

Phylogenetic investigation of the *Baikalodrilus* species flock (Clitellata, Naididae) endemic to Lake Baikal, Siberia

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Abstract

Background: Lake Baikal is the deepest and most voluminous lake in the world, with a unique environment (ultraoligotrophic and well-oxygenated waters at all depths), and is located in a region that is experiencing rapid climate change. It is populated with an endemic genus of oligochaetes (*Baikalodrilus*), which currently comprises 21 morphospecies. However, the validity of many species is questionable; the great similarity in their description and the lack of unequivocal diagnostic characters often lead species identification to an impasse. In order to clarify the systematics of this genus, we analysed one nuclear (ITS) and two mitochondrial (COI and 16S) markers of 33 *Baikalodrilus* specimens and four specimens of the genera *Spirosperma*, *Embolocephalus*, *Rhyacodrilus* and *Haber* as an outgroup. **Results:** Phylogenetic inferences based on parsimony, maximum likelihood and Bayesian analyses showed an early separation between two groups of species that belong to two distinct size classes and helped to re-evaluate the validity of some morphological characters as specific diagnostic characters. Three species identified prior to molecular analyses were consistent with clustering based on DNA sequences. A fourth morphospecies proved to be actually an assemblage of two distinct species. It was also possible to isolate a group of specimens that could be considered as a new species. Other clusters remained ambiguous, not only in terms of molecular clustering but also of morphological distinctness. **Significance:** These results will be useful for a taxonomical revision of the genus and a better assessment of the oligochaete species diversity in a lake environment facing contemporary climatic changes.

A unique environment facing contemporary climatic changes

Lake Baikal is the deepest (1,637 m), the most voluminous (23,000 km³) and the most ancient (25 – 30 Myr) lake in the world, with a unique environment (ultra-oligotrophic and well-oxygenated waters at all depths). It is located in a region that is experiencing rapid climate change. The lake harbours about 192 oligochaete species, of which more than 70% are endemic and species flocks are recognizable or suspected.

