## Some new insights into relations within superfamily Dicrocoeliidae (Digenea) based on molecular data

## Joanna Hildebrand<sup>1</sup>, Zdzisław Laskowski<sup>2</sup>, Vasyl V. Tkach<sup>3</sup>

<sup>1</sup>Department of Parasitology, Institute of Genetics and Microbiology, University of Wrocław, Przybyszewskiego 63, 51-148 Wrocław, Poland

<sup>2</sup>W. Stefański Institute of Parasitology, Polish Academy of Sciences, Twarda 51/55, 00-818 Warszawa, Poland <sup>3</sup>Department of Biology, University of North Dakota, 10 Cornell Street, Grand Forks, North Dakota 58202, USA

Corresponding Author: Joanna Hildebrand; e-mail: joanna.hildebrand@uwr.edu.pl

All digeneans assigned to the superfamily Dicrocoeliidae Looss, 1899, parasitize bile ducts and gallbladders of birds and mammals and represent a considerable morphological variability. The Dicrocoeliidae currently accomodates three families, 47 genera, and over 400 species. It must be emphasized, however that some of those genera, such as *Lyperosomum* or *Brachylecithum* are species rich, while many others include only one or two species. Because of the exceptional variability of morphological patterns within this superfamily, its taxonomic structure has frequently been modified, new genera and new subfamilies or tribes have been proposed as well as separate species were transferred from one genus to the other. The systematic position of some dicrocoeliid species, phylogenetic interrelations, and host associations still remain insufficiently studied.

The aim of our study was to compare the compatibility of the most recent classification of Dicrocoeliidae based on morphology and some biological features with the phylogenetic relations of taxa, based on molecular data. For analysis of relations among genera we used sequences of partial 28S rDNA gene, while for relations within the genera – the sequences of partial region of *cox1* mtDNA gene. For molecular analyses were used specimens identified to species or genus level based on morphological features and the host specificity. New DNA sequences were generated for 85 dicrocoeliids representing mainly two subfamilies, i.e., Dicrocoeliinae and Leipertrematinae. Bayesian inference (BI) and Maximum Likelihood (ML) analyses of the 28S rDNA data were conducted to reveal relations between the taxa, likewise analyses of the *cox1* mtDNA data were used to explain relations within some genera.

The result of our, still preliminary but the first molecular study on a larger number of species, provided new insights into the phylogenetic relationships and classification system within Dicrocoeliidae.