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SUPPLEMENTARY MATERIALS

**Molecular phylogenetics provides unequivocal support for reclassifying *Cathaemasia hians*
longivitellata and *C. h. hians* (Trematoda: Cathaemasiidae) as two valid species with different host
preferences**

Petr Heneberg^{1,*}, Jiljí Sitko²

Affiliations:

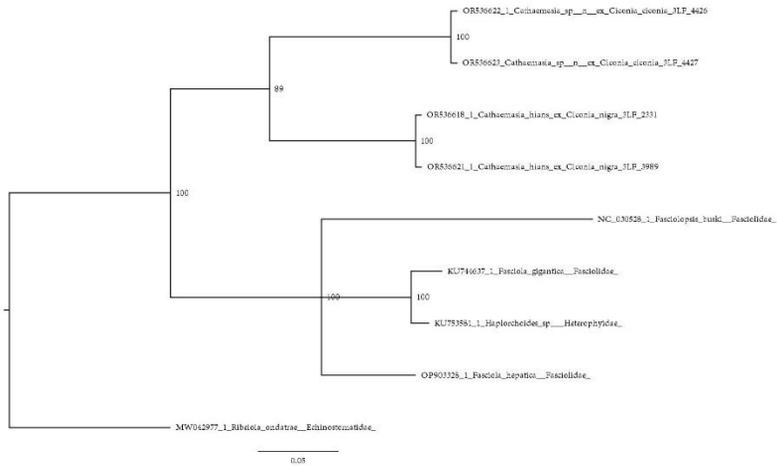
¹ Charles University, Third Faculty of Medicine, Prague, Czechia.

² Comenius Museum, Moravian Ornithological Station, Přerov, Czechia.

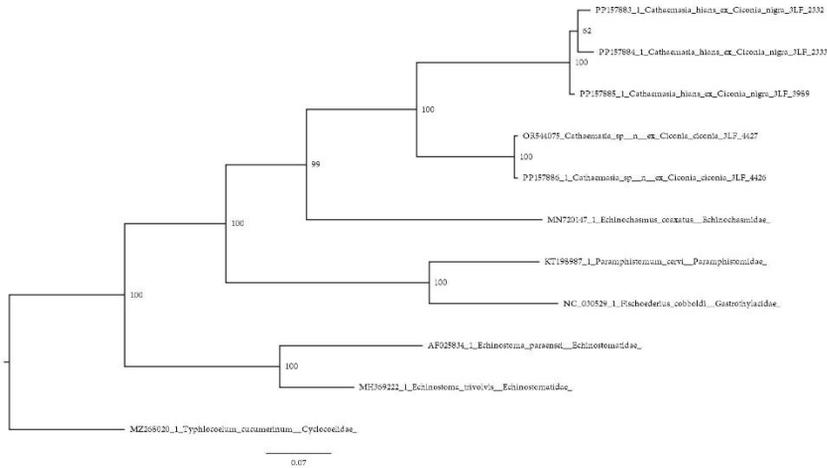
*Correspondence to: petr.heneberg@lf3.cuni.cz.

22 **Supplementary figure legends**

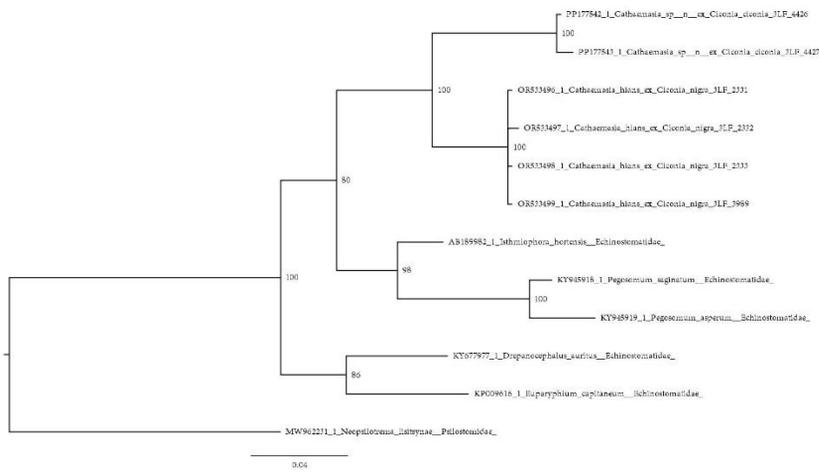
23 **Fig. S1.** Bayesian analyses of the sequences of the mitochondrial and nuclear DNA loci of *Cathaemasia*
24 spp. **(a)** CO1, **(b)** ND1, **(c)** ITS2, and **(d)** 18S rDNA. The bars indicate the number of substitutions per
25 nucleotide. The numbers above internodes indicate the percentage of trees in which the associated taxa
26 clustered together.



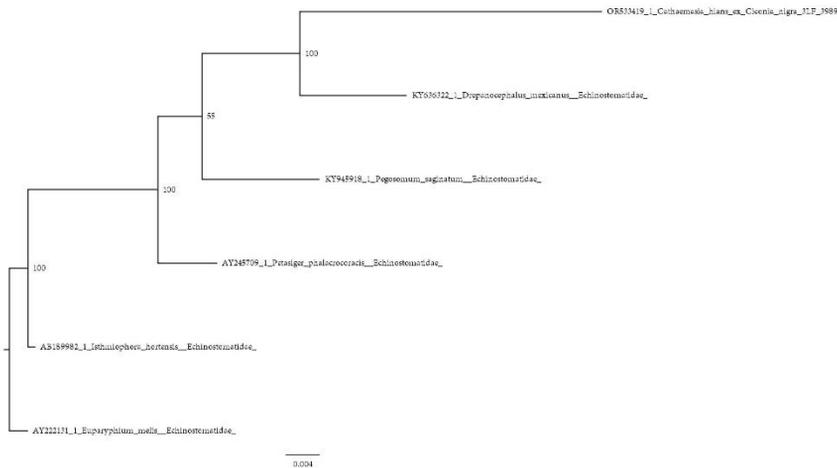
A – CO1



B – ND1



C – ITS2



D – 18S