

**Supplementary material**

**Molecular and morphological systematics of *Bursatella leachii* de Blainville, 1817 and *Stylocheilus striatus* Quoy & Gaimard, 1832 reveal cryptic diversity in pantropically distributed taxa (Mollusca : Gastropoda : Heterobranchia)**

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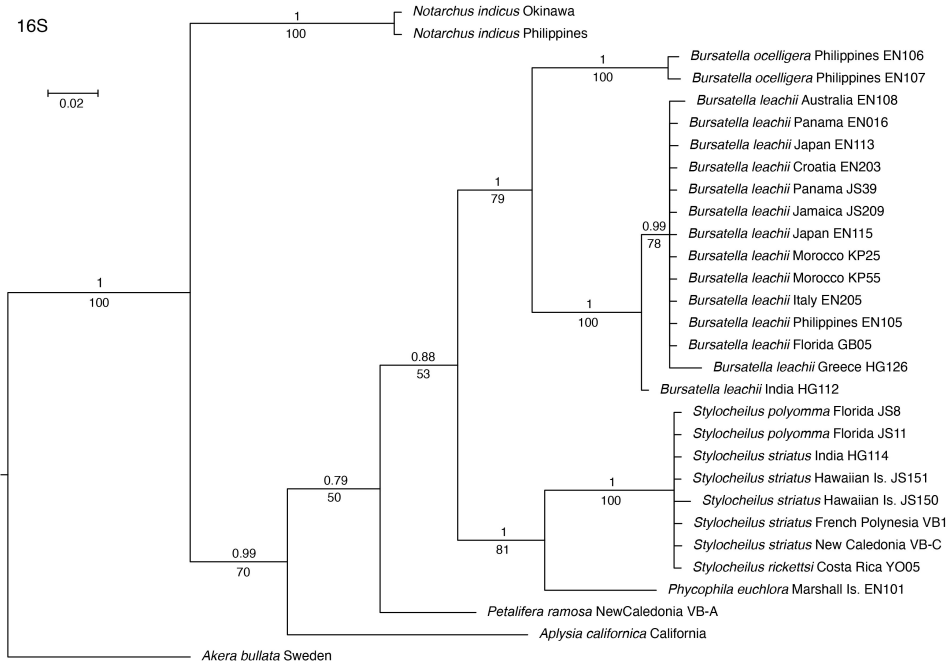
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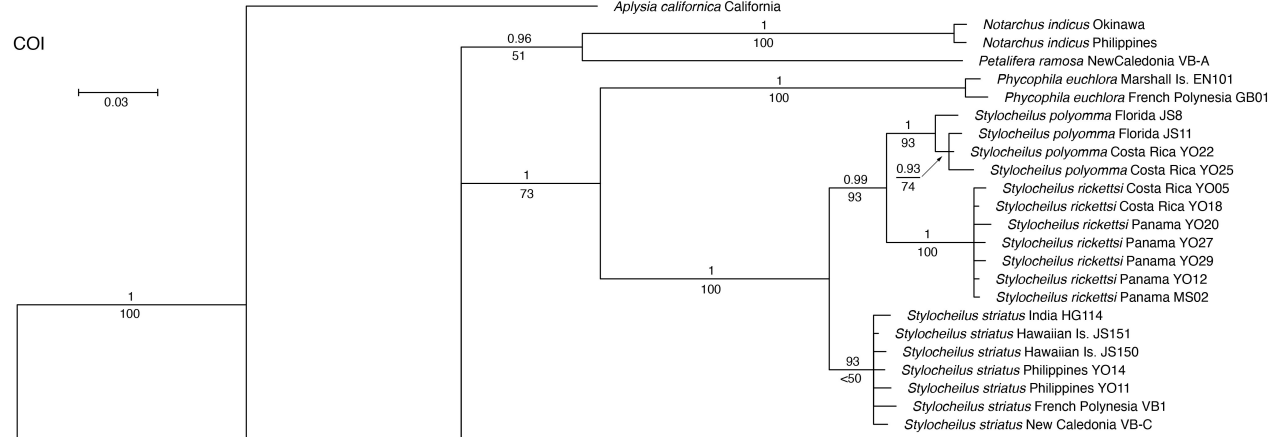
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**Fig. S1.** Individual Bayesian consensus trees of specimens of *Bursatella*, *Stylocheilus*, *Phycophila*, and the outgroup taxa for each gene analysed individually (COI, right; 16S, top left; H3, bottom left), including posterior probabilities (above nodes) and bootstrap support values from the maximum-likelihood analysis (below nodes). (See following page.)

