



**A variety of interactions
in the marine environment**

**ABSTRACTS VOLUME
FROM 49TH EUROPEAN
MARINE BIOLOGY SYMPOSIUM**

September 8–12, 2014
St. Petersburg, Russia

Zoological Institute Russian Academy of Sciences

Zoological Institute Russian Academy of Sciences

**A variety of interactions
in marine environment**

**ABSTRACTS VOLUME
FROM 49TH EUROPEAN
MARINE BIOLOGY SYMPOSIUM**

September 8–12, 2014
St. Petersburg, Russia

St. Petersburg
2014

est as a model for the study of the evolution of shallow water benthic communities due to geological and hydrological changes.

**COMMUNITY COMPOSITION IN REDOX ZONE
OF SALT LAKES SEPARATING FROM THE WHITE SEA
E. D. Krasnova¹, I. A. Milutina², D. A. Voronov^{2, 3}**

¹White Sea Biological Station, Lomonosov Moscow State University, Russia

²A. N. Belozersky Institute of Physico-Chemical Biology, Lomonosov Moscow State University, Russia

³A. A. Kharkevich Institute for Information Transmission Problems RAS, Russia

Because of postglacial isostatic uplift with an average speed of 32 cm per century, many of the White Sea bays are separated gradually from the sea. At the intermediate stages, usually the meromixis is observed. At the boundary of aerobic and anaerobic layers there is of 10-50 cm thick redox zone colored in green or red with sharp physical and chemical gradients. The green layer caused by development of green phototrophic sulfur bacteria was found in three reservoirs that are further advanced in isolation from the sea. The red layer due to blooming of cryptophyte algae *Rhodomonas* sp. was found in three water bodies with regularly seawater inflow.

Large amount of unicellular and multicellular heterotrophic organisms often develop in the redox zone. To identify the organisms we used a molecular genetic approach. Total DNA was extracted, 18S rRNA gene amplified, PCR fragments were purified, extracted using the MinElute Gel Extraction Kit (QIAGEN) and cloned into the vector pTZ57R/T.

Two infusorian species were identified, one heterotrophic protozoan from Cercozoa group, and one cryptophyte algae species. First ciliate species found in the lagoon at Green Cape shows 99% similarity by 18S rRNA gene with *Euplotes elegans* (GenBank No DQ309868) from Mariager Fjord (Schwarz et. al., 2007) and from the fjord Framvaren EF527105; 18S rRNA sequence of another ciliate species from the lagoon on the Zeleny Cape and lake Trekhtzvetnoe has 99% similarity with uncultivated marine eukaryote (EF527105 and DQ103855), and 98% similarity with *Prorodon teres* (X71140.1). Partial sequence of 18S rRNA gene of the heterotrophic protozoan from group Cercozoa found in the Lake Elovoe has high sequence similarity with an uncultivated Cercozoa (FN263034, JQ226494.1) from oxygen-deficient zone in northeast Pacific and JN090864.1 from freshwater lake Karl in Greece (Oikonomou et. al., 2012). The nucleotide sequence of *Rhodomonas* sp. from the lake Kislo-Sladkoe and lagoon at Zeleny Cape has 99% similarity with the strain *Rhodomonas* sp. RCC2020 (JN934672) isolated from the deep chlorophyll maximum in Beaufort Sea at the depth of 40 m.

Bloom of unicellular algae *Euglena* sp. was discovered in the chemocline of Lake Trekhtzvetnoe in February 2014, and massive development of heterotrophic dinoflagellates *Oxyrrhis marina* was revealed in the lagoon at Green Cape at September 2012.

The resulting list of species allows outlining some features of community. At the basis there are different mixotrophic organisms (*Rhodomonas*, *Euglena*) capable of photosynthesis as well as of organic matter nutrition. It is important for adaptation to environment with hydrogen sulfide and big amount of bacterial mass as a potential food source. Three other detected organisms are predators able to consume large cells of algae as well as to phagocytize bacteria. Ciliates *E. elegans* are resistant to oxygen deficiency. The enzyme system of *O. marina* allows it to live in the absence of oxygen (Altenbach et al., 2012).

**MICROBIAL COMMUNITY STRUCTURE
OF TWO ANCHIALINE CAVES ON MLJET ISLAND (ADRIATIC SEA)**

**N. Krstulović¹, M. Solić¹, D. Santić¹,
J. Marsić Lučić², M. Ordulj³, S. Sestanović¹**

¹Institute of Oceanography and Fisheries, Laboratory of Microbiology, Split, Croatia

²Institute of Oceanography, Laboratory for Aquaculture, Split, Croatia

³University of Split, Department of Marine Studies, Split, Croatia

The microbial abundances, including bacteria, viruses, and heterotrophic nanoflagellates, was determined for two anchialine caves located on the Island of Mljet (Adriatic Sea): Bjeajka Cave and Lenga Pit. Both caves are situated approximately 100 m from the coast with extensive subterranean connections to the sea, resulting in noticeable marine and terrestrial influences. Because of the shallow settings of the studied caves, they represent habitats with a minimal light or complete darkness where photosynthesis is minimal or not possible. Thus, during the surveys there was no evidence of cyanobacterial cells in either caves, but the presence of bacteria, viruses and heterotrophic nanoflagellates (HNF) was established. Further, bacterial abundance was higher in caves in comparison to surrounding open seawater. In the surrounding seawater the predominance of the LNA group over HNA is determined, which also indicates the