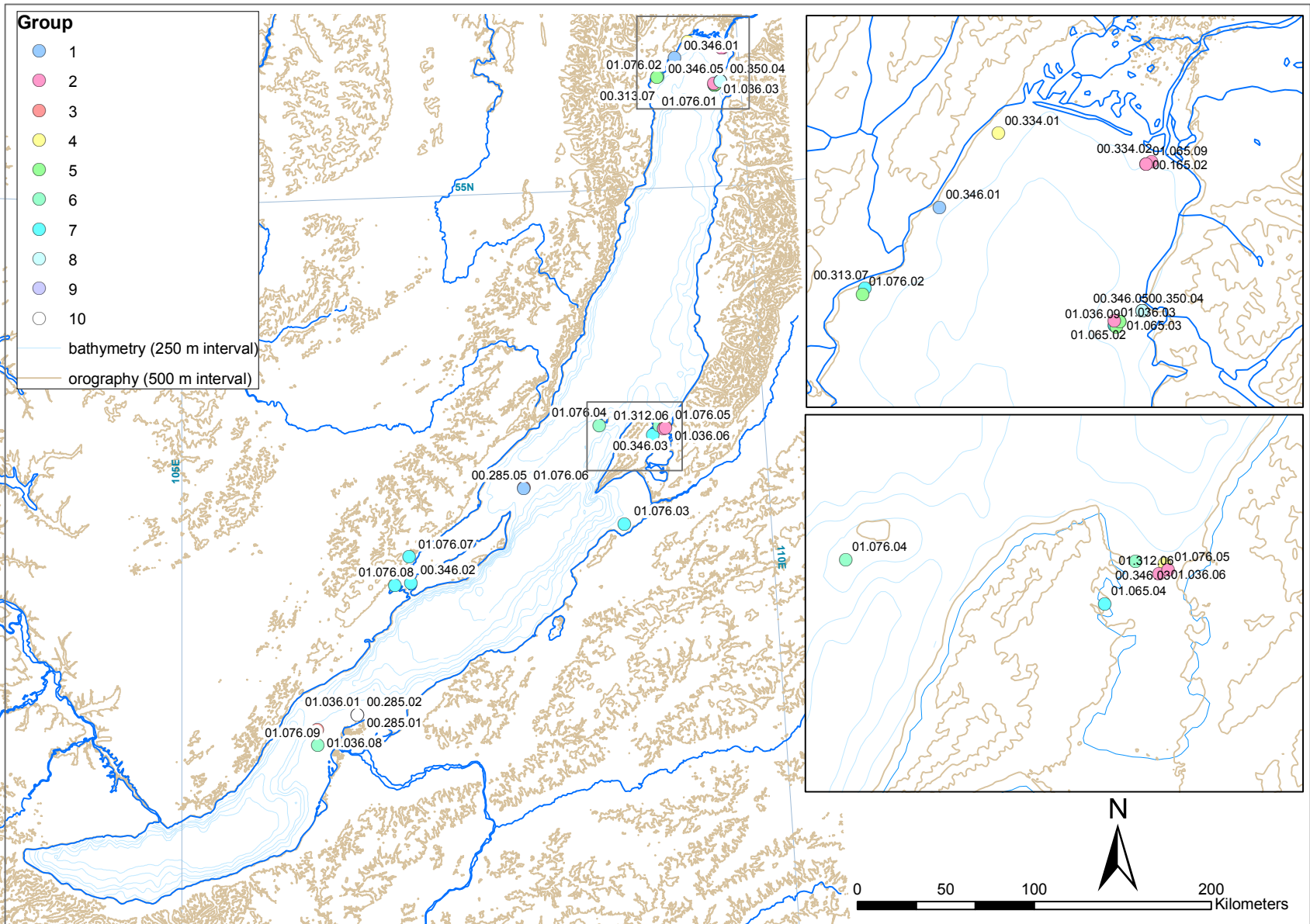


FIGURE 2: Location where individuals were sampled. Colour codes are used in order to match locations and highlighted clusters of Fig. 1

The *Baikalodrilus* species flock

Baikalodrilus is an endemic genus of oligochaetes to Lake Baikal, which currently comprises 21 morphospecies. By its monophyly, endemicity, and speciosity, the genus can be considered as a “species flock”. However, the validity of many species is questionable; the great similarity in their description and the lack of unequivocal diagnostic characters often lead species identification to an impasse.

Phylogenetic inferences

In order to clarify the systematics of this genus, phylogenetic analyses were carried out using one nuclear (ITS) and two mitochondrial (COI and 16S) markers, and complementary phylogenetic reconstructions methods (parsimony, maximum likelihood and Bayesian analyses). The three methods gave congruent results.

Species delineation

Three species identified prior to molecular analyses were consistent with clustering based on DNA sequences. A fourth morphospecies proved to be actually an assemblage of two distinct species. It was also possible to isolate a group of specimens that could be considered as a new species. Other clusters remained ambiguous, not only in terms of molecular clustering but also of morphological distinctness. Morphological characters proved to be of variable usefulness as species diagnostic characters. A taxonomical revision is badly needed but most types are seemingly lost... so that the validity of many species is queried (*species inquirenda*).

Evolutionary history

Phylogenetic inferences showed an early separation between two groups of species that belong to two distinct size classes (see *B. digitatus* and *B. werestschagini* vs. all others). The genetic variability within the flock is low, suggesting a “recent” radiation of *Baikalodrilus*, possibly contemporary with dramatic climatic changes in Baikal environment that occurred at the beginning of the Pleistocene (± 2 Mya).

