**LEGENDS FOR SUPPLEMENTARY MATERIAL**

**Table S1.** Collection sites (coordinates and quadrats of central European zoological mapping grid) pertaining to Cyclocoelidae specimens examined for the analysis of prevalence and intensity of infection, and identification numbers of the examined specimens deposited in the Commenius Museum, Přerov, Czech Republic.

**Table S2.** Alignment of trimmed ITS2 locus corresponding to nt. 3-565 (563 bp) of *Circumvitellatrema**momota*JQ886068, which consisted of partial 5.8S rDNA and partial (close to full-length) ITS2 sequences.

**Table S3.** Alignment of trimmed 18S rDNA locus corresponding to nt. 142-726 (585 bp) of *Cyclocoelum mutabile* AJ287494, which consisted of partial LSU rRNA coding sequence. Note the supposedly incorrect species identification of previously published specimen AJ287494, which probably represents *Harrahium* sp. Also the host species of this specimen (*Calidris canutus*) does not match the original species identification.

**Table S4.** Alignment of trimmed CO1 locus corresponding to nt. 49-351 (303 bp) of *Philophthalmus gralli* JQ675731, which consisted of partial CO1 coding sequence.

**Table S5.** Alignment of trimmed ND1 locus corresponding to nt. 1-435 (435 bp) of *Parafasciolopsis fasciolaemorpha* EF612500, which consisted of partial ND1 coding sequence.

**Table S6.** Maximum likelihood fits of 24 nucleotide substitution models for the ITS2 locus (10 sequences with a total of 593 positions in the final dataset), with all sites used for the analyses, including the gaps. For each model, we calculated the Bayesian information criterion, Akaike information criterion (corrected) and maximum likelihood values.

**Table S7.** Maximum likelihood fits of 24 nucleotide substitution models for the 18S rDNA locus (8 sequences with a total of 587 positions in the final dataset), with all sites used for the analyses, including the gaps. For each model, we calculated the Bayesian information criterion, Akaike information criterion (corrected) and maximum likelihood values.

**Table S8.** Maximum likelihood fits of 24 nucleotide substitution models for the CO1 locus (9 sequences with a total of 306 positions in the final dataset), with all sites used for the analyses, including the gaps. For each model, we calculated the Bayesian information critetion, Akaike information criterion (corrected) and maximum likelihood values.

**Table S9.** Maximum likelihood fits of 24 nucleotide substitution models for the ND1 locus (11 sequences with a total of 435 positions in the final dataset), with all sites used for the analyses, including the gaps. For each model, we calculated the Bayesian information critetion, Akaike information criterion (corrected) and maximum likelihood values.

**Figure S1.** Phylogenetic tree (50% majority-rule consensus) based on Bayesian inference of Cyclocoelidae ITS2 locus. Color of branches indicates Bayesian posterior probabilities.

**Figure S2.** Phylogenetic tree (50% majority-rule consensus) based on Bayesian inference of Cyclocoelidae 18S rDNA locus. Color of branches indicates Bayesian posterior probabilities.

**Figure S3.** Phylogenetic tree (50% majority-rule consensus) based on Bayesian inference of Cyclocoelidae CO1 locus. Color of branches indicates Bayesian posterior probabilities.

**Figure S4.** Phylogenetic tree (50% majority-rule consensus) based on Bayesian inference of Cyclocoelidae ND1 locus. Color of branches indicates Bayesian posterior probabilities.