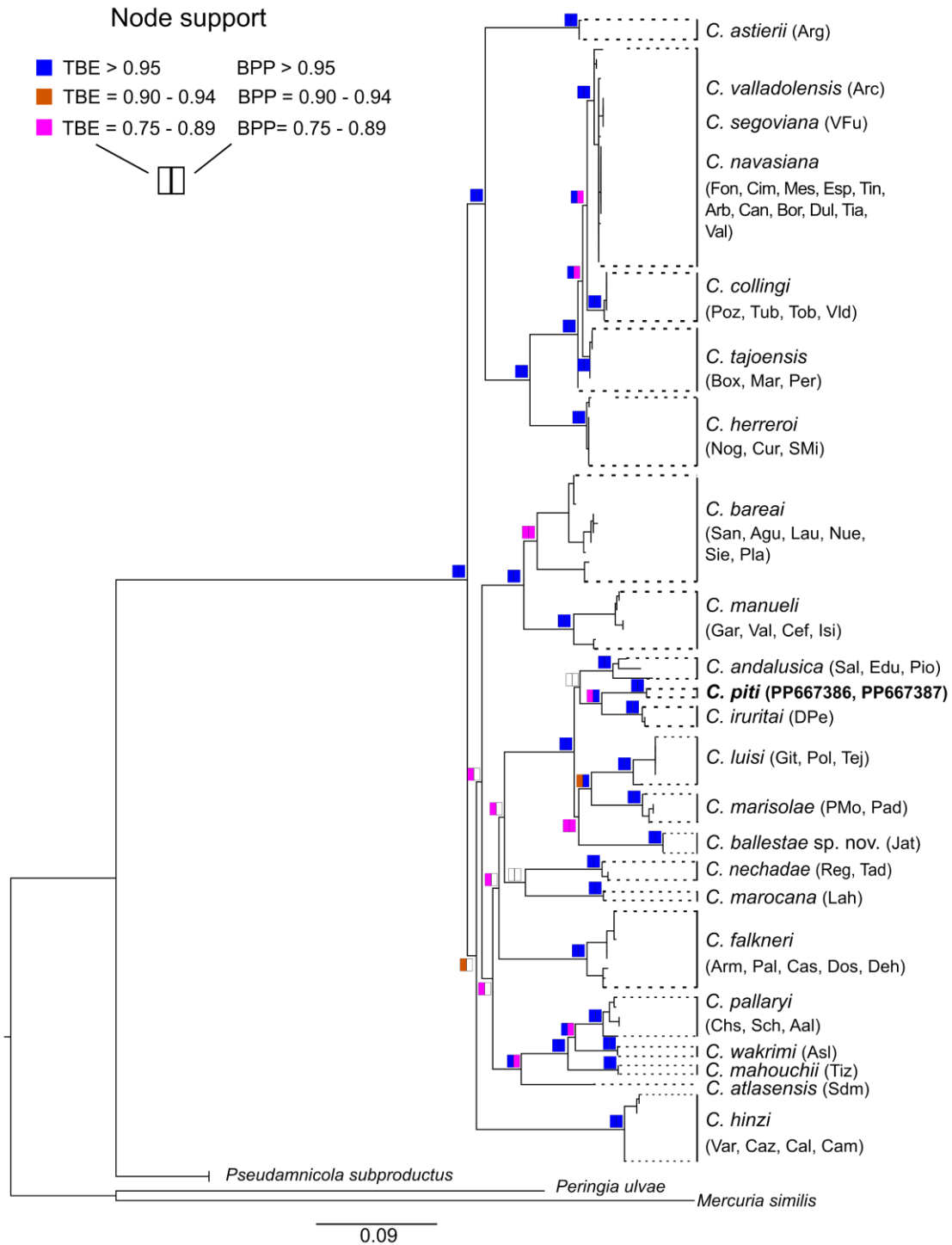


**Figure S1.** Phylogenetic relationships among *Corrosella* species inferred using maximum likelihood based on the concatenated dataset of three gene fragments. Transfer bootstrap expectation (TBE) and Felsenstein bootstrap (FB) support values for key branches are represented by coloured squares. Scale bar below the topology indicates substitutions per site.



**Figure S2.** Phylogenetic relationships among *Corrosella* species inferred using maximum likelihood and Bayesian inference based on the COI dataset, including *C. piti*. Transfer bootstrap expectation (TBE) and Bayesian posterior probability (BPP) support values for nodes above the species level are indicated by coloured squares. The scale bar below the topology represents substitutions per site.