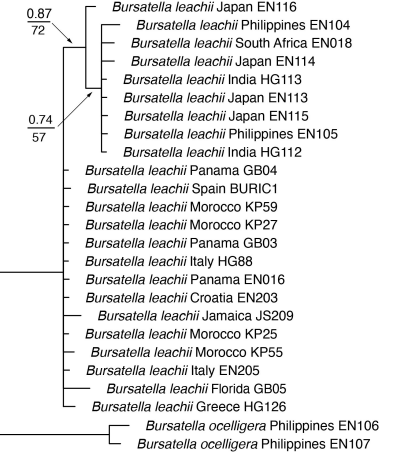
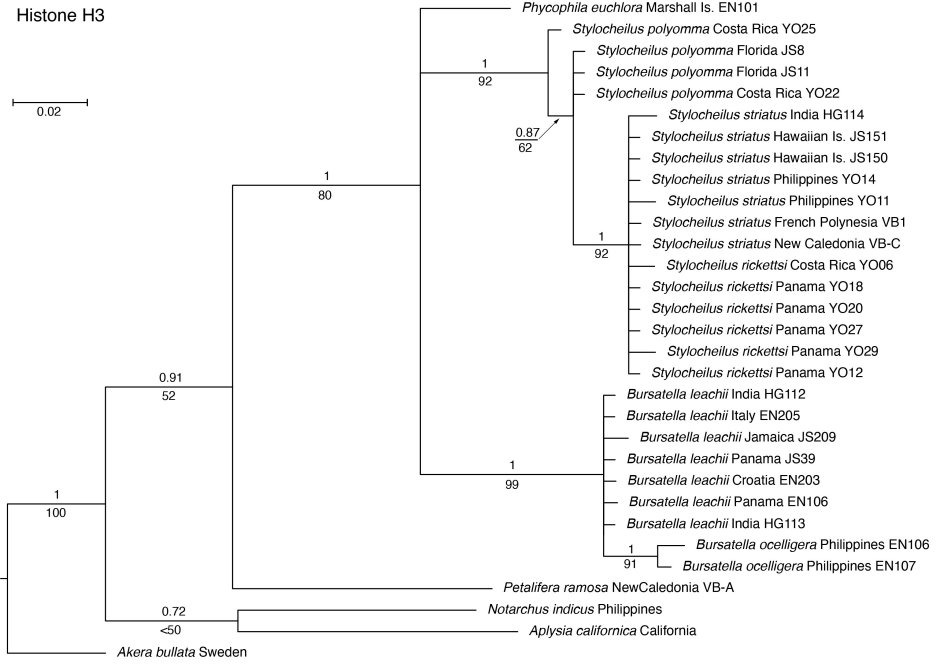
16S



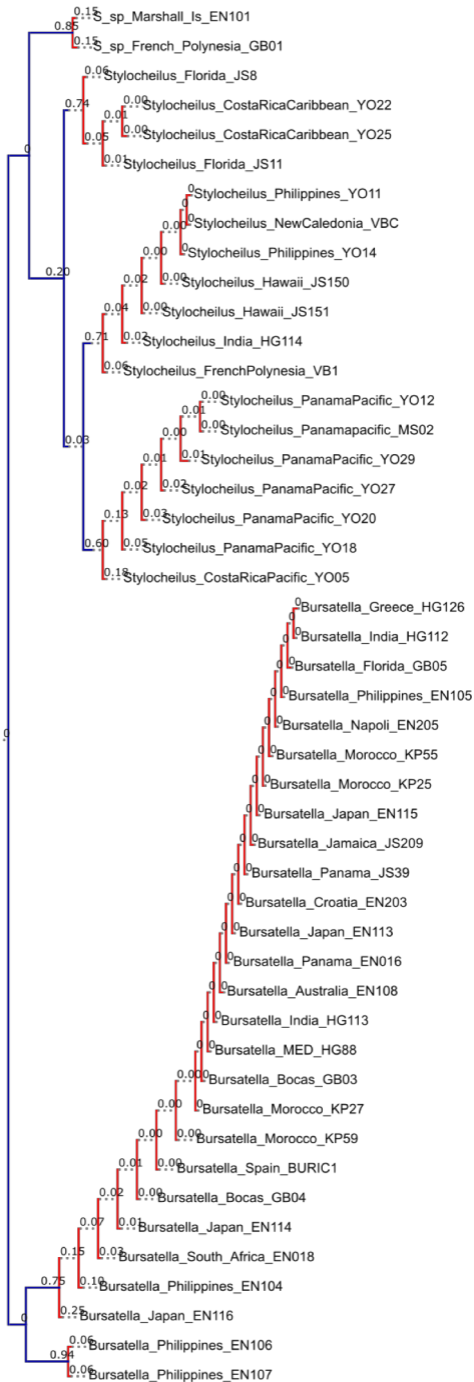
COI



Histone H3



**Fig. S2.** Species delimitation tree generated with the Bayesian Poisson tree processes (bPTP), using the results of the phylogenetic analysis of the concatenated alignment. Branch colours indicate among-species (blue) and within-species (red) branching events. Likelihood scores are reported above the nodes. (See following page.)

