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The results of the species composition, abundance and biomass of heterotrophic nanoflagellates (HNF) were obtained for the first time in the Laptev Sea in August-September 2014-2015. An attempt was made to assess the role of HNF in grazing productions of bacterioplankton (P_B) and virioplankton (P_V). 24 species and forms of HNF 9 taxa and groups of uncertain systematic position were found. Kinetoplastea Honigberg, 1963 were characterized by the highest species diversity. The HNF community dominated by bacteriophages (eighteen species), also found four omnivorous and two carnivorous species. N_{HNF} ranged from 108-651 cells/ml, the biomass — 0.3-3.5 mg C/m³. N_{HNF} was three orders of magnitude lower than N_B , and B_{HNF} was 1.6-63.3% (mean 24.4±4.0%) biomass of bacterioplankton. Between N_{HNF} and N_B were detected high positive correlation ($R=0.63$, $p=0.05$). The virus particles (diameter of 200-531 nm) potentially can be edible objects for HNF. However, the ratio of the number of large viruses at N_{HNF} was low - 42-417. HNF could consume a significant amount of virus attached to the walls and inside bacteria. The number of bacteria with attached viruses was 8.7-26.5% N_B . On bacteria it was up to 11 virus particles. The number of bacteriophage-viruses in infected cells reached 111 particle/cell. Guided by literature data on clearance rates of water by Arctic HNF (Sherr et al., 1997), calculated that in the water column of the Laptev sea the HNF community consumed 1.1-30.4% (average 8.3%) daily P_B and 1.3-77.2% (average 14.9%) the daily P_V . The research supported by the RFBR grant 14-04-00130.

THE STATUS OF THE SPECIES *BALANTIDIUM ELONGATUM* FROM THE GUT OF EUROPEAN COMMON FROG

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The representatives of the genus *Balantidium* Claparède et Lachmann, 1858 have several common morphological features: sacciform or

slightly elongated body completely covered with cilia forming dense longitudinal rows. In the anterior part of the body, there is an opening of vestibulum. Such features are clearly visible under light micro-scope. Because balantidia have very few other morphological characters suitable for taxonomy, their species identity is usually determined using morphometric data. Comparative analysis of several described *Balantidium* spp. indicated that many of these specific names might be synonyms. All balantidia inhabiting the intestine of mammals and birds were recognized to belong to a single species — *Balantidium coli*, recently moved to the genus *Balantioides* Alexeieff, 1931. We supposed that some species from amphibians may be synonyms (balantidia are polymorphic) and some of them may belong to different genera. For solving this issue, we used modern electron microscopic techniques and molecular phylogenetic analysis. We studied the morphology of *Balantidium entozoon* and *B. elongatum* from the gut of European common frog *Rana temporaria* Linnaeus, 1758 using light and electron microscopy. The distinguishing features of *B. elongatum* are the long thin fusiform body and relatively short vestibulum. However, other traits (number of kinetes and the distance between them) are indistinguishable between two species. Their intracellular structures also showed no differences. The sequences of 18S rRNA gene of both species were identical to each other and to that of *B. entozoon* from the GenBank. Thus *B. elongatum* must be considered as a younger synonym of *B. entozoon*.

BRIDGING THE GAP BETWEEN TRADITIONAL TAXONOMY AND TRANSCRIPTOMICS IN ARCELLINIDS (AMOEOBOZOA)

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