

Naked lobose amoebae (Amoebozoa) from marine habitats: implications of comparative data on their occurrence in deep and shallow habitats

Alexander Kudryavtsev^{1,2}, Ekaterina Volkova¹, Anna Gladkikh^{1,3}, Suzana Živaljić⁴, Eckhard Völcker⁵, Steffen Clauß⁵, Hartmut Arndt⁴, and Jan Pawlowski⁶

1. Department of Invertebrate Zoology, Faculty of Biology, St. Petersburg State University, Russia

2. Laboratory of Parasitic Worms and Protistology, Zoological Institute Russian Academy of Sciences, Russia

3. Irkutsk Antiplague Research Institute of Siberia and Far East, Russia

4. Department of General Ecology, Institute for Zoology, University of Cologne, Germany

5. Penard Labs Berlin/Cape Town, Germany/South Africa

6. Molecular Systematics and Environmental Genomics, Department of Genetics and Evolution, University of Geneva, Switzerland

The geographic distribution of the naked lobose amoebae (Amoebozoa) has been little addressed in the past studies, mainly because of challenging and time-consuming identification of morphospecies in this group. The primary goal of the study that we present was to check, whether marine habitats with contrasting conditions (i.e., the deep and shallow biotopes) are inhabited by different species of Amoebozoa. The results of the first sampling campaigns of 2009 and 2010 seemingly supported this hypothesis, yielding several new species in *Vannella*, *Vexillifera*, *Neoparamoeba*; new genera in Vannellida, Dactylopodida and Himatismenida, and several new, deeply-branching amoebozoan lineages. In particular, a unique species *Squamamoeba japonica* (now a separate class Cutosea) was first isolated from the deep bottom sediments of the Sea of Japan. However, further sampling led to the isolation of more identical strains of *Squamamoeba japonica* from marine habitats at different depths and in different oceans. In addition, the isolated strains have identical ranges of salinity tolerance and pressure resistance with one exception. By far, the opposite example is the genus *Cunea* (Dactylopodida), with three morphologically identical species from the deep West Atlantic, the shallow sediments in The Red Sea and a brackish continental habitat without direct connection to the ocean. All these strains show significant differences in the molecular sequences and tolerance ranges against temperature and salinity. The data presented show that various morphospecies of Amoebozoa may have different patterns of distribution in the biosphere, ranging from a single global population consisting of identical, broadly adaptable individuals, to numerous separated populations that may be limited in their distribution areas partly due to the narrow tolerance ranges to environmental conditions. It still remains to be checked to which extent the isolated species represent an active part of the sampled communities. Partially supported by an RFBR grant 15-29-02749-ofi_m.