eastern seas of Russia.

Toxicity of a cultures of *A. tamarense* isolated from different location on the Russian east coast were detected (Orlova et al. 2007). Red tides caused by *A. tamarense* and *A. acatenella* at one million cells per liter were recorded in Avachinskaya Guba Inlet in Kamchatka and in Aniva Bay (Konovalova, 1989).

Data on the qualitative and quantitative composition of resting stages of planktonic microalgae in recent marine sediments from the Russian East coast over the period 2000–2007 revealed cysts of the potentially toxic species *Alexandrium tamarense*, *A. cf. minutum*, *Gymnodinium catenatum* (PSP toxin producers), and *Protoceratium reticulatum* (yessotoxin producer) and cysts of bloom-forming species *Cochlodinium* cf. *polykrikoides* and *Heterosigma* cf. *akashiwo* (Orlova et al., 2004; Orlova,

Morozova, 2009). The cysts of toxic species *Alexandrium tamarense* were the dominant cyst type in the study area.

A recent investigation of benthic dinoflagellates and epiphytic on macrophytes in Peter the Great Bay in the Sea of Japan showed the occurrence of potentially toxic species (*Ostreopsis* cf. *ovata*, *O.* cf. *siamensis*, *Prorocentrum lima*, *Amphidinium carterae* and *A. klebsii*). *Ostreopsis* cf. *ovata* and *Ostreopsis* cf. *siamensis* are known to produce palytoxin-like compounds. *Ostreopsis* spp. were abundant in macrophyte samples and total density varied from 18 to 10970 cells/g dry weight (Selina, Orlova, 2010).

Conclusion

Long-term observations indicated that the occurrence of HABs on the Russian East coast had an increasing trend and significant seasonality. To date we have identified 35 potentially toxic algal species. The appearance of new causative species, especially toxin-producing species, were observed in this period. Toxic algae represent several of the most dominant taxa in both abundance and biomass within study area (e.g. *Alexandrium*, *Pseudo-nitzschia*, *Ostreopsis*). Other taxa, although low density noted, still remain a potential threat as toxic producers. Continued studies of phytoplankton and microbenthic communities in Far Eastern Seas of Russia will no doubt reveal other potentially toxic species. For beneficial management practices, it becomes necessary to maintain programs that will identify and monitor potentially dangerous flora.

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**MORPHOLOGY AND MOLECULAR PHYLOGENY OF THE CILIATE
GENUS *TUNICOTHRIX* AND FAMILY PARABIROJIMIDAE (PROTOZOA,
CILIOPHORA)**

Renhai Dai^{1,2} and Kuidong Xu^{1*}

¹Department of Marine Organism Taxonomy & Phylogeny, Institute of Oceanology,
Chinese Academy of Sciences, Qingdao 266071, China; E-mail: kxu@qdio.ac.cn

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

The morphology and molecular phylogeny of two novel urostylid ciliates, *Tunicothrix brachysticha* and *T. multinucleata*, are investigated using the techniques of living observation, protargol impregnation, and small subunit (SSU) rRNA gene sequencing. Both species are frequent in muddy-sand sediment but very rare in sandy sediment of the intertidal zone of Qingdao Bay, China. *Tunicothrix brachysticha* is on average 90 × 30 μm-sized in vivo, with a broadly clavate body shape, and characterized by the rather short midventral row terminating at 40% of the body length and the right marginal row 1 terminating at mid-body. *Tunicothrix multinucleata* is on average 190 × 30 μm-sized in vivo, and characterized by a clavate body shape and 7-10 macronuclear nodules. Phylogenetic analyses show that the *Tunicothrix* is robustly clustered with *Parabirojimia*, forming a clade that branches off from the Urostylida core clade with high bootstrap values. Based on the morphological and molecular data, we establish a new family Parabirojimidae, which comprises *Parabirojimia* and *Tunicothrix* and is distinguished by a unique roughly T-shaped bipartite adoral zone of membranelles, three enlarged frontal cirri, and a midventral complex with midventral pairs confined to buccal field.

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THE SPECIES DIVERSITY OF THE GENUS *PYRAMIMONAS* (PRASINOPHYCEAE) FROM THE NORTHWESTERN SEA OF JAPAN

I.V. Stonik

A.V. Zhirmunsky Institute of Marine Biology, Far East Branch, Russian Academy of Sciences, Vladivostok, 690041, Russia.

E-mail: innast@imb.dvo.ru

Introduction

The genus *Pyramimonas* Schmarda (Prasinophyceae) comprises more than 60 marine, brackish- and fresh-water species; most of them have a wide distribution all over the biogeographical zones (McFadden et al., 1986). Representatives of the genus inhabit mostly the neritic zone of the sea, some of these algae cause „water bloom“ (Thronsen, 1993). In the northwestern Sea of Japan, where mariculture farms and recreation areas are located, blooms of *Pyramimonas* species have occurred frequently (Konovalova et al., 1989; Stonik, Aizdaicher, 2005). Prasinophytes, like many other groups of unarmored flagellates in the far eastern seas of Russia (including the northwestern Sea of Japan, Okhotsk Sea and Bering Sea), are still poorly studied, which can be explained by technical difficulties of sampling and examination (Konovalova, 2003). The previous information on the representatives of the genus *Pyramimonas* found in the area is limited to morphological descriptions of five species from coastal waters of from the northwestern Sea of Japan and is based on evidences of light microscopic study (Gail, 1950; Konovalova et al., 1989). Scientific literature gives no data on the quantitative composition and seasonal dynamics of the population density and biomass this algal group in the Russian waters of Japan Sea.

The purpose of this work was to study species diversity of the prasinophycean algae of the genus *Pyramimonas* from the northwestern Sea of Japan, and their seasonal dynamics of the population density and biomass.

Results

The study used bathymetric samples collected in in Amurskii Bay and in Golden Horn Bay (Fig. 1). The sampling was performed in a half-closed man-made lagoon within the City of Vladivostok in Amurskii Bay (Station 1), in the neighboring Vtoraya Rechka River (Station 2), and in Golden Horn Bay (Station 3). Samples at Station 1

were collected from January to October of 2003. Samples at Stations 2 and 3 were taken from January 1993 through January 1994.

Samples for quantitative analysis were taken from the surface horizon (0-0.5 m) with the use of a 4-liter Molchanov bathometer. One-liter sample was fixed with Utermöhl's solution and concentrated through sedimentation to a volume of 10-15 ml.

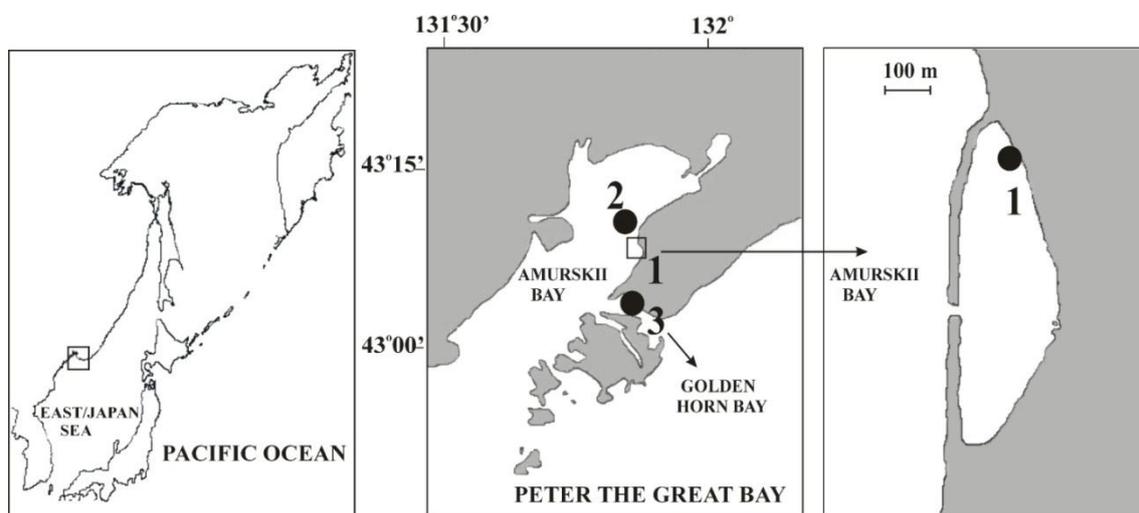


Fig. 1. Location of the sampling stations (1-3).

Algal cells were counted in a 0.05–1 ml Nojott chamber. During water “bloom”, a direct cell counting was done in non-concentrated water samples. Live cells as well as fixed material were examined, photographed and measured using a light microscope (LM) Olympus BX41. Preparations for transmission electron microscopy (TEM) were prepared by the method of “shadow-cast microscopy” proposed by Moestrup and Thomsen (1980); the method involves contrasting of preparations for studying details of the cell fine structure in unarmored flagellates. The material was sprayed with chrome and examined with a TEM JEM-100 B (JEOL, Tokyo, Japan).

According to literature data and the results of our observations, eight species of the genus *Pyramimonas* were found in the Russian waters of the northwestern Sea of Japan: *P. aff. amyliifera* Conrad, *P. aff. cordata* McFadden, Hill et Wetherbee, *P. delicatula* Griffith, *P. grossii* Parke, *P. longicauda* Van Meel, *P. nansenii* Braarud, *P. semiglobosa* Pascher, *P. tetrahynechus* Schmarda (Table 1). As a result of previous studies on the representatives of the genus *Pyramimonas* in the Russian waters of the northwestern Sea of Japan five species were found: *P. delicatula*, *P. grossii*, *P. longicauda*, *P. semiglobosa*, and *P. tetrahynechus* (Gail, 1950; Konovalova et al.,

1989). These records were based on light microscopic studies. It is well known that species of the genus *Pyramimonas* are difficult to identify using routine methods and require, in some cases, electron microscopic examination. So previous data on species identification based on light microscopic studies are not always reliable. Basing on results of our electron microscopic study, the systematic list of the planktonic microalgae for the northwestern Sea of Japan has been supplemented with three species of the genus *Pyramimonas*, new for the region: *P. aff. amyliifera*, *P. aff. cordata*, and *P. nansenii*.

An analysis of the seasonal dynamics showed that the most conspicuous winter peak of the population density of *Pyramimonas* species in Amurskii Bay was clearly distinguishable in February. In winter and early spring, the prasinophycean algae made a considerable contribution of 28 to 60 % into the total population density on the background of a relatively low biomass, 1.1-8.8 % of the total phytoplankton biomass in Amurskii Bay. In the Golden Horn Bay, the summer peak of the population density of *Pyramimonas* species was most intensive in June. In summer, in the period of mass development of the algae of the genus *Pyramimonas* in the Golden Horn Bay, the prasinophycean algae contributed up to 71 % of the total population density and up to 84 % of the total microalgal biomass. An increase was noted in the density and biomass of the *Pyramimonas* species in the polluted waters of Amurskii and Golden Horn bays, in the vicinity of sewage water outlets.

Data of some authors (Gardner, Hargraves, 1979; Hajdu et al., 1996) shows that temperature is a factor affecting the seasonal dynamics of growth of the genus *Pyramimonas* and other groups of unarmoured flagellates in coastal marine ecosystems. For Amurskii Bay, no statistically significant correlations were revealed between the variations in water temperature and population density/biomass of the prasinophytes. But in Golden Horn Bay, we have found a reliable correlation between variations in water temperature and population density ($R_1 = 0.68$, $p = 0.00017$) and biomass ($R_2 = 0.67$, $p = 0.00021$) of the prasinophytes. However, this positive correlation between the temperature rise and the increased population density and biomass of the prasinophytes may be linked also to an impact of some other physical, chemical, and/or biological variables (stratification of the water column, availability of biogenic elements, zooplankton grazing etc.) related to temperature.

We can expect that application of special methods of fixation and electron microscopy will allow researchers to considerably extend our knowledge on flora of the prasinophycean algae in the plankton of Sea of Japan.

Conclusion

Species diversity of the genus *Pyramimonas* Schmarda (Prasinophyceae) and their seasonal dynamics of the population density and biomass from the northwestern Sea of Japan have been studied. To date we have identified eight species of *Pyramimonas*, some of them are new for the northwestern Sea of Japan: *P. aff. amyliifera*, *P. aff. cordata*, and *P. nansenii* Braarud. Blooms of *P. nansenii* were observed in winter, and blooms of *P. aff. cordata* and *P. grossii* were observed in summer, with abundances exceeding 10^6 cells l^{-1} and comprising up to 28-71% of the total phytoplankton abundance. An increase was noted in the density and biomass of the *Pyramimonas* species in the polluted waters of Amurskii and Golden Horn bays, in the vicinity of sewage water outlets.

Table 1. Species composition of the prasinophycean algae of the genus *Pyramimonas*, found in the plankton of Peter the Great bay, Sea of Japan

Species	Length, μm	Width, μm	Maximum population density, ths. cellsL ⁻¹	Reference
<i>Pyramimonas</i> aff. <i>amyliifera</i> Conrad	16-20	11-13	50	Our data
<i>Pyramimonas</i> aff. <i>cordata</i> McFadden, Hill et Wetherbee	7-9	6-8	2524	Our data
<i>Pyramimonas delicatula</i> Griffith	12-15	-	-	Gail 1950
"-	-	-	-	Konovalova 2003
<i>Pyramimonas grossii</i> Parke	7-10	5-6	676	Our data
"-	7.5-8	4.5-6.3	-	Konovalova <i>et al.</i> 1989
<i>Pyramimonas longicauda</i> Van Meel	16-20	10-12	70	Our data
"-	18-20	12-14.5	-	Konovalova <i>et al.</i> 1989
<i>Pyramimonas nansenii</i> Braarud	8.7-13.4	6.1-8.3	94000	Our data
<i>Pyramimonas semiglobosa</i> Pascher	5-6	8-10	0.12	Gail 1950
<i>Pyramimonas tetra-rhynchus</i> Schmarda	16-18	6-10	0.07	Gail 1950

Note: "-", no data

Table 2. Population density (ths. cells L⁻¹) and biomass (mg m⁻³) of *Pyramimonas* species at stations 1-3

Date	Station 1		Date	Station 2		Station 3	
	N	B		N	B	N	B
03 January 2003	-	-	06 January 1993	-	-	-	-
19 January 2003	-	-	26 January 1993	-	-	-	-
01 February 2003	96400	50000	13 February 1993	50	26,2	-	-
14 February 2003	100	5	26 February 1993	-	-	9,2	4,8
03 March 2003	8800	4600	13 March 1993	-	-	-	-
13 March 2003	11200	5800	26 March 1993	0,8	0,4	0,3	0,2
03 April 2003	-	-	09 April 1993	3,7	1,9	0,3	0,2
08 April 2003	-	-	27 April 1993	2,9	1,5	1,2	0,6
15 May 2003	-	-	06 May 1993	0,6	0,3	1,9	1
30 May 2003	14000	7300	30 May 1993	1	0,5	106	55,3
13 June 2003	-	-	18 June 1993	3,2	1,7	100	52,3
21 June 2003	-	-	30 June 1993	-	-	3170	1658
06 July 2003	100	7	14 July 1993	11	5,9	1	0,5
22 July 2003	-	-	31 July 1993	3,1	1,6	854	447
04 August 2003	-	-	20 August 1993	4,2	2,2	0,5	0,3
17 August 2003	-	-	27 August 1993	-	-	2,4	1,3
02 September 2003	-	-	18 September 1993	4,7	2,5	1638	857
22 September 2003	-	-	30 September 1993	5,6	2,9	7,9	4,1
06 October 2003	-	-	12 October 1993	36,4	19	15,1	7,9
			28 October 1993	1,9	1	0,4	0,2
			19 November 1993	1,2	0,6	1	0,5

			1993 29 November	1	0,5	-	-
			1993 13 December	-	-	-	-
			1993 27 December	2	0,9	-	-
			1994 18 January	0,6	0,3	0,5	0,3

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**FLORISTIC CHANGES OF MARINE BENTHIC GREEN ALGAL SPECIES
(CHLOROPHYTA) AT THE SUBTROPICAL ISLAND OF HAINAN (PR CHINA)
BETWEEN 1933 AND 2009 REFLECT ENVIRONMENTAL DEGRADATION**

Eduard A. Titlyanov^{1*}, Tamara V. Titlyanova¹, Inka Bartsch², Bangmei Xia³, Li Xiu
Bao⁴, Huang Hui⁴

¹A.V. Zhirmunsky Institute of Marine Biology, Far Eastern Branch of the Russian
Academy of Sciences, Palchevskogo 17, Vladivostok, 690041, Russia

²Alfred-Wegener-Institute for Polar and Marine Research, Am Handelshafen 12,
27570 Bremerhaven, Germany

³Institute of Oceanology, Chinese Academy of Sciences, 7 Nanhai Road, 266071
Qingdao, PR China

⁴China South Sea Institute of Oceanology Chinese Academy of Science, No 164,
Xingangxi Rd. 510301 Guangzhou, China

Check-list of all findings of green algae (Chlorophyta) in Hainan Island (People Chinese Republic) during the period from 1933 to 2009 was fulfilled. A total of 106 taxa have been recorded including Ulotrichaceae (1 species), Gomontiaceae (1 species), – Ulvellaceae (5 species), Ulvaceae (13 species), Cladophoraceae (24 species, 1 variety), Anadyomenaceae (2 species), – Boodleaceae (5 species), Siphonocladaceae (4 species), Valoniaceae (4 species), Dasycladaceae (3 species), Polyphysaceae (5 species), – Bryopsidaceae (3 species), Caulerpaceae (10 species plus 1 variety plus 3 formae), Udoteaceae (9 species), Codiaceae (10 species plus 1 variety), Derbesiaceae (1 species). 24 species recorded here are new to Hainan Island and 13 species are new records for China. In general, the green algal flora of Hainan Island is very species rich especially in the families Cladophoraceae, Caulerpaceae and Ulvaceae and comparable to other tropical and subtropical regions of the western Pacific. 69 species were found within the period from 1933 to 1935, where Caulerpaceae – 13 species (or amounted to 19% of the flora), Codiaceae – 11 species (16%) and Cladophoraceae – 9 species (13%) were predominated. In 1990 and 1992, 65 species of green algae were collected, where Cladophoraceae – 18 species (25%) and Ulvaceae – 10 species (16%) of the flora predominated. In 2008 and 2009, 50

species were found only in Sanya Bay including 8 species of Ulvaceae (16% of the flora) and 10 species of Cladophoraceae (20%).

During the period from 1930 to 1990, serious changes occurred in green algal flora of Hainan Island. Relative number of Ulvaceae increased 1.6 times, Cladophoraceae increased 1.7 times. At the same time, 8 species of Codiaceae, 8 species of Caulerpaceae and 4 species of Udoteaceae were not found.

In Sanya Bay during the period from 1990 to 2009, green algal numbers increased by 5 species of Cladophoraceae and by 2 species of Ulvaceae. *Ulothrix implexa* (Ulotrichaceae) and *Parvocaulis clavatus* (Polyphysaceae), *Penicillus sibogae* (Udoteaceae), *Chaetomorpha ligustica*, *Cladophora socialis* (Cladophoraceae) were found for the first time in Hainan and the latter 3 species – new for China.

It is assumed that the changes in green algal flora in Hainan within a period from 1933 to 1990 occurred because of coral reefs degradation, while in Sanya Bay within a period from 1992 to 2009 insignificant changes could be evoked by the increased pollution (urban sewages and fish pond waste).

CNIDARIA DIVERSITY IN THE NORTHWEST PACIFIC: PATHWAYS OF THE DISPERSAL

Tatyana N. Dautova

A.V. Zhirmunsky Institute of Marine Biology, Far East Branch,

Russian Academy of Sciences, Vladivostok 690041, Russia

E-mail: tndaut@mail.ru

The main drivers leading to the global biodiversity changing in the coastal marine ecosystems can be discussed as: 1. the possible invasion of the alien species (or group of the species) using the various pathways of the overseas connectivity; 2. the overexploitation of the bioresources with the man-made pollution of the coastal seas; 3. the global climate changing and environmental stress. The joint efforts of the ecologists and taxonomists to trace the global and local trends and perspectives in the marine biodiversity changing could be focused on the main components of marine populations. These components which may be called critical functional groups which are fundamental to understanding resilience of ecosystems and can be used as biomarkers for the possible invasion monitoring. Among the Cnidaria, two main coral groups should be placed in a focus of the careful study and monitoring – stony corals and soft corals (Cnidaria: Octocorallia) and a range of medusae.

The biodiversity Centre and pathways for the soft coral distribution and dispersal.

Since Ekman in 1953 considered the Malay Archipelago as the faunistic centre of Indo-West Pacific from where species dispersed to peripheral areas, the position of this area was discussed by many authors during last decades. For the competent tracing of the trends in the status of the stony corals and soft corals populations the joint efforts of the specialists in the coral taxonomy and ecology together with the analysis of the dispersal ways are needed. The possible dispersal ways by oceanic currents should be analyzed along with the genetic similarity of populations in order to learn how distribution ranges are generated and how they are maintained. The study of distribution patterns requires the good understanding both detailed records of the coral fauna throughout the distribution range and high quality oceanographic data to be correlated with these distributions (Veron and Minchin, 1992; Hoeksema 2007). The warm water of the Kuroshio Current passes east of the Philippines to southern

pacific side of the Japan and intrudes into the South China Sea moving along of southern Taiwan. It can influence on the corals richness on the reefs of the central part of Vietnam as well as southern Taiwanese reefs. The preliminary Alcyonacea list of the soft corals (with *Briareum* genus) of Central Vietnam includes 27 genera; the *Sinularia* species list has 36 “old” species and a range of the new species (Dautova, pers. comm.). The reefs of the southern Taiwan contain 22 genera including *Sinularia*. The presence in Central Vietnam of the most of Nephtheidae genera as well as longer list of *Sinularia* species may be considered as a result of the direct connection of the region with Coral Triangle in addition to the Kuroshio influence. The single finding in SCS of the *Sinularia yamazatoi* which species was before recorded only at Southern Ryukyu shows that this species: a) probably has the dispersal from the Indo-Malayan centre; b) may be rare and due to it is not recorded on Taiwanese reefs; c) can pass into the Vietnamese waters both directly from Coral Triangle and by Kuroshio influx. The recent Indonesian finding of the *S. mammifera* which species was described from Vietnam (Manuputti, Ofwegen 2007) anticipate the same. The coral reefs of Taiwan and Japan are closely linked by the northward flowing Kuroshio Current (Fijiwara et al., 2000). The soft coral fauna of both areas shows a close resemblance between their faunas in terms of generic composition and number of species (Table 1). The finding of *S. higai* and *Sarcophyton nanwanensis* both from Japan and Taiwan anticipate that similar patterns also exist for other important soft coral genera (Benayahu et al., 2004).

The Chinese reefs (mainly on Hainan Island) at the northern part of the SCS, have links with reefs of Vietnam and the Spratly Arch. The geographic location of these reefs close to northern margin of Indo-Pacific coral reef centre of high biodiversity can allow the quite rich coral fauna existing, but there is lack of taxonomic capacity to confirm this. Studies are required to assess the possible important role of these reefs in global reef system. Only reefs around Hong Kong are significantly studied. Lam and Morton (2008) showed the full list of Hong Kong’s Octocorallia studied since the middle of the 19th century. Besides of the needed studying of some taxa, it is interesting to note the total absence of widely spreaded tropical zooxanthellate genera *Sinularia* and *Sarcophyton* along with presence/predominating of azooxanthellate genera, such as *Eleutherobia*, *Paraminabea*, *Scleronephthya*, *Nephtyigorgia* and *Dendronephthya*.

Trends for the Octocorallia dispersal in the temperate waters: the biogeographic boundaries and the retrieval of the cold water biodiversity Centre.

The geographic location of the coral communities which exist in South Korea waters has produced coral fauna of special biogeographical interest. The tropical and the subtropical marine invertebrates are being distributed together with the temperate ones in the southern part of Cheju Island at south of Korea peninsula, as this place is directly being affected by the Kurioshio Current. As a result, 65% of total Korean Anthozoa species are encountered here including 40 species of gorgonians, 12 Alcyonacea and 4 Pennatulacea species. Approximately 20 soft coral species are being distributed downwards 45m deep in subtidal zones surrounding the island such as Munsom and Boemsom forming soft coral beds (Song 2001). The several species of *Dendronephthya* are presented here as well as “tropical” gorgonians *Menella*, *Ellisella* and *Acabaria*, but the temperature restricts here zooxanthellate soft corals, such as *Sinularia* or *Lobophytum*. From the other hand, the Tsushima Current is directed across Korean/Tsusima Strait into the Sea of Japan during summer and winter seasons (Chen et al., 1994). It can limit the dispersal of many temperate Octocorallia to Yellow and East China Seas. By this reason seems to be the temperate gorgonian genus *Primnoa* is not found to the south of Jeodong, Dodong and Sadong Islands in the southern part of the Sea of Japan (Song, 1981). Another temperate gorgonian genus –*Calcigorgia* - has the range restricted to the south by the Sea of Japan too. This genus can indicate the possible dispersal way for temperate Octocorallia in Northern Pacific. Two *Calcigorgia* species including *C. spiculifera* are occurred in Aleutian Islands area. However, the list of gorgonians of Kurile Islands is richer because of includes five new *Calcigorgia* species in addition to *C. spiculifera* (T. N. Dautova, pers comm). The waters of the Oyashio Current form probably the richest fishery in the world owing to the extremely high nutrient content of the cold water. This current circulating counterclockwise in the western North Pacific by Kurile Islands had the intrusion into the Japan Sea across the Tsugaru Strait during the Holocene history (Takei et al., 2002). Does the centre of temperate coral diversity take place in North Pacific as the source of dispersal? It can be the subject of the future investigations using model taxa which are well revised equally with molecular and paleoceanography data.

The invasion: soft coral *Carijoa* and *Rhopilema* medusae.

The soft coral *Carijoa riisei* (Duchassaing and Michelotti, 1860), or Snowflake coral, has native range in the Western Atlantic, from Florida to Brazil. In Hawaii, *Carijoa* coral was firstly found in 1966. In present, the coral is noted outside of harbors, on shipwrecks or in sheltered and shaded crevices or shallow caves on the deeper reefs. The invasive characteristics of the *Carijoa* include: low mortality, the absence of the superior competitors and significant predators, fast population growth and the fast growth of the coral individuals (1cm per week), continuous reproduction (Concepcion, 2006). The target for this fouler can be not only the artificial or natural substrata, but the several coral species of the Hawaiian reefs may under the *Carijoa* pressure. Grigg (2003) states that not only can this species be found on pier pilings in shallow water, but that it is also abundant in much deeper water (down to 120 m), particularly in shaded environments. The newest data on the southern Vietnam coral reefs are show that *Carijoa riisei* inhabits the shallows in the Nha Trang Bay, South China Sea (T. N. Dautova, pers. comm.). The settlements are found at the 6 collecting stations in the range of depth 8-16 m. At the moment, this coral could be discussed as common in Nha Trang Bay, but not abundant. The further monitoring is needed to trace the possible emission of the species. At the same time, recent molecular sequencing work in progress is now casting doubt on the Caribbean/Atlantic origin for the Hawai'ian population (Samuel Kahng., pers. comm., 2005). The taxonomy of the species needs a revision because of the phylogeography data showed that the *Carijoa riisei* didn't come to Hawaii from the Caribbean. From the other hand, the haplotypes of the Hawaiian *Carijoa* are found in the Pacific, so the multiple introductions from Pacific are more likely (Concepcion, 2006).

Scyphozoan medusa *Rhopilema esculentum* is popular seafood in eastern and southern Asian nations where there is a high market demand that stimulates large-scale jellyfish production. Due to its economic importance in China, many biological studies have focused on the jellyfish *R. esculentum* Kishinouye in terms of the biology and taxonomy, environmental impact of aquaculture activities and culture techniques (numerous publications, for example Chen et al., 1987, Chen et al., 1984a, b, 1985; Chen et al., 2004; Ding et al., 1981; Li et al., 2005; Lu, 1995; 1997; Wang, 1992, 1995; Zhang, 2006). Since 1999 year the medusa appeared at the coast of Primorye, its commercial catch began in 2001. Possible paths of this species penetration into Peter the Great Bay and distribution were defined with the northward drift from the East China Sea through Korea Strait by streams in the sea surface layer. Due to these

streams, the jellyfishes could reach Peter the Great Bay in 23 weeks. It was concluded, the *Rhopilema* does not enter the Amur Bay under condition of north or southeast wind, but its stock in the Bay is redistributed. On the contrary, the *Rhopilema* pass into the Ussuri Bay under south, southeast, and north winds, therefore volume of its catch in the Ussuri Bay is 3 times higher than in the Amur Bay. The period of the *Rhopilema* presence in Peter the Great Bay could be divided in four stages: 1 - the approach of small clumps of jellyfishes (late August - early September); 2 - sharp increasing of jellyfishes numbers; 3 - stable high abundance of jellyfishes within several weeks; 4 - sharp decline of abundance (Borodin et al., 2003). Since 2008 that medusa is found in the Peter the Great Bay seasonally earlier, moreover, its amount is increased significantly (Trofimov, 2009). *Rhopilema* was suggested as seasonal migrant in the Peter the Great Bay, however, the finding of the young medusae in the June 2010 year can lead to the idea on the naturalization of that medusa population in the area. Further survey should be focused on the biology/dynamics of the species in Russian waters and molecular investigations to clear the origin of that jellyfish from Chinese population.

Conclusions

For a good understanding of processes regulating species diversity we need to understand how species disperse and which factors restrict their settlement and survival. We may need to know more about oceanic currents but also about the genetic similarity of populations in order to learn how distribution ranges are generated and how they are maintained. In addition, we need to know about the ecological factors that regulate species diversity. Although various hypothetical models have been proposed for explaining how the centre of maximum diversity originated, a combination of various models offers the most satisfying solution as clarification for the position and shape of the most likely centre of maximum marine diversity (Hoeksema, 2007).

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COMPARATIVE STUDY OF THE BIODIVERSITY OF GAMMARIDEAN FAUNA OF THE YELLOW SEA AND THE RUSSIAN FAR EASTERN SEAS

Xianqiu Ren

Institute of Oceanology, Chinese Academy of Sciences, Qingdao 266071, China

A total of 109 species of benthic Gammaridea belonging to 22 families and 54 genera have been recorded from the Yellow Sea. Among these 30 species (about 27.5% of the total) found from the Yellow Sea Cold Water Mass over 40-50 m deep are the components of the North Pacific Temperate Fauna, while 79 species (72.5%) distributed in the shallow coastal areas are mainly warm water components of the Indo-West-Pacific Fauna. Of the cold-water 30 species, 2 belong to the north hemisphere coldwater species which are found also in the Arctic, 3 are Amphi-boreal species found in both north Atlantic and north Pacific, 8 are north Pacific temperate species, 4 are Amphi-Pacific temperate species, and 3 are Northwest Pacific temperate species found in Russia Far East sea—Japan—Yellow Sea. Besides, three temperate species are endemic to the Yellow Sea—northern Japan, and seven temperate species are probably endemic to the Yellow Sea.

Of the 79 warm water species (72.5%), 54 are West Pacific warm water species and dominated in the Yellow Sea; 29 of them are found only in China seas, probably endemic (10 species in the Yellow Sea, 7 in the Yellow—East China Sea, 12 in the Yellow—East—South China Seas). And 25 are Sino-Japanese warm water elements: 6 species are Indo-west-Pacific species, 7 are widely distributed in three oceans, and 3 are cosmopolitan. Moreover, there are another 10 warm water species of the Yellow Sea fauna, 4 of which are found from the East and West Pacific, 5 are recorded from warm waters of the Atlantic and Pacific Oceans, and one species is common to West Pacific and North Africa.

Budnikova & Besrukov (2008) recorded 349 species (with 299 identified to species level) of Gammaridea collected from the Peter the Great Bay, western Sea of Japan. They distinguished the fauna into 12 biogeographic complex, and indicated that 290 species are boreal: 1) Pacific Near-Asian low-boreal species, 68 spp., 2) Pacific Near-Asian wide-boreal species, 94 spp., 3) Pacific Near-Asian high-boreal species, 1 spp., 4) Boreal Arctic spp. 57 spp., 5) Boreal Arctic Circumpolar species 23 spp., and

6) Amphiboreal species 25 spp.). And only 9 species are warm water in nature (tropical, subtropical): 1) Pacific Near-Asian subtropical-low-boreal species, 4 spp., 2) Amphipacific subtropical low boreal species, 1 sp., 3) Boreal-tropical species, 1 sp., and 4) Pan-oceanic species, 3 spp.). The data distinctly showed the high percentage of the cold water species of the Russian Far Eastern fauna, and the high percentage of warm water elements in the Yellow Sea. The Russian Far Eastern species should be affiliated to the North Pacific Temperate Fauna, the Yellow Sea Fauna is warm temperate and the western Sea of Japan, cold temperate.

**THE SEA ANEMONE GENUS *NEMANTHUS* CARLGREN, 1940
(ACTINIARIA: NEMANTHIDAE): SPECIES COMPOSITION AND
GEOGRAPHICAL DISTRIBUTION**

Elena E. Kostina¹, Irina N. Gladkikh², Elena V. Leychenko²

¹A.V. Zhirmunsky Institute of Marine Biology, Far Eastern Branch,
Russian Academy of Sciences, Vladivostok 690041, Russia

E-mail: cnidopus@mail primorye.ru

²Pacific Institute of Bioorganic Chemistry, Far Eastern Branch,
Russian Academy of Sciences, Vladivostok 690022, Russia

E-mail: irinagladkikh@gmail.com

The present work is based mainly on the literature data and samples taken in the coastal areas of Vietnam (South China Sea) during a marine expeditions aboard the research vessel «Academik Oparin» of the Pacific Institute of Bioorganic Chemistry and A.V. Zhirmunsky Institute of Marine Biology of the Far Eastern Branch of the Russian Academy of Sciences in 2007 and 2010. At present, there is no less than 3 species *Nemanthus*: *N. nitidus* (Wassilieff, 1908), *N. californicus* Carlgren, 1940 and *N. annamensis* Carlgren, 1943 (See Table). These species are distinguished mainly by the coloration of their column, development of muscles of the oral disc, mesenteries, sphincter and the abundance of nematocysts in the acontia-like organs. Solitary or grouped sea anemones normally live attached to the branches of gorgonians, black corals and to the carapace of Decapoda (See Figure).

