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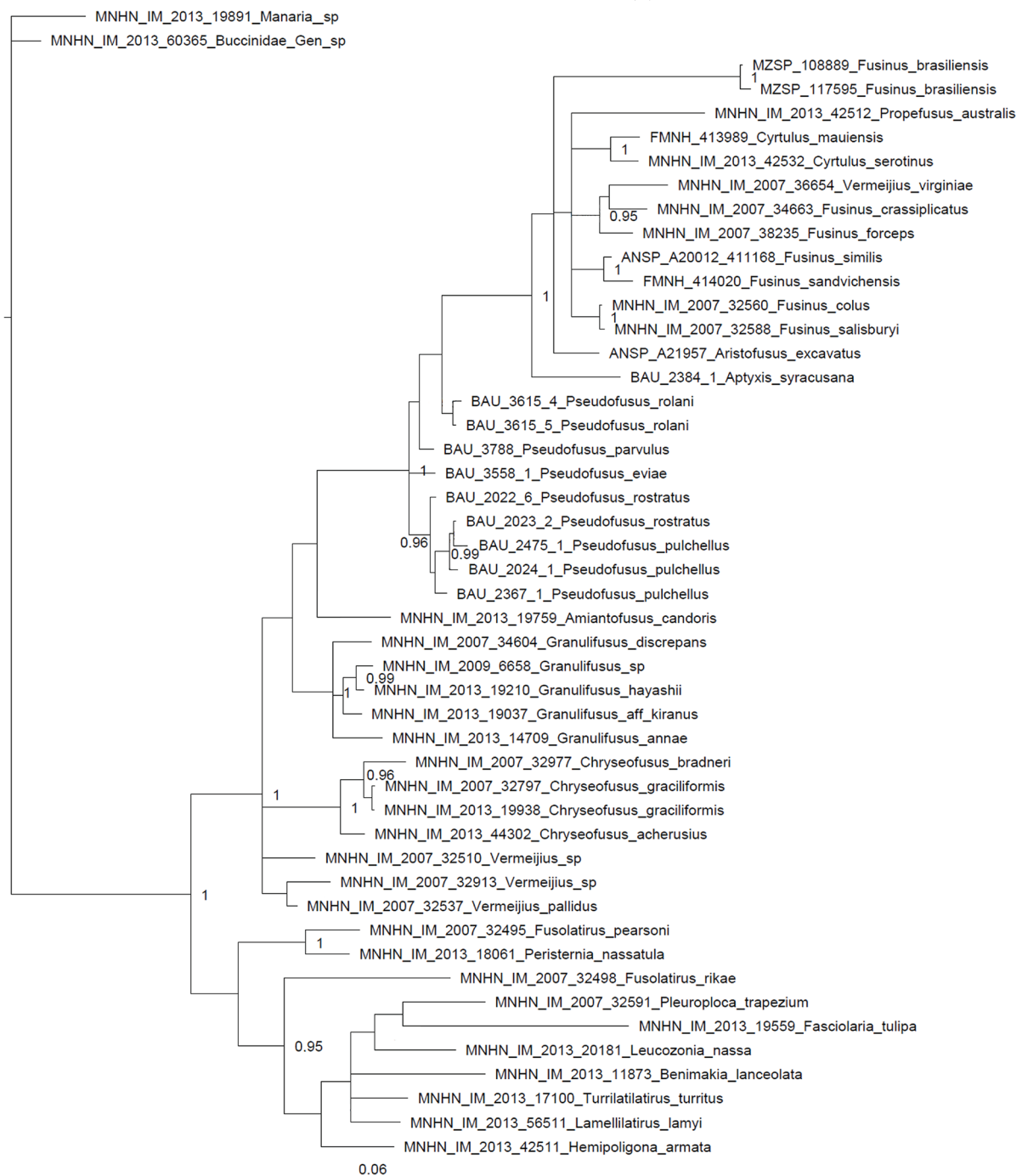
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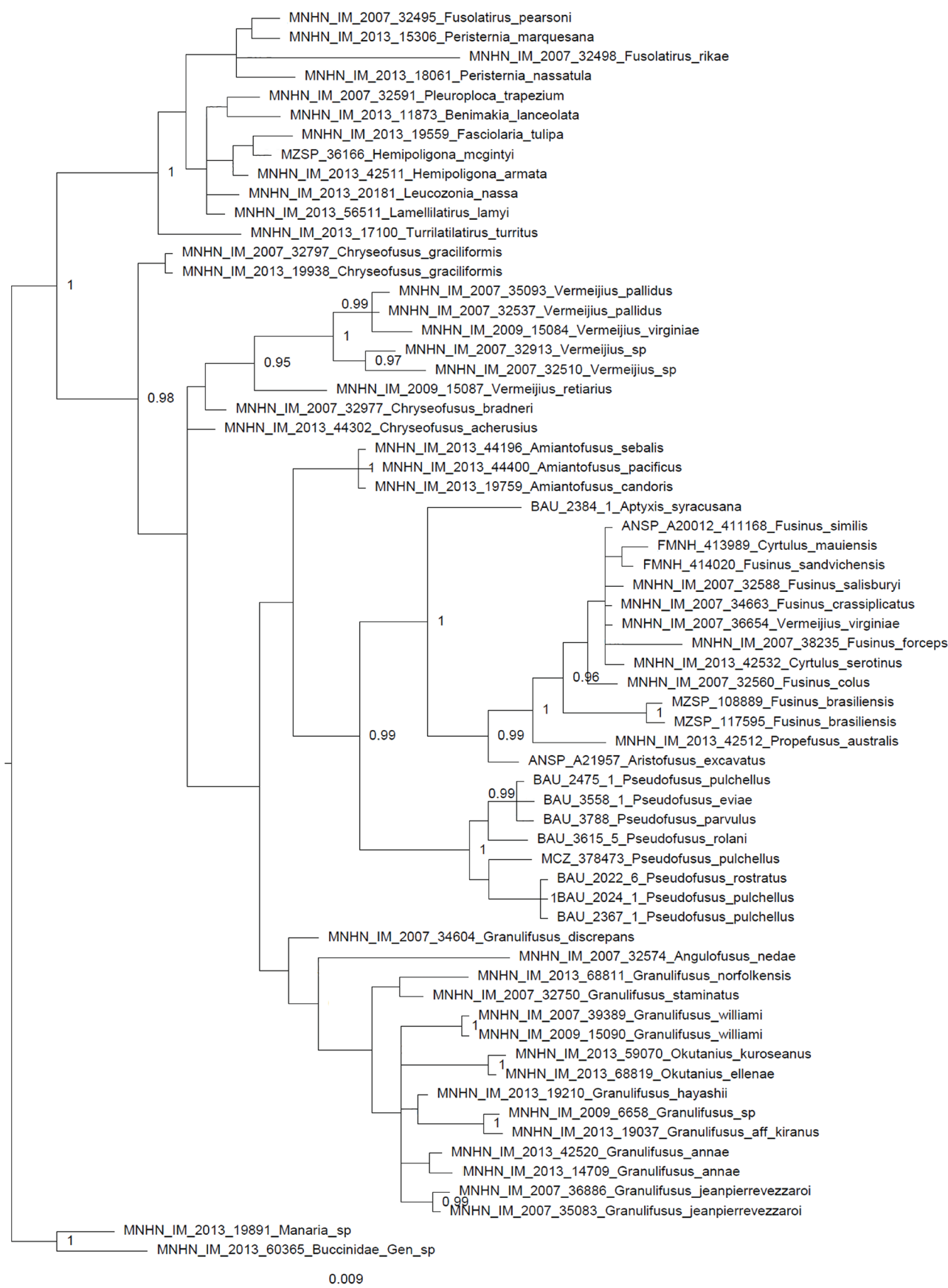
## A molecular framework for the systematics of the Mediterranean spindle-shells (Gastropoda, Neogastropoda, Fasciolaridae, Fusininae)

**Giulia FASSIO, Paolo RUSSO, Giuseppe BONOMOLO, Alexander E. FEDOSOV, Maria Vittoria MODICA, Elisa NOCELLA and Marco OLIVERIO**

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**Fig. S1:** Phylogenetic relationships among fasciolariaids as illustrated by the **Bayesian** majority consensus tree of the **16S** alignment. The tree is rooted on two buccinoideans (the Eosiphonidae *Manaria* sp., voucher MNHN-IM-013-19891, and an undetermined Buccinidae, voucher MNHN-IM-013-60365). Support values are given as posterior probabilities for the Bayesian analysis based on 107 generations, 25% burnin (only values  $\geq 0.95$  are shown).