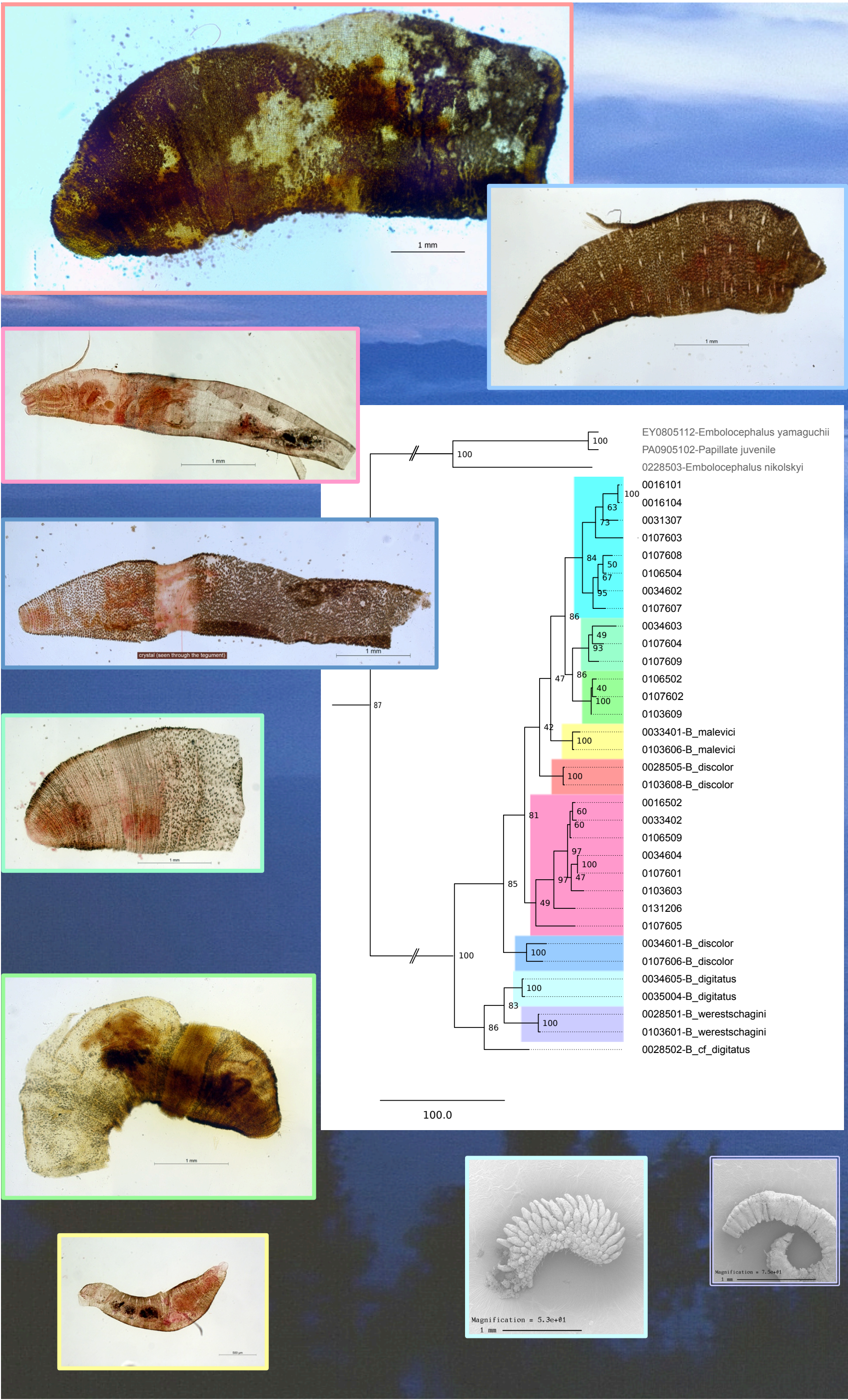


FIGURE 1: Phylogenetic tree based on the concatenation of COI, 16S and 18S-ITS1-5.8S-ITS2-28S and reconstructed using the maximum likelihood method with 1000 bootstrap pseudoreplicates.

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