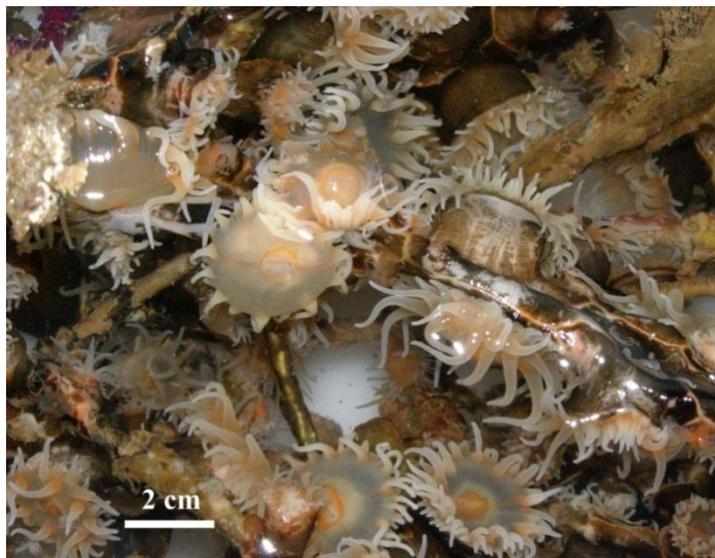


Fig. The sea anemones *Nemanthus* sp. on the Gorgonacea from South China Sea, Cham Island

Distribution and habitat of the sea anemone genus *Nemanthus*

Species	Area	Actinian partner, depth	References
<i>Nemanthus nitidus</i> (Wassilieff, 1908)	Sagami Bay, Bonin Islands (Port Lloyd), Japan	6–128 m	Carlgren, 1940, 1949; Yanagi, 2006
	Seychelles Islands	–	den Hartog, 1994
	Geojedo Isl., Korea	Gorgonacea <i>Acalycigorgia inermis</i> , <i>Euplexaura</i> sp.; 30–60 m	Song, Lee, 1998; Song, 2004
	Izu Peninsula, Honshu Isl., Japan	Decapoda <i>Izucaris</i> <i>masudai</i> ; 20 m	Okuno, 1999; Marin, 2006
	Jeju Isl., Korea Strait; Yellow Sea; Mipo, Korea	<i>Antipatharia Antipathes</i> <i>densa</i> ; 10–40 m	Song, 2000; Cha, Song, 2001; Song, 2004; Moon, Song, 2005
	Honshu, Hokkaido, Kyushu Islands, Japan	Gorgonacea; 10–30 m	Uchida, Soyama, 2001
	Tokyo Bay, Japan	470 m	Yanagi, 2006
<i>Nemanthus californicus</i> Carlgren, 1940	Arena Bank, Sea of Cortez, California	82 m	Carlgren, 1940, 1949
	Isla San Jos é Archip éago Islas Murci éago, Guanacaste, Costa Rica	<i>Antipatharia</i> <i>Myriopathes</i> <i>panamensis</i> ; 30 m	Excoffon et al., 2009
<i>Nemanthus annamensis</i> Carlgren, 1943	Nhatrang Bay, Vietnam; R éam, Cambodia	Gorgonacea	Carlgren, 1943, 1949
	Kenya; Seychelles and Maldives Islands	Decapoda <i>Lauridromia</i> <i>intermedia</i> ; 53 m	Lavaleye, den Hartog, 1995
	Indonesia	–	den Hartog, 1997
	Guam Isl., Mariana Islands	–	Paulay et al., 2003
	Bach Long Vi Isl., Gulf of Tonkin, Vietnam	Gorgonacea; 5–22 m	Our data, 2007

<i>Nemanthus</i> sp.	Pulau Tioman, Malaysia	Antipatharia	England, 1987
	Honshu, Hokkaido, Kyushu Islands, Japan	10–30 m	Uchida, Soyama, 2001
	North Sulawesi, Indonesia	Antipatharia <i>Antipathes</i> sp.; 10 m	Tazioli et al., 2007
	Cham Isl., Vietnam	Gorgonacea; 12 m	Our data, 2010

Note. «–» – data are not available.

Thus, species of the genus *Nemanthus* are widely distributed in the Pacific and Indian Oceans. It is believed that the three species are unidentifiable on the basis of morphological and anatomic available descriptions and therefore possibly *Nemanthus* could be a monospecific genus with a wide Indo-Pacific distribution (Lavaleye, den Hartog, 1995; Yanagi, 2006; Excoffon et al., 2009).

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COMPOSITION OF LITTORAL MACROBENTHOS OF TAUISK BAY OF THE SEA OF OKHOTSK

M.B. Ivanova, A.P. Tsurpalo

A.V. Zhirmunsky Institute of Marine Biology FEB RAS, Vladivostok
690041, Russia

E-mail: m_ivanova_imb@mail.ru

Tauisk Bay cuts approximately 74 km deep in the north coast of the Sea of Okhotsk between Cape Shestakov in the west and Cape Alevin in the east. The Bay width between them makes almost 150 km. The Bay coast is mainly high and indented by bays and bights, among which Motykleisky, Amakhtonsky, Odian Bays and Nagaev Bight are the biggest. Many rivers flow into the Bay. Tauy, Yana, Arman and Ola are the biggest among them. Reefs and rising kekurs stretch along the western coast of the Bay near the Capes.

Tides in the Bay are irregular semidiurnal, their maximum amplitude makes 4.9 m [13]. Tidal fluctuations and wind effect create a complicated system of currents in Tauisk Bay: in summer the major volume of water is carried out of the Bay through Likhachev Channel (between Cape Shestakov and Spafariev Island) [9].

In Tauisk Bay ice formation starts in the early November. Fast ice is formed only in closed bays: Motykleisky, Odian and in Nagaev Bight; the rest area is covered by drifting ice. Ice melting begins in the Bay in the late May; it is partially carried out to the sea, where currents take it to the west. A complete liberation of the Bay from ice takes place approximately in the middle of June [12].

Sharp fluctuations of salinity are typical for Tauisk Bay. Beginning from the spring (April-May) water salinity in the western part of the Bay falls to 27‰. In June-July salinity reduction is extended to the entire water area of the Bay. And only in August salinity of surface water reaches 30-31‰. In September-October salinity again drops to 24-28‰ under the effect of autumn floods [3]. Salinity of coastal waters, surrounding the intertidal zone, is also highly variable.

Data on animals and plants of the intertidal zone of Tauisk Bay are presented in works of P.V. Ushakov [14], and later on they were substantially supplemented by A.V. Ilyichev and I.A. Ryazantseva [4], D.A. Galanin [3] and K.V. Regel [10, 11]. Studies on separate groups of organisms are also available. Some littoral algae are

mentioned in works by I.A. Kashin [6], and T.L. Kalita [5] presents quite a complete list of macrophytes of Rechnoy Bay of Tauisk Bay. As to animals of the littoral macrobenthos of Tauisk Bay, Amphipoda [8], some Bivalvia and Gastropoda [15] and fishes [1, 2] are described.

Samples collected by the joint expedition of the Department of Marine Biology of the FEB SD AS USSR and the Far Eastern State University in the intertidal zone of Tauisk Bay in 1969 served as a material for the present paper. 21 hydrobiological sections were made, and 191 samples of macrobenthos were collected, including 161 quantitative and 30 qualitative ones.

During the expedition period (from June 24 to August 2, 1969) maximum water temperature (23 °C) in the intertidal zone of Tauisk Bay was registered in Motykleisky Bight on July 15 (littoral bath). Maximum temperature along the shore line (21.1 °C) was recorded at the same place on July 14. Maximum water temperature in the open part of the Bay - 19 °C – was registered on July 28 (Olsky Reid). Minimum temperature was fixed on June 13 in the open Bay (Staritsky Peninsula) - 5 °C. Maximum air temperature was recorded on July 30 (Olsky Reid) – 28.1 °C, minimum air temperature – on July 1 in the open part of the Bay (Staritsky Peninsula) – 10.3 °C.

We collected 176 macrobenthic species in the intertidal zone of Tauisk Bay (Table). Among them 36 species belong to tree algal type and 1 species – to flowering plants. The portion of all plants makes 20.5% of the total number of species. Maximum number (19 species) falls on red algae. Animals of the intertidal zone of the Bay include 139 species. Among them Polychaeta include 41 species (23.3%), Amphipoda – 28 species (16%), Gastropoda – 16 species (9.1%), Bivalvia – 15 (8.5%), and hydroids – 14 species (8%). The other animal groups are represented by insignificant numbers (less than 4 species).

Table .1. Taxonomic composition of macrobenthos of the intertidal zone of Tauisk Bay

Type/subtype	Classis	Order	Family	Genus	Species
Plants	5	14	31	55	60
Rhodophyta	Bangiophyceae	1	1	1	2
	Florideophyceae	5	14	25	26
Chlorophyta	Ulvophyceae	3	6	11	13
Magnoliophyta	Monocots	1	1	1	1
Heterokontophyta	Phaeophyceae	4	9	17	18

Animals	30	57	166	253	337	
Spongia	Calcispongiae	1	1	3	3	
	Demospongiae	4	5	6	8	
Cnidaria	Hydrozoa	2	10	14	20	
	Scyphozoa	2	3	4	5	
	Anthozoa	1	6	7	10	
Ctenophora	Atentaculata	1	1	1	1	
Plathelminthes	Turbellaria	–	–	–	+	
Nemertinea	Anopla	1	1	2	2	
	Enopla	1	1	3	3	
Sipuncula	Phascolosomatidea	1	1	1	1	
	Sipunculidea	1	1	1	1	
Echiurida	Echiuroidea	–	1	1	1	
Annelida	Polychaeta	–	32	61	79	
	Oligochaeta	–	–	–	+	
Mollusca	Polyplacophora	2	4	4	4	
	Gastropoda	9	18	28	40	
	Bivalvia	6	11	14	18	
Arthropoda	Maxillopoda (infraclassis Cirripedia)	1	3	5	6	
	Malacostraca	Mysidacea	1	1	2	4
		Euphausiacea	1	1	1	1
		Cumacea	2	2	2	5
		Amphipoda	22	22	35	53
		Isopoda	3	3	5	5
		Decapoda	7	7	9	12
Pantopoda	1	1	1	1		
Nemathelminthes	Nematoda	–	–	–	+	
Cephalorhyncha	Priapulida	1	1	1	1	
Chaetognata	Sagittoidea	1	1	1	1	
Bryozoa	Flustrata	3	5	5	5	
Echinodermata	Holothuroidea	3	3	4	4	
	Asteroidea	2	2	4	7	
	Echinoidea	2	2	2	3	
	Ophiuroidea	1	2	2	2	
Hemichordata	Enteropneusta	–	1	2	2	
Chordata	Ascidiaceae	2	3	3	3	
	Teleostomi	3	10	19	26	
Total: 21	35	72	197	308	398	

According to our own and published data 398 macrobenthic species were revealed in the intertidal zone of Tauisk Bay, including 60 plant and 338 animal species (Table), attributed to 308 genera, 197 families, 72 orders, 35 classes, 19 types and 4 kingdoms.

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UNEXPECTED DOMINANCE OF THE SUBTROPICAL COPEPOD *TEMORA TURBINATA* IN THE TEMPERATE CHANGJIANG RIVER ESTUARY AND ITS POSSIBLE CAUSES

Guang-Tao Zhang¹, Song Sun¹, Zhao-Li Xu², and Qi-Long Zhang¹

¹Institute of Oceanology, Chinese Academy of Sciences, Qingdao 266071, China

²East China Sea Fisheries Research Institute, Chinese Academy of Fisheries Sciences, Shanghai 200090, China

The zooplankton community in the Changjiang (Yangtze) River estuary (CRE) was sampled quarterly in 2004, the 1st yr after the Three Gorges Reservoir was impounded to a water level of 135 m, in order to investigate possible changes in the community structure after freshwater control upstream at the dam. Zooplankton assemblages were consistent with previous studies in all seasons except summer. A tropical-subtropical copepod species, *Temora turbinata*, was found to be the most abundant zooplankton species in this area for the 1st time in Aug. 2004, while previously dominant species, such as *Calanus sinicus*, *Euchaeta concinna*, and *Labidocera euchaeta*, decreased in abundance and appearance frequency. From historical data, *T. turbinata* was never dominant in this area before 2003. It was present only in summer, in accordance with the northerly invasion of the Taiwan Warm Current (TWC). In this study, the range of the Changjiang River Diluted Water was found to have shrunk in summer, and the TWC occupied a larger area of both the bottom and surface layers, compared to the long-term average. Our results indicate that *T. turbinata* in the CRE area was recruited from the southern part of the East China Sea by the TWC. Its unexpected dominance suggests a northward extension of warm-water species resulting from global warming, although it appeared immediately following water control at the Three Gorges Reservoir.

Key Words: *Temora turbinata*, Three Gorges Reservoir, Taiwan Warm Current, Global warming, Northward extension.

Table 1. Dominant zooplankton species and their dominance index (Y) in the Changjiang River Estuary in August in this and three previous studies.

Taxon	Aug. 1959	Aug. 1986	Aug. 2002	Aug. 2004
Copepoda				
Calanus sinicus	0.06	0.11	0.50	
<i>Labidocera euchaeta</i>	0.09	0.03		
<i>Tortanus vermiculus</i>	0.03			
<i>Centropages dorsispinatus</i>		0.03		0.07
Paracalanus spp.				0.04
<i>Euchaeta larvae</i>	0.12		0.04	
<i>Temora turbinata</i>				0.09
<i>T. discaudata</i>			0.02	
Acartia pacifica		0.04	0.04	0.08
Chaetognath				
Sagitta betodi	0.13			
<i>S. enflata</i>	0.09	0.06	0.05	0.08
S. nage		0.09		
Siphonophora				
<i>Muggiaea atlantica</i>		0.04		
<i>Diphyes chamissonis</i>		0.03		
Cladocera				
<i>Penilia avirostris</i>		0.03		
Euphausidii				
<i>Pseudoeuphausia latifrons</i>	0.03			

Decapods			
<i>Lucifer intermedius</i>	0.02	0.03	0.03
Decapoda larvae			0.03
Thaliceae			
<i>Doliolum denticulatum</i>			0.03

THE SPECIES DIVERSITY AND ITS FLORA OF ORDER SPHACELARIALES (PHAEOPHYTA) FROM CHINA COAST

Lanping Ding^{1*} and Rixiao Luan^{1,2}

¹Institute of Oceanology, Chinese Academy of Sciences, Qingdao 266071,
China

²Dalian Museum of Natural History, Liaoning Province, Dalian 116023, China
Corresponding author: lpd2118@hotmail.com

Thallis of Order Sphacelariales are small, erect branching filament composed by multiserial cells, apical growth, cell long longitudinally and arranged regularly, and contains numerous and disk-shaped chromatophores. The propagule can give rise to new plant. This order only contains one family, Sphacelariaceae Decaisne.

In the recent past years, with some dried specimens preserved in Marine Biological Museum of IOCAS and Dalian Museum of Natural History, Liaoning Province and samples collected by authors along the coast of China, authors carried on the morphological taxonomy study of this order. By classification and identification, 8 species of genus *Sphacelaria* are described (not include *S. californica*, reported abroad, absence of feature description), vs. (1) *S. carolinensis* Trono, (2) *S. cornuta* Sauvageau, (3) *S. divaricata* Montagne, (4) *S. fusca* (Hudson)S.Gray, (5) *S. novae-hollandiae* Sonder, (6) *S. rigidula* Kuetzing, (7) *S. subfusca* Setchell et Gardner and (8) *S. tribuloides* Meneghini, including 2 new record and 2 new modified species. It is introduced to the species' characteristic, habitats and geographical distribution with a key referring to family, genus and species.

The coastal waters of China mainly are divided into three marine flora. The species distributes into three marine flora. There are 5 in the flora of South China Sea, with extra overlapping species 1 for Yellow-Bo Sea and East China Sea, 1 for East China Sea and South China Sea, and 1 for these three intact flora.

Key Words: species diversity, Sphacelariales, China coast, flora

**THE PHYTOPLANKTON CONTRIBUTION TO THE DIET OF SOME
MUSSEL SPECIES (MOLLUSCA: BIVALVIA) FROM DIFFERENT PARTS
OF THE SEA OF JAPAN**

Evgeniya E. Vekhova¹, Mikhail I. Kusaykin² and Konstantin V. Kiselev³

¹Laboratory of Invertebrates Ecology, A.V. Zhirmunsky Institute of Marine Biology
FEB RAS, 17 Palchevskogo St., Vladivostok, 690041, Russia. E-mail:

evechova@mail.ru

²Laboratory of Enzyme Chemistry, Pacific Institute of BioOrganic Chemistry FEB
RAS, Pr. 100-letiya Vladivostoka 159, Vladivostok 690022, Russia

³Biotechnology Department, Institute of Biology and Soil Science FEB RAS,
Vladivostok, 690022, Russia

Bivalve mollusks are one of the most dominant filter-feeders in coastal marine environments, and many investigations were focused on studying the feeding and diet of this important group of marine invertebrates (Seed, Suchanek, 1992). Mussels obtain nutrients from dissolved organic substances, bacteria, phytoplankton, and a number of zooplankton species of various sizes (Davenport et al., 2000; Wong et al., 2003). Phytoplankton is known as the main component of the diet of many suspension-feeders including bivalves in shallow marine environments (Bricelj, Shumway, 1991; Mac Donald, Ward, 1994). Modern methods applied to study trophic structure of an ecosystem are mostly aimed to identify food sources (Kharlamenko et al., 2001), and not the quantity of phytoplankton. Phytoplankton is a key link between primary production and the higher trophic levels. Both the quality and quantity of seston are important determinants of food resources of bivalves, and both these factors are highly variable in shallow marine environments (Bayne, 1993). Therefore, modern analytic methods should be developed to estimate the portion of phytoplankton in the diet of marine invertebrates.

Bivalve mollusks of the family Mytilidae, including such species as Grayan's mussels *Crenomytilus grayanus* (Dunker, 1853), Pacific mussels *Mytilus trossulus* Gould, 1950 and the northern horse mussel, *Modiolus modiolus* (Linnaeus, 1758), are considered the main components of coastal marine benthic communities and they play an important role in functioning of the marine ecosystem. (Skarlato, 1981). Also, these common mussel species have commercial value in the Far East of Russia. At the

present time, studying the mytilid's role as consumers of seston is required for understanding the trophic structure of the marine coastal communities, especially that in areas where Mytilidae are abundant. However, little is known about the seston composition in the mussel's diet, as well as their feeding behavior in its trophic relationships with phytoplankton communities. So, the purpose of this study was to investigate the contribution of phytoplankton to the diet of some mytilid species collected from different parts of the Sea of Japan by analyzing of the level of specific activity of the digestive enzyme 1,3- β -D-glucanases, which catalyze cleavage of the major polysaccharides found in phytoplankton (1,3;1,6- β -D-glucan or laminaran). We will develop novel approach to study trophic structure of marine ecosystems.

All specimens of mussels were sampled in August 2008, 2009 from the mussel beds in different parts of Peter the Great Bay, the Sea of Japan. The material was made by means of SCUBA diving at three open sites of its typical habitats (Fig.).

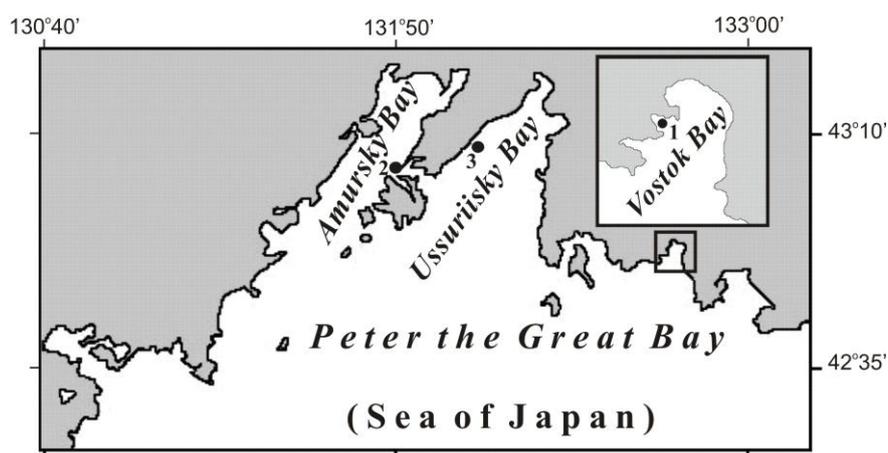


Fig. Map of the study area and the positions of the sampling sites.

The activity of 1,3- β -D-glucanases activity was determined by an increase of the amount of reducing sugars with the Nelson method (Nelson, 1944). Each sample was carefully disintegrated and extracted with 0.05 M Na-succinate buffer (pH 5.2) in ratio 1:3. Extract was centrifuged during 15 min at 9000 overturn/min, at the temperature 4 °C; 1 ml of supernatant was applied on column with Sephadex G-25 to remove of the low-molecular weight substances. The digestive activity of the mussels was estimated on the level of enzymatic activity 1,3- β -D-glucanases (laminarinases), which was the most high in comparison with remainder enzymes O-glycoside hydrolases. The amount of the enzyme that catalyzed formation of 1 nmol of product during 1 h was taken as an activity unit. To estimate the digestive enzymes activity depending on the mollusks age mussels with different shell length were used. To

determine the age of each mussel, growth rings on the outer shell surface and structural marks on the longitudinal sawn face of the valve were examined (Zolotarev, 1989). Each sample of the digestive system tissues of 3–5 living specimens was analyzed three times. Statistical analysis employed the Statistica 8.0 program. The results were represented as mean \pm standard error and were tested by paired Student's t-test. The 0.05 level was selected as the point of minimal statistical significance in all analyses.

We explored the diets of *C. grayanus*, *M. trossulus* and *M. modiolus* collected within mussel beds in different parts of Peter the Great Bay (northwestern part of the Sea of Japan). The analysis of 1,3- β -D-glucanases activity showed that the contribution of phytoplankton to the mussels' diet is different for each species collected from different parts of Peter the Great Bay. At different stages of development *C. grayanus*, *M. trossulus* and *M. modiolus* consume different amount of phytoplankton independently from their location. The comparative analysis of specific activities level in mussels with shell length 50 mm showed that the highest level of specific activity of 1,3- β -D-glucanases was detected in *M. trossulus*. The level of specific activity of the digestive enzymes 1,3- β -D-glucanases in *C. grayanus* was two times lower and in *M. modiolus* in three times lower than in *M. trossulus*. To establish carefully consuming of phytoplankton by mussels in different bays of the Sea of Japan in Grayan's mussels *C. grayanus* the level of specific activity of the digestive enzymes 1,3- β -D-glucanases and sequence analysis of glucanase gene were studied. Both methods showed the same results independently. Among these three bays the highest level of specific activity of 1,3- β -D-glucanases and the glucanase expression were detected in the mussels from Amursky Bay: the differences were significantly increased (*ANOVA*, $p < 0.05$) compared with one's in the mussels from Vostok Bay and Ussuriisky Bay. The levels of specific activity of 1,3- β -D-glucanases in *M. trossulus* and *M. modiolus* collected from Amursky bay were significantly higher than in the mussels collected from Vostok Bay and Ussuriisky Bay.

So, phytoplankton makes an essential component of *C. grayanus*, *M. trossulus* and *M. modiolus* diet. However, the amount of phytoplankton consumed by mussels depends on their habitat and age. Perhaps, it is due to the diet of these bivalves, which usually includes diverse species of phytoplankton, and depends on temporal changes in environmental conditions (Bayne, 1993). The two substantive factors that determine mussel's diet are the seston's quality and amount. These factors considerably vary in

the unsteady environmental conditions of the marine coastal zone. In response to the unstable nutritional environment, many filter feeding invertebrates, including such widespread groups of bivalves as mytilids, have developed an elaborate and selective feeding strategy (Prins et al., 1991). Thus, investigation of the levels of activity and expression of the genes of digestive enzymes 1,3- β -D-glucanases in mussels can be successfully used as a new method to determine the extent of phytoplankton as nutritional source for marine invertebrates.

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DISTRIBUTION OF MACROBENTHIC COMMUNITIES IN THE INTERTIDAL ZONE OF THE VIETNAMESE ISLANDS

Elena E. Kostina

A.V. Zhirmunsky Institute of Marine Biology, Far Eastern Branch,
Russian Academy of Sciences, Vladivostok 690041, Russia

E-mail: cnidopus@mail primorye.ru

The present work is based on 120 qualitative and quantitative samples of the macrobenthos taken in the intertidal zone of the Vietnamese Islands (South China Sea) during a marine expedition aboard the research vessel «Professor Bogorov» of the A.V. Zhirmunsky Institute of Marine Biology of the Far Eastern Branch of the Russian Academy of Sciences in August–October 1988. It was investigated intertidal zone of Catwick Islands (10 ° N, 109 °09' E), Thu Island (10 °32' N, 108 °56' E), Re Island (15 °20' N, 108 °40' E), Thiam Island (15 °40' N, 108 °30' E), Ze Island (17 °08' N, 107 °20' E), Daochao Island (20 °50' N, 107 °20' E) and Zanzola Island (20 °40' N, 107 °20' E).

Five bionomical types of the intertidal zone (Gurjanova, Fyong Chzhan Khyu, 1972; Gulbin et al., 1987, 1988; Nguen Van Chung et al., 1988) were studied on the basis of the substrate features, wave action, influence of the water-freshening and also specific factors (pools, ground vegetation) (See Table).

Distribution of the intertidal communities in the Vietnamese Islands

Type of the intertidal zone	Communities	Biomass of macrobenthos, g wet wt m ⁻²	Island
Rocky intertidal zone	Bivalve mollusc <i>Saccostrea mordax</i> (upper horizon)	7200	Catwick Small Island
		12000	Catwick Big Island
		10764	Thiam Island
	Barnacle <i>Megabalanus tintinnabulum</i> (middle horizon, lower horizon)	11205	Catwick Small Island
		5527	Catwick

			Big Island
	Barnacle <i>Tetraclita squamosa squamosa</i> (middle horizon, lower horizon)	10257	Thiam Island
	Coral <i>Tubastraea coccinea</i> (middle horizon)	1985	Catwick Big Island
	Gastropoda <i>Cellana testudinaria</i> (upper horizon)	657	Thiam Island
Rocky-blocky-bouldery intertidal zone	Gastropoda <i>Nodilittorina millegrana</i> (upper horizon)	648	Thiam Island
	Barnacle <i>Tetraclita squamosa squamosa</i> (upper horizon)	3066	Ze Island
	Green algae <i>Halimeda</i> spp.+ <i>Caulerpa</i> spp. (middle horizon)	245	Thu Island
	Bivalve mollusc <i>Saccostrea mordax</i> (middle horizon)	11574	Thiam Island
		5520	Ze Island
Dead coral reef	Bivalve mollusc <i>Saccostrea mordax</i> (upper horizon)	3442	Re Island
	Angiosperm <i>Thalassia hemprichii</i> (middle horizon)	3240	
Silty-stony intertidal zone	Bivalve mollusc <i>Ostrea foliolum</i> (upper horizon)	2733	Daochao Island
	Bivalve molluscs <i>Isognomon ephippium</i> + <i>Hormomya mutabilis</i> (upper horizon)	430	Zanzola Island
	Bivalve mollusc <i>Saccostrea echinata</i> (middle horizon)	897	Daochao Island
	Bivalve molluscs <i>Gafrarium pectinatum</i> + <i>Annomalocardia squamosa</i> (middle horizon)	1263	Zanzola Island
Sea pools	Gastropods <i>Vermetes planorbis</i> + <i>Macrophragmus tokyoensis</i> (upper horizon)	5646	Catwick Small Island

In the intertidal zone of Vietnamese Islands 101 plant and 268 animal species were found. Zonal-biogeographical composition of biota is typical for tropical region of the Pacific Ocean. Macrobenθος of hard substrates was the richest in qualitative and

quantitative compositions. Population of crumbly substrates was the poorest. It did not find any macrophytic algae in the upper horizon and the major part of the middle horizon of surf-open sandy beaches.

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**ABOUT COINCIDENCE OF BORDERS OF BIOGEOGRAPHICAL AREAS
AND ASYNCHRONOUS DYNAMICS OF SEA INVERTEBRATE
ABUNDANCE**

Gabaev D.D.

A.V.Zhirmunsky Institute of Marine Biology FEB RAS, Vladivostok 690041

Abiotic environmental factors, among which temperature is the most important parameter (Bigon et al., 1986), affect all stages of life cycle of sea dwellers. Thermopathia affects successful reproduction of a species in a specific year (Gabaev, 1987), as well as species settling (Kafanov, Kudriashov, 2000). That is why two water areas, having significant distinctions in temperature and other abiotic factors, contain mainly those animals and plants, which are the most adjusted to these habitats. A border, dividing these two water areas, is a biogeographic one, and different arrays of living organisms can be found along the both sides of this border (Kubanin, 1984; Bagaveeva, 1988; Plekhov, 2000). However, air and water masses depend on climate-forming forces, which are highly changeable, whereas conditions of successful reproduction of sea dwellers are stable (Libikh-Shelford law). In the result of this conflict different sea areas demonstrate successful reproduction, whereas many mariculture farms, being in an area unfavorable for reproduction in a specific year, incur losses due to the low abundance of spat. Knowledge about reasons, affecting reproduction of commercial species, will permit us to forecast the dynamics of their abundance, as some important abiotic factors can be predicted (Reznikov, 1980). If a forecast of spat collection proves to be correct, mariculture farms can exchange planting stocks between water areas, having different spat abundance.

Materials for this paper were collected in 1981-1989 in Possyet Bay and at mariculture farms of Primorye (Sea of Japan/Eastern Sea), engaged in cultivation of the Japanese scallop *Patinopecten (Mizuhopecten) yessoensis* (Jay). In the process of observation over the conditions of its reproduction we took adult scallops from the two water areas once in 10 days in order to determine gonadal index by the method of Ito et al. (1975). The spawning time of the mollusk was determined by reduction of this index. In a week after the spawning start, once in 2-3 days, we took plankton samples and installed scallop collectors. On the rest 4 stations productivity of a year

was determined by the contents of scallop collectors, installed by farmers for spat collection.

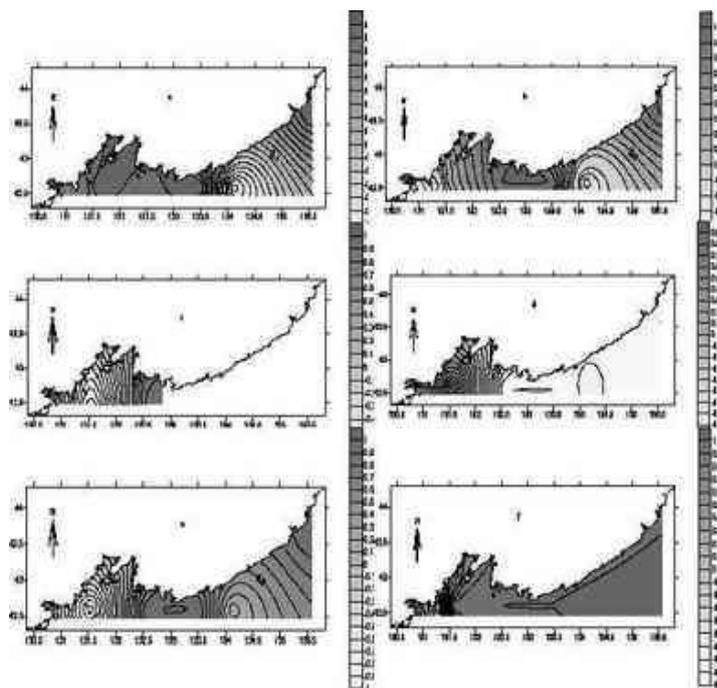


Fig. Location of stations at which Pearson correlation coefficients of abundance dynamics of invertebrates coincide and not coincide with that of Minonosok Inlet, Possyet Bay. A – *P. yessoensis*; b – *M. trossulus*; c – *H. arctica*; d – *Ch. nipponensis*; e – *S. swifti*; f – *A. amurensis*.

Results and discussion

In the result of our observation we found that the entire Peter the Great Bay demonstrates uniformity of conditions, determining reproduction of the Japanese scallop and accompanying invertebrates (Gabaev, 1989). At the same time, comparison of abundance dynamics of several bivalve species in Minonosok Bay, Possyet Bay, and Kit Bay (Middle Primorye) showed asynchrony of its dynamics (Fig.). Pearson correlation coefficient of abundance dynamics of the Japanese scallop *P. yessoensis*, the Pacific mussel *Mytilus trossulus*, the scallop *Swiftopecten swifti* and *Hiatella arctica* in Minonosok Bay and Kit Bay has negative values. The Japanese scallop from Kit Bay has higher gonadal index and abundance of young individuals, inhabiting collectors, as compared to the same age Japanese scallop from Minonosok Bay. A similar dynamics of the Japanese scallop abundance is observed in Vladimir Bay, which is situated southward of Kit Bay. A border between the two water areas, displaying different dynamics of bivalves abundance, runs near Olarovsky Cape

(Gabaev, 1989), situated near 43 °N, and the border between two faunistic provinces – South Primorye and North Primorye – runs in the same place (Kubanin, 1984; Bagaveeva, 1988; Plekhov, 2000; Golovan, 2009; Sukhanov, Ivanov, 2009; Ivanov, 2009; Kafanof et al., 2000). This is a border of impact of two currents: a cold one, Primorsky, and a warm one, Korean. Various temperature tendencies and precipitation abundance in summer arise from these hydrological peculiarities (Pokudov, Vlasov, 1980; Birman, 1985), and mists, not typical for Primorye, can be frequently observed near Tumanny Cape in summer.

A border between the boreal and subtropical zones runs along Sangar Strait (Japan). This Strait is also a border between the Northern neutral zone and the Northern circumcentral zone, as well as between Manchurian Province and Japanese Province according to Forbes. 64% of drainage from the Sea of Japan runs through this Strait, and about one third of that – through Laperuz Strait (Shuntov, 2001). Such a great flow of warm waters created a border between two climatic zones, and at the same time this Strait separates two zones with asynchronous dynamics of abundance of the Japanese scallop. Processing of data on scallop spat sampling at sea farms from Mutsu Bay (Honshu Island) and Lake Saroma (Hokkaido Island), presented in Materials...(1973) and Ventilla (1982), permitted us to determine that Pearson correlation coefficient between two abundance dynamics has negative value (Gabaev, 1988). Mollusks reproduction asynchrony on water areas, separated by a specific water mass, is possibly connected with inter-annual changeability of warm water flow going to the north. It changes the location of a place, favorable for reproduction, and causes differences in spat abundance. At present, as it was expected (Gabaev, 1989), the farm, cultivating scallop near Olarovsky Cape, in lean years acquires planting stock in Possyet Bay.

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**SPECIES COMPOSITION AND FAUNAL CHARACTERISTICS OF
BUCCINACEA (MOLLUSCA, GASTROPODA) OF THE YELLOW SEA AND
BOHAI SEA**

Suping Zhang and Zhiyun Chen

Institute of Oceanology, Chinese Academy of Sciences, Qingdao 266071, China

In order to further understand the species composition and geographical distribution of Buccinacea of the Yellow Sea and Bohai Sea where some species are abundantly distributed, and to reasonably exploit the natural shell-fish resources, we analyzed the data obtained by the biological investigation of the Yellow Sea and Bohai Sea over the years by the Institute of Oceanology, Chinese Academy of Sciences. The results showed that there were 21 species of Buccinacea which attributed to 3 families and 9 genera in the sea area. Some species of the 3 families, Columbelloidea, Nassariidae and Buccinidae, are of high economic value. Among these species, 10 are warm water species, and 4 of them are distributed southward to the East China Sea, and 6 of them are eurythermal and euryhaline species distributed from the Yellow Sea and Bohai Sea to the Guangdong Province coast of the South China Sea, even along the whole China coast. Among the recorded species in the Yellow Sea and Bohai Sea, 11 species are boreal faunal elements, such as the cold water species, *Buccinum undatum plectrum* and *Buccinum pemphigum* are also distributed throughout Hokkaido, Japan and Bering Sea. Seven other boreal species, which are also distributed in Japan and Korean Peninsula, occur only in the Yellow Sea in China.

The list of species of various geographical groups of Buccinacea of the Yellow Sea and Bohai Sea is as follows:

I . Warm water species (10 species):

1. Bohai Sea—Yellow Sea—East China Sea (4 species):

Mitrella burchardi (Dunker, 1877)

Siphonalia spadicea (Reeve, 1846)

Nassarius (Zeuxis) sinarus (Philippi, 1851)

Nassarius (Hima) pauperus (Gould, 1850)

2. Eurythermal and euryhaline species, Bohai Sea—South China Sea (6 species):

Mitrella bella (Reeve, 1859)

Zafra mitriformis A. Adams, 1860

Cantharus cecillei (Philippi, 1844)

Nassarius (Varicinassa) variciferus (A. Adams, 1851)

Nassarius (Zeuxis) succinctus (A. Adams, 1851)

Nassarius (Hima) festivus (Powys, 1835)

II. Boreal species (11 species)

1. Cold water species, Bering Sea—Hokkaido, Japan—Yellow Sea (2 species)

Buccinium undatum plectrum Stimpson, 1865

Buccinium pemphigum (Dall, 1907)

2. Japan—Yellow Sea (7 species)

Japelion latus (Dall, 1918)

Neptunea arthritica cumingii Crosse, 1862

Siphonalia subdilatata Yen, 1936

Buccinium yokomaruae Yamashita et Habe, 1965

Volutharpa ampullaceal perryi (Jay, 1857)

Nassarius (Hima) multigranosus (Dunker, 1847)

Nassarius (Hima) fraterculus (Dunker, 1860)

3. Yellow Sea and Bohai Sea (2 species):

Plicifusus sp.

