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Comparative molecular-genetic analysis of some species of genus *Crepidostomum* (Digenea: Allocreadiidae) by means of rDNA sequence data

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The present study raises the question of the taxonomic state of some species of parasitic flat worms from genus *Crepidostomum* (Digenea: Allocreadiidae), collected in Europe and in the Far East. We also included in research some representatives from genus Bunodera. Moreover, several species of *Crepidostomum*, provided by prof. Takeshi Shimazu, was used. In previous molecular-genetic studies on these species, an inadequate number of taxa were used for more complete comparison and further analysis, namely: several species from the genus *Crepidostomum*: *C. farionis, C. metoecus, C. auriculatum, C. chaenogobii and C. nemacheilus*; one species from Bunodera – B. acerinae; and also the gene bank data were used. Due to the difficult definition of taxonomic status, we decided to increase the sample and added the same species of *Crepidostomum* from the Kamchatka territory. In view of the use of only one site in early studies, 28S, it was necessary to include in the analysis of one more rDNA marker - ITS. For the taxonomic revision, we applied two genetic markers of ribosomal DNA, ITS and 28S, and a morphological description of some of the species studied, with the exception of the Far Eastern forms, whose morphological description had not previously been reported. We sequenced 188 individuals from the genera Bunodera and *Crepidostomum*. According to the data obtained, we aligned all sequences with the total length of 880 bp (base pairs) and reconstructed phylogenetic tree using ML method (Maximum Likelihood), including, the genetic distances between each individual species were calculated. Phylogenetic analysis revealed interspecific differences between species of the genus *Crepidostomum* on intrageneric level. One of the species, C. auriculatum, is distinguished by genetic isolation with regard to the members of this genus, as previously mentioned by many authors. And one species, earlier identified as Bunodera acerinae, was identical with the B. luciopercae forming one common well-supported clade. Previously validity of B. luciopercae was confirmed. Thus, the increase of the number of studied individuals from different geographical points will help us to determine the pattern of their variability, to make assumptions about their genetic divergence, which will bring us, closer to

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