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Genetic diversity of bryozoan relict *Hislopia placoides* (Gymnolaemata: Hislopiidae) in Lake Baikal

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Motivation and Aim: Bryozoans (phylum Bryozoa) are simple aquatic invertebrates living in sedentary colonies. The bryozoans are classified as the Stenolaemata, Phylactolemata and Gymnolemata. Members of Gymnolemata usually occur in seas and brackish water, but there are families, inhabiting fresh water (Paludicellidae, Hislopiidae). The only representative of Gymnolemata described from Lake Baikal is endemic species *Hislopia placoides* (Korotneff, 1901). In Lake Baikal, this species is regarded as a relic of past, warmer, geological periods. *H. placoides* is characterized by ecological plasticity. In the lake Baikal, several morphs of *H. placoides* have been described that differ from each other in the form of colonies and zooids, confined to certain habitat conditions. At the same time, the genetic diversity of *H. placoides* morphs has not yet been studied. Thus, the aim of this investigation was to study the genetic polymorphism and evolutionary history of different morphs of *H. placoides*.

Results: Representatives of two morphs of *H. placoides* were studied. *H. placoides* m. *sabulosa* were collected in the open littoral of Lake Baikal (near Babushkin, depth 18–60 m). *H. placoides* m. *ripariensis* were collected from Posolsky Sor (depth 1–3 m) and Angara River (depth 3–5 m). A total of 18 bryozoan colonies were analyzed. For molecular genetic studies, the gene fragments of the COI and 16S rDNA of mitochondrial DNA were used. The four COI haplotypes and two 16S rDNA haplotypes were revealed among the *H. placoides* specimens studied. Moreover, the shared haplotypes were found in the different morphs. Thus, morphological variability and geographic distances are not related to genetic polymorphism and, possibly, due to the ecological features of local habitats, inducing the modification variability of the colonies.

In addition, during the DNA sequencing, we encountered ambiguous peak profile on the some electrophoregrams, which did not allow us to build a nucleotide sequence. To solve this problem, we performed nanopore sequencing of two colonies for the COI marker and one colony for the 16S marker using the portable DNA-sequencer MinION (Oford Nanopore Technologies). A total of 146,117 and 89,504 reads were obtained for COI amplicon, and 346,016 reads were revealed for 16S rDNA amplicon. Analysis of the nucleotide sequences showed that within each colony, both for the COI amplicon and for the 16S rDNA amplicon, reads were reliably divided into two clusters in a ratio of 1:4. This indicates the presence of mitochondrial DNA polymorphism within each of the clones studied. It is possible that the obtained results are related to the fact that mitochondria in *H. placoides* are inherited both maternally and paternally during sexual reproduction. The method of sequencing of the single molecules through the MinION has shown its effectiveness for detecting mitochondrial DNA polymorphism within a single colonial organism.

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