Nassarius sp.

TAXONOMIC COMPOSITION OF THE MEIOBENTHOS COMMUNITY IN KOZMINO BAY (PETER THE GREAT BAY, SEA OF JAPAN)

Ludmila S. Belogurova

A.V. Zhirmunsky Institute of Marine Biology, Far East Branch,
Russian Academy of Sciences, Vladivostok 690041, Russia

E-mail: iralevenetz@rambler.ru

Kozmino Bay is situated in the south-east of Nakhodka Bay in the Sea of Japan. The special sea oil terminal Kozmino has been recently built here, and an urgent task arose of establishing proper environmental control, i.e. to organize and regularly conduct the biological monitoring of the surrounding area. For this purpose, a study was undertaken to investigate a background ecological characteristics of the biota in Kozmino Bay and Ozero Vtoroe Bight (Fig.1). Meiobenthos is an abundant group of animals that are of a great variety in the sea bottom sediments, they are a convenient object for ecological research.

Meiobenthic organisms are divided into two groups: eumeiobenthos and temporary meiobenthos (Bougis, 1950). This work was aimed at determination of the structure and composition of the meiobenthic community for organization of biological monitoring in Kozmino Bay.



Fig. 1. The scheme of sampling of bottom sediments in the area under an impact of construction of mooring and port facilities in Kozmino and Ozero Vtoroe bights. Numbers indicate the sampling stations.

Seventeen samples of meiobenthos collected in September-October 2008 in the area of the construction of the mooring and port facilities in Kozmino Bay were used as material for our study. The depths in the area of the study were from 1.5 to 28 m. For quantitative estimation of meiobenthos, samples of bottom sediments were taken with a modified Van Veen grab (collection area of 0, 2 m²). Subsamples for meiofaunal analysis from the grab were collected using a tubular bottom sampler (soil core 20 cm² in diameter, 5 cm in length). The samples were washed through 1-mm and 63- μ m sieves, fixed in 4% formalin and stained with "Rose Bengal". Bottom sediments were classified according to the traditional nomenclature (Parsons *et al.*, 1982). Biomass of the animals was calculated with the use of the data obtained by Galtsova and Pavlyuk (1987) from the nomograms of Chislenko (Chislenko, 1986).

It is known that taxonomic composition and population density of meiobenthic animals depend mostly on the properties of sediments (Galtsova, 1991, Schratzberger *et al.*, 2000). Bottom sediments in Kozmino Bay are presented with gravel, gravel-and-pebbles deposits, medium-and fine-grained sands with a high content of silt particles, aleurite and pelite.

Meiobenthos of the study area was represented by 16 taxonomic groups. Eumeiobenthos included many groups: Harpacticoidea, Foraminifera, Acarina, Turbellaria, Ostracoda, Nematoda; temporary meiobenthos included immature Oligochaeta, Polychaeta, Ophiuroidea, Bivalvia and Gastropoda larvae, juvenile crustacean Amphipoda, Caprellidae, Isopoda, Tanaidacea, and Cumacea.

The total density of the meiobenthos population varied among the stations from 26.01 to 720.12 thousand ind./m², 171.15 thousand ind./m² on the average. Representatives of eumeiobenthos dominated at all the stations (78%), nematodes were dominant among them (42%). Foraminifera were responsible for 21%, harpacticides for 11%. The shares of other groups (halacarides, turbellaria and ostracods) did not exceed 1–2%. In temporary meiobenthos was dominated by polychaetes (10%), oligochaetes (3%), and amphipods (3%). Caprellids, isopods, gastropods, bivalves, tanaides, ophiures, and cumacean crabs constituted from 1 to 2% (Fig. 2).

The eumeiobenthos was dominated by nematodes, they occurred on all the bottom types. The share of nematodes varied among the stations from 7.4 to 81.4%, contributing on the average 42% to the total population density of meiobenthos. The highest population density of nematodes (362 thousand ind./m² and 323 thousand ind./m²) were recorded on medium-grained sands with a high content of silt fractions (St. 6, 9). On silty sands, the population density of nematodes was lower: from 26 to 112 thousand ind./m² (St. 1, 8, 11, 12, 14, 15, 16, and 17). The lowest population density of nematodes was in pelite-aleurite grounds and on outcrops of the rock (from 8 to 9 thousand ind./m²) (St. 2, 5, 7).

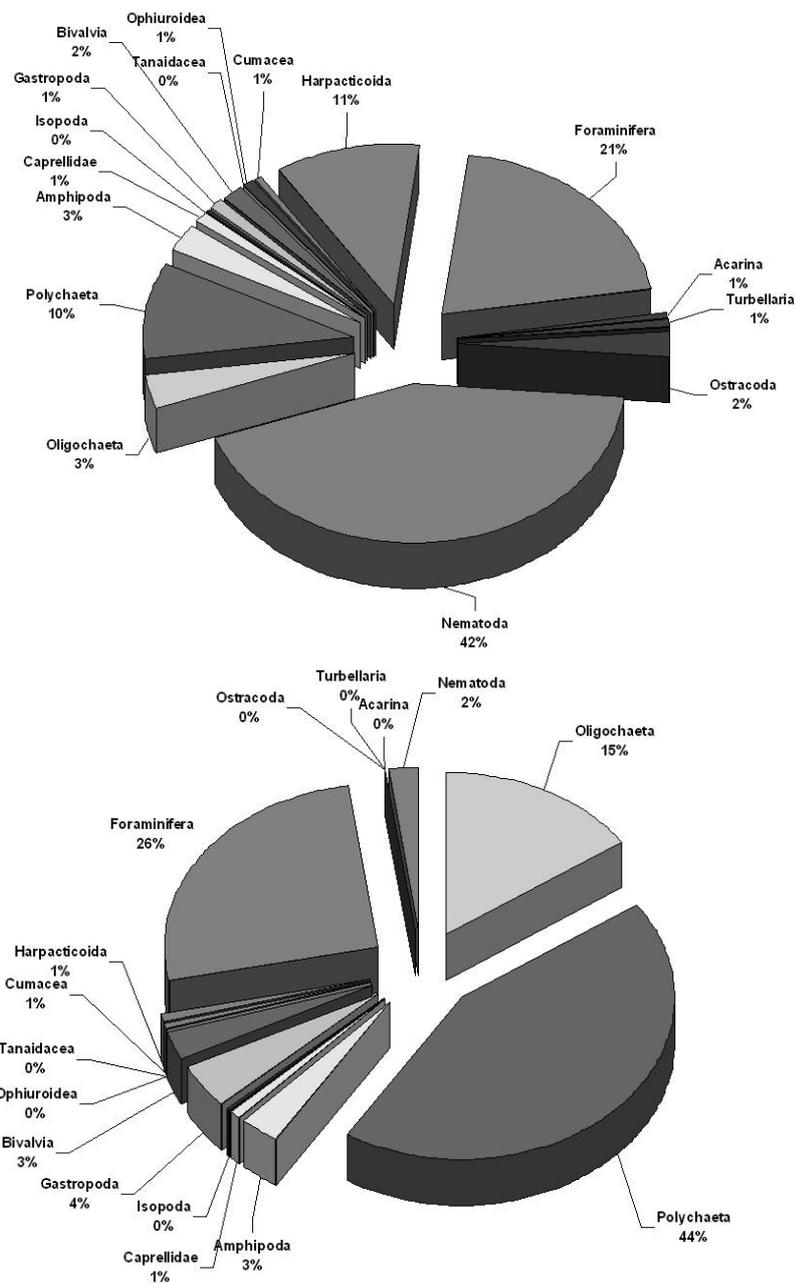


Fig. 2. Percentages for population density (above) and biomass (below) of the main groups of meiobenthos in the area of study.

Foraminifera is the second dominant group of meiobenthos, their shares on stations made 3.9–40.5%, on the average 21% of the total population density of meiobenthos. Their maximum population density, 195 840 ind./m², was recorded for pebble-sandy slightly silty soil at 7-m depth (St. 6), the minimal population density, 3570 ind./m², was recorded on sands with low contents of silt particles at 23-m depth (St. 13).

Population density of harpacticides was lower than that of foraminiferae, varying from 3.5 to 37% among stations. The average share of harpacticides constituted 11% of the total density of meiobenthos. The maximal population density (54 570 ind./m²) of harpacticides was found on a rock outcrop (St. 7) overgrown with the algae *Ulva lactuca* and *Desmarestia viridis*, the minimum population density, 2550 ind./m², was recorded on silty sands (St. 3), at 8.8 m depth.

Ostracoda were found at 13 stations, their shares did not exceed 2 % of the total population density of meiobenthos. The maximum population density of ostracods, 21420 ind./m², was recorded for pebble-sandy poorly silty soils (St. 6), 7-m depth, the minimum value, 1020 ind./m², at 4-m depth (St. 10) on gravel-pebble soils.

Turbellaria and Halacarida did not exceed 2% of the total meiobenthos population. They were found at 10 and 9 Stations, respectively. The maximum number of turbellaria (5 610 ind./m²) was recorded on pebble-sandy ground at 7-m depth (St. 11), and the maximum number of halacarides (5 610 ind./m²) on pebbles at 1,5-m depth (St. 4). The minimum population density of turbellaria and halacarida, 510 ind./m², were recorded for pebble-sandy grounds at depths of 7 and 4 m (St. 10 and 11, respectively).

The share of temporary meiobenthos varied from 1 to 22% of the total meiobenthos population. At all depths and at all the stations, temporary meiobenthos was dominated by polychaetes. The maximum density of polychaeta population (72 420 ind./m²) was recorded at a depth of 21 m on silty sands (St. 9), the minimum, 3 060 ind./m², at 4-m depth on pebble-gravel grounds (St. 10). The shares of oligochetes, amphipods-gammarids, caprellids, ophiurae, isopods, cummacean crabs, larval gastropod and bivalve mollusks did not exceed 1–3% of total meiobenthos sampled.

The share of temporary meiobenthos in biomass was considerably higher than the share of eumeiobenthos owing to the development of Polychaeta и Oligochaeta. On

all the stations temporary meiobenthos reached 71% of the total biomass. The maximum biomass of the temporary meiobenthos ($12\ 053.14\ \text{g/m}^2$) was measured at 7-m depth (St. 6) on medium-grain sands with a high content of silt particles. In temporary meiobenthos, the highest values for biomass at all the stations were recorded for Polychaeta, their shares were as high as 13.8 to 79.9% of the total biomass. The second place in biomass belonged to Oligochaeta. The maximum biomass of oligochaetes, $1927\ \text{g/m}^2$, was registered at 3-m depth in pelito-aleurite sediments (St. 1). Biomass of amphipods-gammarids, carpellids, ophiuræ, isopods, cumaceans, larval gastropods and bivalves did not exceed 12% in total.

Biomass of eumeiobenthos made 29 % of the total biomass of meiobenthos. From all groups of eumeiofauna, the highest biomass was recorded for Foraminifera (26%). The maximum biomass of foraminiferae (40.6%) was recorded for Station 6 (depth of 7 m) on medium-grained sand. Other groups of eumeiobenthos (Harpacticoida, Acarina, Turbellaria, Ostracoda, Nematoda) had lower biomass values (Fig. 2).

Thus, our studies have shown that meiobenthos of the subtidal zone of Kozmino Bight is dominated in population density by eumeiobenthos and in biomass by temporary meiobenthos. Meiobenthos was dominated by nematodes; this observation will make it possible to use nematodes as an indicator of the state of the marine ecosystem. The population of nematodes is rather stable; therefore, any changes in the population structure of nematodes can be related to disturbances in the natural environments.

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***ACILA DIVARICATA* (HINDS, 1843) AND *A. MIRABILIS* (ADAMS ET REEVE, 1850) ARE ONE? EVIDENCE FROM COI AND 16S MITOCHONDRIAL DNA**

Zhongli Sha, Junlong Zhang, Fengshan Xu

Institute of Oceanology, Chinese Academy of Sciences, Qingdao 266071, China

Acila divaricata (Hinds, 1843) and *Acila mirabilis* (Adams et Reeve, 1850) are common benthic bivalves in China Seas, which are difficult to identify because of the morphological similarity. Many authors have treated the later as junior synonym of *Acila divaricata* (Hanley, 1860; Dall, 1898; Schenck, 1934, 1935, 1936; Habe, 1958, 1977; Knudsen, 1967; Kuroda et Habe, 1981).

The existing research reveals barcodes from COI will be useful in distinguishing bivalves. In the present paper, mitochondrial COI and 16S sequences were used to investigate the divergence between *A. divaricata* and *A. mirabilis*. The results showed that no overlap was found between pairwise intra- and inter-specific genetic distances. Pairwise intraspecific distances of 16S ranged from 0.000 to 0.008, while pairwise interspecific genetic distances ranged from 0.067 to 0.078. Pairwise intraspecific distances of COI ranged from 0.002 to 0.017, while pairwise interspecific distances ranged from 0.128 to 0.134. The present results evidenced that *A. divaricata* (Hinds, 1843) and *A. mirabilis* (Adams et Reeve, 1850) should be treated as two distinct and valid species.

Acila divaricata was discovered in 1843. The original description ambiguously indicated that the holotype was from China seas with a depth of 154 meters. The localities exceed 100 meters can be found only in the East and South China Seas. This revealed the specimens from the East China Sea is *A. divaricata* (Hinds, 1843), but not *A. mirabilis*, whose distribution is limited to the Yellow Sea. The two species can be distinguished by the following morphological characteristics: the ridge of *A. mirabilis* from the umbone to posterior-ventral margin is rather distinct; the sculpture of the ridge is the extension of the surface sculpture. Furthermore, the two species are different in size. *A. divaricata* is smaller, no more than 15 mm in length, while *A. mirabilis* can be 30 mm long. For individuals in the same size, *A. divaricata* has more teeth and the teeth are stronger.

**BIODIVERSITY OF EPIBIONTS OF THE SCALLOP *MIZUCHOPECTEN*
YESSOENSIS IN PETER THE GREAT BAY, SEA OF JAPAN**

Ida I. Ovsyannikova

A.V. Zhirmunsky Institute of Marine Biology, Far Eastern Branch,

Russian Academy of Sciences, Vladivostok 690041, Russia;

E-mail: inmarbio@mail.ru

The Japanese scallop *Mizuhopecten yessoensis* (Jay) is one of the main objects of fishery and mariculture in Primorye. This species has an Asian low boreal area of habitat. The scallop forms assemblages in the upper sublittoral zone of Peter the Great Bay. On a soft bottom the scallop shells form an additional hard substrate and shelter for marine organisms. Macroepibiosis can serve as a simplified model of bottom communities, and scallop communities are additional centers of biodiversity. Investigation of diversity of epibionts is especially urgent in view of intensification of recreation stress in the sea water areas of the southern Primorye and reduction of biodiversity because of anthropogenic intervention in natural processes. The aim of this work is to reveal and compare scallop epibiosis composition in various sites of Peter the Great Bay.

Samplings of living different-age scallops collected in the upper sublittoral zone of five areas of Peter the Great Bay within the period from 1979 to 2007 served as a material for our study (Figure). Totally 930 scallop individuals were selected. The samples were fixed in 4% neutral formaldehyde solution. Macroepibionts from natural and cultivated scallop settlements were taken stock of according to the improved standard technique (Ovsyannikova, Levenets, 2004; Levenets et al., 2005).

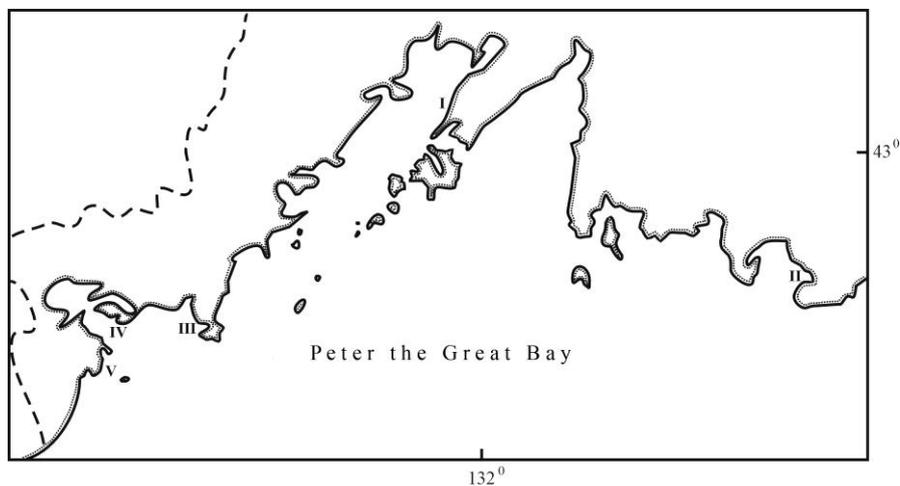


Fig. The map of Peter the Great Bay. Areas: I - Amursky Bay, II - Nakhodka Bay, III - eastern Possyet Bay, IV - central Possyet Bay, V - south-western Peter the Great Bay.

We identified 56 epibiont species from 13 phyla in scallop population from area I (northeastern part of Amursky Bay). Polychaetes (11 species, including 7 drilling ones), red algae and bivalves prevail in number. Cirripedes, polychaetes and brown algae occur the most frequently on scallop shells. Wide boreal (30%), low boreal (27%) and subtropic-low boreal (23%) species determine zonal-geographical composition of epibiosis. About 12% falls at the boreal arctic species. Biogeographical analysis shows the prevalence of Pacific Asian species (53%) among epibionts. Portions of species widely distributed in the World Ocean and in the Pacific are approximately equal: about 20% of the total number of species.

In scallop population from area II (Nakhodka Bay) 17 epibiont species from 8 phyla were recorded. Barnacles, red algae, mollusks and sea anemones the most frequently occur. Zonal-geographical composition is determined by wide boreal (44%) and low boreal (31%) species. Portions of cold-water and warm-water species are close: 12 and 13% respectively. Pacific Asian species significantly prevail in biogeographical composition (62%). About 25% of the total species number fall at species widely distributed in the Pacific, and 13% - at species widely distributed in the World Ocean.

In area III (the eastern part of Posyet Bay) 19 epibiont species from 9 phyla were found on young scallop shells in the period of their bottom growing (7-18 months). Among them 53% fall at algae. Occurrence frequency of the most species does not exceed 10%. Wide boreal and low boreal species make the bulk of zonal-geographical composition. Portions of cold water and warm water species are low: each makes 6% of the total number of species. Pacific Asian species prevail in biogeographical composition of epibiosis. A portion of widely distributed in the Pacific species is considerable.

In area IV (the central part of Posyet Bay) 27 species and 10 phyla, including 15 algal species, were met in populations of cultivated scallop. Analysis of zonal-geographical groups of epibionts shows the prevalence of wide boreal (42%) and relatively warm-water (25%) species. A portion of cold-water species is equal to 4%. Biogeographical composition is determined by Pacific Asian and widely distributed Pacific species. The presence of amphiboreal species is noticeable here.

In area V (south-western part of Peter the Great Bay) 59 epibiotic species from 13 phyla were observed. Macroalgae make 62% of the total number of species. From animals polychaetes prevail by abundance. Occurrence frequency of the most species does not exceed 5-10%. Zonal-geographical composition is determined mainly by low boreal and wide boreal species. Pacific Asian species prevail in biogeographical composition. However, the presence of prevailing in the World Ocean, amphiboreal and widely distributed Pacific species is noticeable in this area.

According to long-term investigations, a tendency to the increase of algae importance in scallop epibiosis both by species number and by biomass can be observed in Sivuchya Bay (area V). Algal contribution in species richness of epibiosis made on the average 53%, and varied between 43% in 1999 and 60% in 2003 on sandy bottom. Prevalence of algae over animals by species number was observed in 1996 (57%), 1998 (52%), 1999 (55% on silty sand and 60% on sand), and in 2007 (53%). Prevalence of animals over algae was registered only in 1999 on sand.

Dominance of temperate-water boreal species is typical for biogeographical composition of epibiosis in Sivuchya Bay. Wide boreal (24% of the total number of species) and low boreal (28%) species make more than a half of epibionts, and determine a boreal character of this community. Presence of warm-water (subtropical-low boreal and boreal-tropical) species, which portion makes in total 21%, is considerable. Widely distributed in the World Ocean species make about 18%, including boreal-tropical-notal ones (13%). Cold-water boreal-Arctic species make about 9% in epibiosis of Sivuchya Bay. In some years zonal and biogeographic composition of epibiosis was slightly different. A portion of boreal-Arctic species varied considerably: from 15% in 1999 to 0% in 2003 and 2007. Disappearance of cold water species from epibionts can indirectly testify to warming of waters of the studied area. In the adjacent waters of this area, the central part of Posyet Bay, a gradual rise of mean annual water temperature is observed (Gayko, 1999, 2002).

Thus, taxonomic diversity of epibiosis of the Japanese scallop *M. yessoensis* in Peter the Great Bay is rather great: about 100 species of hydrobionts from 13 phyla, including 52 algal and 45 animal species. The bulk of flora species diversity is formed by red algae and that of fauna – by polychaetes and mollusks. The presence of some species of red and green algae, serpulid polychaetes, boring polychaetes and sponges, ectoparasitic gastropods, barnacles, bryozoans and ascidians is typical for all areas. In different areas of Peter the Great Bay epibiosis composition varied from 17 species

(area II) to 59 species (area V). Species composition of areas I and V, at a similar total number of species, differed mainly by algal composition.

Zonal-geographical composition of epibiosis in all areas of Peter the Great Bay is mainly determined by low boreal and wide boreal species. Hydrothermic features of separate water areas determine variations in number of relatively cold-water or warm-water species. The bulk of biogeographical composition of the Japanese scallop epibionts is formed by Pacific Asian and widely distributed Pacific species. Presence of species, prevalent in the northern or in the both hemispheres, is noticeable in the southwestern and southeastern parts of Peter the Great Bay, probably due to the presence of permanent currents coming from the open sea.

Earlier we observed an obvious prevalence of algae over the other groups of organisms (Levenetz, Ovsyannikova, 2004). A high mortality and low quantitative parameters of barnacles in scallop epibiosis is possibly a consequence of competitive interrelation with macrophytes. Sometimes an earlier algal spores settling on scallop shells, as compared to barnacle larvae, is observed in this water area. Algae often form a continuous cover on the upper scallop shell. Occasionally they are also met along the edge of the lower flap. Consequently young barnacles, preferring the abdominal edge of a shell, lack free space for settling. Rapid growth of algae degrades living conditions of barnacles and can result in their oppression and death. In separate years in Peter the Great Bay forcing of barnacle *Hesperibalanus hesperius* from scallop shells by algae can be the result of insufficient larvae number for reproduction (Dautov et al., 2001).

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LONG TERM CHANGES IN THE ECOSYSTEM OF JIAOZHOU BAY, CHINA

Xiaoxia Sun, Song Sun

Institute of Oceanology, Chinese Academy of Sciences

7 Nanhai Road, Qingdao, China

Based on the long-term field observation and history data, the long-range changes of Jiaozhou Bay (Fig. 1) ecosystem were studied. The main result is as follows:

The air temperature in the area of Jiaozhou Bay showed a trend of increasing with fluctuation during the past 100 years. The increase in temperature was the most significant in the winter and least in the summer. It was also found that there were significant correlation relationship between the variation of annual mean temperature and PDO (Pacific Decadal Oscillation) index. The changing trend of the water temperature was in consistent with the air temperature, especially in winter. The salinity showed a trend of decreasing since 1981, especially in the summer. The variation rate of the surface salinity was $-0.064/\text{yr}$ for the annual mean, and $-0.131/\text{yr}$ in August. The changing trend of salinity was contrary to the adjacent sea area, such as the Bohai Sea and some area of the Yellow Sea.

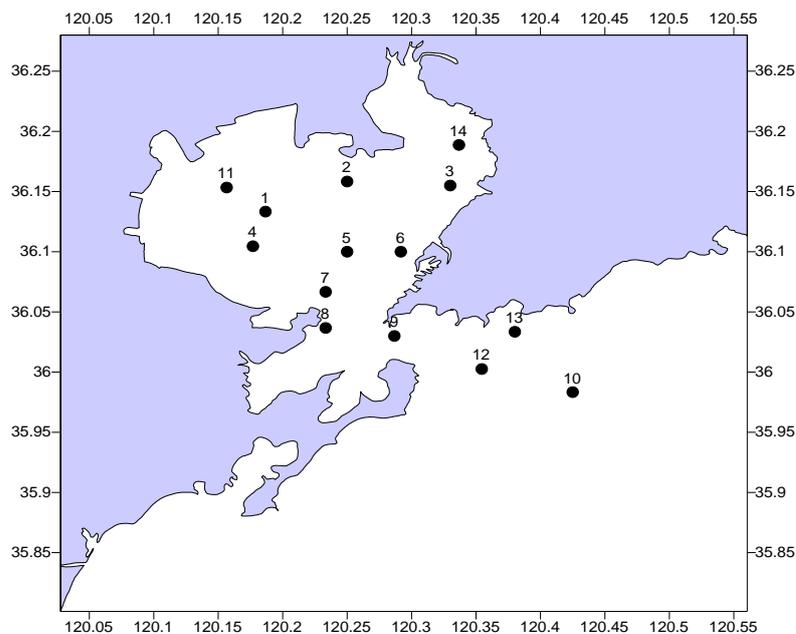


Figure 1. Sampling stations in Jiaozhou Bay

Results indicated that the concentrations of all of the five kind of nutrients showed a trend of increasing during the last several decades. The concentration of ammonium increased gradually from 1980s, reaching a peak in 2001 and decreased since then. The increasing trend of the concentration of nitrite and nitrate was significant from 1990s, especially after 2000. The concentration of phosphate and silicate was increased mainly after 1998. Although the imbalance state of the nutrient was alleviated comparing to the 1990s, it is still necessary to control the increase of DIN. It is also important to pay attention to the dramatic increase of nitrate and phosphate concentration due to the excessive use of the fertilizer.

Results indicated that there was no significant change on the spatial distribution pattern of chlorophyll a concentration during the last 20 years. The concentration of Chl a showed a decreasing trend from the north-eastern and north-western part to the center area, the southern part, the mouth and the outer area of the bay. The change on the seasonal characteristics of Chl a concentration was evident. The Chl a concentration increased in the winter and summer, but decreased in the spring and autumn. In the long term frame, the Chl a concentration was fluctuated, ranging from 1 to 4.76 mg m⁻³. The long term changes of the Chl a concentration and primary productivity were affected by the increase of nutrient concentration and the filtering pressure of maricultured shellfish in Jiaozhou Bay.

Results indicated that the micro- and nano-phytoplankton was the main composition of the phytoplankton in the surface water in Jiaozhou Bay. The nano-phytoplankton was dominant in the bottom layer, and the percentage was higher than 90%. The seasonal change of the size composition in the surface water was significant, with the micro-phytoplankton dominating in the winter and autumn and the nano-phytoplankton dominating in the spring and summer. No apparent seasonal change was observed on the size composition in the bottom layer, and the nano-phytoplankton was the dominant component at all seasons. During the past 20 years, the percentage of micro-plankton increased gradually, which was thought to be affected by the long term change of nutrient concentration and structure.

The total abundance of phytoplankton was increasing in Jiaozhou Bay since 1981, and the increase was evident since 2000, especially in the winter. No clear changes presented in the distributional pattern of total abundance of phytoplankton. As for dominant phytoplankton species, they changed in recent years, e.g. the dominant species included all along *Skeletonema costatum*, *Chaetoceros Curvisetus*,

Coscinodiscus asteromphalus, *Chaetoceros debilis*, *Pseudonitzschia pungens*, *Eucampia zoodiacus* et al. in the recent fifty years, while some phytoplankton species which was ever dominated before 1990's, including *Guinardia striata*, *Rhizosolenia alata f. Indica*, *Hemiaulus sinensis* et al., was not dominant any more since 2000. Furthermore, the new dominant species (e.g. *Chaetoceros lorenzianus*, *Chaetoceros densus*, *Lithodesmium undulatus*, *Ceratium furca*, *Ceratium fusus* et al.) were appeared in the recent five years. The variation of the community structure of phytoplankton in Jiaozhou Bay was related to the increase of temperature, the dramatic increasing concentration of total inorganic nitrogen and changes of proportion of nutrient composition in the winter and spring.

The biomass of zooplankton was pronouncedly increasing in recent years in the Jiaozhou Bay. The average biomass was up to 0.361 g/m³ from 2001 to 2008, equaled to 3.54 times biomass of them in 1990's. The abundance of zooplankton was increasing before 2000, and was fluctuant after 2000, which was related to variation of zooplankton species composition. The seasonal variation pattern of biomass and abundance of zooplankton also changed. In 1990's, the biomass and abundance were highest in summer, while they were highest in spring, secondly in summer since 2000. Results of studies about the long term changes of key functional groups of zooplankton showed that the abundance of medusae and tunicate was increasing, especially the medusae in the recent 20 years. The variation of abundance of copepods and chaetognaths was fluctuant during this period.

**GEOGRAPHICAL DISTRIBUTION OF CHEILOSTOME BRYOZOANS OF
THE SUBORDERS INVICELLINA, SCRUPARIINA, MALACOSTEGINA
AND NEOCHEILOSTOMINA IN CHINA SEAS**

Huilian Liu, Xixing Liu

Department of Marine Organism Taxonomy and Phylogeny, Institute of Oceanology,
Chinese Academy of Sciences, Qingdao, 266071, China.

E-mail: hlliu@ms.qdio.ac.cn

Up to now, 302 species of cheilostome Bryozoans belonging to the four suborders, Inovicellina, Scrupariina, Malacostegina and Neocheilostomina, have been found along China coast. Among these, 25 species are distributed in the Bohai Sea, 52 in the Yellow Sea, 119 in the East China Sea, and 218 in the South China Sea. These bryozoans have the following distributional patterns: (1) 2 species found only in the Bohai Sea; (2) 16 species found only in the Yellow Sea; (3) 29 species found only in the East China Sea; (4) 143 species found only in the South China Sea; (5) 6 species were common to the Bohai and the Yellow Sea; (6) 3 species were common to the Bohai Sea, the Yellow Sea and the East China Sea; (7) 31 species were common to the Yellow Sea and the East China Sea; (8) 3 species were common to the Yellow Sea, the East China Sea and the South China Sea; (9) 4 species were common to the East China Sea and the South China Sea; and (10) 14 species were common to the Bohai Sea, the Yellow Sea, the East China Sea and the South China Sea. In conclusion, the bryozoan of suborders Inovicellina, Scrupariina, Malacostegina and Neocheilostomina found from China Seas are dominant by warm water species, and mainly distributed in the East China Sea and the South China Sea.

THE DEEP-WATER FISH FAUNA OF THE SEA OF JAPAN: CONNECTION WITH ITS ENVIRONMENTAL CONDITIONS AND ORIGIN

Pavel A. Saveliev

A.V. Zhirmunsky Institute of Marine Biology, Far Eastern Branch,
Russian Academy of Sciences, Vladivostok, Palchevsky street 17, 690041

E-mail: tomthumb@mail.ru

The zoogeography characteristic of marginal seas of the North-West Pacific (the Okhotsk, Japan and Yellow seas) is determined of variations of oceanography and bottom topography (Nishimura, 1983). The Sea of Japan is the most isolated because of the shallow sill depth (less than 140m) in narrow straits while the depth in the deep part of the Sea exceeds 3800 m (The main characteristics of geology and hydrochemistry of the Sea of Japan, 1961).

These peculiarities are responsible for unusual hydrography especially as to the deep-water system occupied (85%) by so-called “Japan Sea proper water” (JSPW). The JSPW has low temperatures (0° – 1.5° C) and high salinity (34.04–34.10‰) and low oxygen concentration (220 – $250 \mu\text{mol/kg}^{-1}$) (Asaoka, 1987).

Tritium and chlorofluorocarbons distributions in the Sea of Japan (Noriki et al., 1988) testify that JSPW is produced in the northern shallow part of the Sea. According to Nishiyama et al. (1990) warm eddies which have generated with high salinity waters of the upper layer in the Warm Current Region move into the Cold Current Region and increase their density cooled by the surrounding cold waters. Consequently these waters being cooled by surrounding cold waters must have sunk into the deep layer and formed JSPW (Nishiyama et al., 1993). The residence time of deep water in the Sea is 50-60 years.

Resulting zoogeographical peculiarities were thoroughly reviewed by Nishimura (1965-1969) in which the extremely poor fauna below a depth of 200-300 m belonging to the “taraba-community III” was considered to the deepest assemblages of the sea including fishes. The absence of so-called ancient type deep sea demersal fishes *sensu* Andriashev (1953) was also emphasized there. Although the features were confirmed later (Ogata et al., 1973; Okiyama, 1993; Okiyama et al., 2004) details of the functional mechanisms of this deep water communities and structure is required further thorough inquiry.

Materials and methods

Sampling were carried out within the Russian exclusive economic zone in the Sea of Japan on board R/V “Akademic A.M. Lavrentyev” (SoJaBio International Expedition, August-September, 2010) using Agassiz 3.5 m trawl (AGT) with 1 cm mesh size and small experimental 1.35 m trawl (ST) covering 506 to 3428 m depths and epibenthos sledge (EBS) covering depths from 455 to 3666 m. The speed was from 0.3 to 1.5 knots. The hauling time varied from 2 to 20 minutes. There were 22 AGT/ST and 23 EBS stations but only 9 AGT/ST and 4 EBS trawl haulings yielded fishes. It must be noticed that all the gear cited are not adapted for fishing but nevertheless we had some success. Comparing AGT and ST the former fishing efficiency was greater than in the letter.

Results and discussion

According to Okiyama (2004) the deep sea demersal fish community below 500 m depth is presented by 20 species in 7 families. His point of view that possible addition of new forms to this community is less likely has confirmed by our short survey captured the depths below 3000 m. Some species share eurybathial distributions from depths shallower than 3000 m but the majority of them are occasional occurrence and only a few species of abundant occurrence extend their habitats downward beyond 1000 m.

Representatives of 3 families, namely Psychrolutidae, Zoarcidae, and Liparidae have been met. The unique caught Psychrolutidae was one individual of *Malacocottus zonurus* species 170 mm in total length (TL) caught at 634 m depth. Among zoarcid fishes *Lycodes tanakae*, *Lycodes uschakovi* and *Bothrocara hollandi* have been caught in trawls and EBS. From the point of view of study of Zoarcidae biology captures of *Lycodes* genus both are very valuable. For example, *Lycodes tanakae* specimen 72 cm TL, caught at 1034 m depth (station B6-9) is apparently one of rare finds of this species at that depths. Toyoshima (1983), Sheiko and Fedorov (2000). shown broad bathymetric range for considered species including the 30-1130 m depth. Our individual is apparently the only one that has been found out and fixed at depths over 1000 m. Discovery of another lycodid fish, young *Lycodes uschakovi* about 30 mm TL at 519 m depth is not less interestingly (station B7-6) as the direct evidence of recent hatching. Since the activity of individuals of small size is small we have obtained simultaneously the data on depth of spawning and development of eggs. The age of caught individual apparently was no more than month from the birth.

Bothrocara hollandi was the most prosperous and occurred at most stations during SoJaBio Expedition. Vertical distribution of the species is remarkably eurybathial while it is usually more abundant at the depths shallower than 500 m (Ogata et al., 1973). Our survey revealed again that this species clearly represents the deepest fish fauna in the Sea of Japan. In the base of our data along with Okiyama (2004) we confirm that this species was rather abundantly obtained near the lower limit of its bathymetric range, although there are no available records of the species beyond 2000 m as usual. The depths range for the species was 499-1527 m.

