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Ecological zonation of the Baikal endemic piscine leeches of the genus *Baicalobdella* (Hirudinea, Piscicolidae)

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ABSTRACT. Molecular delimitation methods have revealed that the morphological homogenous species of the Baikal endemic fish leeches, *Baicalobdella torquata* (Grube, 1871), is a cryptic complex. The identified level of genetic differences allows us to assume the existence in Lake Baikal of two species within this complex, which are clearly separated geographically.

Keywords: molecular delimitation, fish leeches, *Baicalobdella*, Lake Baikal

1. Introduction

The hirudofauna of Lake Baikal consists of 31 species of parasitic and non-parasitic leeches, among which10 species, according to recent data, belong to Piscicolidae, the family of fish leeches (Kaygorodova, 2012; Kaygorodova and Pronin, 2013; Kaygorodova, 2015). Two species represent the genus *Baicalobdella* (Dogiel, 1957): *B. torquata* and *B. cottidarum*, which E.I. Lukin (1976) combined into one species, but cytogenetic studies restored them (Kaygorodova and Natyaganova, 2012; 2015).

In this study, we analysed extensive collections of the *B. torquata* samples parasitizing on amphipods to identify boundaries between the populations.

2. Materials and methods

Biological material was collected during the Baikal expeditions from 2011 to 2013 within the depth range from 0 to 285 m. Samples were collected throughout the lake and in the upper course of the Angara River. Potential hosts were caught by trawling at depths from 50 to 285; at depths from 3 to 50 m, samples were collected by divers, and in the coastal areas (from 0 to 2 m), a dip net was used or samples were collected by hand. The found *Baicalobdella* were fixed with 80% ethanol. Morphological analysis and species identification were carried out according to the initial and additional descriptions of the species (Grube, 1871; Epshtein, 1987). Bioinformatic analysis was carried out based on nucleotide sequences of the gene fragment coding mitochondrial cytochrome oxidase I (mtCOI) using computer programs from the MEGA 7 package (Kumar et al., 2016).

3. Results and discussion

Morphological analysis of the collected material allowed us to identify 65 leeches as *B. torquata*. For molecular delimitation, we amplified and decoded the mtCOI sequences of all samples. Based on the obtained data, we constructed a phylogenetic tree (Fig.).

The nucleotide sequences of amphipod ectoparasites form two well-divided phylogenetic lineages, between which a zonal fixation can be traced: branch I contains a group of leeches inhabiting the northern and central Baikal basins, and branch II includes a group of leeches collected in the central and southern basins of the lake, including the samples from the upper course of the Angara River. We have revealed that the populations are geographically separated, and the border between then runs along the Malyoe More Strait.

Further analysis of the molecular data array indicated the genetic polymorphism (p) of the northern and southern population in the range of 0.0103 and 0.0174, respectively. The genetic p-distance between the detected populations is 0.089 ± 0.010, which is very high for the population level according to the provisions of molecular taxonomy. The identified level of genetic differences allows us to assume the existence of two separate species within the morphological species *Baicalobdella torquata*. The description of new species will require additional morphological analysis.

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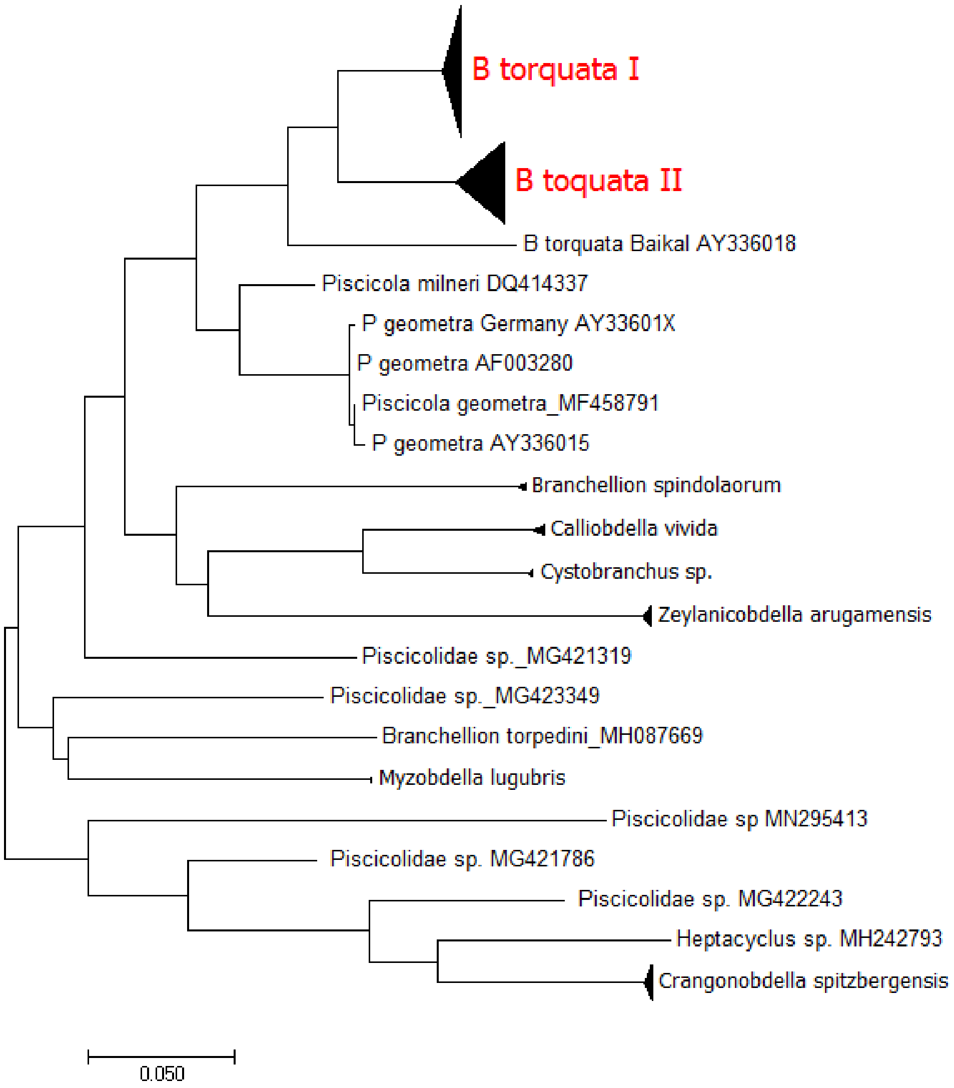

Fig. COI phylogeny visualizing the presence of two species within *B. torquata*.

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