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Intraspecific genetic variation in gastropods *Liobaikalia stiedae* (Dybowski, 1875) in BaikalKovalenkova M.V.^{1*}, Sitnikova T.Ya.¹, Sherbakov D.Yu.^{1,2}¹ Limnological Institute, Siberian Branch of the Russian Academy of Sciences, Ulan-Batorskaya Str., 3, Irkutsk, 664033, Russia² Irkutsk State University, Karl Marx Str., 1, Irkutsk, 664003, Russia**ABSTRACT.** Genetic variation of Baikal endemic gastropods *Liobaikalia stiedae* was analyzed using the nucleotide sequence of the COI mitochondrial gene fragment. High intraspecific mtDNA differentiation is revealed, while local populations can be more similar to related species than to other populations.**Keywords:** sand-dwelling, Baicaliidae, gene flow**1. Introduction**

Intraspecific diversity sheds light on scales and mechanisms of the geographic and ecological isolation in speciation. The prosobranch snail family Baicaliidae includes more than 40 species. It is the largest endemic molluscan group of Lake Baikal. Some species widely distributed in the lake; the habitat of a few species is limited to a single geographical part (northern or southern) of the lake. Baicaliids are found on all types of sediments in different macro- and microhabitats. "Southern" *Liobaikalia stiedae* (Dybowski, 1875) burrows in soft substrates and lays eggs on sand grains. Thereby viscous population structure of this species can be expected. Previous study using mitochondrial DNA sequences indicated that the monotypic genus *Liobaikalia* was low genetically differentiated from related genera *Korotnewia* and *Parabaikalia* (< 1% of nucleotide substitutions at Folmer region) (Zubakov et al., 1997; Kovalenkova et al., 2015). Observed discrepancies between the species tree and current taxonomy of the group were explained by fast morphological evolution in the Baicaliidae family (Kovalenkova et al., 2015).

2. Material and methods

Ten specimens of *L. stiedae* were collected from three locations in the South Baikal basin with dredging (13-45 m). We used universal primers for amplification and sequencing fragments of the mitochondrial gene COI (Folmer et al. 1994). The best-fit model of sequence evolution was inferred based on the Bayesian information criterion with IQ-tree v. 1.6.10 (Nguyen et al., 2014). Medians of paired interspecific and interlocal genetic distances were estimated with the HKY model for COI in the "ape" package R (Paradis et al., 2004). To

estimate divergence times of *L. stiedae* haplotypes and related baicaliids, we used earlier suggested divergence rate of the "Folmer region" $1.83\% \pm 0.21/\text{Myr}$ for hydrobioid gastropods (Wilke, 2003). The phylogenetic tree was reconstructed based on unique haplotypes of the COI gene from *L. stiedae* and closely related species using BEAST v. 1.8.4 (Drummond and Rambaut, 2007). Haplotypes of *Baicalia carinata* and *Maackia herderiana* were used as outgroups. The different combinations of the speciation models were used for the analysis: Yule or birth-death process with strict clock or uncorrelated lognormal relaxed clock.

3. Results and discussion

A total of 4 unique CO haplotypes was detected. Every local population had one (Koty, Posolskaya bank) or two haplotypes (Babushkin). Median genetic distances between local populations ranged from 1.8 to 3.9% of nucleotide substitutions. Genetic distance is highest between COI haplotypes from Babushkin and Koty (> 3.5% substitutions), whereas median interspecific variation for baicaliids is ab. 5%.

The phylogenetic reconstructions have indicated speciation birth-death process with relaxed molecular clock as the most optimal model. Haplotypes of *L. stiedae* from Babushkin diverged from a common ancestor of *Liobaikalia* and closely related species about 1.5 myr. These estimates of the divergence times coincide with the beginning of the significant climatic and geomorphological changes caused reduction of inflow of biogenic elements to the lake (Kachukov et al., 1998; Goldberg et al., 2005). The other *Liobaikalia* sequences form a clade, whose age is estimated at 0.32-1.09 my. However haplotypes of *K. korotnewi* and *P. elata* collected in Maloe More clustered with sequences

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of *L. stiedae* from Koty within *Liobaikalia* clade (< 1% substitutions).

Previously it was shown that intraspecific genetic variation of the other psammobiont baicaliid snail *Baicalia carinata* exceeds interspecific distances as well as mito-nuclear discordance exists within the genus *Baicalia* (Peretolchina et al., 2007). *Baicalia carinata* had two populations boundaries of which partially coincide with big river estuaries. Relation of *Liobaikalia* intraspecific structuring and geography barriers is not apparent.

4. Conclusions

Genetic analysis of cytochrome c oxidase sequences *L. stiedae* disclosed divergent genetic groups represented by local populations. Observed differences between geographically distant populations prove viscous population structure of this species. Phylogenetic relations between different groups of *L. stiedae* and closely related species may indicate the interspecific gene flow or retention of the ancestral polymorphism. Our results highlight the potential problems of relying on a single-locus-marker for delineating baicaliids' species.

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