Another interesting feature of the species is the presence of two morphotypes tentatively termed as “white type” and “black type” (Kojima et al., 2001; Okiyama, 2004; Kodama et al., 2008; Kodama, Kojima, 2009). The former have pale body coloration and the latter is obscure. Both of them were recognized among *Bothrocara hollandi* individuals obtained from different depths. White morphotype represented by shallow living individuals that are gradually replaced by deep-dwelling obscure specimens at 1000 m depths. According to the data presented by Okiyama (2004) the two morphotypes differ in body sizes namely the black type is distinctly smaller than 26 cm whereas white one grows to 36 cm. Basing on the data of the expedition and previous fishing surveys the obscure specimens are affirmed to be smaller than the pale since the largest representative of the black type in stock reaches 212 mm in TL. There were either juvenile or II-III maturity stage individuals. The length at maturity was approximately the same as in previous study (Okiyama, 2004).

The underwater observations which have been carried out during the SoJaBio Expedition from a video camera established on the EBS frame have allowed to realize for the first time to trace the behavior of one of the most deep-water Sea of Japan species, *Bothrocara hollandi*. The preliminary analysis allows to make a conclusion that the individuals of this species spend the slow-moving mode of life that should be typical for inhabitants of extreme depths where the absence of a rich forage reserve does not permits to have another life strategy. Fishes lie on the bottom and keep quite behavior even at the moment when EBS approaches, trying to leave the capture zone only if the close contact with the device will be inevitable. The reaction to the light and powerful flashes of a camera is absent, but for all that fishes remain motionless. It is possible to explain such behavior only by two reasons. Firstly, inhabitants of depths never encountered with deep-water gears and do not feel a threat from their direction, and secondly some degree of a sight reduction is obvious.

The last of the families noticed is Liparidae that was represented by the extremely rare *Careproctus batialis* (stations B2-5 and B2-6 on Bogorov's ridge) at the depths 1700 and 1781 m. For today there are only two specimens of the species are conserved in the Zoological Museum (Zoological Institute RAN, Sankt-Petersburg) caught in 1932 at depths between 1940 and 2300 m in Tatar strait (Popov, 1933; Derjugin, 1939; Lindberg, Krasukova, 1987). So there are two additional individuals now to describe the variability of the morphological characters and some peculiarities of the species biology.

Another Liparidae species was obtained by one of the EBS hauling (station B6-6, 982 m). It is suggested to be the *Careproctus colletti* that inhabits the depth range between 60 and 1350 m (Amaoka et al., 1995). The total length of our young specimen reaches about 50 mm.

There were no any fishes beyond 2000 m depths. This phenomenon is well agreed with the conception of origin and evolution of the Sea of Japan (Nishimura, 1964). Probably the time that elapsed is insufficient for the development of rich deep-sea fish and invertebrate's fauna in this area in spite of favorable hydrochemical conditions down to the extreme depths. All findings are believed to help in discovering of some aspects of the Japan Sea origin which is still considered at least from two different positions (The main characteristics of the geology and hydrochemistry of the Sea of Japan, 1961).

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**MORPHOLOGICAL AND MOLECULAR ANALYSIS OF TWO SPECIES OF
CHAETOMORPHA, *C. AEREA* AND *C. LINUM* FROM CHINA COAST**

Linhong Teng^{1,2}, Bingxin Huang³, Lanping Ding^{1*}

¹ Institute of Oceanology, Chinese Academy of Science, Qingdao 266071,
China

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

³ Shantou University, Shantou 515063, China

Corresponding author: lpd2118@hotmail.com.

The taxonomic separation of *Chaetomorpha aerea* and *C. linum* was evaluated by morphological and molecular analysis in this study. The two species are different from each other in frond dimension, cell wall constricted or not and their mean length/width ratios (LWR). *C. aerea* attenuate basipetally, with diameter 270-400 µm at upper portion, 200-400 µm at middle portion, 160-240 µm at basal portion. Cell walls usually constrict. In contrast, *C. linum* usually have a consistent cell diameter, 150-300 µm, and cell wall don't constrict. The LWR is smaller than that of *C. aerea*. The different plants of the two species are molecularly analyzed by ITS region and 18S rRNA gene. Through ITS region alignment, it is shown that *C. aerea* has marked variation in thallus diameter, in that the thin plants with diameter 100-120 µm has identical ITS sequence with the thick ones. The pairwise distance between the two species is 15.4% for ITS region and 2.5% for 18S rRNA gene. It confirms the genetic divergence at molecular level.

Key Words: *Chaetomorpha aerea*; *Chaetomorpha linum*; morphology; 18S rRNA gene; ITS region; phylogeny

**MORPHOLOGY AND SYSTEMATIC IMPLICATIONS OF JUVENILE
LITIOPIIDS (CAENOGASTROPODA: CERITHIOIDEA: LITIOPIDAE)
FROM THE SOUTHERN RUSSIAN FAR EAST**

Larisa A. Prozorova¹, Tatiana Ya. Sitnikova²

¹Institute of Biology and Soil Science, Far Eastern Branch of Russian Academy of Sciences, Vladivostok, 690022, Russia. Email: lprozorova@mail.ru

²Limnological Institute of the Siberian Branch of Russian Academy of Sciences, Irkutsk, 664033, Russia. Email: sit@lin.irk.ru

In autumn 2006 small unidentified gastropods with shell height nearly 3 mm were collected in Vostok Bay (Peter the Great Bay, the Sea of Japan) by I.A. Kashin and A.Yu. Zvyagintsev (A.V. Zhirmunsky Institute of Marine Biology, FEB RAS). Mollusks inhabited in bulk surface of buoy exposed three month before collecting to study biofouling. Hydrological conditions: salinity 25-35 ‰, depth 4 m, stone bottom. Firstly, these microgastropods were regarded to Assimineidae. However, Dr. A. Chernyshev (IMB FEB RAS), who observed alive snails, noted long cephalic tentacles, unusual for assimineids (personal communication). To make more precise taxonomical identification of collected mollusks their morphological study was conducted. Overall examination of shell and soft body was made using a MBS-10 binocular with scales. Detailed examination of operculum was carried out using a Philips 525 Scanning Electron Microscope.

Shell is small, not exceeding 3 mm, thin, semitransparent when fresh, oval conical, with six slightly tumid whorls; last whorl is weakly angulated; aperture drop-like, without columellar tooth; umbilicus is absent. Operculum ovate, paucispiral, transparent, with eccentric nuclei and fine ridge-like attachment scar below the nuclei. Protoconch comprising 3,0-3,5 whorls is smooth, glossy, transparent, light brown in contrast to dull, yellowish teleoconch, sculptured by fine growth lines crossed by slight, strap-like spiral striae.

Radula is taenioglossate (R- | - [I + (L)] - | - 2 M) and typically cerithioid. Hourglass-shaped rachidian tooth with triangular buttress is wider than long. Cutting edge of rachidial has large central cusp and four smaller denticles, by a pair on each side. Marginal teeth are scythe-shaped, with cusped tips.

External morphology. The small head has a short bilobed snout and a pair of long cephalic tentacles. Tiny black eyes are located on the outer edge of the tentacular peduncles. Foot is long, narrow, but extensible, supplied by two mucous glands, located similar that in *Alaba incerta* (Orbigny, 1842) and *Litiopa melanostoma* Rang, 1829 [Houbrich, 1987]. Long and deep propodial mucous gland lies along the leading edge of the sole and large mesopodial mucous gland is on the center of posterior part of the sole. The leading edge of propodium has a pair of tentacles, one of each side. These propodial tentacles are shorter than cephalic ones. Epipodial tentacles are inconspicuous and the most probably absent. Mantle edge is smooth.

Mantle cavity organs. Mantle cavity is deep, dominated by a large ctenidium having wide, triangular filaments. A ridge-like osphradium extends nearly full length of the ctenidium. Pallial gonoduct is not developed because of juvenile stage of studied mollusks.

Based on combination of characters described above, studied microgastropods should be referred to the family Litiopidae. Their long active foot is used to climb out algae. Long cephalic and podial tentacles as well as podial mucous glands are adaptations for algal habitat. Produced mucous thread attaches the snail to the substrate or surface film of the water. Operculum with a narrow spiral ridge on the attached surface, many-whorled protoconch and shape of rachidials are a conspicuous features in the Litiopidae as well [Houbrich, 1987]. However, smooth protoconch and absence of epipodial tentacles found in Vostok Bay litiopids differ them strongly from two other morphologically studied species of the group belonging to *Alaba* H. et A. Adams, 1853 and *Litiopa* Rang, 1829. These species are characterized by “long retractible epipodial tentacles along the side of the posterior of the foot” and “protoconchs sculptured with numerous axial riblets and subsutural plaits” [Houbrich, 1987, p. 17].

The only litiopid species is known on the Southern Russian Far East - *Diffalaba vladivostokensis* (Bartsch, 1929) [Golikov & Scarlato, 1967]. Sometimes the species is included in *Alaba* [Volova et al., 1979; Kulikova et al., 2000 and others] or cited as a junior synonym of the *Diffalaba picta* (A. Adams, 1961) [Gulbin, 2006; Kantor & Sysoev, 2006 and others].

No comprehensive morphological study of the *D. vladivostokensis* have previously been made. Precise data on its reproduction and larval development [Kulikova et al.,

2000] were published without morphological description of both larval and juvenile stages.

Generic identification of the Primoryen litiopid is a rather doubtful. Original description by of the *Diffalaba* Iredale, 1936 is very brief [Iredale, 1936]. Soft body and larval shell morphology of type species of the genus *D. opiniosa* Iredale, 1936 from Australia is not yet described. Finally, T. Habe [1960] cited *D. picta* as belonging to the *Astrolaba* Laseron, 1956, while Houbrich [1987] excluded this genus from Litiopidae.

Concerning to specific identification, we should conclude that the *Diffalaba vladivostokensis*, which found to be lacking in epipodial tentacles, is not synonym of the *D. picta*. The main reason is that *D. picta* has four epipodial tentacles – a pair on each side of the foot and a posterior pair [A. Adams, 1962]. Besides that, there are essential differences in shell morphology between *D. vladivostokensis* and *D. picta* [Golikov & Scarlato, 1967; personal observation].

So, a further investigation is necessary to ascertain taxonomical position of litiopids from the Vostok Bay and adjacent area. Especially as a rather diverse litiopid fauna is recorded around Japan Islands [Higo & Goto, 1993 and many others]. That is why, comparative morphological study of “*Diffalaba picta*” sensu lato from Japan, Korea, North East China and South East Russia is highly advisable.

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**THE TEMPERATURE CHARACTERISTICS OF *CHAETOMORPHA VALIDA*
(CLADOPHORALES, CHLOROPHYTA), WITH ANALYSIS OF ITS
DIFFUSION POTENTIAL IN THE FLORA OF CHINA SEAWEEDS**

Yunyan Deng^{1,2}, Xiaorong Tang³ and Lanping Ding^{1*}

¹ Institute of Oceanology, Chinese Academy of Sciences, Qingdao 266071, China

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

³ Marine Genetics and Breeding Laboratory, Ocean University of China, Qingdao
266003, China

Corresponding author: lpd2118@hotmail.com

A marine green alga which formed large biomass at coast of Rongcheng city, Shandong province was studied. The green alga was identified as *Chaetomorpha valida* (Hooker et Harvey) Kützing (Cladophoraceae, Chlorophyta) by morphological features. Based on the unialgal culture, suitable temperature range for growth and reproduction of the alga's sample were examined. The suitable temperature range lied in 21~29°C. As the result of the suitable temperature range, this species was placed into warm-water in temperature characteristics. Among this temperature characteristics, this species will present potential possibility of southward diffusion along China coast.

Key Words: *Chaetomorpha valida*, temperature characteristics, diffusion, flora, China coast

**COMMUNITY STRUCTURE AND SPATIAL DISTRIBUTION OF MARINE
BENTHIC NEMATODES AT THE LATE STAGE OF THE YELLOW SEA
MACROALGAL BLOOM IN 2008**

Xiuqin Wu¹, Kuidong Xu^{1*}, Yong Huang²

¹Institute of Oceanology, Chinese Academy of Sciences, Qingdao 266071, China;

E-mail: kxu@qdio.ac.cn

²College of Life Sciences, Liaocheng University, Liaocheng 252059, China

The Yellow Sea experienced the world largest green tide due to the macroalgal bloom of *Enteromorpha prolifera* from May through July, 2008. To evaluate the environmental effect of the green tide, the community structure and spatial distribution of marine benthic nematodes were investigated at the late stage of the macroalgal bloom. The abundance of nematodes ranged from 186 inds./10 cm² to 3177 inds./10 cm², with an average of 1193 ± 689 inds./10 cm² in total 31 stations. Compared with the data obtained in 2007, the abundance decreased by about 1/3 in stations heavily affected by the *Enteromorpha prolifera* bloom, while it is slightly increased in stations in the Yellow Sea cold water mass apart from the macroalgal bloom. This resulted in an unusual trend of nematode standing crop decreasing from the central to the coastal area of the southern Yellow Sea. A total of 294 putative species/taxa belonging to 110 genera and 28 families were observed. The communities exhibited a high degree of dominance by *Dorylaimopsis rabalaisi*, *Dorylaimopsis* sp. 4, *Sphaerolaimus* sp. 7, *Sabatieria* sp. 8, *Parodontophora marina*, *Paramesacanthion* sp. 3, *Daptonema* sp. 10, *Chromadora* sp. 2, *Vasostoma longispicula*, *Paramarylynna* sp. 1. The epistrate feeders were the most predominant nematode feeding type, accounting for 36.3% of total nematodes. The macroalgal bloom resulted in obvious changes in structural and functional parameters of nematodes, especially in stations heavily affected by the macroalgal bloom. BIOENV analysis showed that the combination of phaeophytin-a and organic matter contents was most relevant to explain nematode species composition and diversity. In comparison with data obtained from the southern Yellow Sea in 2003, the more species observed should be attributed to the increasing sampling intensity and taxonomic knowledge, while the fewer genera were largely due to the effect of macroalgal bloom. Our study indicated that macroalgal bloom distinctly inhibited the

standing crop of nematodes as well as meiofauna in the inshore area. The decrease was likely not due to the deficiency of food concentration, but caused by the deposition and degradation process after the *E. prolifera* bloom.

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**COMMUNITY OF FREE-LIVING MARINE NEMATODES ON
MACROPHYTES (STARKA STRAIT, PETER THE GREAT BAY, SEA OF
JAPAN)**

Yulia A. Trebukhova¹, Olga N. Pavlyuk², Valentina V. Galtsova³

¹Far Eastern Marine Biosphere State Natural Reserve, Far East Branch, Russian
Academy of Sciences, Vladivostok 690041, Russia

²A.V. Zhirmunsky Institute of Marine Biology, Far East Branch, Russian Academy of
Sciences, Vladivostok 690041 Russia

³Russian State Hydrometeorological University, St. Petersburg 195196, Russia

The structure of nematode communities have been studied in the layer of algae *Ahnfeltia tobuchiensis* in the different years of observations. In Starka Strait the unattached stratum of *A. tobuchiensis*, up to 1 m thick, forms the mobile friable layer at depth from 1 m to 30 m. The layer of *A. tobuchiensis* is under the influence of complex system of currents. The motion of water determines the configuration, the integrity and the thickness of the layer *A. tobuchiensis* (Ivanova et al 1994). The totality of all plants and animals inhabiting the layer of *A. tobuchiensis* represents a uniform specific community. Numerous studies are done on communities living on *A. tobuchiensis* with an attention accent on composition and the distribution of bottom macrophytes and macrofauna. Practically there are no studies done on meiobenthos and nematodes, in particular, in the layer of *A. tobuchiensis*.

Materials and Methods

Meiobenthos samples collected in August 2007 and in July 2009 in the Starka Strait in the layer of *A. tobuchiensis* (at depth 10 m) were used for this research (Fig. 1). The thickness of *A. tobuchiensis* layer reached up to 50 cm. The samples were collected by scuba divers using a tubular bottom sampler with a mouth diameter of 5 cm and the height of the sediment sample columns measuring 5 cm. In total, 16 samples have been collected. Algae were collected by frame with the area 0.5m². The Shannon-Wiener

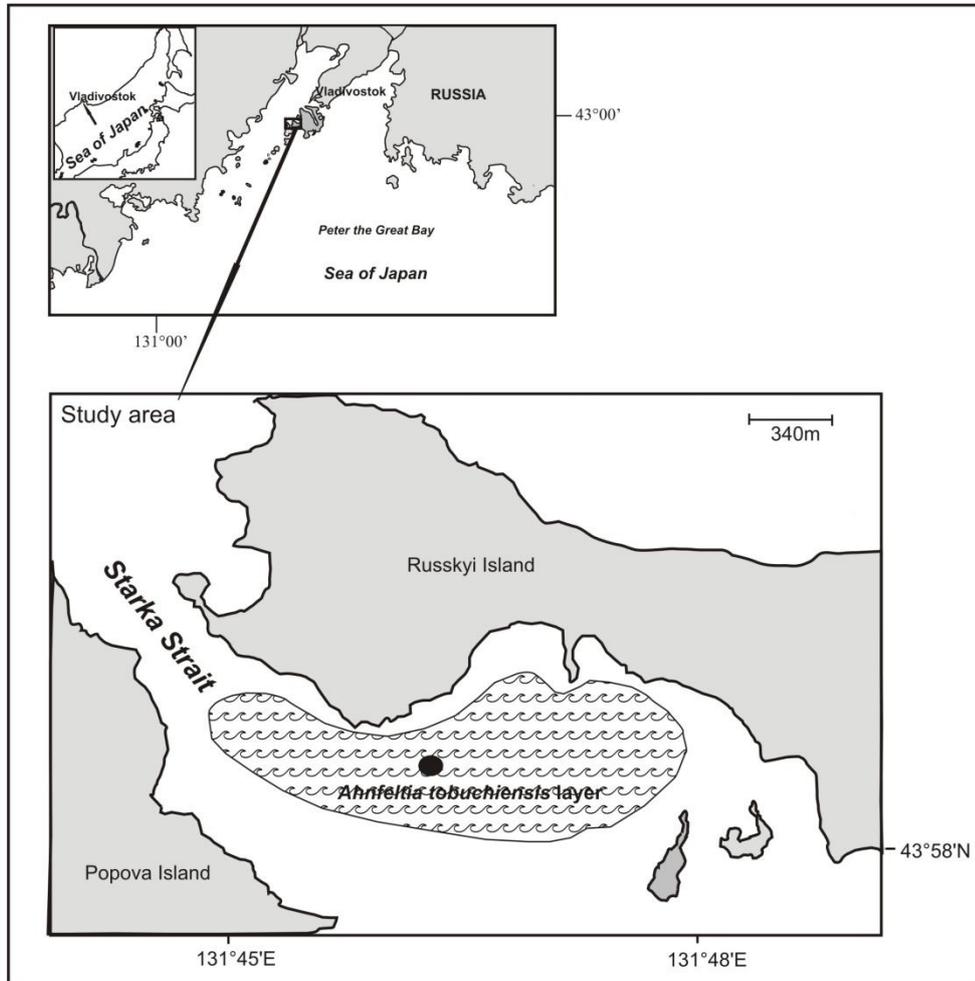


Fig. 1. A schematic map of study area inside of Peter the Great Bay (Sea of Japan).

diversity index (H), the Simpson domination index (C) and Pielou evenness index (e) were used in the characterization of the nematodes taxocenoses structure:

$$H = -\sum n_i / N \log_2 n_i / N;$$

$$c = \sum (n_i / N)^2;$$

$$e = H / \log S,$$

where n_i – is the density of each species, N – the total density of the taxocenosis, H – index of Shannon-Wiener, S – number of species.

The Wieser classification (Wieser 1953), based on the structure of the mouth cavity of animals, was used for the estimation of the trophic structure of the nematode community. According to this classification four groups of feeders were defined: selective deposit feeders (1A), non-selective deposit-feeders (1B), epistratum feeders (2A) and omnivores (2B).

Results and discussion

In 2007 the density of nematodes on the alga was low and composed 1.2% of the meiobenthos density (Fig. 2). Species composition of Nematodes was poor and counted 9 species. Dominant species was *Draconema japonicum* whose density was 55.9 % of the total density of nematodes. Juvenile forms composed the main part of the population of this species (58%). *Anticoma possjetica* took the second place on the density (12.3 %). Prevailing trophic grouping were selective deposit-feeders (1A, 68.2 %). The Shannon-Wiener diversity index (2.26), and Pielou evenness index (1.16) were relatively low, while the Simpson domination index (0.33) was very high.

In 2009 the density of nematodes on the alga composed 4.1% of the total density of meiobenthos (Fig. 2). The species composition of nematodes practically did not change but the change of the dominant species occurred. In June 2009 *A. possjetica* prevailed, the density of this species composed 51.4% of the total density of nematodes. Immature forms predominated (67%). *D. japonicum* occupied the second place on the density – 25.7%. The dominant trophic group was selective deposit feeders (1A, 87.7%). The Shannon-Wiener diversity index (1.97), and Pielou evenness index (1.01) were relatively low, while the Simpson domination index (0.34) was very high.

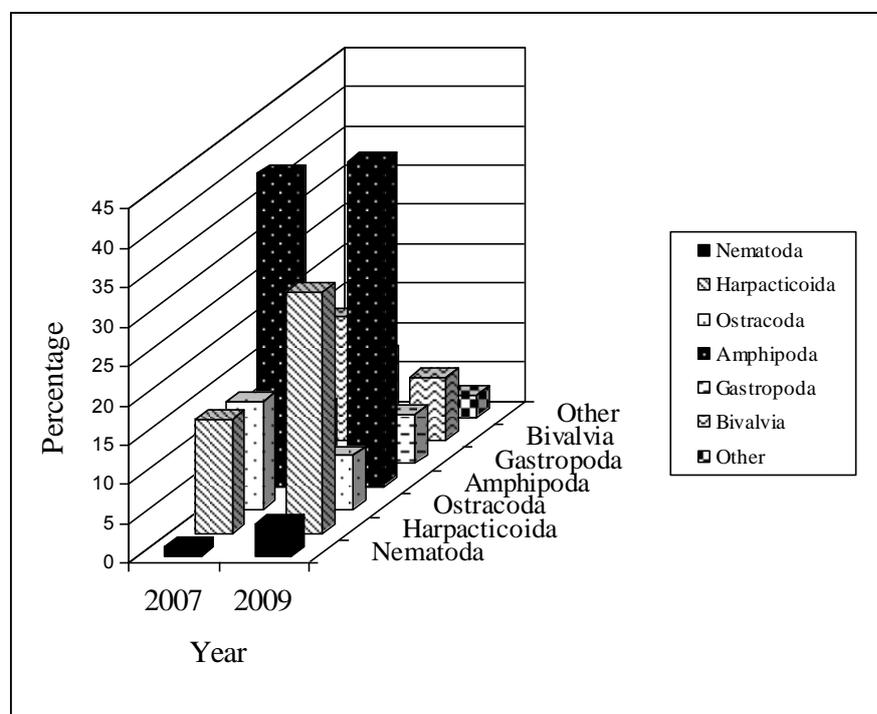


Fig. 2. Percent meiofauna composition in the *A. tobuchiensis* layer.

The taxonomic composition and the population density of nematodes in phytal communities associated with the characteristics of the algae: size, shape, the degree of branching and texture (Kito, 1982). In the community of *A. tobuchiensis* in meiobenthos crustaceans predominated, the proportion of nematodes was 1.2%–4.1%. Along with crustaceans, some nematodes have the ability to fasten to the substrate through the caudal glands and kept on moving objects using setae (Galtsova 1991). Probably, for this reason in the layer *A. tobuchiensis* species *D. japonicum* prevailed in the taxocenosis of nematodes. Species *A. possjetica* is retained on the alga due to the long tail and the tailed glands. The nematodes community on macrophytes is influenced by various factors of environment: speed of a water current, quantity of a food material in the form of deposit parts etc. (Tchesunov 2006). The layer of *A. tobuchiensis* provides epiphytic organisms, including nematodes, by organic matter which tightly accumulates in the branched space of seaweed. The complex structure of alga and the variety of food material increase the potential usefulness of resources for the population of alga (Kito 1982). The source of various organic compounds is also dead tissue of algae, suspended matter of which is delayed by interlocking thallus of algae. In taxocenosis of nematodes, inhabited in the layer of *A. tobuchiensis*, the prevailing trophic group was selective deposit-feeders (1A). Probably, such conditions are favorable for the development in the taxocenoses of nematodes of this trophic group. It was revealed that *A. tobuchiensis* influences on the meiobenthos animals living in a layer. In our opinion, sufficiently steady conditions with a constant granulometric composition of the sediment under the layer of *A. tobuchiensis* were formed, in which for the duration of long time there are the specific community of meiobenthic organisms and the special community of nematodes.

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**CORAL BLEACHING ON LUHUITOU FRINGING REEF, SANYA BAY,
HAINAN ISLAND, CHINA**

Xiubao Li, ^{1,2} Hui Huang, ^{1,*} Sheng Liu, ¹ Eduard A. Titlyanov, ³ Liangmin Huang, ¹
Tamara V. Titlyanova ³

¹Key Laboratory of Marine Bio-resources Sustainable Utilizing, South China Sea
Institute of Oceanology, Chinese Academy of Sciences, Guangzhou 510301, China

²Tropical Marine Biological Research Station in Hainan, CAS, Sanya 572000, China

³A.V. Zhirmunsky Institute of Marine Biology, Far Eastern Branch of the Russian,
Academy of Sciences, Palchevskogo 17, Vladivostok, 690041, Russia

*Corresponding author: coralreef@scsio.ac.cn

Luhuitou fringing reef was seriously affected by human activities and terrestrial runoff and no coral bleaching due to high thermal stress was recorded in literature. Bottom seawater temperature (BSTs) recording indicated that Qiongdong upwelling may significantly influence Luhuitou fringing reef, resulting in an apparent decrease in monthly means of BSTs in August in 2007-2009. However, along with less impact from upwelling in 2010, a slight increase in BSTs in August induced the first observed coral bleaching in Luhuitou fringing reef. Bleaching survey demonstrated that *Montipora* was the most susceptible taxon, whereas *Galaxea fascicularis* and *Pocillopora damicornis* were among the least susceptible taxa. Juvenile corals showed very few bleaching and most taxa showed relatively higher Bleaching Response in large size classes. Only loose relationships between coral recruitment and adult coral community were observed. Recent new findings from other studies demonstrated that abundant DIN would significantly reduce the upper thermal bleaching thresholds of inshore reefs. So it is suggested that improved coral reef management (i.e. sedimentation, DIN, overfishing and destructive fishing) will increase the regional-scale survival prospects of coral reefs to global climate change.

Key Words: coral bleaching, high thermal stress, upwelling, Luhuitou fringing reef

**SEASONAL DYNAMICS OF THE CRAB LARVAE IN MINONOSOK INLET
(POSYET BAY, PETER THE GREAT BAY, THE SEA OF JAPAN) IN
2000–2004**

Nina I. Grigoryeva

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

E-mail: grigoryeva04@mail.ru

The studies of seasonal dynamics of the crab larvae are of primary importance in assessing the reproduction success of populations. The success of the larvae development in the plankton and their settling to the bottom or substrates determine the population density and the abundance of further generations. Furthermore, the monitoring data on the larvae distribution may allow evaluating the abiotic factors impacting the species reproduction and registering the variability of the biological processes in different years.

The studies of the marine zooplankton of the near shore area of Peter the Great Bay were started in the late 1920s to the early 1930s (Tagats, 1933; Kasyanov et al., 1978; Korn, Kulikova, 1997; Kulikova et al., 1999; Maslennikov, Korn, 1999; Dolganova et al., 2004). However, the decapod larvae and, especially, the crab larvae were not taken into account in these studies. The zooplankton studies included only the plankton surveys in 1962–1971 in Posyet Bay (most of them were performed in the western shallow part of the bay) (Sveshnikov, Kryuchkova, 1971; Kos, 1977; Vyshkvartsev et al., 1979; Brodskii, 1981). The first studies of the spatial distribution of the crab larvae were performed in 1990–1992, when the water current impact was assessed for the larvae distribution of two commercial species - the red king crab *Paralithodes camtschaticus* (Tilesius, 1815) and the snow crab *Chionocetes opilio* (Fabricius, 1788) (Fedoseev, Grigoryeva, 2001a,b; Grigoryeva, Fedoseev, 2001b). According to these studies, the crab larvae first appeared in the open part of Posyet Bay close to Kitovy Bay and the Raid Pallada Inlet, and only after that did they spread in the whole bay. Some larvae were registered in the inner inlets; however, their survival rate was quite low due to the strong freshwater input and the high water temperatures in these areas. These data allowed recalculate the temperature, the dissolved oxygen, and the salinity optima for the crab larvae for the first time

(Grigoryeva et al., 2001; Grigoryeva, Fedoseev, 2001a). The interannual variability of the red king crab larvae population density and their settling to the artificial substrates in the aquaculture farms was described in further investigations (Fedoseev, Grigoryeva, 2001a,b, 2004). The present research was aimed to describe the seasonal dynamics of the crab larvae in Minonosok Inlet (Posyet Bay, Peter the Great Bay) in the spring and summer periods.

Materials and Methods

The analysis of the crab larvae's seasonal dynamics in 2000–2002, 2004 was targeted at six Brachyura crab species: the Japanese swimming crab *Charybdis japonicus* (A. Milne-Edwards, 1861), the pea crab *Pinnixa rathbuni* (Sakai, 1934), the Arctic lyre crab *Hyas coarctatus ursinus* (Rathbun, 1924), the kelp crab *Pugettia quadridens* (de Haan, 1839), the shy crab *Paradorippe granulata* (de Haan, 1841), and the porcelain crab *Pachycheles stevensii* (Stimpson, 1858). The plankton surveys were performed in Minonosok Inlet in the period from May 24 through all September at two stations. Zooplankton samples were taken by means of an MTA net (45 cm mouth opening) and an Apshtein net (25 cm mouth opening) using standard methods (Volkov et al., 1980). Vertical tows from the bottom to the surface were performed. 58 samples were taken in total. The larvae were identified using the drawings of Sato (1958), and Konishi & Shikatani (1999, 2000) and by comparing them with the larvae reared in the shore laboratory.

Results and Discussion

The crab larvae occurred in plankton of the area studied during observation period taking into with account that their taxonomic composition and the total density were greatly varied. The greatest crab density was observed in the open part of the Minonosok Inlet in June and August. Their maximal population density was 45.3 and 48.2 ind. per m⁻³, respectively. The taxonomic composition and number of crab larvae significantly differed at the two stations.

The decapod larvae population density also increased up to 245.3 ind. m⁻³. Four abundance peaks were registered: at the end of May, in the middle of June, at the end of June - the beginning of July, and at the end of July - early of August. The biodiversity of the decapod larvae increased and included shrimp larvae and larvae of some neritic crab species, such as the pea and the Japanese swimming crabs. They first appeared in the shallow near the shore areas in the middle of June.

The pea crab larvae were registered through the whole period of the observations - from the middle of June through September, as was also described for Vostok Bay (Kornienko, Korn, 2005). Larvae of *Pinnixa rathbuni* dominated in the plankton in the studied area season round, with two maxima of density (in the middle of June (26.3 ind. per m⁻³) and, the minor one - at the end of June (19.0 ind. per m⁻³)). The other peak of that species was recorded in the beginning of July - 10.2 ind. per m⁻³. Individual larvae of that species appeared in plankton in August and September. Concurrently with the pea crab larvae the Japanese swimming crab larvae occurred with a maximum density of 13.6 ind. per m⁻³ from the middle of June to the beginning of September. The density of the larvae reached its maximum at the end of June and gradually decreased in July; the late larvae incidentally occurred at the end of August. Larvae of the Arctic lyre crab were recorded in plankton from June 24 up to the middle of July, with their density reaching 11.9 ind. per m⁻³. They were recorded in small numbers (1.7-2.9 ind. per m⁻³) from the middle August to the beginning of September. Larvae of the shy crab occurred individually in plankton for the most part of the season. Their density reached 2.9 ind. per m⁻³ only in the middle of July and in the middle of August. Larvae of the kelp crab occurred in plankton in very small numbers (1.7 ind. per m⁻³) from June 16 until June 27. The maximum density was recorded in June 24 (8.7 ind. per m⁻³). Some individuals of the porcelain crab larvae were recorded in the plankton in July 11 (0.6 ind. per m⁻³).

The larvae of the deep-water crab species like the red king crab, the blue king crab, and the neritic helmet crab *Telmessus cheiragonus* (Tilesius, 1812) were not found here. The larvae of the two main commercial species like the red king crab and the snow crab were found in May of 2000 and 2001 only in the bay mouth of the Raid Pallada Inlet. Their maximal population density was 0.29 and 0.63 ind. per m⁻³, respectively. In Kitovy Bay, only some aggregations of the snow crab (0.31 ind. m⁻³) larvae were found. All these larvae were of the presetting developmental stages. One glaucotoe larva of a red king crab was even found. The larvae of the blue king crab *Paralithodes platypus* (Brant, 1850) were not registered at all. Thus, strong seasonality of the reproduction periods of the different crab species was observed. It was found out the deep-water species started their reproduction earlier followed by the neritic ones.

2000-2004 were characterized by cold winters and early springs compared to the average weather conditions of the last ten-day period (here and further, the hydrology

data are given according to Aschepkov et al. (2004)). The monthly average in April of 2000-2004 was 4.7-6.0 °C. In May it was 10.9-13.3 °C. The increasing of the water temperature was observed through the summer, and the highest monthly average values were registered in August. The average water temperature for the period from June to August also exceeded the interannual averages and was 16.6–25.1 °C. It constituted above 20.0 °C for September. The same tendency was observed in all regions of the Far East (Danchenkov et al., 2003; Glebova, 2005; Kim et al., 2006).

It is well known that the hatching of the crab larvae depends on the water temperature, and a water temperature increase speeds up the process of the embryonic development as well as decreases the periods between molting. In the seas of the Far East, the larvae hatching is observed earlier in the “warm” years compared to the “average” ones. The years with warm springs and hot summers are the most unfavorable for the larvae of the red king crab and helmet crab and favorable for the larvae of the small neritic species, as follows from the analysis of original and published data on long-term observations. Early hatching was observed in 2000-2004 for almost all the crab species. The red king crab larvae started to settle down quite early, in the end of May, when they already reached the glaucotoe developmental stage. In the previous years, they usually started settling down in the end of June – the beginning of July (Fedoseev, Grigoryeva, 2001a,b; Grigoryeva, Fedoseev, 2004).

The well-pronounced patchiness of the crab larvae distribution was observed for the whole period of the investigations, especially in June and July, when the population density reached the maximal values. This phenomenon was observed earlier by a number of authors also in Peter the Great Bay and in other areas of the Sea of Japan (Molotkov, Baenkhayeva, 1980; Dolganova et al., 2004; Shkoldina, 2004; Shkoldina et al., 2004). It is well-known that crab larvae perform diel vertical migrations, staying in the deeper water layers during the daytime and migrating to the surface at night where their abundance there may increase by tenfold (Melnikov, 1980; Forward, Douglass, 1986; Dolganova, 1998). The zooplankton sampling in the present study was performed during the daytime; that is why we assume some larvae were not caught. Further investigations are necessary with performing obligatory diel sampling stations.

