**Supp. file 1.** Phylogenetic trees. Outgroup taxa were pruned off. Specimens identified by two-digit locality code in bold, four digit individual DNA code, and orographic unit (see Table 1) or GenBank accession number; posterior probabilities or bootstrap support values at nodes; scale bars in substitutions per site; the sequence of *H. tellinii* (Pollonera, 1898) was generated by Ponder *et al*. (2008). <https://doi.org/10.5852/ejt.2021.775.1555.5329>



**Figure S1.** Phylogenetic tree from Bayesian analysis in MrBayes based on 16S rRNA. Bold capitals denote haplotypes of *H. kissdalmae* from statistical parsimony network in Figure 9.



**Figure S2.** Phylogenetic tree from maximum likelihood (ML) analysis in W-IQ-TREE based on 16S rRNA.



**Figure S3.** Phylogenetic tree from Bayesian analysis in MrBayes based on ITS2.

****

**Figure S4.** Phylogenetic tree from maximum likelihood (ML) analysis in W-IQ-TREE based on ITS2.



**Figure S5.** Phylogenetic tree from maximum likelihood (ML) analysis in W-IQ-TREE based on COI, 16S rRNA and ITS2.



**Figure S6.** Phylogenetic tree from Bayesian analysis in MrBayes based on COI.



**Figure S7.** Phylogenetic tree from maximum likelihood (ML) analysis in W-IQ-TREE based on COI.

Reference

Ponder W.F., Wilke T., Zhang W.-H., Golding R.E., Fukuda H. & Mason R.A.B. 2008. *Edgbastonia alanwillsi* n. gen. & n. sp. (Tateinae: Hydrobiidae *s.l.*: Rissooidea: Caenogastropoda); a snail from an artesian spring group in western Queensland, Australia, convergent with some Asian Amnicolidae. *Molluscan Research* 28: 89-106.