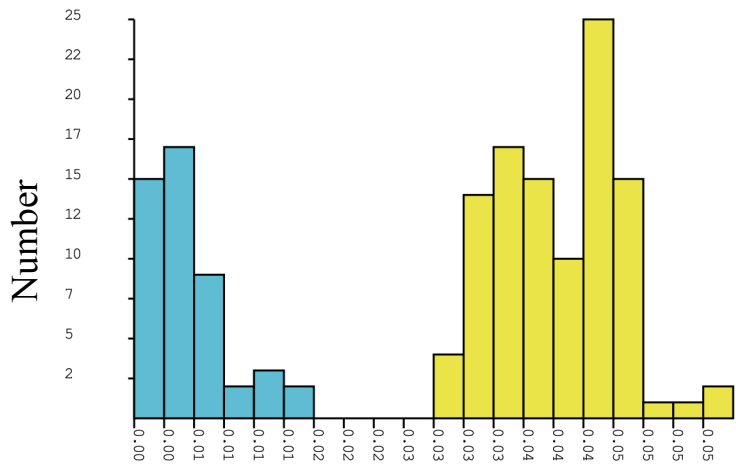


**Fig. S3.** Frequency histogram of intraspecific (blue) and interspecific (yellow) pair-wise genetic distances calculated with Automatic Barcode Gap Discovery (ABGD) for cytochrome *c* oxidase I (COI) sequences of *Stylocheilus* (left), and *Bursatella* (right) specimens, using the Jukes–Cantor (top) and the Kimura (bottom) models. The barcoding gap between the highest intraspecific distance values and lowest interspecific distance values is highlighted by a black dotted line. (See following page.)

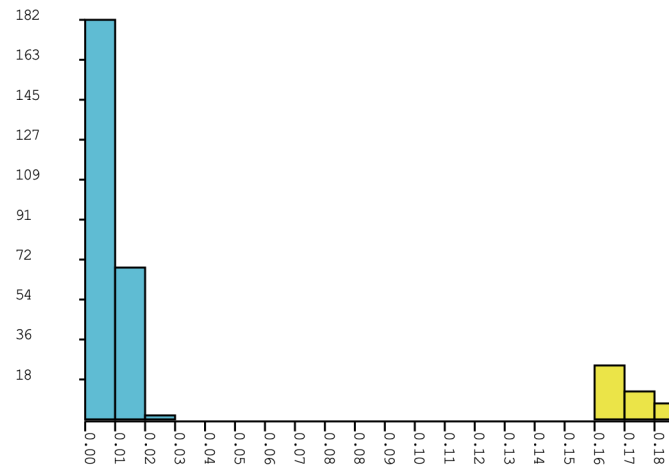
*Stylocheilus*

*Bursatella*

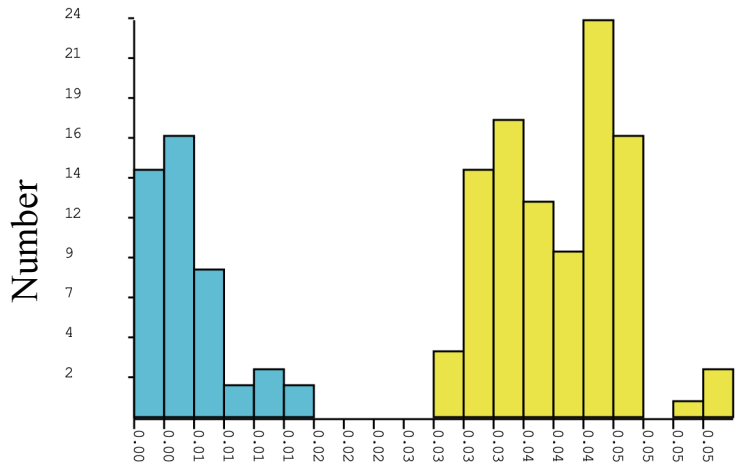
JC69



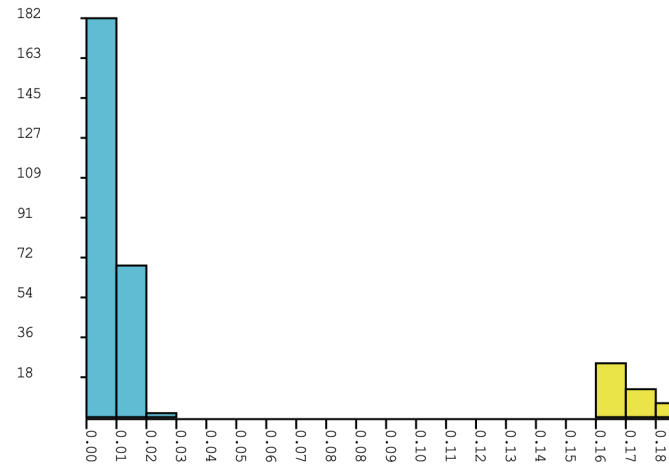
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K80



K80



Distance value

Distance value