Additionally, a relatively low crab larvae abundance was observed which did not exceed 48.2 ind. m⁻³. The interannual variability of the crab larvae population density is possible to analyze using the original and published data, We do not have any data

on Posyet Bay; thus, we compared the information on the larvae distribution and abundance for the other shallow bays of Peter the Great Bay. The crab larvae population density reached 68 ind. m⁻³ in 1973–1974 in the Alexeev Inlet (Mikulich, Biryulina, 1977). The decapod larvae were not studied, but their abundance was usually higher. In 1976 the decapod zoea abundance was 159 ind. m⁻³ in the Melkovodnaya Inlet (Molotkov, Baenkhaeva, 1980); in Vostok Bay, it reached even 1200 ind. m⁻³ in July of 1975–1976 (Kasyanov et al., 1978). The 1980s was a period of the total decline of the crab larvae population density; for example, the average abundance of the crab larvae was 20 ind. m⁻³ in 1986–1990 in the Alexeev Inlet (Maslennikov et al., 1994). The decapod larvae were found around Reineke Island from April through September of 1990 with the maximal abundance of 12 ind. m⁻³ (Maslennikov, Korn, 1999). The decapod larvae abundance was also low for the period of 1990–1996; only in 1996 there was a slight increase occur in the shallow part of Amur Bay in June (35 ind. m⁻³) and August (93 ind. m⁻³) (Kulikova et al., 1999). However, in the southwestern part of Peter the Great Bay, the average decapod larvae abundance did not exceed 2.21–21.9 ind. m⁻³ in the same year (1996) (Shkoldina, 2004; Shkoldina et al., 2004). The maximal larvae abundance was observed in July – August in the near shore areas and constituted 18.5–67.0 ind. m⁻³ (Shkoldina, 2004; Shkoldina et al., 2004). Thus, the maximal decapod larvae abundance was registered for the 1970s; it declined in the end of the 1980s and stayed low until now. The interannual variability of the zooplankton communities was defined by the water temperature and salinity. We assume that the significant decline in the total decapod larvae abundance and crab larvae abundance is defined mostly by the climatic (probably, planetary) factors and the anthropogenic load; and the local water temperature and salinity play an insignificant role.

Conclusion

In Minonosok Inlet (Posyet Bay), the total abundance of the decapod larvae was in June 24 in 2000–2004 with the maximum being 245.3 ind. m⁻³. The crab larvae were the most abundant in June and August (45.3 and 48.2 ind. per m⁻³, respectively). Three abundance peaks were registered: in the middle of June, at the end of June - early of July, and at the end of July - early of August. The studies of the seasonal dynamics of the crab larvae in Posyet Bay revealed their low biodiversity at the beginning of the season, when they are mostly represented by red king crab and snow crab larvae. The larvae of the other species appeared later. The larvae of the

deep-water species like the red king crab and snow crab dominated in May, while the larvae of the neritic crab species (the Japanese swimming crab and the pea crab) had the highest population density in June. A well-pronounced patchiness of crab larvae distribution was observed, especially in the period of their maximal abundance. The shift of the spawning period was observed in 2000–2004, according to the hydrological data analysis. The period of the investigations was characterized by an early warm spring and a hot summer; thus, the crab larvae hatching started earlier than in past years. The red king crab larvae started to settle down quite early. That is in the end of May when they already reached the glaucotoe developmental stage. The maximal abundance in Peter the Great bay was observed in the 1970s, it declined in the 1980s and has stayed low until now. We assume that the significant decline of the total decapod larvae abundance and the crab larvae abundance is defined mostly by the climatic (probably, planetary) factors and the anthropogenic load; the local water temperature and salinity play an insignificant role.

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POPULATION DYNAMICS AND BODY SIZE *CALANUS SINICUS* IN THE SUBTROPIC COASTAL WATERS OF HONG KONG

G.-T. Zhang¹ and C. K. Wong²

¹ Key Lab of Marine Ecology & Environmental Science, Institute of Oceanology,
Chinese Academy of Sciences, Qingdao, China and

²Department of Biology, The Chinese University of Hong Kong, Shatin, Hong Kong

The range of *Calanus sinicus* along the Chinese coast extends from the Yellow Sea and the East China Sea to the northern part of the South China Sea. Previous studies on the seasonal dynamics of *C. sinicus* have focused on populations in the temperate waters. Far less information is available on populations in the subtropical waters of the South China Sea. We studied seasonal variations in the population structure and body size of *C. sinicus* in two sheltered bays in the subtropical coastal areas of Hong Kong.

Tolo Harbor is a sheltered bay in the northeastern part of Hong Kong. It opens into Mirs Bay which is exposed to water currents from the South China Sea. Adults and copepodids appeared first in low numbers in Mirs Bay in December. Abundance in the entire area increased markedly in early January and reached a peak in late January and early February, but densities were always much higher in Mirs Bay than in the inner parts of Tolo Harbor. Numbers decreased to very low levels in April and no individual was collected after May.

Females, males and CV collected in January and February had longer prosome length than those collected in March, April and May. In addition, prosome length of females, males and CV tended to be longer in Mirs Bay and shorter in Tolo Harbor. The average prosome length of females collected before February was comparable to that of females collected in November from the southern part of the Yellow Sea. In contrast, females collected after mid-March were smaller than the smallest individuals collected from the Yellow Sea.

Our results suggest that the occurrence of *C. sinicus* in near-shore areas around Hong Kong in winter and early spring is associated with the NE monsoon and intrusion of cold waters from the East China Sea. *C. sinicus* is introduced into Mirs Bay and Tolo Harbor by water currents in late autumn or early winter. Individuals reproduce locally

mainly between January and March. After March, individuals develop smaller size as water temperature increases and environmental conditions become unfavorable.

Key Words: *Calanus sinicus*, population, body size, coastal waters

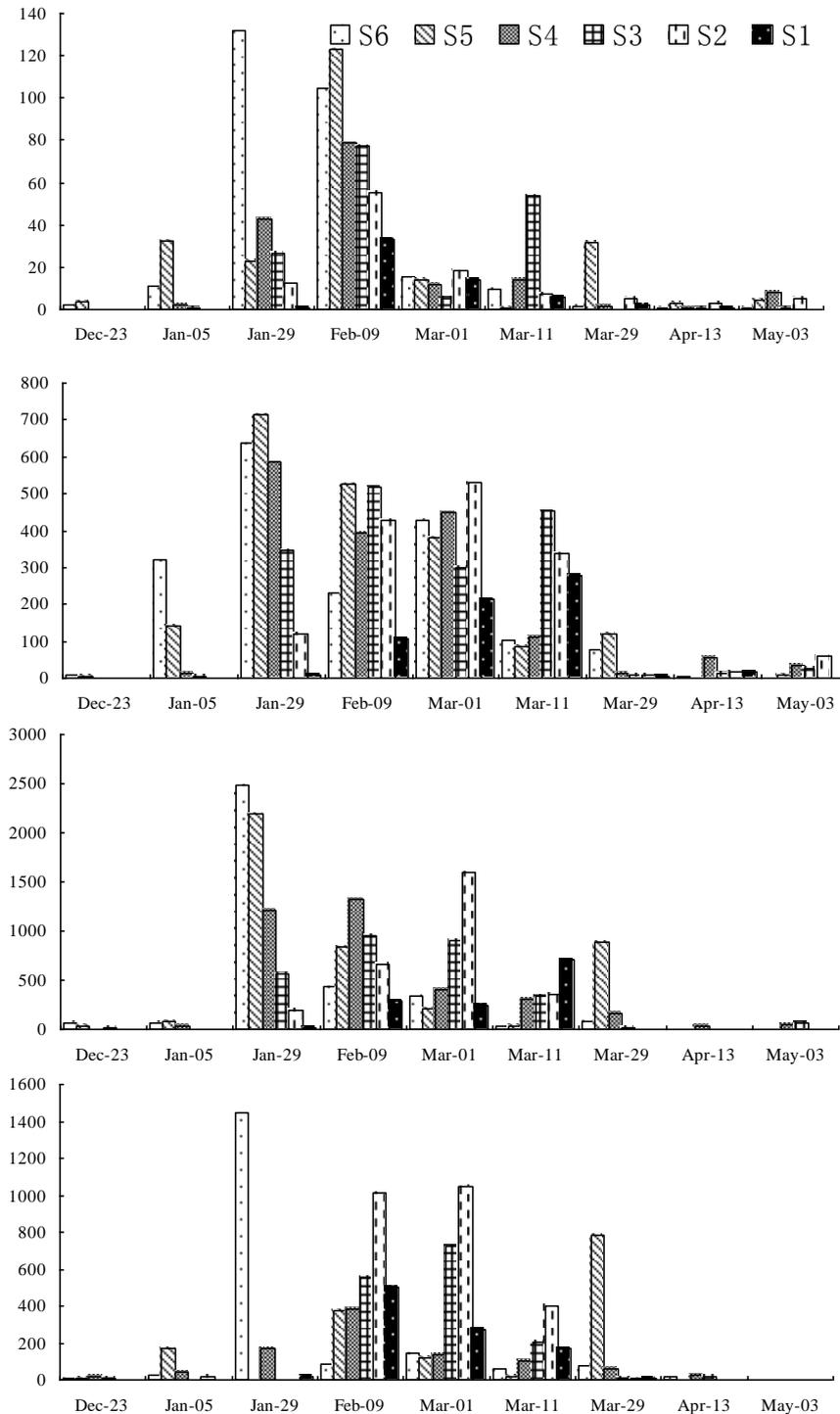


Fig. 1. *Calanus sinicus*: Seasonal variation of density of different developmental stages at each station (From top: adults, copepodites, nauplii, eggs)

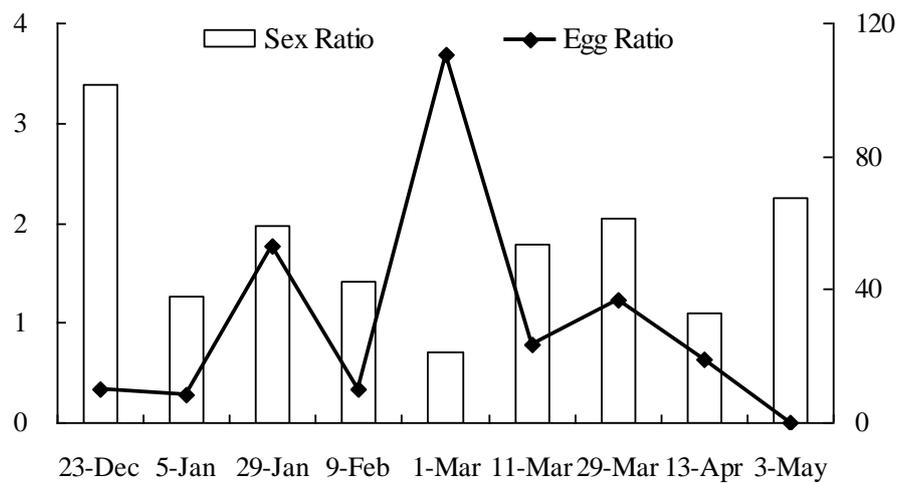


Fig. 2. Sex ratio (Female/Male) and Egg ratio (Egg/Female) of *Calanus sinicus* in each cruise.

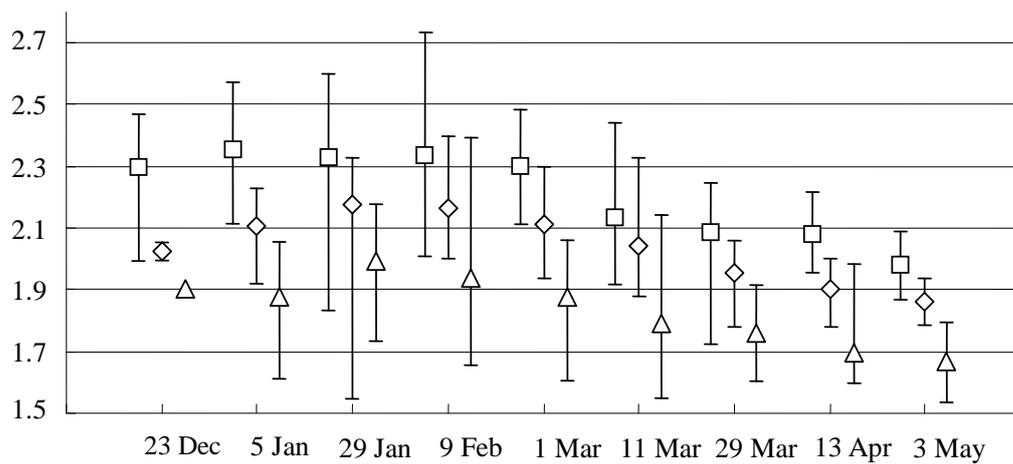


Fig. 3. *Calanus sinicus*: Seasonal variation of average prosome length (mm) of females (\square), males (\diamond) and CVs (\triangle). Vertical lines represent the maximum and minimum values.

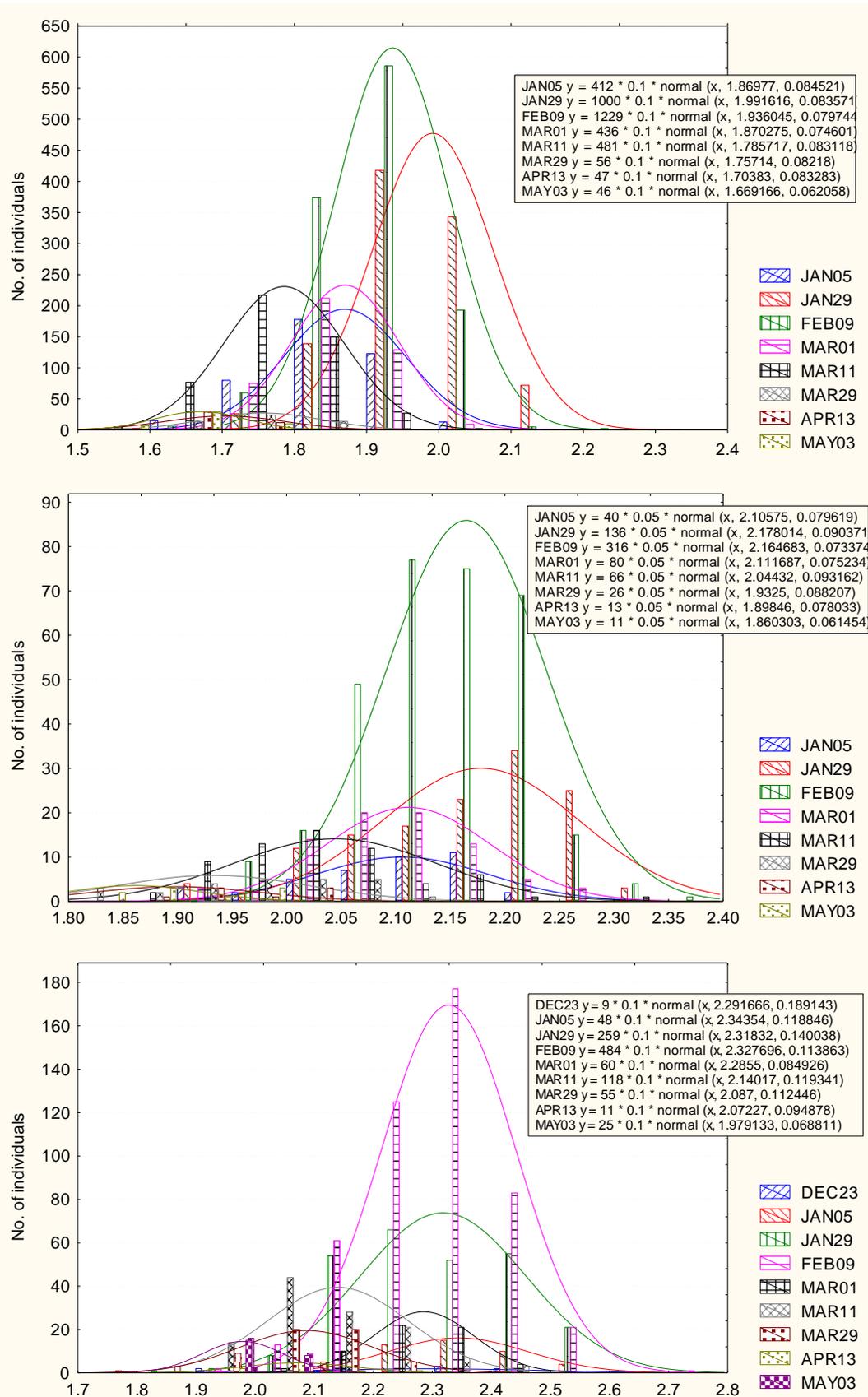


Fig. 4. *Calanus sinicus*: Size frequency distribution of CVs (top), Males and Females (bottom) in each cruise.

**DIVERSITY OF SOFT-BOTTOM MOLLUSKS IN THE FAR EASTERN
MARINE RESERVE (PETER THE GREAT BAY, SEA OF JAPAN)**

E.B. Lebedev

Far Eastern State Nature Marine Biosphere Reserve, Far East Branch,
Russian Academy of Sciences, Vladivostok 690041, Russia

E-mail: ev-lebedev@mail.ru

Peter the Great Bay is situated in the southwestern part of the Sea of Japan. A great diversity of its biota is determined by complicated hydrological conditions in the Bay. Cold-water boreal-arctic and warm-water subtropical species inhabit the Bay. Regular investigations of fauna and flora of Peter the Great Bay were started about 100 years ago.

About 30 years ago the Far Eastern State Nature Marine Biosphere Reserve was founded in the Bay. One of the major tasks of the Reserve is investigation and preservation of biodiversity.

Realization of this task requires a thorough inventory of flora and fauna, as well as revelation of rare species and species requiring protection. Mollusks are one of the main groups of macrobenthos, and quite often they determine the pattern of soft bottom population. Lately the Far Eastern

Marine Reserve accumulated faunistic studies which enlarge species lists of gastropods and bivalves (Gulbin, 1990; Klimova, 1984; Moskalets, 1984, 1990).

We determined a contemporary composition of fauna (about 80 species) of bivalves and gastropods from the soft bottom of the Eastern and Southern areas of the Far Eastern Marine Reserve in Peter the Great Bay, Sea of Japan. Samples of macrobenthos, collected from the soft bottom in the depth range from 2 to 36 m in summer of 2005-2007, served as materials for our work (see the Figure). The samples were taken using a Van Win dredger with a catching area of 0.11 m². The samples were washed through a sieve with 1 mm mesh, and fixed in 4% formaldehyde solution. Mollusks were identified to a species or genus.

Totally 51 mollusk species were found on soft bottoms of the Eastern site, and 64 species – in the Southern site. Bivalves of the East site include 34 species, and that of the Southern site – 43 species. On the whole, fauna of Bivalvia is sufficiently diverse. Examined mollusks are attributed to 54 species, 40 genera, 22 families and 6 orders.

The most prominent position is occupied by representatives of the order Veneroida (12 families, 25 genera and 32 species). The second place is occupied by the order Myoida (3 families, 3 genera and 7 species). The order Arcoida contains 2 families, 6 genera and 6 species. The order Pholadomyida includes 2 families, 2 genera and 5 species. The rest orders include 1-2 families, 1-3 genera and 1-3 species. At the family level Tellinidae (3 genera and 9 species), Veneridae (6 genera and 6 species), as well as Mactridae and Mytilidae (5 genera and 5 species), include the maximum number of taxa. 9 families (41%) and 35 genera (88%) had 1 species. Thus, overwhelming majority of genera and a half of families of bivalves (Nuculanidae, Glycymerididae, Pectinidae, Hiatellidae, Kelliellidae, Solenidae, Astartidae, Lucinidae, Psammobiidae, Corbulidae and Pharidae) on soft bottoms of the studied area were represented by minimum number of species.

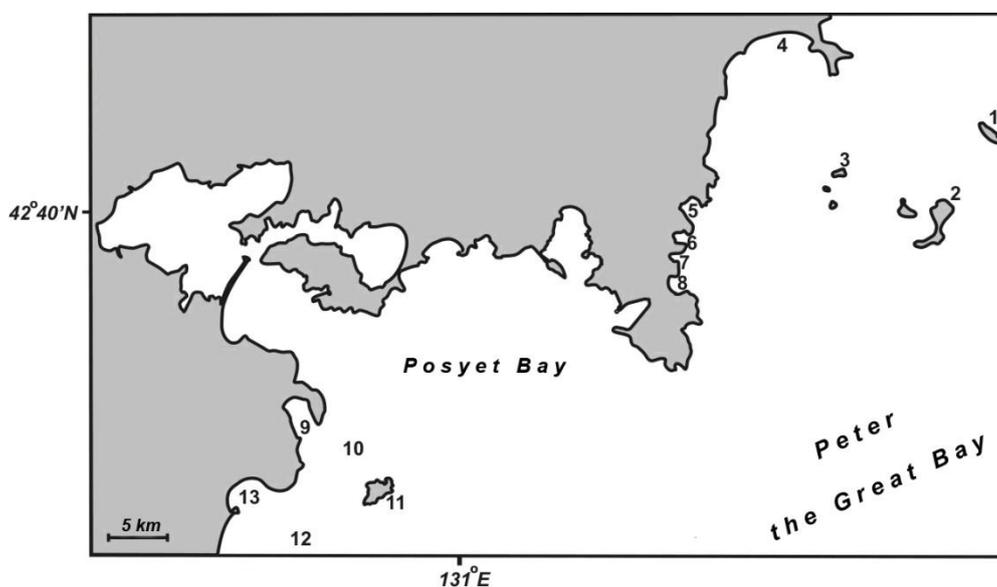


Fig. The map of study area. Figures designate places of taking quantitative samples.

Bivalve species, preferring silty and sandy bottoms and inhabiting the upper bottom layers, were basically met at the Eastern site. These are *Acila insignis*, *Nucula ovatotruncata*, *Diplodonta semiasperoides* and *Alveinus ojianus*. *Mactra chinensis*, *Yoldia keppeliana*, *Axinopsida subquadrata*, *Felaniella usta*, *Liocyma fluctuosa*, and *Spisula sachalinensis* occurred frequently. *A. insignis*, *L. ovatotruncata*, and *D. semiasperoides* were found at the Southern site more frequently as compared to the others, whereas *A. ojianus*, *Y. keppeliana*, *A. subquadrata*, *Callithaca adamsii*, and

Mya sp. occurred somewhat rarer. About a half of Bivalvia species (67%) were rare ones. The majority of rare species were Asian low boreal, and more seldom – subtropical low boreal. Large families – Tellinidae and Veneridae – included mainly Asian low boreal species. Families Mytilidae and Mactridae contained mainly wide boreal and subtropic-boreal species.

The majority of species has local Pacific origin and is characterized by a narrow distribution within the limits of the boreal zone. Species from the Asian low boreal area made 50% of all

Bivalvia at the Eastern site, and 34% - at the Southern site. The portion of relatively warm-water species – subtropical and subtropical-low boreal – was smaller at the Eastern site (25%) as compared to the Southern site (32%). Species wide distributed in the boreal waters of Pacific, make 11% of all bivalves at the Eastern site. Their portion at the Southern site is 13%. Cold-water species include 14% of all bivalves at the Eastern site, and 18% at the Southern site. As is obvious, Bivalvia fauna of the Southern site of the Reserve is more diverse and rich in warm water and temperate water components. At the both sites the bulk of bivalves fauna is formed by Pacific Asian low boreal and subtropical species (Lutaenko, 2002, 2003).

Gastropoda mollusks at the Eastern site include 17 species, and at the Southern site – 21 species. Gastropoda fauna is less diverse. Found mollusks are attributed to 27 species, 23 genera, 14 families, 11 superfamilies and 6 clades. Representatives of Neogastropoda (4 superfamilies, 4 families, 7 genera and 7 species) and Littorinimorpha (3 superfamilies, 4 families, 7 genera and 7 species) occupy the most prominent position. The rest 4 clades include 1-2 families, 1-3 genera and 1-3 (5) species. At the family level, Trochidae (2 genera and 4 species), as well as Rissoidae and Pyramidellidae (3 genera and 3 species each), contain the largest number of taxa. One species was found in 4 superfamilies (36%), 6 families (42%) and 19 genera (82%). Thus, the majority of genera and almost a half of families of gastropods from the soft bottom of the studied area (Turbinidae, Littorinidae, Truncatellidae, Olivellidae, Muricidae and Philinidae) were represented by one species.

In the most habitats at the both sites of the Reserve small silt-loving mollusks *Setia candida* and *Pyrgolampros rufofasciata* from Asian low boreal area were met. Common species of gastropods were: at the Eastern site – Asian low boreal *Bela erosa*; at the Southern site – Asian subtropical *Philine scalpta* and Asian wide boreal

Cryptonatica janthostoma. About a half (48% species) of Gastropoda were rare. Most rare species were Asian low boreal and, more seldom, subtropical-low boreal species. Large families - Trochidae, Rissoidae and Pyramidellidae – also included basically Asian low boreal species.

Overwhelming majority of the found species has local Pacific origin and is characterized by narrow distribution within the range of the boreal zone. Species from Asian low boreal area make 79% of all Gastropoda at the Eastern, and 65% - at the Southern sites. The portion of relatively warm water species – subtropical and subtropical low boreal – at the Eastern site was lower (14%) than at the Southern site (20%). Species, prevailing in the boreal waters of Pacific, were represented by few species number at the Eastern site, and made only 7% of all Gastropoda. At the Southern site their portion was twice greater – 15%. As one can see, gastropodal fauna of the Southern site of the Reserve is more diverse and rich in warm water and temperate water components.

Thus, our results confirm preservation of a significant biological diversity of mollusk fauna from soft bottoms in water area of the Far Eastern Marine Biosphere Reserve, as compared to the previous studies. The author is grateful to the workers of A.V. Zhirmunsky Institute of Marine Biology FEB RAS V.V. Gulbin and M.B. Ivanova for consultations on species identification. The study was supported by FEB-1 grant N 09-I-II23-08.

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**SEASONAL AND GEOGRAPHICAL DISTRIBUTION OF PLANKTONIC
COPEPODS IN TOLO HARBOUR AND ADJACENT AREA: RESPONSES
TO POLLUTANT CONTROL PROJECTS**

G.-T. Zhang^{1,2}, C. K. Wong¹

¹ Department of Biology, The Chinese University of Hong Kong, Shatin, N.T.,
Hong Kong SAR, China

² Key Lab of Marine Ecology & Environmental Science, Institute of Oceanology,
Chinese Academy of Sciences, Qingdao, China

Tolo Harbor is a poorly flushed bay in the northeastern corner of Hong Kong. Eutrophication caused by excessive introduction of untreated and secondarily treated sewage began in the 1970s. Increased nutrient input led to noticeable increase in algal biomass and algal bloom occurrences. Pollution reduction measures were introduced in 1986. Decline in water quality has been halted after actions implemented to control and reduce nutrient inputs became fully operational in 1998. Zooplankton samples collected in 2003–2004 revealed that Tolo Harbor contained higher density and lower diversity of planktonic copepods compared to Mirs Bay, a less polluted sea area outside Tolo Harbor. The impact of nutrient reduction on the copepod communities in Tolo Harbor was also studied by comparing data collected in this study to those collected in 1987–1991. Average copepod density decreased from 7,528 ind. m⁻³ in 1987–1991 to 4,410 ind. m⁻³ in 2003–2004, but the total number of recorded species increased from 48 in 1987–1991 to 52 in 2003–2004. Small copepods, notably species of *Paracalanus* and *Oithona*, dominated the copepod communities in both periods, but there was an increase in species evenness, caused by an increase in the number of dominant species, in 2003–2004. These observations confirm that eutrophication may lead to increases in copepod densities accompanied by increased dominance of small species.

Keywords: Eutrophication; copepods; community composition; species diversity; abundance; Hong Kong

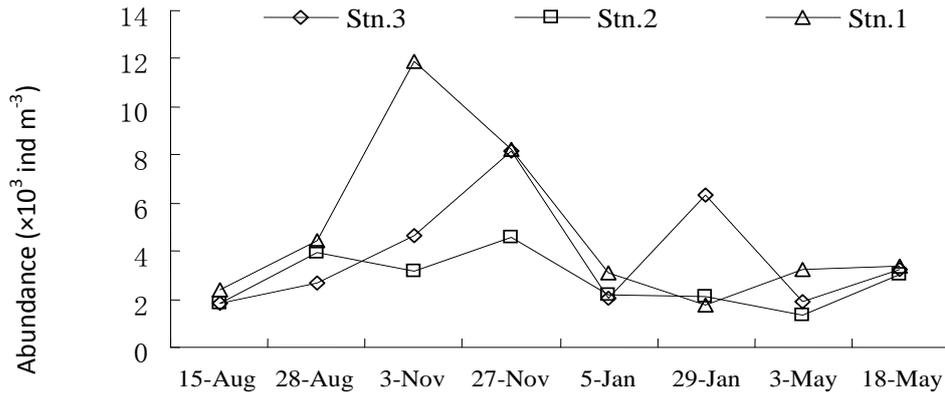


Fig. 1. Seasonal variation of copepods abundance ($\times 10^3 \text{ ind m}^{-3}$) at each station

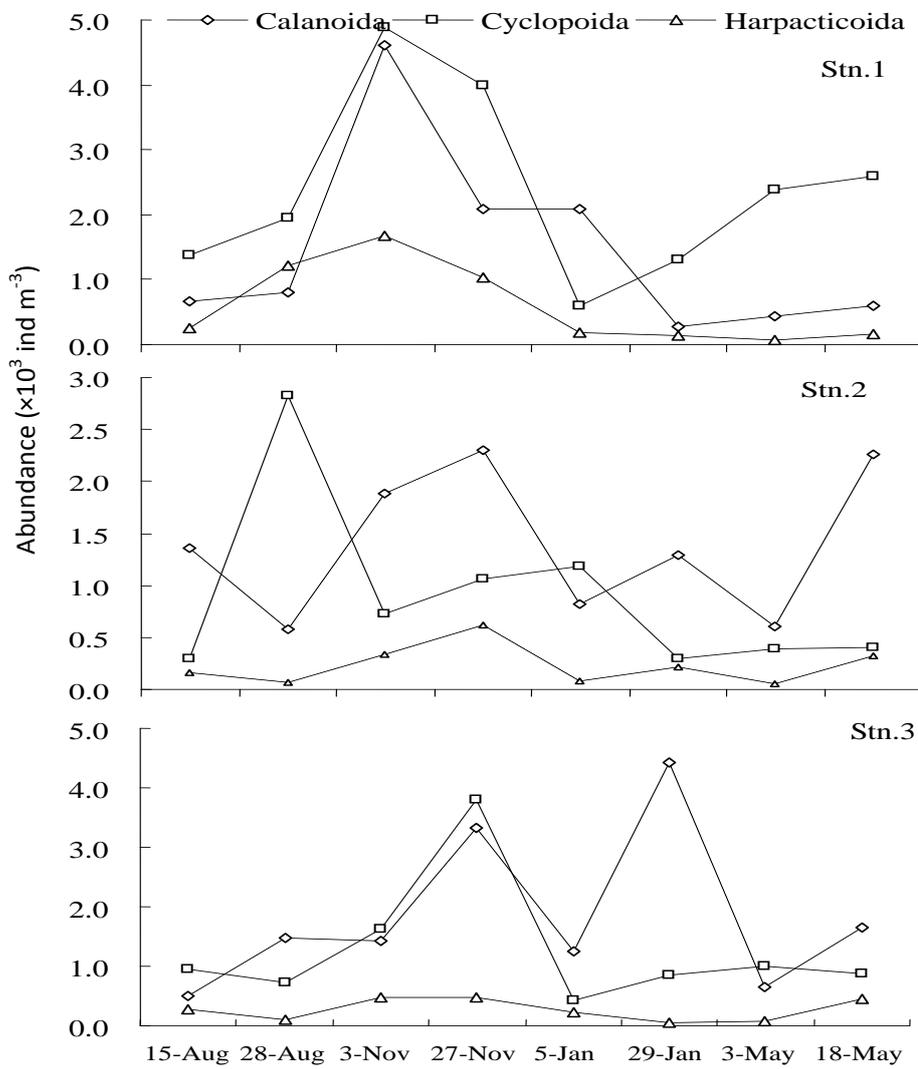


Fig. 2. Seasonal variation of abundance ($\times 10^3 \text{ ind m}^{-3}$) of different taxon (Calanoida, Cyclopoida and Harpacticoida) at each station

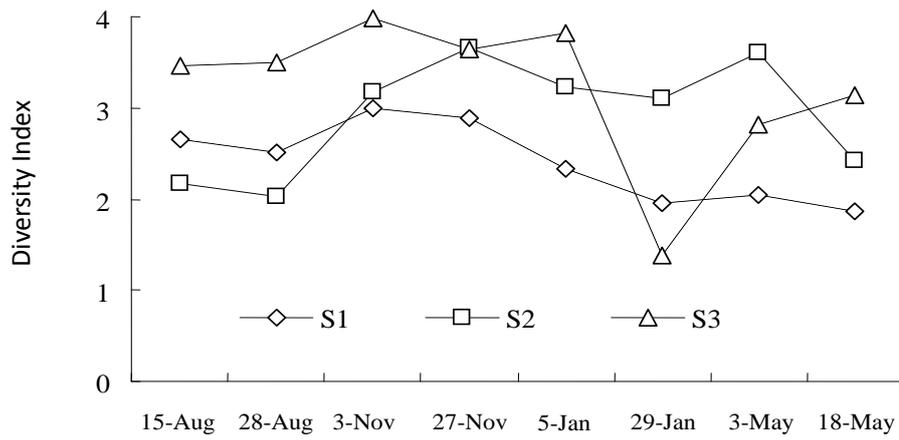


Fig. 3. Seasonal variation of Shannon-Wiener's index in each cruise

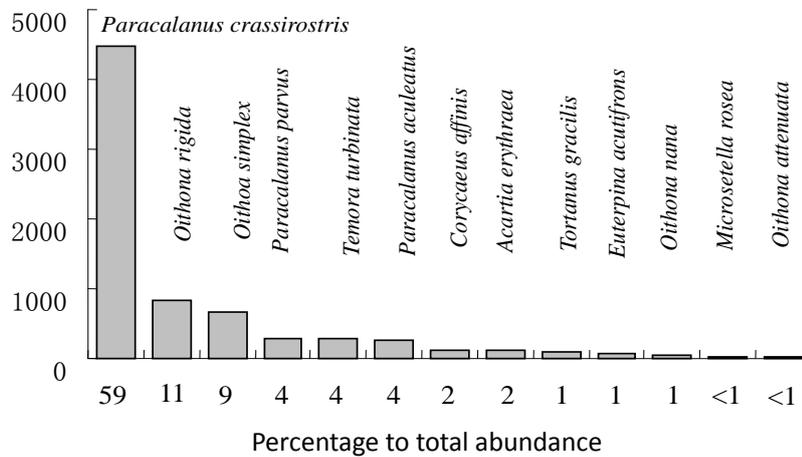


Fig. 4. Average density of dominant species at station 1 from 1988 to 1991 (with data from Wong *et al.*, 1993). Species were ranked according to their proportion in total copepod abundance.

STRUCTURE AND GEOGRAPHIC DISTRIBUTION OF ZOOPLANKTON COMMUNITIES IN WESTERN ARCTIC OCEAN IN SUMMER 2003

Guangtao Zhang, Song Sun

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

Based on species composition and abundance of zooplankton from 43 stations in the Western Arctic Ocean, community structure and geographic distribution, as well as relation between zooplankton communities and environmental conditions were investigated. Three zooplankton communities were identified with cluster analysis: high latitude deep ocean community located in the Canadian Basin and Chuchi Plateau, shelf community located in the central Chukchi Sea and neritic transition community including station along the Alaska Coast and in the north of Chukchi Sea. The deep ocean community was least in total zooplankton abundance, and dominated by copepods. Dominant species includes *Oithona spp.*, *Scolecithricella minor*, *Calanus hyperboreus* and *Metridia longa*. The major difference between the other two communities was abundance of Ostracods, which was 573.2 ind m⁻³ on average in shelf community and 20 time higher than the neritic transition community. Dominant species in shelf community were, from the highest dominance index, Ostracods, *Calanus glacialis*, *Pseudocalanus newmani*, and those in neritic transition community were *P. newmani*, Banaracle larvae and *Acartia longiremis*. The deep ocean community inhabited in high latitude area characterized by low temperature and chlorophyll a concentration. The shelf community distributed in mainly central Chukchi Sea with high temperature and low chlorophyll a concentration and several stations with low temperature and high chlorophyll a concentration. Stations from all these three habitats were included in neritic transition community. It was indicated that zooplankton community in western Arctic Ocean received influences from both the sub-arctic Bering Sea and high latitude areas, but determined by different population recruit rates among species, as only those adapted well to local environmental conditions can thrive.

Keywords: Western Arctic Ocean; zooplankton; community structure; dominant species; Ostracods

Table 1. Dominant species (taxon) and dominance index (Y) of each community.

Community III	Y	CommunityII	Y	CommunityI	Y
<i>Pseudocalanus newmani</i>	0.19	Ostracods	0.51	<i>Oithona spp.</i>	0.35
Barnacle larvae	0.18	<i>Calanus glacilis</i>	0.14	<i>Scoletthicella minor</i>	0.15
<i>Acartia longiremis</i>	0.08	<i>Pseudocalanus newmani</i>	0.10	<i>Calanus hyperboreus</i>	0.12
<i>Oithona spp.</i>	0.06	Banercle larvae	0.09	<i>Metridia longa</i>	0.10
<i>Calanus glacilis</i>	0.06	<i>Acartia longiremis</i>	0.04	<i>Calanus glacilis</i>	0.06
<i>Oikopleura sp.</i>	0.05	<i>Oikopleura sp.</i>	0.02	<i>Pseudocalanus newmani</i>	0.04
<i>Calanus hyperboreus</i>	0.05			Ostracods	0.04
Ostracods	0.03			<i>Microcalanus pygmaeus</i>	0.02
				Nauplii	0.02

43个站位的聚类分布图

Ward's method
1-Pearson r

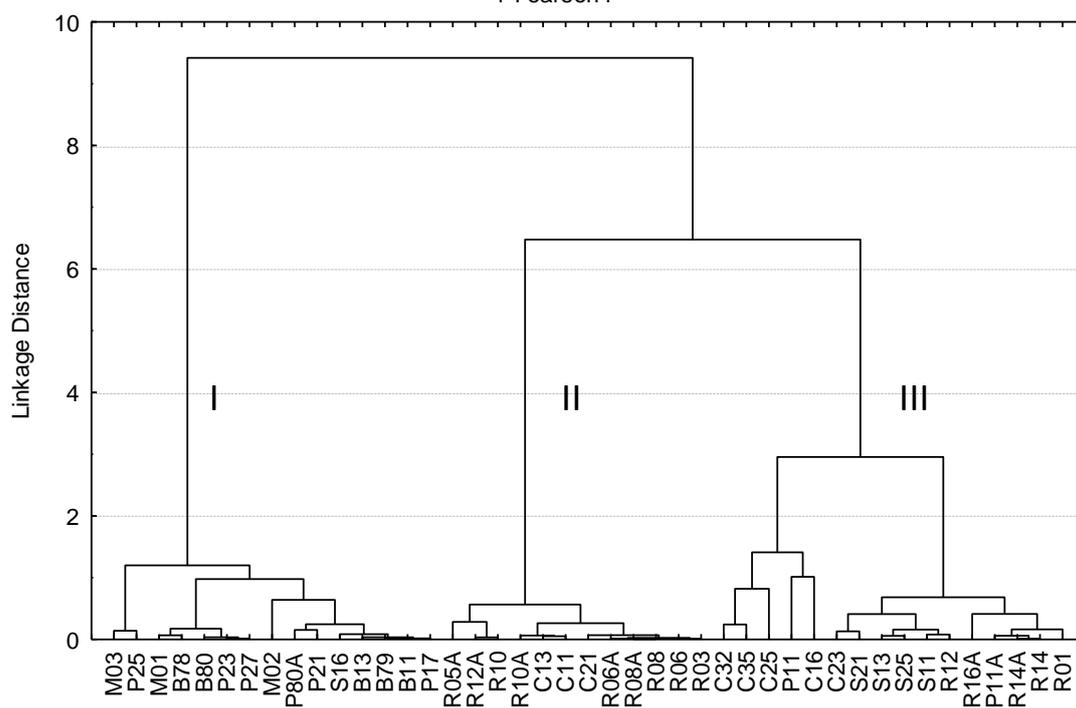


Fig. 1. Station similarity determined by cluster analysis.

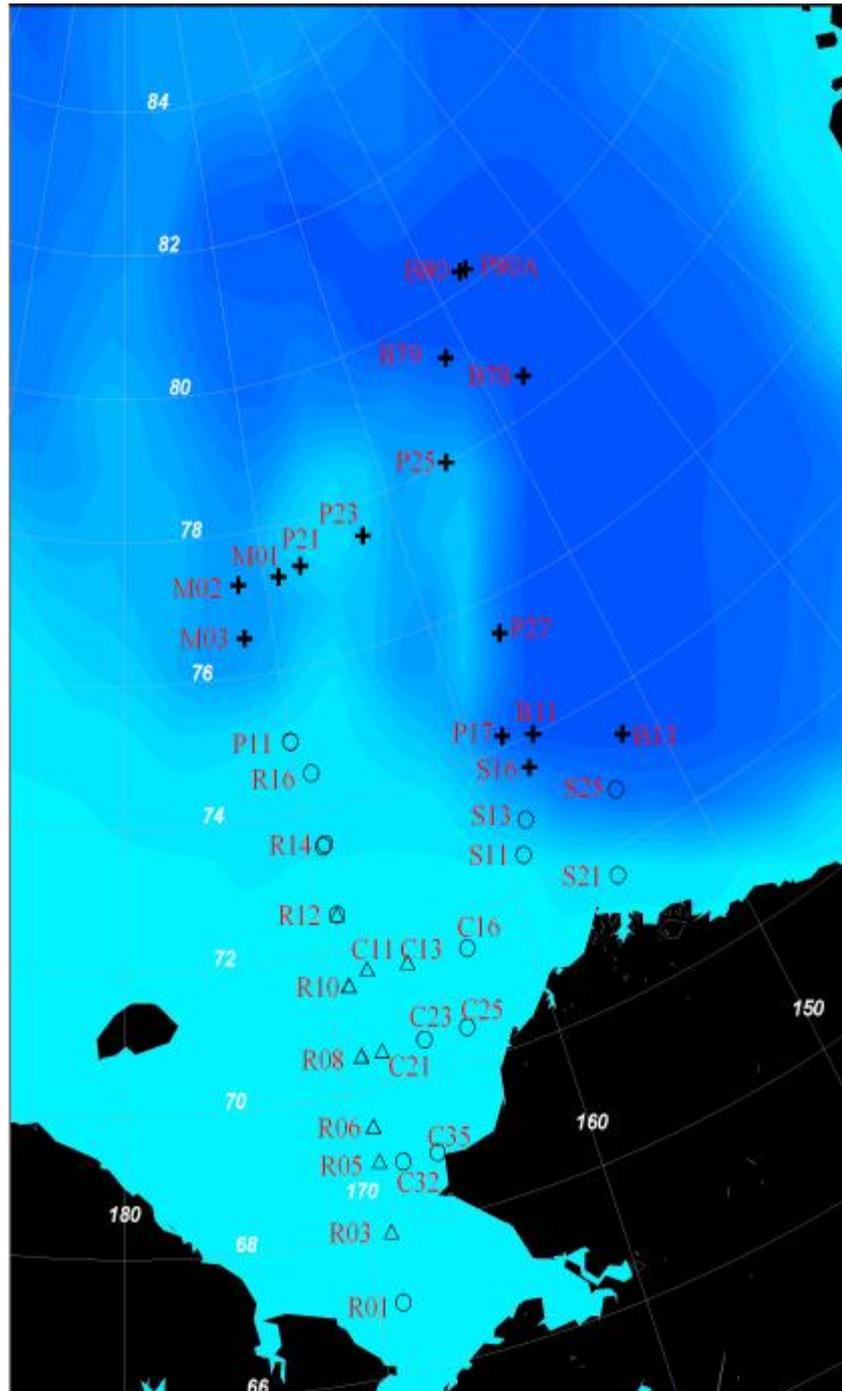


Fig. 2. Geographical distribution of three communities defined by cluster analysis

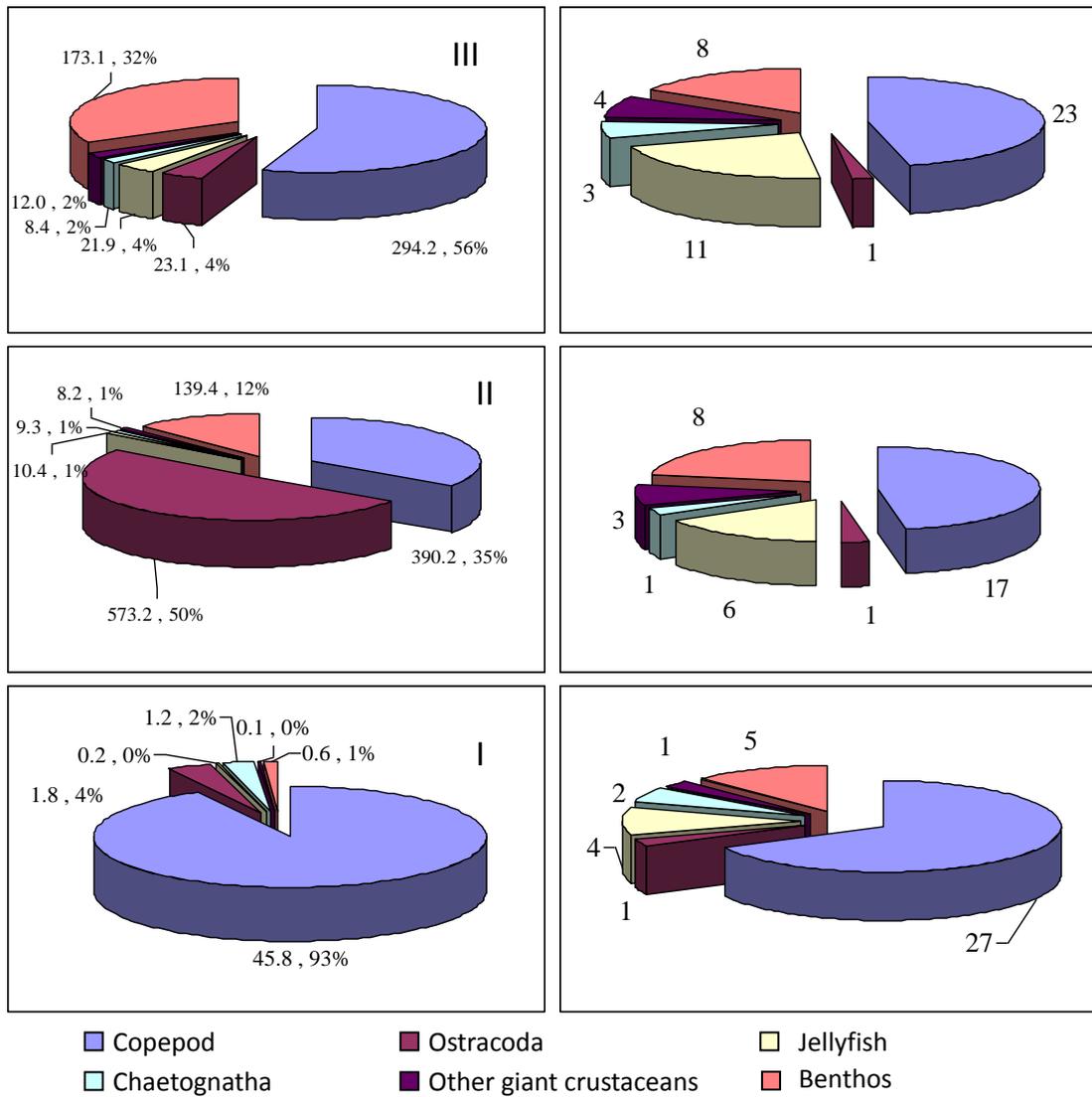


Fig. 3. Proportion, average density (Left collumn) and species number (Right collumn) of different taxonomic groups

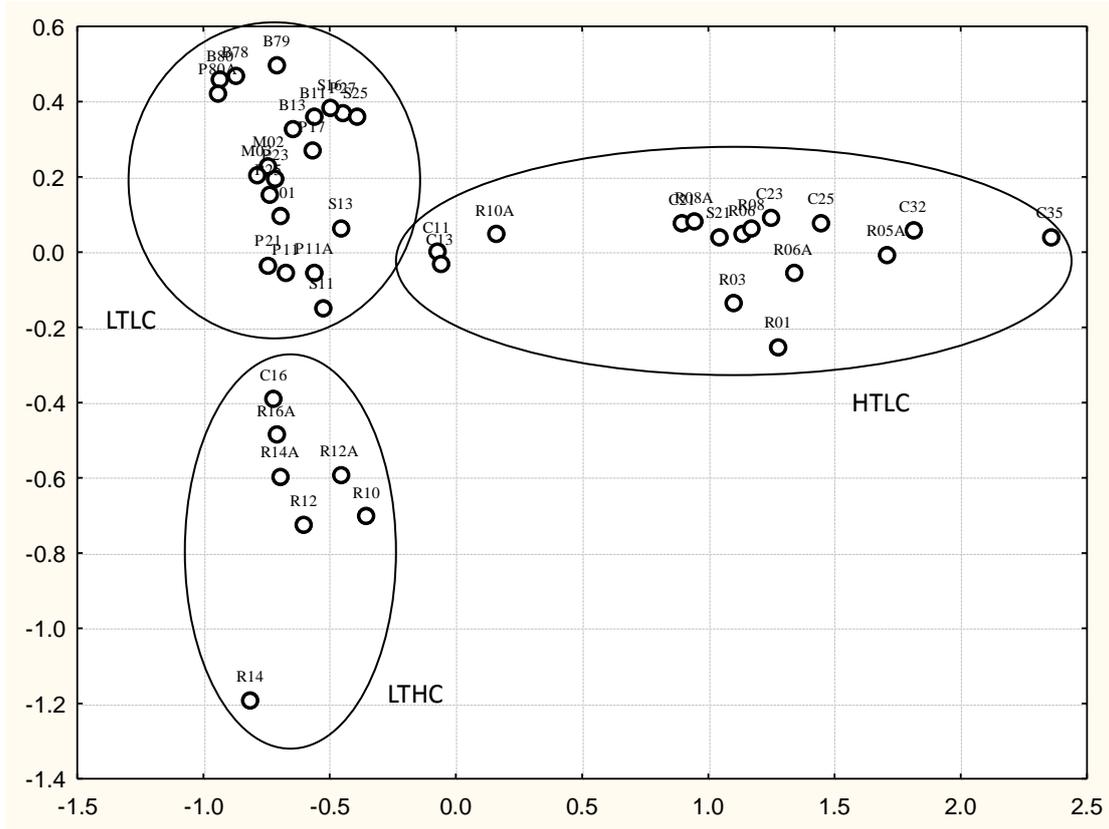


Fig. 4. MDS of all sampling stations. L- Low; H-High; T-Temperature ; C-Chlorophyll (Statistica 6.0)

**COMPOSITION AND SEASONAL VARIABILITY OF
ICHTHYOPLANKTON COLLECTED USING FISHING LIGHTS IN
VOSTOK BAY (PETER THE GREAT BAY, SEA OF JAPAN)**

T.G. Sokolovskaya, A.S. Sokolovsky, I.V. Epur

Institute of Marine Biology, Far Eastern Branch of the Russian Academy of Sciences,
Vladivostok 690041
E-mail: iraepur@mail.ru

Peter the Great Bay was suggested by the Institute of Marine Biology and chosen a control site for monitoring the coastal biodiversity according to the DIWPA (Diversitas in the Western Pacific and Asia) program. The same type of work had been previously conducted for several years at a less regular basis in Vostok Bay (Adrianov, 2004). Starting from 2003, well-planned regular works have been carried out on the inventory and monitoring of ichthyofauna.

One of effective collecting methods in Vostok Bay was catching of ichthyoplankton, young and adult fish using fishing light mounted on a pier of the Vostok scientific station of the Institute of Marine Biology.

The inventory of ichthyoplankton by use of fishing lights was not carried out in Russia before, and out long-term investigations are therefore important both for scientific and practical purposes.

Materials and Methods

Fish attracted to the illuminated zone were caught with a gauze net an hour after light switching at night (from 9 a.m. to 6 p.m.). Illumination was provided by a mercury vapour lamp DRL 500 fastened to a pole mounted on the pier located at the Vostok scientific station. Water depth near the side of the pier is 1.5–1.7 m.

The fish material collected was fixed with 4% formaldehyde solution and was later processed in the laboratory. Species were identified both with our original keys (Sokolovsky, Sokolovskaya, 2008) and with the earlier published keys, particularly *An Atlas of the Early Stages) Fishes in Japan* (1988).

All fish larvae and fries were measured and counted. Data on each sample were registered in ichthyoplankton cards and later were analysed and added to a computer database.

A total of 584 ichthyoplankton samples was collected and processed. Usually catches began in the middle of March or in early April, depending on the time when sea ice melted in Vostok Bay, and ended in October–November (Table 1).

Table 1. The number of fauna samples collected using fishing lights in Vostok Bay from 2003 to 2010

Year	Number of samples per month								n
	III	IV	V	VI	VII	VIII	IX	X	
2003	-	6	10	14	9	6	6	6	57
2004	4	8	14	12	10	8	4	6	66
2005	7	11	12	10	11	7	5	4	67
2006	-	10	12	11	9	7	5	4	58
2007	7	7	13	12	10	8	6	5	67
2008	9	12	16	12	12	13	12	11	97
2009	3	10	12	13	11	12	14	14	89
2010*	11	11	16	19	17	9	–	–	83
Total									584

*The samples of 2010 are processed until 15.08.2010.

Results and Discussion

The processed ichthyoplankton samples totally contained fish larvae and fries of 72 species belonging to 31 families of fishes having pelagic larvae and juveniles.

The major part of the ichthyoplankton collected in Vostok Bay consisted of the larvae and fries of the following families: Stichaeidae (13 species), Cottidae (10), Agonidae (6), Clupeidae (3), Salmonidae (3), Hemitripterae (3), and Gobiidae (3). The other families were represented by one or two species in the samples.

Rather high species diversity in the ichthyoplankton community is recorded for the spring period: 24 species in March, 41 species in April, and 42 species in May (Table 2). It may be explained by the fact that the ichthyofauna of Peter the Great Bay mostly consists of boreal and Arctic boreal species, which spawn at low water temperature, usually in autumn–winter or in winter–spring. These species belong to two orders with almost equal contributions: Scorpaeniformes 27 species and Perciformes 24 species. The species composition of the ichthyoplankton changes most considerably in April and May as compared to March: it shows an almost twofold increase. Starting from June the number of species in the ichthyoplankton gradually decreases to eight species in October.

In June and July most members of families with high number of species (Cottidae, Agonidae, Psychrolutidae, Liparidae, and Salmonidae), which made up the bulk of the

spring catches, disappear from the samples. In this period they get grown up enough to leave warm shallow waters and to go to greater depths.

In spring and autumn (from June to September) the ichthyoplankton includes the larvae and fries of both local resident species and southern migrants spawning in the bay: *Konosirus punctatus*, *Sardinops melanostictus*, *Engraulis japonicus*, *Cololabis saira*, *Hyporhamphus sajori*, and *Strongylura anastomella*.

Though the dynamics of the number of species has a distinct seasonal trend with a maximum in April–May, the number of families, to which these species belong, has a slightly different trend with a maximum in June–July. Members of the Clupeidae family are present in the ichthyoplankton samples longer than the others (seven months of the eight months of sampling): at the end of summer the larvae of *Clupea pallasii* are joined by the larvae of southern species, *K. punctatus* and *S. melanostictus*. Species belonging to the families Osmeridae, Stichaeidae, Pholidae, and Gasterosteidae, the larvae of which live in the pelagic zone, are found in the samples for five to six months. Members of the Cottidae family, on the contrary, have a short planktonic stage and then assume benthic mode of life. Sea poachers (fam. Agonidae) have a similar life cycle.

The larvae of many fish species are characterized by a positive phototaxis, i.e. they readily move to sources of light and aggregate in illuminated places. They are generally abundant in ichthyoplankton samples and comprise over 100 specimens per a sample. There are 19 such species in Vostok Bay, first of all commercially important *C. pallasii*, *S. melanostictus*, *E. japonicus*, *Hypomesus japonicus*, *Mallotus villosus*, *Salangichthys microdon*, *C. saira*, *Sebastes taczanovskii*, *Stichaeus grigorievi*, *Pleurogrammus azonus*, and *Limanda aspera*.

Among non-exploited species the most abundant are the larvae and fries of *Gasterosteus aculeatus*, *Syngnathus schlegeli*, *Porocottus allisi*, *Liparis agassizii*, *Lumpenus sagitta*, *Stichaeus nozawae*, *Opisthocentrus ocellatus*, and *Gymnogobius heptacanthus* from the family Gobiidae. The species with a weak phototactic response are found in the samples in very low numbers, up to ten specimens, or singly.

In 2009 and 2010 the ichthyoplankton included the fish species, which rarely occur in these waters: *Eleutherochir mirabilis*, *Davidijordania lacertina*, and *Liparis tessellatus*.

Several years of observation are insufficient to draw firm conclusions on interannual fluctuations in the ichthyoplankton community in Vostok Bay. Still, some inferences

can be made at least for abundant species: these are objects, in which long-term changes in the composition and numbers of ichthyoplankton are most significant. Thus, the larvae of *M. villosus* were abundant in the samples in June–July, 2008, but were absent from them in the previous and subsequent years. Similarly, the larvae of *S. melanostictus* are found in the ichthyoplankton of the bay rather irregularly.

Table 2. Seasonal changes in the number of fish families and the number of species of these families found in ichthyoplankton samples collected in Vostok Bay in 2003–2010

№	Fish family	Month							
		III	IV	V	VI	VII	VIII	IX	X
1.	Clupeidae	-	1	1	1	3	3	3	3
2.	Engraulidae	-	-	-	1	1	1	1	1
3.	Osmeridae	-	-	2	3	3	1	1	-
4.	Salangidae	-	-	-	-	1	1	1	1
5.	Salmonidae	-	1	2	-	-	-	-	-
6.	Cyprinidae	-	-	-	-	-	1	1	1
7.	Gadidae	1	1	2	2	1	-	-	-
8.	Scombesocidae	-	-	-	1	1	1	1	-
9.	Belonidae	-	-	-	-	-	1	1	-
10.	Hemirhamphidae	-	-	-	-	1	1	1	-
11.	Gasterosteidae	-	-	-	1	1	1	1	1
12.	Hypoptychidae	-	-	-	-	1	-	-	-
13.	Syngnathydae	-	-	-	1	1	1	1	-
14.	Scorpaenidae	-	-	1	2	2	-	-	-
15.	Hexagrammidae	-	2	2	2	-	-	-	1
16.	Cottidae	6	9	9	1	-	-	-	-
17.	Hemitripterae	1	1	1	1	-	-	-	-
18.	Psychrolutidae	1	1	1	-	-	-	-	-
19.	Agonidae	4	6	4	1	-	-	-	-
20.	Cyclopteridae	-	1	-	-	-	-	-	-
21.	Liparidae	1	2	2	1	-	-	-	-
22.	Mugilidae	-	-	-	-	1	1	-	-
23.	Zoarcidae	-	1	-	-	-	-	-	-
24.	Stichaeidae	6	11	10	8	2	1	-	-
25.	Pholidae	2	2	2	3	3	1	-	-
26.	Cryptacanthoididae	1	1	-	-	-	-	-	-
27.	Trichodontidae	1	1	1	-	-	-	-	-
28.	Ammodytidae	-	-	1	1	-	-	-	-
29.	Callyonimidae	-	-	-	-	1	-	-	-
30.	Gobiidae	-	-	-	1	3	2	2	-
31.	Pleuronectidae	-	-	-	1	1	-	-	-
Total number of species		24	41	42	33	27	17	14	8
Total number of families		10	15	15	18	17	13	11	6

Ichthyoplankton sampling by use of fishing lights was a part of the general fish fauna investigations in Vostok Bay. Other methods of collection were also applied, but attracting fish with light proved to be the most effective and the least-cost way of getting primary material for the assessment of ichthyofauna biodiversity in the area. Therefore, ichthyoplankton sampling using fishing lights may be recommended as one of the methods for biodiversity monitoring.

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**DISTINCTIVE MITOCHONDRIAL GENOME OF THE CALANOID
COPEPOD *CALANUS SINICUS*, A USEFUL MOLECULAR MARKER FOR
PHYLOGENETIC AND POPULATION STUDIES**

Minxiao Wang¹, Song Sun¹, Chaolun Li¹ and Xin Shen²

¹ Institute of Oceanology, Chinese Academy of Sciences, Qingdao 266071, P.R. China

² Huaihai Institute of Technology, Lianyungang, 222005, P.R. China

Introduction

With greatest diversity and richest abundance, copepods exhibit extensive ecological radiation in the marine ecosystem. *Calanus sinicus* dominates continental shelf waters in the Northwest Pacific Ocean and plays an important role in local ecosystem by linking primary production to higher trophic levels. Lacking effective molecular markers, several phylogenetic issues on copepods are still elusive from population to higher levels such as their phylogenetic position within Pancrustacea as well as phylogenetic relationships of their component orders. Recent ambiguous status of copepod phylogenetic research is at least partly due to the limited morphological characters, difficulty in accessing morphological homology and a poor fossil record. Being genome-level informative, mitochondrial DNA sequences are used as markers not only for population genetic studies but also for phylogenetic studies. Here we present the first nearly complete mitochondrial genome of *C. sinicus* and character it in detail. Gene order of *C. sinicus* was compared with other crustacean to add light on the evolution of mitochondrial gene of the group. Combining the new mitogenome and the previously published mitogenomes of arthropods, we reconstruct a preliminary phylogeny of Copepoda with deduced amino acid sequences of the 12 mitochondrial protein coding genes apart from ATP8. In addition to a better understanding of phylogenetic position of copepod, we compared intraspecific polymorphism of major loci in 11 *C. sinicus* mitogenomes from 4 populations to exploit proper SNP markers for population studies.

Materials and methods

C. sinicus for charactering mitogenome were collected in the Yellow Sea (35.9N, 122.9E). To compare intraspecific polymorphism pattern of different loci among populations, *C. sinicus* from Yangtze estuary (28.6N, 122.1E; n=4), North Yellow Sea (38.9N, 122.9E; n=3) and Korea (36.9N, 126.3E; n=3) were picked out. Complete

mitochondrial genome of the species was determined as described in Lang et al. (Lang and Burger 2007).

Results

The 20,460bp contig assembled (Fig. 1) consists of all but 2 tRNA genes (*trnR* and *trnC*), including 13 protein coding genes (*COX1-3*, *ND1-6*, *ND4L*, *ATP6*, *ATP8* and *CYTB*), 2 rRNA genes (*srRNA* and *lrRNA*) and 20 tRNAs. In addition, one of the long noncoding regions (LNR) between *trnH* and *trnA* is postulated as control region (CR) due to the conserved elements within. Different from most mitogenomes in metazoan, the abutting gene blocks *ND4* / *ND4L* and *srRNA* / *lrRNA* are separated distantly. The 35 genes are located in 3 clusters interleaved by long noncoding regions (LNR1, LNR3 and LNR5). Unlike *Tigriopus sp.* (Burton, Byrne et al. 2007), mitochondrial genes are encoded on both strands in *C. sinicus*. As in *D. farina* (Klimov and OConnor 2009), the minority of the genes (*lrRNA*, *trnV*, *trnD*, *trnT*, *ND4L*, *ND5*, *trnH*, *trnA*, *trnY*, *ND3*, *ND4*, *trnK*, *ND2*, *ATP8* and *ATP6*) lie on the H-strand (as defined by molecular weight). Seventeen of 20 tRNAs are arranged in 3 main clusters, which are V-D-T-S₁, F-I and A-F-Y-E-Q-L₁-P-M-K-W-S₂-N clock-wisely. Compactness is a characteristic feature of mitochondrial genomes (Boore 1999). There are small gene overlaps at 3 gene borders. The largest is found between *trnY* and *trnE* with the length of 5 nucleotides.

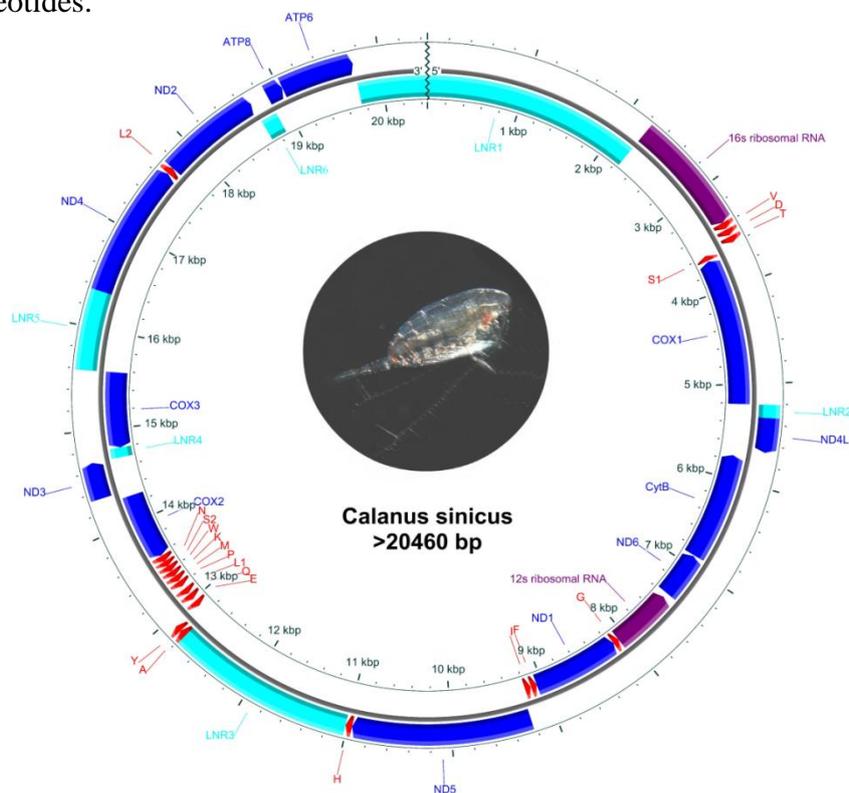


Fig. 1. Mitochondrial genome organization of calanoid copepod *Calanus sinicus*.

With regard to copepods, 5 species representing separate orders clustered together, forming a monophyletic clade with high confidence support (BP, 100; PP, 99). *T. japonicus* (Harpacticoida) and *L. salmonis* (Siphonostomatoida) grouped together, with the cluster containing *S. polycolpus* (Poecilostomatoida) and *P. nana* (Cyclopoida) as their sister clade. The arrangement of the 4 orders excluding Calanoida in both trees confirms the monophyly of Podoplea, which is characteristically tagged by the podoplean tagmosis (Rony Huys and Boxshall 1991). The basal splitting of Copepoda separate Calanoida from Podoplea, reflecting primary status of Calanoida within copepods. As to interordinal phylogenetic relationships within Podoplea, Cyclopoida and Poecilostomatoida exhibit closest affinity in our study, supporting Boxshall's hypothesis to reunite Poecilostomatoida into Cyclopoida, which is gaining support from several independent analysis (Boxshall and Halsey 2004; Huys, Llewellyn-Hughes et al. 2006).

No evidence for recombination in mitogenome of *C. sinicus* was detected in our analysis. Within the 16670 bp alignment there are a total of 191 single nucleotide polymorphism (SNPS) and 108 insertion/deletion polymorphic sites in addition to 3 microsatellite motifs. A sliding-window analysis was performed to map the distribution variable sites among 11 individuals (Fig. 3). The mean frequency of the variable sites in 11 *C. sinicus* partial mitogenomes is relatively low, being approximate 0.024. LNR3 harboring 2 microsatellite motifs is most variable while ND4L is most conserved with no sites changed. The "hotspots" bearing highest frequency of variable sites are bases 11216-12260 with 226 variable sites in 1045 bases (1 in 4.6), 1848-2235 with 22 variable sites in 388 bases (1 in 17.6), 649-862 with 10 variable sites in 214 bases (1 in 21.4). The former corresponds to LNR3 and the others span LNR1 and upstream of 16S rRNA gene. Conversely, a 752 bp stretch spanning 4016-4767 carries no variable site, which is sheltered within COX1 gene. COX1 is a popular marker in analysis at population level (Nuwer, Frost et al. 2008). However, our result unveils the conserved nature of the gene and eliminates the possibility of its utility in population genetics for *C. sinicus*. Constant phylogenetic signal distinguishing haplotype groups was detected in all hypervariable regions (unpublished data), which underpin their utility for population analysis.

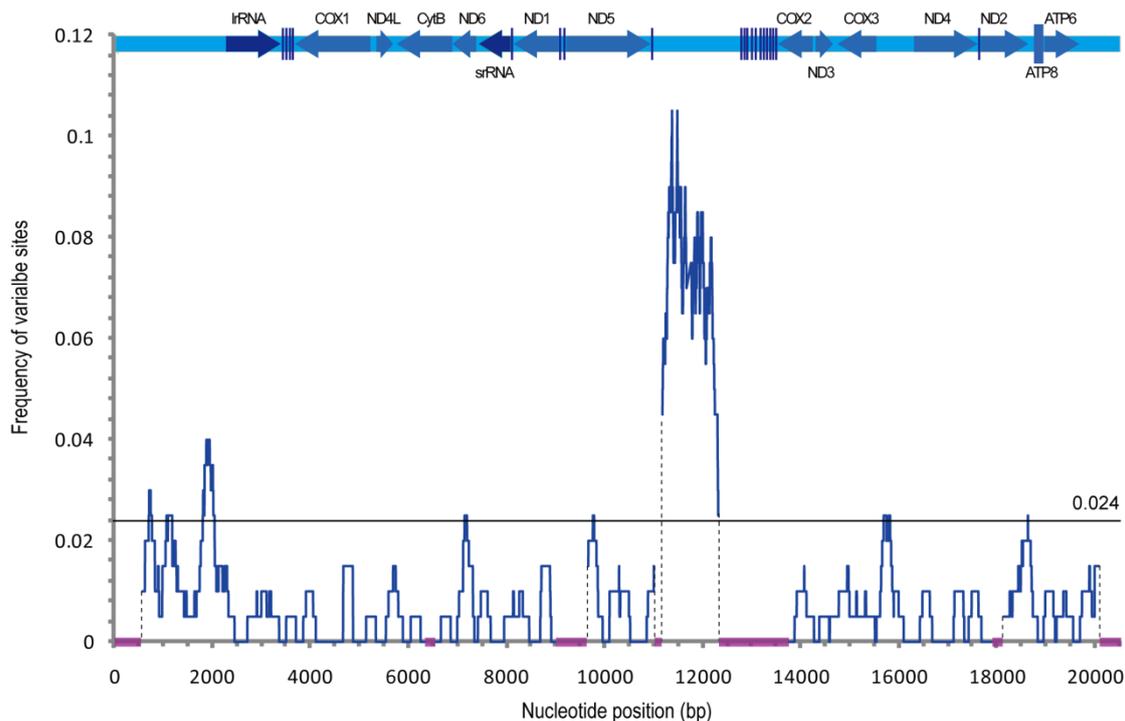


Fig. 3. Plot representation of the frequency of variable sites across the mitochondrial genome of *C. sinicus*.

Conclusion

The concurrence of multiple noncoding regions and reshuffled gene arrangement makes the mitochondrial genome of *C. sinicus* remarkably distinctive from other arthropods. Furthermore, there is another suite of particularities found in the mitochondrial genome (mitogenome) of *C. sinicus*, such as low AT content, symmetrical nucleotide composition between strands, abbreviated stop codons for some protein coding genes (PCGs) and extended length of ATP6 and ATP8 relative to other copepods. Monophyly of copepods and basal split between Calanoida and Podoplea were well resolved. However, Maxillopoda were resolved polyphyletic. The closest affinity between Cyclopoida and Poecilostomatoida supports Boxshall in reassigning the latter subordinate to the former. Within the alignment of 11 *C. sinicus* mitogenomes, there are 401 variable sites harbouring 3 hotspots of variable sites and 3 microsatellite loci.

The occurrence of the sub-genomic fragment (mosaic cyler sequence) during laboratory work calls attention to the application of La PCR to mitogenome sequencing in copepods, and may give an additional evidence of mitochondrial recombination. The accelerated mutational rates within copepods as well as the synergistic interaction of non-coding regions with recombination in *C. sinicus*

mitogenome may give rise to the highly rearranged mitogenome herein. Finally, mitogenomes are proved valuable markers to resolve deep phylogenetic relationships among copepods. The variable sites map of *C. sinicus* mitogenomes provides a solid foundation for population genetic studies.

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**TAXONOMIC IDENTIFICATION AND POPULATION DENSITY OF
APPENDICULARIAN FOUND IN VOSTOK BAY OF THE JAPAN SEA
(TUNICATA, APPENDICULARIA)**

Savelieva A.V. & Dautov S.Sh.

Vladivostok, A.V. Zhirmunsky Institute of Marine Biology FEB RAS

14 Palchevsky Str

E-mail: an.bystrova@mail.ru, daut49shakir@mail.ru

Abstract

The identification, describing and analyzing were made of the appendicularian species *Oikopleura gracilis* (fam. Oikopleuridae) found in plankton samples collected from Vostok Bay State Natural Complex Marine Restricted Basin (VBSNMRB) (Peter the Great Bay, Sea of Japan). This species was defined using the general taxonomic traits of appendicularians: trunk length and shape, tail length and shape, presence or absence of buccal glands and subchordal cells, position and shape of gonads and presence or absence the Eisen's and Foll's oikoplasts. Using the amount of individuals in each of plankton samples it was estimated their abundance.

Key Words: Appendicularia, *Oikopleura gracilis*, Vostok Bay

Introduction

Vostok Bay Restricted Basin is settled down in the Vostok Bay - one of five inner bays of Peter the Great Bay. The Vostok Bay situated in the west of peninsula Trudnii and Nahodka city (<http://ru.wikipedia.org/wiki/>). It has small area, but marine fauna diversity rather high owing to climatic and hydrology specifics of the water area. These circumstances have influenced on the variability of zooplankton. There are many investigations devoted to Crustacean, Echinodermata larvae and some groups of holoplankton, but information about Chordate taxon especially on Appendicularia is limited. First finding of appendicularian in this bay was made 1992 (Dautov, unpublished) during the investigation of the zooplankton distribution in waters of Vostok, Srednyaya, Anna bays.

Appendicularians are most common in holoplankton samples in all oceans and they with copepods and ostracods occupied one of the main positions in marine trophic chains. Appendicularians are the general component of 'marine snow' – the remnants of the plankton organisms which fall down onto sea bottom – and they take large part

in ocean carbon cycle (Sato, Tanaka and Ishimaru, 2001). They are the food of many species of economical important marine fishes. We suggest that our data add important information to the appendicularians' taxonomy and will help other scientists who studied on chordates.

Materials and Methods

Earlier it was shown that appendicularians being the seasonal component of holoplankton in this area, they present summer time when the south winds prevailed. Plankton samples were collected August 2010 early mornings by plankton net of Jedi (#100 μm) at Vostok Bay using speed-boat. We took three samples from each station. Stations coordinates were determined by GPS-navigator.

Samples were obtained from 10 m to 5 m depth. We processed them under stereomicroscope using Bogorov chamber just after catching. Identification of species was created with illustrated Guide to Marine Plankton in Japan (Appendicularia: p. 1393-1414) Chihara M., Murano M., 1997; Appendicularia by A. Buckmann, 1969; Appendicularia of Japanese Waters by T. Aida, 1908. and Fenaux R. The Classification of Appendicularia (Tunicata): history and current state, 1993.

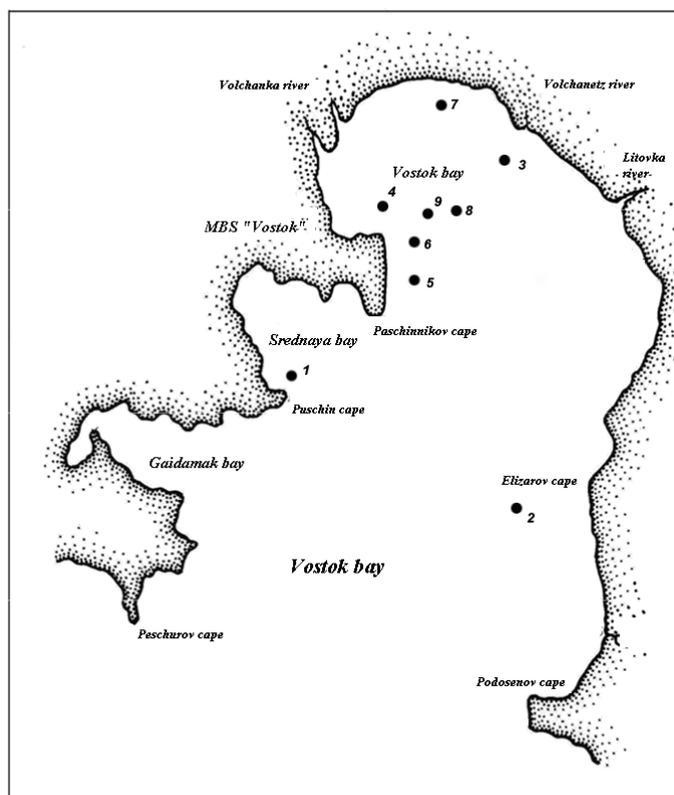


Fig.1. Vostok bay. Points show the stations, where we were get a samples.

Results

General morphology

Appendiculariae are pelagic tunicates and compose a large part of holoplankton. They have notochord (Nishino and Satoh, 2001). During their life cycle they lack dramatic metamorphosis. They have constant cell composition (Fenaux, 1993). Body of Appendicularia is subdivided into trunk and tail. Trunk contains digestive, nerve, reproductive systems and sensitive organs. It can subdivide into three parts: pharynx-brachial, digestive and reproductive (Aravena and Palma, 2002). Tail is a locomotory organ, which possesses by good developed muscles and fins. Mouth conducts inside large pharynx. Pharynx has one pair openings – spiracles. There is endostyle on ventral side of pharynx, both sides of it present or absent buccal glands. Short esophagus follows behind pharynx, which leads into stomach with two lobes. Left lobe has a small protrusion (Burighel et al., 2001), sometimes this one is absent. After stomach food comes to intestine and then – to the rectum. Rectum is ended by anal papilla. There is not atrial cavity or cloaca. Commonly Appendiculariae are hermaphrodites, but one species – *Oikopleura dioica* – is dioecious. Gonads are situated at posterior part of the trunk that increases according to maturing of them. Testes consist of two parts, which situated both side of ovary. The tails' length is six times of trunks' length. On both sides of posterior part of tail sometimes solitary subchordal cells can happen sometimes not, the presence of these cells depends on to species of this family (Fredriksson and Olsson, 1991a).

Taxonomic classification

Phylum Chordata

Subphylum Tunicata (Urochordata)

Class Appendicularia

Order Appendiculariae

Family Oikopleuridae Mertens

Genus *Oikopleura*: body is compact, organs compacted densely in inner trunk. Oikoplast is arranged on dorsal side of trunk, under gut. Pharynx at both sides opens through pair of spiracles and follows into cavity of the gelatinous house. Stomach has two lobes: right and left. Esophagus continues into the last one. Anus is situated under stomach.

Subphylum Oikopleura (Coecaria) Lohmann: buccal glands are absent. There are not subchordal cells (Aida, 1908). Gonads after maturing cover posterior part of stomach lobes.

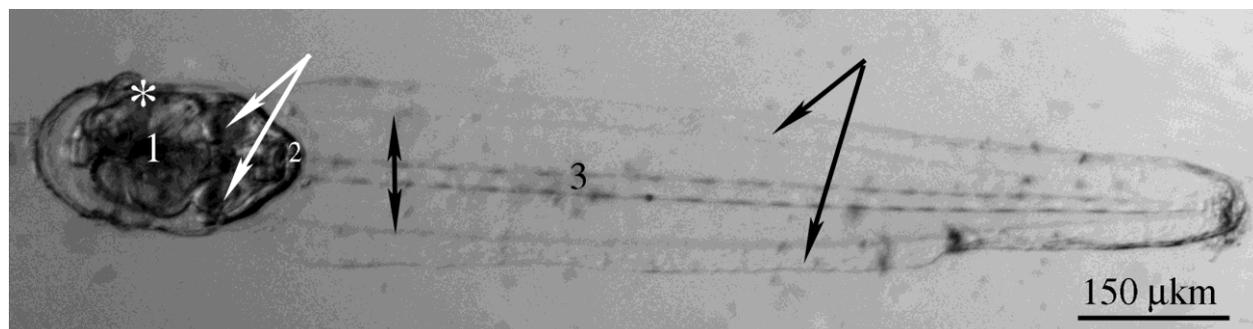


Fig. 2. Appendicularia *O.gracilis* body plan. Other individual that possesses visible tail fins. 1 – Gut, 2 – mouth, 3 – notochord, * - trunk, black double arrow – muscles bunds, black arrows – fins.

Basic characteristics of *O.gracilis*: trunk length – 200-250 mkm. Length of tail – 900-1500 mkm. Upper lip has ciliar epithelium. Tail is elegant and narrow on his end, with narrow fin (Fig.2). Gonad consists of testis and ovary. Testis consists of two equal parts and they occupy upper part of gonad. Ovaries arranges under testis between its parts. There is Eisen’s oikoplast (Aravena and Palma, 2002). Trunk has an elongated form, and little bit flattened with his dorsal surface. Spiracles are arranged in a middle part of pharynx. Mouth opens on the middle trunk axis (Bucmann, 1969). Width of tail on it anterior part is more than tail width on his posterior end. Tail end is narrow. There are not subchordal cells. Buccal glands are absent (Fredriksson and Olsson, 1991b). Width of muscle bend is approximately 15 mkm. Left stomach lobe like a bean and has not protrusion. But we were found non-specific characteristic for this species. There is some gelatinous hood covering *O. gracilis* trunk (Fig.3). This hood repeats all form of trunk and it secreted very fast. Some species from Oicopleuridae family possess the same gelatinous hoods (*O.longicauda*, *O.intermedia*, *O. labrodariensis* and etceteras), but for *O.gracilis* it is not marked (Chihara, Murano, 1997; Buckmann, 1969; Aida, 1908, Fenaux 1993).

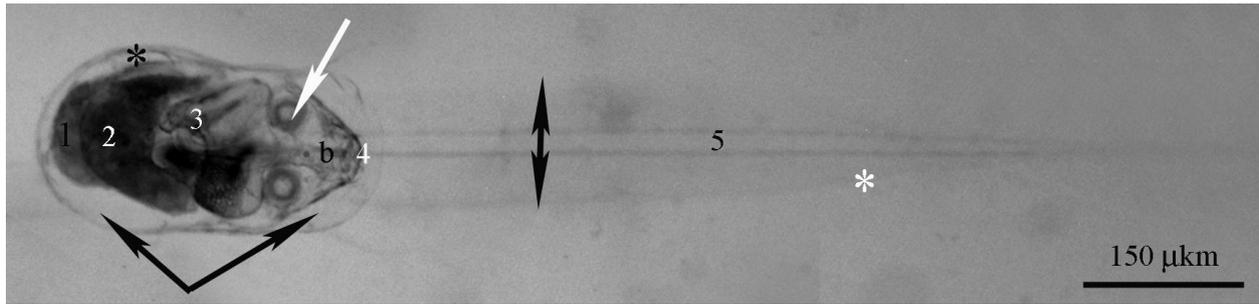


Fig. 3. Appendicularia *O.gracilis* body plan. Individual, that possesses rather visible hood. 1 – gonads, 2 – left stomach lob, 3 – intestine , 4 – mouth, 5 – notochord, white star – tail, b – brain, * - trunk, white arrow – spiracles, black arrow – hood, double black arrow – muscle bend.

These characteristics coincide not completely with just said above particulars, so we can not conclude exactly that our finding species is *O.gracilis*. Probably, it is connected with not well visible hood and some investigators can not found this one earlier.

Distribution: this species inhabit coastal marine water. They was found in Atlantic, European waters, Indian Oceans, Mediterranean Sea, North West Atlantic, Antarctic waters (Capitano et. al., 2003), Pacific Oceans (in particular, in Northern Pacific Coast (Strathmann, 1987)), Red Sea and Japan Sea (Aida, 1908; <http://www.marinespecies.org/aphia.php?p=taxdetails&id=103410>). *O. gracilis* is a circum global species.

Population density

Table. Concentration of the *O. gracilis* at Vostok Bay in August 2010

Numbers of stations	A number of other appendicularia species	Density of <i>O.gracilis</i> (a number of individuals / m ³)
1	0	0,02
2	10	0,509
3	0	0,113
4	0	0,067
5	0	0,018
6	2	0,015

7	0	0,088
8	0	0
9	0	0,005

From Table one can concludes that distribution of *O.gracilis* is not equal. Station 2 has a highest population density and Station 8 nihil habit. A number at all other stations are not equal too. Such unequal population density can be explained with the help of currents in Vostok Bay, because holoplankton can move very slowly and it depends on the water streams. In winter season we can not find any specimens of appendicularia. But also appendicularian commonly posses some movements that help them to join for improve reproductive processes, connected with allogamy.

Discussion

Appendicularia distributed in all oceans. They are the second or third most abundant component in marine mesozooplankton communities (Gorsky and Fenaux, 1998). This tunicates introduce in seas and bays due to the sea currents. But for many bays their presence is not usual. They appear only at summer season when the sea water becomes warmer. This being the case in our investigation, because *O.gracilis* was found in Vostok bay only during summer seasons of 2006-2010. For instance, we can catch only two individuals during the summer long 2008. Their revealings are very important, because our knowledge about Appendicularia family Oikopleuridea, especially *O.gracilis*, is very poor. It is connect with difficulties to investigate and determine this species, due to their transparency and it is very complicated to define in accordance with the main classification characteristics rather under stereomicroscope. Most investigations realize on dioecious species *O. dioica* (Bouquet et. al., 2009), so information about it quite a few. In this article we attempt to attract an attention to *O. gracilis* as species, which common in our region and have high number in summer time.

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**LATITUDINAL SPECIES DIVERSITY GRADIENT OF POLYCHAETES ON
THE SHALLOW COASTAL AREAS OF THE EASTERN SAKHALIN
ISLAND, THE SEA OF OKHOTSK**

I.L. Alalykina, V.I. Fadeev

A.V. Zhirmunsky Institute of Marine Biology,

Far East Branch of the Russian Academy of Sciences, Vladivostok 690041, Russia

E-mail: Inna L. Alalykina <alalykina@mail.ru>

Introduction

The evidence for the existence of a latitudinal species diversity gradient for the shallow-water benthos came from the early studies of Thorson. The pattern shown so clearly by molluscs may (Kafanov, 1991), however, not be a general one, for investigations of other taxa have failed to find such clear patterns. Unfortunately data are too few and scarce for other taxa to undertake similar analyses.

The fauna and distribution of polychaetes on the East Sakhalin Island shelf were studied by a number of authors (Ushakov, 1950, 1959; Koblikov, 1978; 1985; Buzhinsky, 1985). These faunistic and hydrobiological researches have been performed in 40-70th years of the last century. Any work devoted to studying of a biological variety of this group, for the given region till now it was not spent. Considering the increased interest of researchers to a biodiversity problem, including the presence or absence of its latitudinal species diversity gradient for various groups of organisms (Hillebrand, Azovsky, 2001; Mokievsky, Azovsky, 2002; Volvenko, 2008; *Chertoprud et al*, 2007), it is interesting to study latitudinal diversity gradient of polychaetes through the eastern coast of Sakhalin Island. The main goal of this report is the analysis of the change of polychaete species richness and biodiversity of the shallow-water zone of the Eastern Sakhalin Island coast.

Materials and methods

During July - September 2003-2009 the samples were collected in southern (Aniva Bay), north-eastern (coastal zones near Lunskey, Piltun and Chayvo Bay) and northern (Severniy Bay) Sakhalin Island shelf using a 0.25m² Van -Veen bottom grab. In this report only data obtained from stations placed at depths to 30 m with similar sediment type (sand) were used. Three replicate samples were taken at each station (all 580 stations). In the laboratory polychaetes were first sorted to family, and than to the

species level. For each species was determined average abundance (N , ind/m²) and biomass (B , g/m²).

Margalef diversity index ($D = (S-1)/\ln N$), where S – the number of species, N – abundance of all species), Shannon – Wiener diversity index ($H = - \sum p_i \log_2 p_i$ (bit/ind)) and Pielou evenness index ($J = H/\log_2 S$) were calculated for polychaete taxa at each station.

Results and Discussion

In the present study, a total of 152 species of polychaetes belonging to 96 genera and 32 families were recorded in sandy sediments of the upper sublittoral zone of the eastern Sakhalin Island. The greatest polychaete taxonomic richness (102 species, 74 genera and 32 families) were reported on the southern Sakhalin Island (Aniva Bay). The number of taxa decreases regularly towards the north. So, 87 species of polychaetes belonging to 60 genera and 25 families were found at the shallow-water of the North-Eastern Sakhalin and only 29 species, 23 genera and 16 families were recorded from the Severniy Bay (Fig. 1).

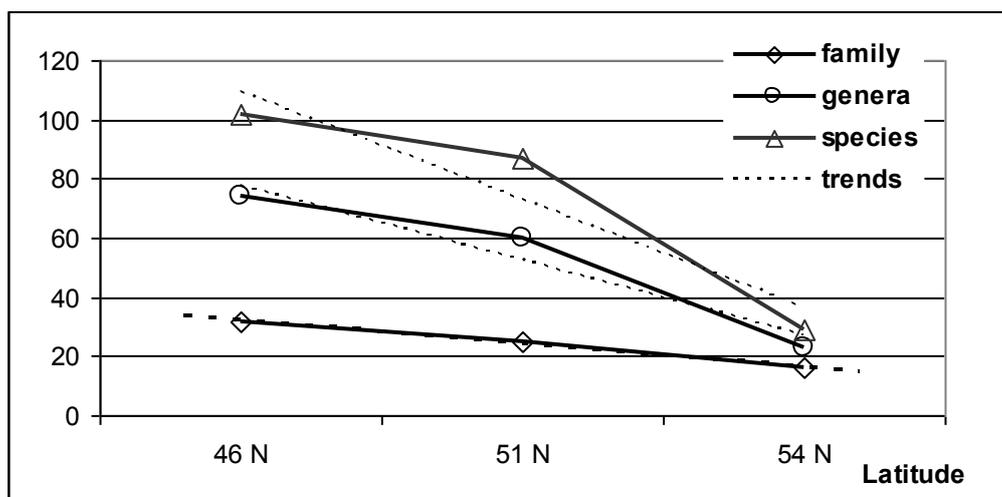


Fig. 1. Latitudinal changes of the number polychaete species, genera and families through the Eastern coast of Sakhalin Island.

The axis y is the number of taxa, axis x – the latitudes of the Southern, North-Eastern and Northern coast of the Sakhalin Island correspondingly.

In shallow waters of this region latitudinal trends of the number of species (multiple $R^2=0.89$ is significant), genera ($R^2=0.94$) and families ($R^2=0.99$) have been revealed. These results agree with earlier studies of polychaete species performed from this region (Koblikov, 1978, 1985).

However, the greater species number of recorded at any area not always testifies about the high diversity. It is known, the recorded species number on the area more, than more surveyed area (number of samples) (Mokievsky, Azovsky, 2002; Chertoprud et al, 2007; Volvenko, 2008).

In comparison with others regions the polychaete species richness of the East Sakhalin Island coast is sufficiently high. Margalef and Shannon diversity indexes at Odessa port are estimated the polychaete diversity as 1.08-2.41 and 0.19-2.11 correspondingly (Losovskaya, 2005). In the Barents Sea Shannon diversity index is equal to 3.68 (based on \log_2) (Ambrose et al, 2009). According to our data the diversity of polychaetes of the all Eastern Sakhalin Island coast value at 7.17 by Margalef indexes, 4.29 by Shannon indexes (based on \log_2) and 0,79 by Pielou evenness index.

The data on abundance (N , ind/m²), species richness (S) and diversity indexes of polychaetes calculated for each station are shows in Table 1.

Table 1. Diversity indexes and abundance (N , ind/m²) of polychaetes on the shallow coastal areas of the Eastern Sakhalin Island, the Sea of Okhotsk.

46 N (Aniva Bay - 43 stations)					
	S	N, ind/m²	D	H (bit/ind)	J
mean	13,86	215,19	2,41	2,84	0,86
Standard error	1,34	22,46	0,24	0,17	0,01
min - max	1 - 30	26 - 680	0 - 5,17	0 - 4,33	0,71 - 1
51 N (coastal zones near Lunsky Bay (79 st.), Chayvo Bay (100 st.), Piltun Bay (351 st.))					
mean	4,09	47,79	0,94	1,42	0,81
Standard error	0,11	5,93	0,03	0,04	0,01
min - max	1 - 20	2 - 2053	0 - 3,32	0 - 3,5	0,46- 1
54 N (Severny Bay - 7 st.)					
mean	7,29	44,71	1,56	1,96	0,83
Standard error	1,92	13,00	0,42	0,49	0,06
min - max	1 - 13	3 - 90	0 - 2,76	0 - 3,36	0,64 - 1

The species richness estimated by Margalef diversity index increases with depth at all researched areas and is run up to maximum at the stations from Aniva Bay (Southern Sakhalin Island) (Fig. 2).

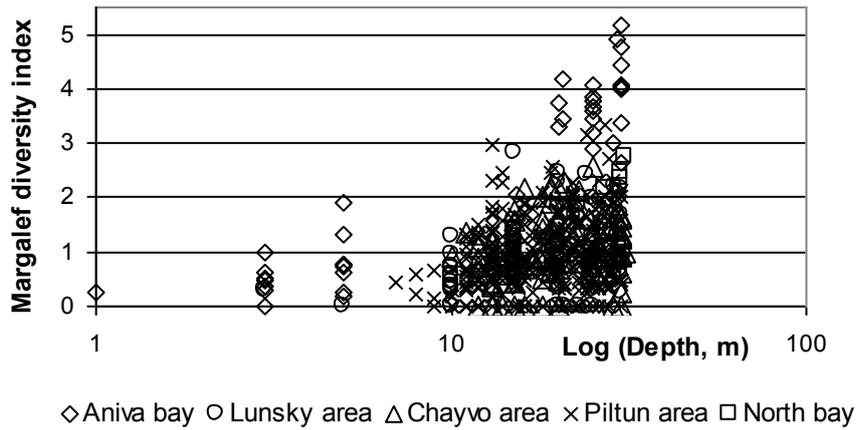


Fig. 2. The change of the Margalef diversity index with depth at others areas of the Eastern Sakhalin Island.

It is necessary to underline that the polychaete fauna of both Aniva Bay and Severny Bay is studied insufficiently. It should expect the increasing of the species number in the future investigations. On the contrary polychaete fauna of the Piltun area is research enough well.

The species accumulation curve for all stations of Piltun area shows indication of reaching an asymptote (Fig. 3). The composite curve demonstrates the high examined degree of the investigated area.

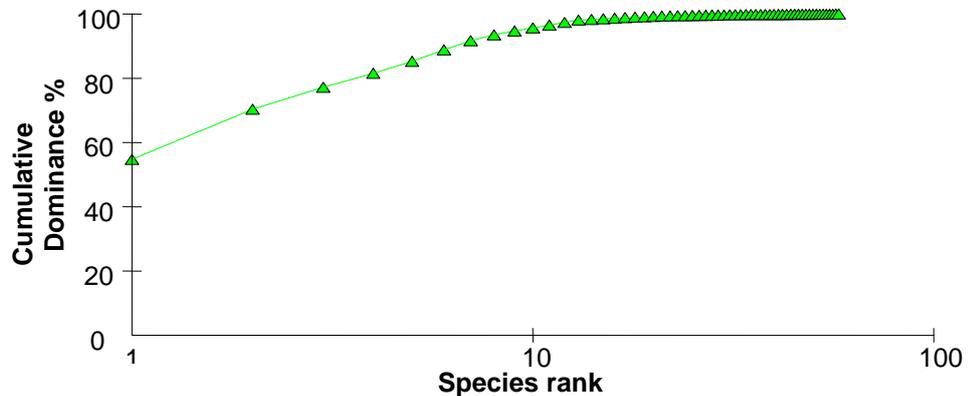


Fig. 3. Species accumulation curve for polychaetes from 351 stations sampled in the Piltun area of the North-Eastern Sakhalin Island.

According to Fig. 4, the polychaete richness (S , $R^2=0.89$) and Margalef diversity index (D , $R^2=0.83$) calculated for each separated area are significant decreased towards the high latitudes. Shannon diversity index (H , $R^2= 0.39$) is also decreased.

Evenness index may be less suitable than species richness for comparing alpha diversity between large scales such as regions.

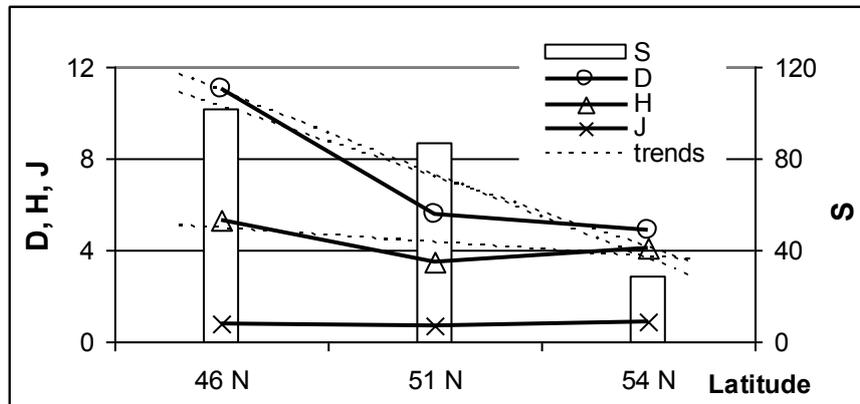


Fig. 4. Latitudinal species diversity gradient of polychaetes on the shallow coastal areas of the Eastern Sakhalin Island.

This fact may be explained by changing of the biogeographical group ratio on the polychaete fauna of the upper sublittoral towards the North (Fig. 5). The ratio of the warm-water elements of the polychaete fauna (low boreal and tropical - subtropical boreal species) is considerably reduced toward the high latitudes (on 20%). The ratio of the cold-water species is increased on similar value (on 19%). It is known, Aniva Bay is been regarded to the low boreal area by many researchers (Buzhinskaja, 1985; Kafanov, 1991 and others). It is zone of the mingling of different zoogeographic elements which are given the high species richness and diversity.

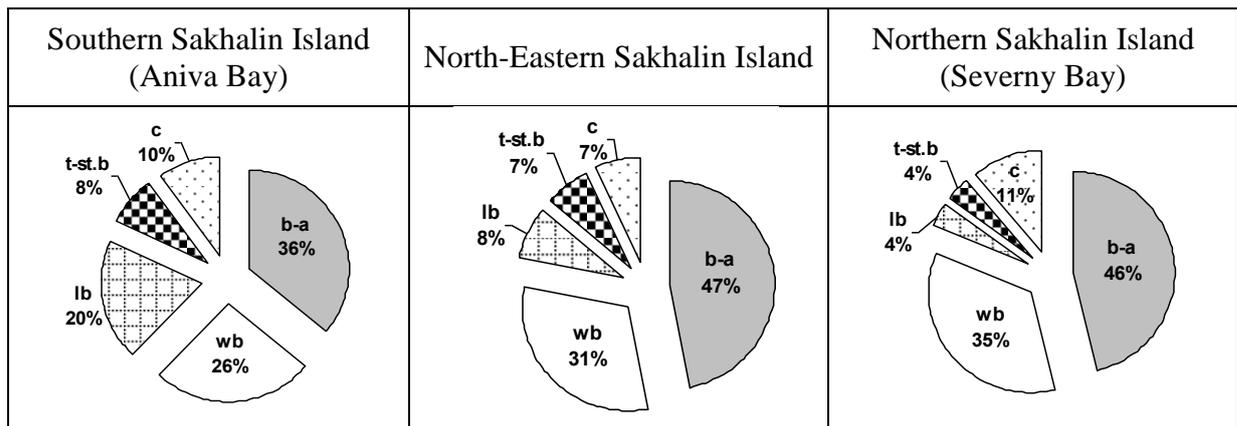


Fig. 5. The polychaete biogeographical group ratio on the species number on the shallow coastal areas of the Eastern Sakhalin Island.

b-a - boreal-arctic; wb - widely distributed boreal; lb - low boreal; t-st.b – tropical - subtropical boreal; c – cosmopolitan species.

We conclude that polychaete diversity is significantly different among the large-scale shallow biotopes chosen for this study. This study lends more evidence to the recent view that latitudinal gradient is sustained general tendency of the biodiversity. As new information will be gathered, complementary analysis should be done further for other regions of the Okhotsk Sea.

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MACROALGAE OF FOULING, SCALLOP EPIBIOSIS AND BENTHOS IN THE SOUTHERN PRIMORYE, SEA OF JAPAN

Irina R. Levenets

A.V. Zhirmunsky Institute of Marine Biology, Far Eastern Branch,

Russian Academy of Sciences, Vladivostok 690041, Russia

E-mail: iralevenetz@rambler.ru

Being an initial link of the trophic chains, finally algae provide for both productivity and biodiversity of water bodies. At present investigation of species composition of macroalgae is absolutely urgent because of intensification of recreation stress on sea waters of the southern Primorye and reduction of biodiversity of sea biota in the result of interference in the natural processes. Macroalgae dwell in sea on various natural and anthropogenic substrates: hard and soft bottoms, shells of alive mollusks, mariculture installations, piers, navigation barriers, ships, and others. A degree of contact of algae with the bottom, along with the other environmental factors, determines composition and structure a particular flora. The aim of the present work is to study taxonomic composition of flora of fouling and epibiosis of the southern Primorye waters in comparison with the benthic flora of this area.

Over 2000 samples of fouling and epibiotic algae of the southern Primorye waters were collected by the scientists of the Institute of Marine Biology FEB RAS within the period from 1979 to 2007 and provided to the author of the given paper for treatment. Samples were taken from hydrotechnical structures – piers, mooring lines and platforms; from hydrobiotechnical structures – installations for algae and mollusks mariculture; in epibiosis – on shells of the Japanese scallop *Mizuhopecten yessoensis* Jay in benthos and bottom culture. Own collections of phytobenthos, collections of the Laboratory of shelf communities ecology IMB FEB RAS and published data were used for comparison.

Identification of the collected material permitted us to establish taxonomic composition of fouling algae from various anthropogenic substrates and epibiotic algae of the Japanese scallop from the coastal waters of the southern Primorye. Totally, taking into account own and published data on fouling and epibiosis, 145 species and taxa of algae from three departments (red algae – 73, brown algae - 36, green algae – 36) were recorded. Nine algal species are new for sea flora of the

southern Primorye. These are red algae *Rhodophysemma odonthaliae* Masuda & M. Ohta and *Neorhodomela sachalinensis* (Masuda) Perest., brown algae *Ectocarpus fasciculatus* Harv., *Chondaria gracilis* Setch. & N.L. Gardn. and *Compsonea* sp., green algae *Acrochaete ramose* (N.L.Gardn.) O'Kelly, *A. flustrae* (Reinke) O'Kelly, *Pseudendoclonium submarinum* Wille and *Zygomitus reticulatus* Bornet & Flahault. Three algal species in fouling were identified only by the published data (Zvyagintsev, 2005).

In phytobenthos of the southern Primorye waters, both in relatively clean and polluted areas, the portion of red algae varies from 48 to 60% of the total number of species, that of brown algae – from 11 to 30%, and green algae – from 15 to 29% (Kashenko, 1999, 2004; Levenets, Skriptsova, 2008; Perestenko, 1994). A comparative analysis of floras of fouling, benthos and epibiosis shows that Rhodophyta prevail in all investigated benthic floras: in Vostok Bay, in the middle part of Ussurijsky Bay, in the inner part of Amursky Bay and in the western part of Peter the Great Bay. Green algae have here minimum abundance: from 15 to 22%. The portion of brown algae varies from 27 to 30%. Flora of the inner part of Amur Bay is an exception: it was transformed in conditions of anthropogenic stress (Levenetz, Skriptsova, 2008). The portion of brown algae is reduced in it (11%), and that of green algae is growing (29%).

Rhodophyta species prevail by species number (54%) in fouling flora of waterfront structures of Peter the Great Bay. In epibiotic flora red algae noticeably prevail over the others by species number (60%). Brown algae are presented by minimum species number both in hydrotechnical structures and in epibiosis (22 and 15% respectively). The main algal departments are presented by approximately equal species number in fouling of installations for *Saccharina japonica* (Aresch.) C.E.Lane, C.Mayes, Druehl & G.A.Saunders cultivation. Green algae slightly exceed the others by species number (37%). Red algae are presented by minimum species number (30%). In fouling of installations for Japanese scallop *Mizuhopecten yessoensis* mariculture the red algae prevail by species number (40%) (fig.1). Green and brown algae are presented by the same number of species.



Fig.1. View of red alga *Ceramium* in fouling of mariculture installation.

According to data of A.Yu. Zvyagintsev (2005), brown algae, making 50% of the total number of macrophytes, prevail by species number in fouling of coastwise trade vessels in the studied area. Red algae are presented by minimum number of species: their portion is equal to 20% of the total number of macrophytes species.

When comparing floras of fouling, epibiosis and benthos, it can be seen that red algae make a half and more of the total species composition in bottom or directly contacting the bottom floras of fouling of waterfront structures and scallop epibiosis. Maximum Rhodophyta superiority was observed in epibiotic flora, as well as in anthropogenically disturbed benthic flora. Brown algae are presented by minimum species number in floras of fouling of waterfront structures, scallop epibiosis and transformed benthic flora. Prevalence of green algae over the other groups was observed in fouling of installations for *S. japonica* mariculture (fig. 2). Brown algae domination is the most typical for ship fouling, i. e. for constructions not having a direct contact with the bottom.



Fig.2. View of green alga *Ulva* in fouling of mariculture installation.

The maximum number of algal species – 98 – was registered in fouling of hydrotechnical structures. Taxonomic diversity of algae is also great: the occurred species are attributed to 20 orders, 34 families, and 65 genera. The biggest families are as follows: Rhodomelaceae, Ceramiaceae and Gigartinaceae from red algae; Chordariaceae from brown algae, and Ulothrichaceae and Ulvaceae from green algae. The biggest genera among red algae are *Ceramium* (4 species) and *Laurencia* (3); from brown algae – *Saccharina* (3), and from green algae – *Bryopsis* (3) and *Ulva* (6 species). Different species dominated among algae by biomass: *Gloiopeltis furcata*, *Callophyllis rhynchocarpa*, *Ptilota filicina*, *Polysiphonia morrowii* from red algae; *Scytosiphon lomentaria*, *Costaria costata*, *Saccharina cichorioides*, *S. gurjanovae*, *S. japonica* from brown algae, and *Monostroma grevillei*, *Ulva flexuosa*, *U. lactuca*, *U. linza* and *Ulvaria splendens* from green algae.

In fouling flora from installations for *S. japonica* mariculture 62 macrophytic species from 18 orders, 29 families and 48 genera were met. The following families were the most numerous: Ceramiaceae from red algae; Chordariaceae from brown algae; Ulothrichaceae, Ulvaceae and Ulvellaceae from green algae. *Ulva* (4 species) and *Acrochaete* (3 species) are the biggest genera. Spectrum of dominating species is rather diverse: *Porphyra seriata*, *Neosiphonia japonica*, *P. morrowii* (red); *Ectocarpus siliculosus*, *Halothrix lumbricalis*, *Chordaria* spp., *Petalonia fascia*, *S. lomentaria*, *Sphaerotrichia divaricata*, *C. costata*, *Saccharina* spp. (brown); *Kornmannia leptoderma*, *U. lactuca* and *U. splendens* (green algae).

In fouling from installations for *M. yessoensis* mariculture the following families were the biggest: Ceramiaceae, Rhodomelaceae; Scytosiphonaceae; Ulvaceae and Cladophoraceae. *Ulva* (4 species) was the richest genus. *Cladophora*, *Saccharina*, *Neosiphonia* and *Ceramium* genera contain 2 species each, the rest – 1 species each. Fouling flora from installations for the Japanese scallop mariculture was the least numerous and diverse. It includes 45 algal species from 16 orders, 21 families and 37 genera. Dominating species were not numerous: *N. japonica*; *S. lomentaria*, *S. cichorioides*, *S. japonica*; *U. flexuosa* and *U. lactuca*.

Flora of the scallop epibiosis was rather diverse. It included 52 macrophytic species from 20 orders, 31 families and 43 genera. Ceramiaceae, Rhodomelaceae and Ulvaceae are the biggest families of this flora. *Ulva*, containing 3 species, was the biggest genus. The following species dominated: *P. morrowii* and *Palmaria stenogona*; *S. japonica* and *Ralfsia* sp.; *U. splendens* and species of *Codium* genera: *Codium fragile* and *C. yessoense* (fig. 3).



Fig. 3. View of green alga *Codium* in scallop epibiosis.

Thus, taxonomical structures of fouling and epibiotic floras are close by proportion of supra-specific taxa of red algae, and differ by contribution of separate families of brown and green algae. Structures of floras of mariculture installations fouling differ among themselves by the proportion of supra-specific taxa in all algal groups. Floras of waterside structures fouling and scallop epibiosis are the closest to the benthic flora of the studied area by contribution of Rhodophyta families to taxonomic structure. Contribution of orders of brown and green algae to the structure of fouling floras of

all types of anthropogenic substrates is the most different from that of sea benthic flora of the southern Primorye.

Thus, proportion of the main algal megataxa in the structure of fouling and epibiosis floras in most cases has slightly different shape as compared to typical benthic floras.

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SPECIES COMPOSITION OF THE CRAB FAUNA OF THE YELLOW SEA

Wei Jiang

Institute of Oceanology, Chinese Academy of Sciences, Qingdao 266071, China

Based on the crab collection of the Marine Biological Museum, Chinese Academy of Sciences and the cruises for the investigations of the Yellow Sea biota from 2007 to 2009, as well as literature data, a preliminary study was conducted on the species composition of the crab fauna of the Yellow Sea. The results showed that there are a total of 102 crab species distributed in the Yellow Sea and can be divided into two categories: 89.2% belong to the warm water species of subtropical and tropical Indo-West Pacific warm water fauna, while the others belong to cold water species of the North Pacific temperate fauna. The 89 warm water species which accounted for 89.2% of total species can be subdivided into 7 types:

1. Indo - West Pacific, West Pacific Species, 34 species, accounting for 33.3%;
2. China Seas - Japan - Far Eastern Seas Species, 2 species, 2.0%;
3. China Seas Endemic Species, 13 species, 12.7%;
4. China Seas - Japan Species, 16 species, 15.7%;
5. Yellow Sea and East China Sea - Japan Species, 11 species, 10.8%;
6. Yellow Sea - Japan Species, 4 species, 3.9%;
7. Yellow Sea Endemic Species, 9 species, 8.8%.

The rest 13 species are cold water species with the following faunal composition:

1. Amphi - Pacific Boreal Species, 2 species, 1.9%;
2. Yellow Sea - Japan Warm Temperate Species, 8 species, 7.8%;
3. Yellow Sea Endemic Species, 3 species, 2.9%.

It should be emphasized that there are 8 pinnotherid species among the Yellow Sea endemic type (from both warm and cold water), including a recently discovered species of *Sakaina* (unpublished) from the northern Yellow Sea.

FILAMENTOUS FUNGI IN THE EPIGROWTH OF THE PACIFIC OYSTER *CRASSOSTREA GIGAS* (BIVALVIA) IN PETER THE GREAT BAY, SEA OF JAPAN

L.V. Zvereva, O.G. Borzykh

A. V. Zhirmunsky Institute of Marine Biology, Far Eastern Branch of the Russian
Academy of Sciences, 17 Palchevskogo Ul., Vladivostok, 690041 Russia

E-mail: zvereva_lv@mail.ru

A mycological investigation of the Pacific (giant) oyster *Crassostrea gigas* (Thunberg, 1793) (Bivalvia) has been for the first time conducted in Peter the Great Bay of the Sea of Japan. The taxonomic composition of filamentous fungi in the epigrowth of the shells of this mollusk has been studied.

The Pacific oyster is a commercially important bivalve mollusk, which is harvested and farmed in Primorsky Krai (Regulev, 2009).

Microscopic fungi growing on oyster shells attract the attention of researchers because both wild and cultured oysters are susceptible to the so-called shell disease caused by the parasitic fungus *Ostracoblabe implexa* (McGladdery et al., 1993). In the Black Sea, up to 80% oysters in oyster beds have shell disease (Gubanov, 1988; Pirkova, Demenko, 2008).

This work studies the taxonomic composition of filamentous fungi growing on the shells of the Pacific oyster.

Materials and Methods

Oysters were collected by divers in the open part of Peter the Great Bay near Rikord Island in 3–4 m of depth in April, 2010.

Pieces of oyster shells were washed three times with sterile sea water, soaked for two hours in sterile sea water with antibiotics (penicillin 500 thousand U/l and streptomycin 0.5 g/l) to suppress bacterial growth. Then the pieces of shells were washed to remove antibiotics and placed onto the surface of agar medium: wort agar or Czapek agar with peptone (Litvinov, Dudka, 1975; Artemchuk, 1981).

Fungal colonies grown up on the media were identified by the keys (Thom, Raper, 1949; Ellis, 1971; Ainsworth et al., 1973; Egorova, 1986; Integration of Modern Taxonomic..., 2000; Pivkin, Zvereva, 2000; etc.).

Results and Discussion

The total number of species found on the shell surface of *Crassostrea gigas* is eleven; seven species were identified (see table). The identified species are anamorphic fungi of the following families: *Dematiaceae* (3 species: *Alternaria alternata*, *A. litorea*, *A. tenuissima*), *Moniliaceae* (2 species: *Penicillium digitatum* var. *californicum*, *Trichoderma aureoviride*), *Tuberculariaceae* (2 species: *Fusarium oxisporum* var. *orthoceras*, *F. lateritium*) (table). The four species denoted as Mycelia Sterilia formed only mycelium and did not produce spores; however, the colonies of these species differed from each other (table).

The species diversity of filamentous fungi found on the shells of the Pacific oyster is low, which can be explained by the peculiarities of this bivalve's biology. The Pacific oyster inhabits hard bottoms: rocks, pebbles, boulders, etc. The composition of filamentous fungi associated with marine organisms correlates with the fungal composition of marine bottoms in the habitats of these organisms (Pivkin, 2000; Zvereva, Vysotskaya, 2007; Zvereva, 2007). According to the data obtained by Pivkin et al. (2005), the species composition of filamentous fungi on different bottoms depends on the grain size composition and organic content of these bottoms: the greatest number of fungal species is recorded from muddy and muddy-sand bottoms and the least number of fungi from stony bottoms.

Table The taxonomic composition of filamentous fungi in the epigrowth of the Pacific oyster *Crassostrea gigas* (Thunberg, 1793) in Peter the Great Bay of the Sea of Japan

Taxon of fungi	<i>Crassostrea gigas</i> shell	
	Wort agar	Czapek's agar with peptone
<i>Alternaria alternata</i> (Fr.) Keissler	+	-
<i>A. litorea</i> (Pivkin et Zvereva) Ging.	+	-
<i>A. tenuissima</i> (Kunze ex Pers.) Wiltshire	-	+
<i>Fusarium oxisporum</i> var. <i>orthoceras</i> (App. Et Wr.) Bilai	+	+
<i>F. lateritium</i> Nees	+	-
<i>Penicillium digitatum</i> Sacc. var. <i>californicum</i> Thom.	-	+
<i>Trichoderma aureoviride</i> Rifai	+	-
Mycelia Sterilia 1	-	+
Mycelia Sterilia 2	-	+

Mycelia Sterilia 3	-	+
Mycelia Sterilia 4	-	+
Total: 11	5	7

The filamentous fungi found on the oyster shells belong to opportunistic microorganisms able to produce mycoses and mycotoxicoses; particularly, species of the genera *Penicillium* and *Trichoderma* (Sallenave-Namont et al., 2000) and species of the genus *Fusarium*, causing infections in young crustaceans (Sindermann, Lightner, 1988).

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Conclusions

1. Fungi on the shells of the Pacific oyster *Crassostrea gigas* have been for the first time studied in Peter the Great Bay of the Sea of Japan. A total of eleven species of filamentous anamorphic fungi have been found, seven of them have been identified, and four species formed only sterile mycelium.
2. The identified species are opportunistic or toxic fungi.

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**FUNGAL COMPLEXES ASSOCIATED WITH THE PRIMORSKY SCALLOP
MIZUHOPECTEN YESSOENSIS AND THE MUSSEL *MYTILUS TROSSULUS*
(BIVALVIA) FROM POLLUTED AND CLEAN AREAS OF PETER THE
GREAT BAY, SEA OF JAPAN**

L.V. Zvereva, O.G. Borzykh

A. V. Zhirmunsky Institute of Marine Biology, Far Eastern Branch of the Russian
Academy of Sciences, Palchevskogo Ul., Vladivostok, 690041 Russia

E-mail: zvereva_lv@mail.ru

A mycological investigation of two bivalve mollusks, the Primorsky scallop *Mizuhopecten yessoensis* (Jay) and the bay mussel *Mytilus trossulus* (Gould), from two areas of Peter the Great Bay (Sea of Japan) has been conducted. The studied bivalves are commercially harvested and farmed in many countries, including the coastal waters of the Russian Far East (Ivin et al., 2006).

The goal of this work was to study the taxonomic composition of filamentous fungi associated with the bivalve mollusks, the Primorsky scallop *Mizuhopecten yessoensis* and the bay mussel *Mytilus trossulus*, from the two areas of Peter the Great Bay (Sea of Japan) differing in the degree of anthropogenic pollution.

Mollusks were collected in Amursky Bay, affected by domestic sewage and industrial effluents from Vladivostok and in relatively clean Vostok Bay (Ogorodnikova, 2001).

Results and Discussion

The taxonomic composition of filamentous fungi associated with the Mizuhopecten yessoensis scallop. The internal organs of the Primorsky scallop from relatively clean biotopes of Vostok Bay contains 18 species of filamentous fungi from 7 genera, including 17 species of anamorphic fungi from the genera *Penicillium* (5 species), *Cladosporium* (5), *Aspergillus* (3), *Trichoderma* (1), *Alternaria* (2), and *Aureobasidium* (1), and 1 zygomycete from the genus *Rhizopus* (table).

The fungal complex associated with the Primorsky scallops from the biotopes of Amursky Bay contains 29 species belonging to 17 genera. This complex includes anamorphic fungi from the genera *Penicillium* (5 species), *Aspergillus* (5), *Acremonium* (4), *Scopulariopsis* (2), and ten more genera, each represented by one species; two species of ascomycetes from the genera *Arachnotheca* and *Chaetomium*; and one zygomycete from the genus *Pilaira* (table).

The taxonomic composition of filamentous fungi associated with the *Mytilus trossulus* mussel. The internal organs of the bay mussel from relatively clean biotopes of Vostok Bay contains 16 species of filamentous fungi from 6 genera, including 14 species of anamorphic fungi from the genera *Penicillium* (7 species), *Cladosporium* (3), *Aspergillus* (3), and *Trichoderma* (1); one ascomycete from the genus *Chaetomium*; and one zygomycete from the genus *Rhizopus* (table).

The fungal complex associated with the bay mussel from the biotopes of Amursky Bay contains 20 species belonging to 10 genera. This complex includes 18 species of anamorphic fungi from the genera *Penicillium* (6 species), *Aspergillus* (4), *Cladosporium* (2), and six more genera, each represented by one species; and two species of ascomycetes from the genus *Chaetomium* (table).

The species of the genera *Aspergillus*, *Penicillium*, *Cladosporium*, *Chaetomium*, and some others found in the studied bivalve mollusks are opportunistic and toxic fungi capable of causing mycoses and mycotoxicoses in marine organisms. The immune-enzyme analysis of the Primorsky scallop *Mizuhopecten yessoensis* showed that the internal organs of these bivalves accumulated mycotoxins, particularly aflatoxin produced by the filamentous fungus *Aspergillus flavus* Link (Zvereva et al., 2009).

Mycotoxicological investigations of the muscles of *Mytilus edulis* show that the presence of fungi in these bivalves represents a real risk of poisoning through the consumption of contaminated shellfish (Sallenave-Namont et al., 2000; Grovel et al., 2003).

Microbiological monitoring of mollusks from different parts of Peter the Great Bay (Sea of Japan) demonstrated that the biodiversity of opportunistic and toxin-producing filamentous fungi, primarily from the genus *Aspergillus*, found in the internal organs of bivalve mollusks increases with the increase of pollution in the coastal waters (Zvereva, 2007a, 2007b, 2008; Zvereva, Vysotskaya, 2005, 2007; Zvereva, Usheva, 2009).

Comparison between the fungal complexes associated with the bivalve mollusks *Mizuhopecten yessoensis* and *Mytilus trossulus* from polluted and clean areas of Peter the Great Bay, Sea of Japan

Genus of fungi	<i>Mizuhopecten yessoensis</i>		<i>Mytilus trossulus</i>	
	Amursky Bay	Vostok Bay	Amursky Bay	Vostok Bay
	Number of	Number of	Number of	Number of

	species	species	species	species
Ascomycota				
<i>Arachnotheca</i>	1	-	-	-
<i>Chaetomium</i>	1	-	2	1
Anamorphic fungi				
<i>Acremonium</i>	4	-	1	-
<i>Alternaria</i>	-	2	1	-
<i>Aspergillus</i>	5	3	4	3
<i>Aureobasidium</i>	-	1	-	-
<i>Beauveria</i>	1	-	-	-
<i>Blastobotrys</i>	1	-	-	-
<i>Chrysosporium</i>	1	-	-	-
<i>Cladosporium</i>	1	5	2	3
<i>Geomyces</i>	1	-	1	-
<i>Monilia</i>	1	-	-	-
<i>Myriotheceium</i>	1	-	-	-
<i>Oidiiodendron</i>	1	-	1	-
<i>Penicillium</i>	5	5	6	7
<i>Periconia</i>	1	-	-	-
<i>Phialophorophoma</i>	1	-	-	-
<i>Scopulariopsis</i>	2	-	1	-
<i>Trichoderma</i>	-	1	1	1
Zygomycota				
<i>Pilaira</i>	1	-	-	-
<i>Rhizopus</i>	-	1	-	1
Total:	29	18	20	16
21				

Investigations of marine filamentous fungi have been supported with the grants from the Presidium of the Russian Academy of Sciences (RAS) and from the Far-Eastern Branch of the Russian Academy of Sciences (FEB RAS) “Microbial biosphere” DVO-1 No. 09-I-P15-04, DVO-3 No. 09-III-A-06-201, DVO-1 “Biodiversity monitoring in Peter the Great Bay of the Sea of Japan” No. 09-I-P23-01, DVO-1 No. 09-I-P15-03, Special Federal Program "World Ocean" No. 01.420.1.2.0003, 2008-2012.

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DEAD PROPORTION OF DOMINANT COPEPOD SPECIES IN THE JIAOZHOU BAY

Aiyong, Wan^{1,2}, Guangtao Zhang^{1*} and Song Sun¹

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

² Graduate University, Chinese Academy of Sciences, 19 Yuquan Road, Beijing 100049, China

* Corresponding author: gtzhang@qdio.ac.cn

Planktonic copepods are perhaps the most numerous metazoans on earth and the most important primary consumers in the ocean. Over the last 30 years much effort has gone into examining the growth and fecundity, but only relatively few investigations have quantified rates of mortality. Dead proportion of these copepods of *Calanus sinicus*, *Paracalanus parvus* and *Oithona similis* population were investigated monthly with neutral red staining method at 12 stations from December 2008 to November 2009 in and around Jiaozhou Bay, China.

Calanus sinicus appeared all through the year, with extremely low abundance in summer. Dead females were observed in five months, accounting for no higher than 5% of total female abundance. Proportion of dead females was high in April and November, when total abundance peaked and egg production was most active, but seawater temperature was not exceeding its thermal limits, it was likely that their death was caused by unfavorable temperature, death of females occurred most possibly as reproduction "cost"; Dead copepodites presented in all but three months, with higher proportion from 1.1% to 15.4%. According to correlation coefficient between monthly average of dead proportion and environmental conditions in different areas of the bay, including seawater temperature, salinity and Chl a concentration, dead proportion of copepodites decreased significantly with Chl a concentration increase only outside the bay, but negatively related to seawater and salinity. Comparing with other studies, the proportion of deaths in this study was noticeably higher than the other station.

Paracalanus parvus occurred throughout the year, with a large abundance peak in summer and small peaks in winter. The mean level of dead percent varied between 3.8 %

and 12.4% for the females (average 6.5%), 2.6-11.4% for male (average 6.4%), 4.9-14.1% for copepodites (average 7.2%) all through the year. Dead proportion of adult was significantly lower than that of copepodites. Dead proportion of *P. parvus* was significantly higher in winter and summer. According to correlation coefficient between average of dead proportion and environmental conditions in different areas of the bay, dead proportion of adult and copepodites were correlation significant correlation with seawater temperature in all bay, higher dead proportion should resulted from seawater temperature exceeding its thermal limits, but it was negative correlation with Chl and salinity.

Oithona similis appeared all through the year, with extremely low abundance in summer. The mean level of dead percent varied between 0.7% and 7.6% for the females (average 1.7%), 5.5-33.3% for male (average 19.1%), 2.9- 8.7% for copepodites (average 4.9%) all through the year. dead proportion of female was significantly lower than that of male observed simultaneously, the deaths of males have 11 times greater than that of female. It is unlikely that these difference can be attributed simply to the males shorter physiological longevity. *O. similis* is a marine, pelagic, cyclopoid copepod distributed from the subtropics to polar waters, according to correlation coefficient between average of dead proportion and environmental conditions in different areas of the bay, but it was negative correlation with Chl, seawater and salinity.

Our study showed that, the death of these copepods were not significant higher than the other station. It is suggested that environments in Jiaozhou Bay was suitable for living although this semi-closed embayment was usually thought heavily influence by human activities.

Key Words: Copepods, Dead proportion, Neutral Red, Jiaozhou Bay

**OPPORTUNISTIC FILAMENTOUS FUNGI ISOLATED FROM
PATHOLOGICALLY CHANGED INTERNAL ORGANS OF THE MUSSEL
MYTILUS TROSSULUS (BIVALVIA) FROM PETER THE GREAT BAY, SEA
OF JAPAN**

L.V. Zvereva, L.N. Usheva

A. V. Zhirmunsky Institute of Marine Biology, Far Eastern Branch of the Russian
Academy of Sciences, 17 Palchevskogo Ul., Vladivostok, 690041 Russia

E-mail: zvereva_lv@mail.ru

Mycological and histological investigations of the bivalves having pathological changes of internal organs have been conducted for several years in Peter the Great Bay (Zvereva, Usheva, 2009). *Mytilus trossulus* (Gould), one of the investigated bivalves, is commercially harvested and farmed in many countries, including the Russian Far East (Ivin et al., 2006).

The chief aim of the present work is to study the taxonomic composition of opportunistic filamentous fungi isolated from pathologically changed internal organs of the bay mussel *Mytilus trossulus*. The main tasks of the work are as follows:

1. To reveal pathologies in the internal organs of the collected mussels;
2. To isolate pure cultures of the filamentous fungi from the pathologically changed organs;
3. To study the taxonomic composition of the filamentous fungi isolated from the mussels;
4. To determine the distribution of opportunistic and toxic filamentous fungi over the internal organs of mussels.

Materials and Methods

The mussels were collected in Vostok Bay (Peter the Great Bay of the Sea of Japan) in August 2004.

Mycological studies. Samples of pathologically changed shells and internal organs (gills, mantles, digestive glands, muscles, and gonads) were soaked in a solution of antibiotics (penicillin 500 thousand U/l and streptomycin 0.5 g/l) for two hours to inhibit the growth of bacteria and then rinsed with sterile sea water. Liquid media with pieces of shells and organs were incubated at 20 °C. The colonies, which had grown up in liquid nutrient media, were transferred to agar media of similar composition for

identification. The following nutrient media were used for incubation: wort agar (15 g/l); solution of standard Czapek medium (25 g/l), Tubaki medium (glucose 30 g/l, peptone 1.0 g/l, yeast extract 0.5 g/l, MgSO₄ 0.24 g/l, FeSO₄ x 7H₂O 0.01 g/l, K₂HPO₄ 1.0 g/l), and Saburo agar medium (Artemchuk, 1981; Methods of..., 1982). All nutrient media were based on filtered sea water. The fungi were identified by use of the classical identification keys (Ainsworth et al., 1973; Bilai, Koval', 1988; Egorova, 1986; Integration of Modern Taxonomic..., 2000; etc.).

The strains of filamentous fungi isolated during these investigations have been added to the Collection of Marine Fungal Cultures belonging to the Zhirmunsky Institute of Marine Biology (Far Eastern Branch of the Russian Academy of Sciences).

Histopathological studies. The work was performed using the classical methods of histological analysis of invertebrate organs and tissues (Lilly, 1969; Pearse, 1962).

Materials for histopathological analysis were fixed in 10% formaldehyde dissolved with sea water for one or two days. Samples of the mollusk tissues and fungal strains were then embedded in paraffin by standard procedures. Five to six micrometer sections were stained with hematoxylin and eosin, with Heidenhain's azan, and with Mallory's trichrome stain for general tissue morphology analysis, and with periodic acid-Schiff (PAS) - special stain of fungi.

Results and Discussion

Mytilus trossulus mussels had malformations of shells and histopathological changes in the internal organs: hemodynamic disorders in the circulatory system (dilatation of blood vessels, excessive filling with blood and thrombosis of blood vessels in gills), inflammatory responses (granulomas), proliferative disorders of gill epithelium (hyperplasia and coalescence of gill filaments).

Seventeen colonies of filamentous fungi were isolated from the examined mollusks (table). The isolated fungi are eurybiontic, facultative marine organisms, widespread in terrestrial and marine habitats.

Table The taxonomic composition and distribution of filamentous fungi over the shell surface and in the internal organs of *Mytilus trossulus*

Species of fungi	<i>Mytilus trossulus</i>					
	1*	2	3	4	5	6
<i>Acremonium charticola</i> (Lindau) W.Gams		+	+	+	+	
<i>Alternaria alternata</i> (Fr.) Keissl.	+					
<i>Aspergillus flavus</i> Link		+	+	+	+	+
<i>A. niger</i> v. Tiegh.		+		+	+	
<i>A. ochraceus</i> K. Wilh.		+	+	+		

<i>Aureobasidium pullulans</i> (de Bary) G. Arnaud	+					
<i>Botrytis cinerea</i> Pers.	+					
<i>Cladosporium cladosporioides</i> (Fresen.) B.G. de Vries	+					
<i>C. sphaerospermum</i> Penz.	+	+	+	+	+	
<i>Geomyces pannorum</i> (Link) Singler et J.W. Carmichl.	+					
<i>Penicillium chrysogenum</i> Thom		+	+	+	+	+
<i>P. commune</i> Thom		+		+	+	+
<i>P. verrucosum</i> Dierckx var <i>verrucosum</i> Samson, Stolk et Hadlock	+	+			+	
<i>Penicillium</i> sp.	+		+	+		+
<i>Trichoderma koningii</i> Oudem.		+	+	+		
<i>Chaetomium globosum</i> Kunze	+					
<i>Rhizopus nigricans</i> Ehrenb.	+					
Total: 17	10	9	7	9	7	4

* (1) shell surface, (2) mantle, (3) muscle, (4) gills, (5) digestive gland, and (6) male and female gonads.

Most fungi found in the mussels are opportunistic species belonging to the genera *Aspergillus*, *Penicillium*, *Acremonium*, *Cladosporium*, *Alternaria*, *Trichoderma*, *Chaetomium*, and *Rhizopus*. It is common knowledge that these fungi can produce mycotoxins and cause mycoses and mycotoxicoses in terrestrial and marine animals. For example, *A. flavus* caused chronic aflatoxicosis followed by often malignant tumour of the liver (hepatoma) in the rainbow trout farmed in the USA, Great Britain, and Italy; *A. flavus* and *A. parasiticus* caused aflatoxicosis, resulting in digestive gland necrosis, in cultivated crustaceans (Sindermann, Lightner, 1988). The fungi from the genus *Cladosporium* were previously isolated from the hyperplastic gill epithelium of cod, and *Hormoconis* (*Cladosporium*) *resinae* produced lesions in the musculature of plaice (Strongman et al., 1997). *A. fumigatus* releases gliotoxin, which have been shown to accumulate in the soft tissues of the *Mytilus edulis* mussel cultivated in France (Grovel et al., 2003). The fungi of the genus *Chaetomium* produce hemolytic toxins and antibiotic metabolites (Pivkin, 2000).

The distribution of filamentous fungi over the shell surface and in the internal organs of the examined mollusks is presented in the table.

The greatest number of fungal species was found on the shell surface, in the mantle, digestive gland, and gills, and the lowest number in the gonads (table).

To sum up, the analysis of taxonomic composition and distribution of filamentous fungi in the internal organs of the bay mussel showed that the organisms of mollusks

having immunodeficiency disorders and pathologies of internal organs accumulate opportunistic and toxic filamentous fungi.

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SEASONAL PATTERNS OF FATTY ACIDS IN SESTON AND THE COPEPOD *CALANUS SINICUS* IN JIAOZHOU BAY AND ITS TROPHIC IMPLICATIONS

Mengtian Liu², Chaolun Li^{1*}, Song Sun^{1,2}

1 Key Laboratory of Marine Ecology and Environmental Sciences, Institute of Oceanology, Chinese Academy of Sciences, 7 Nanhai Road, Qingdao 266071, China
2 Jiaozhou Bay Marine Ecosystem Research Station, Chinese Academy of Sciences, 7 Nanhai Road, Qingdao 266071, China

*Corresponding Author, Email: lcl@qdio.ac.cn

Jiaozhou Bay is a semi-enclosed bay which lies in the northwest of the southern Yellow Sea (35°43'-36°18'N, 120°04'-120°23'E). Under the impacts of both natural processes and human activities, this temperate bay exhibits complex hydrographic features. Seston and *Calanus sinicus* were investigated in Jiaozhou Bay in view of their fatty acid compositions to study the trophic relationships in this moderate plankton ecosystem. Sampling was carried out in D7, C3 and A5 monthly from November 2007 to November 2008 (Fig. 1). All samples were processed according to Folch *et al.* (Folch *et al.*, 1957) and Parrish (Parrish, 1999). Analysis of fatty acid composition was carried out with an Agilent 7890A GC instrument.

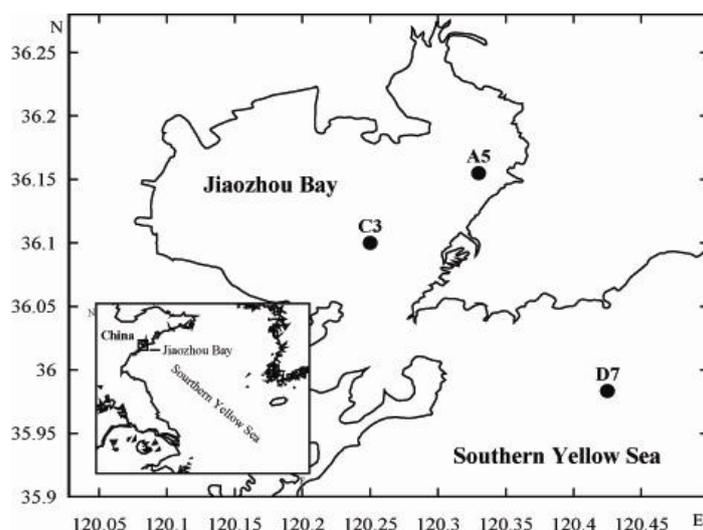


Fig. 1. Map of the study area showing the sampling stations and the location of Jiaozhou Bay.

Principal component analysis was carried out to ordinate the fatty acid patterns of seston according to stations and months (Fig. 2). The results showed that diatom

contributed most to A5 (northwest of the bay) and least to D7 (out of the bay) with dinoflagellates contributed most to D7 and least to A5. According to 16:1 ω 7 and 18:4 ω 3/16:1 ω 7, diatom mainly flourished in spring and summer while dinoflagellates bloomed exclusively in summer, which was generally in accordance with the phytoplankton abundance.

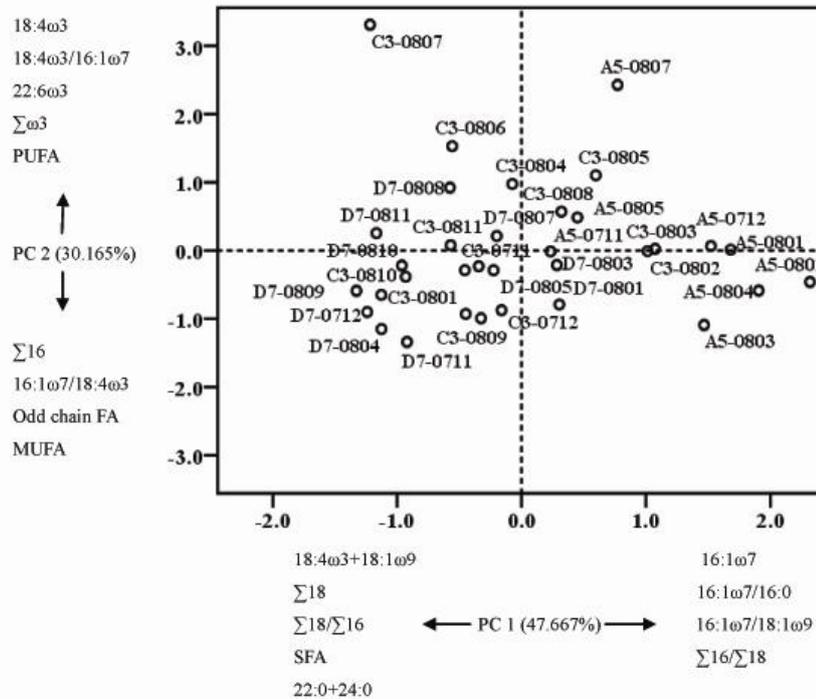


Fig. 2. PCA ordination of seston based on all fatty acid markers from D7, C3 and A5. PC1 (principal component 1) explained 47.667% of the total variations. PC2 (principal component 2) explained 30.165%. Arrows paralleling to each axis denoted the specified fatty acid markers contributing most to the variations.

A distinctive feature of the fatty acid composition of *C. sinicus* (Fig. 3) was the prevalent of 20:5 ω 3 and 22:6 ω 3. The obvious advantage of 16:1 ω 7 over 18:4 ω 3 in female indicated that diatom contributed far more than dinoflagellates in the diets of *C. sinicus*. Annually, the feeding intensity of *C. sinicus* on diatom was higher in spring and autumn than in other seasons. The comparatively low levels of the monounsaturates 20:1 and 22:1 allowed the conclusion to be drawn that besides phytoplankton, *C. sinicus* might feed on a wider range of particles including organic detritus, bacteria, small copepods etc.

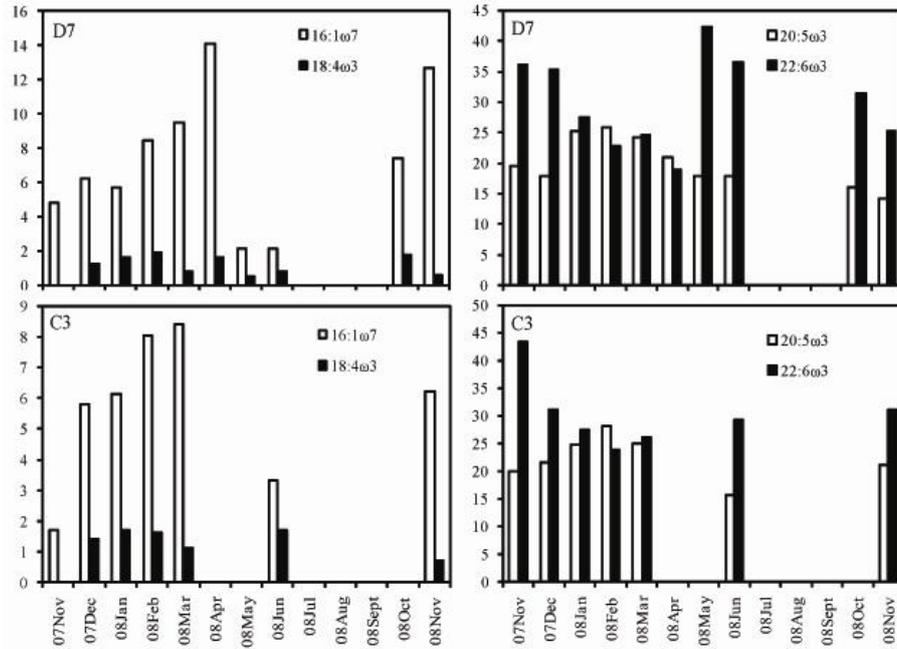
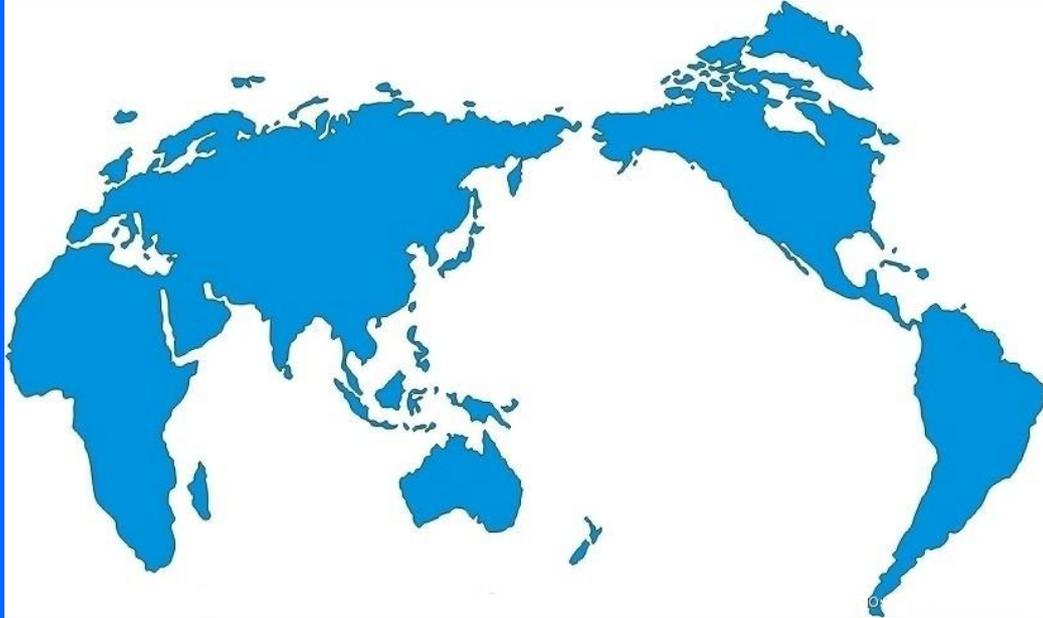


Fig. 3. Temporal changes of selected fatty acids (%) in the female *C.sinicus* in D7 and C3.

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