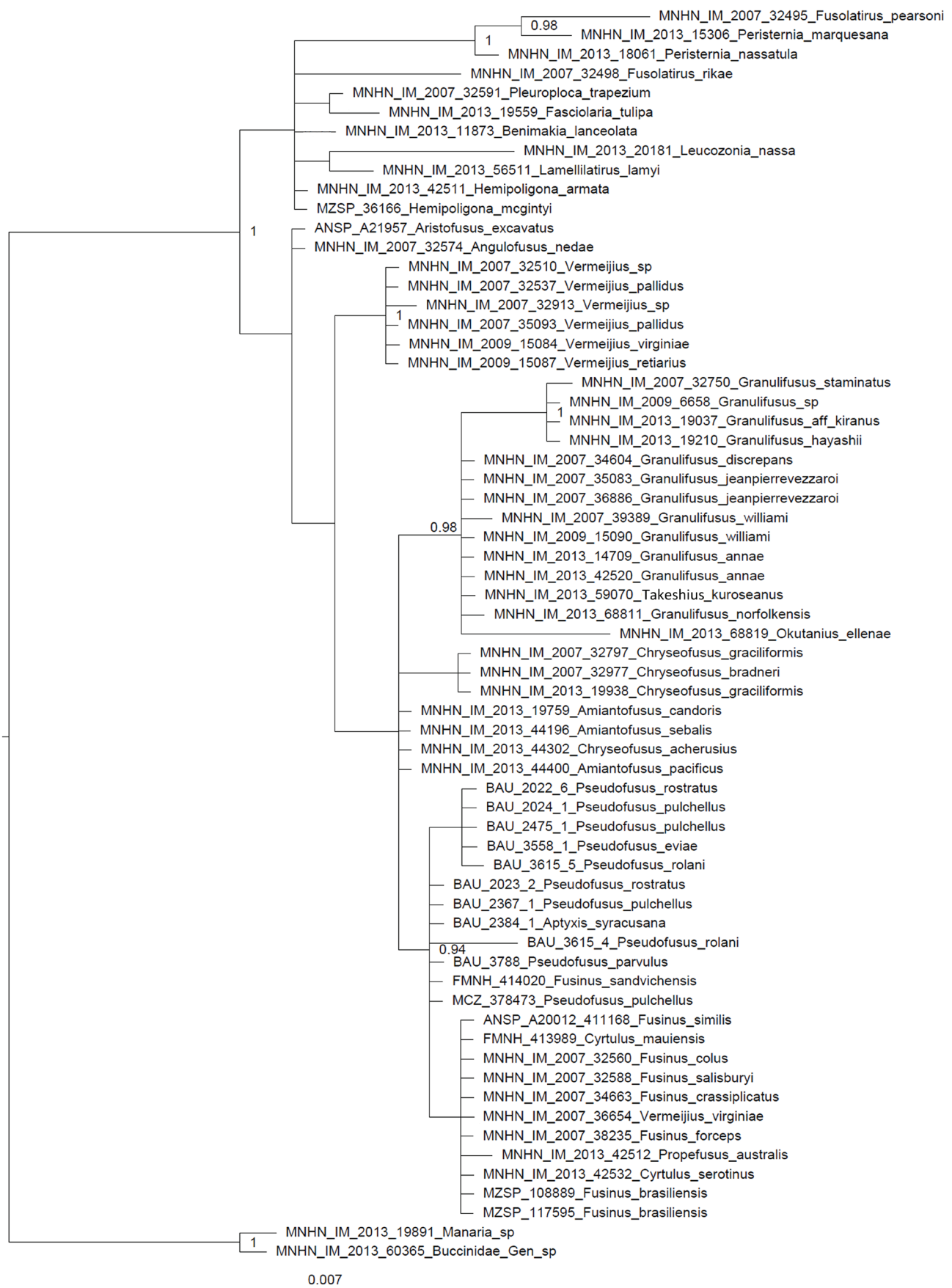


**Fig. S2:** Phylogenetic relationships among fascioliids as illustrated by the **Bayesian** majority consensus tree of the **28S** alignment. The tree is rooted on two buccinoideans (the Eosiphonidae *Manaria* sp., voucher MNHN-IM-2013-19891, and an undetermined Buccinidae, voucher MNHN-IM-2013-60365). Support values are given as posterior probabilities for the Bayesian analysis based on 107 generations, 25% burnin (only values  $\geq 0.95$  are shown).

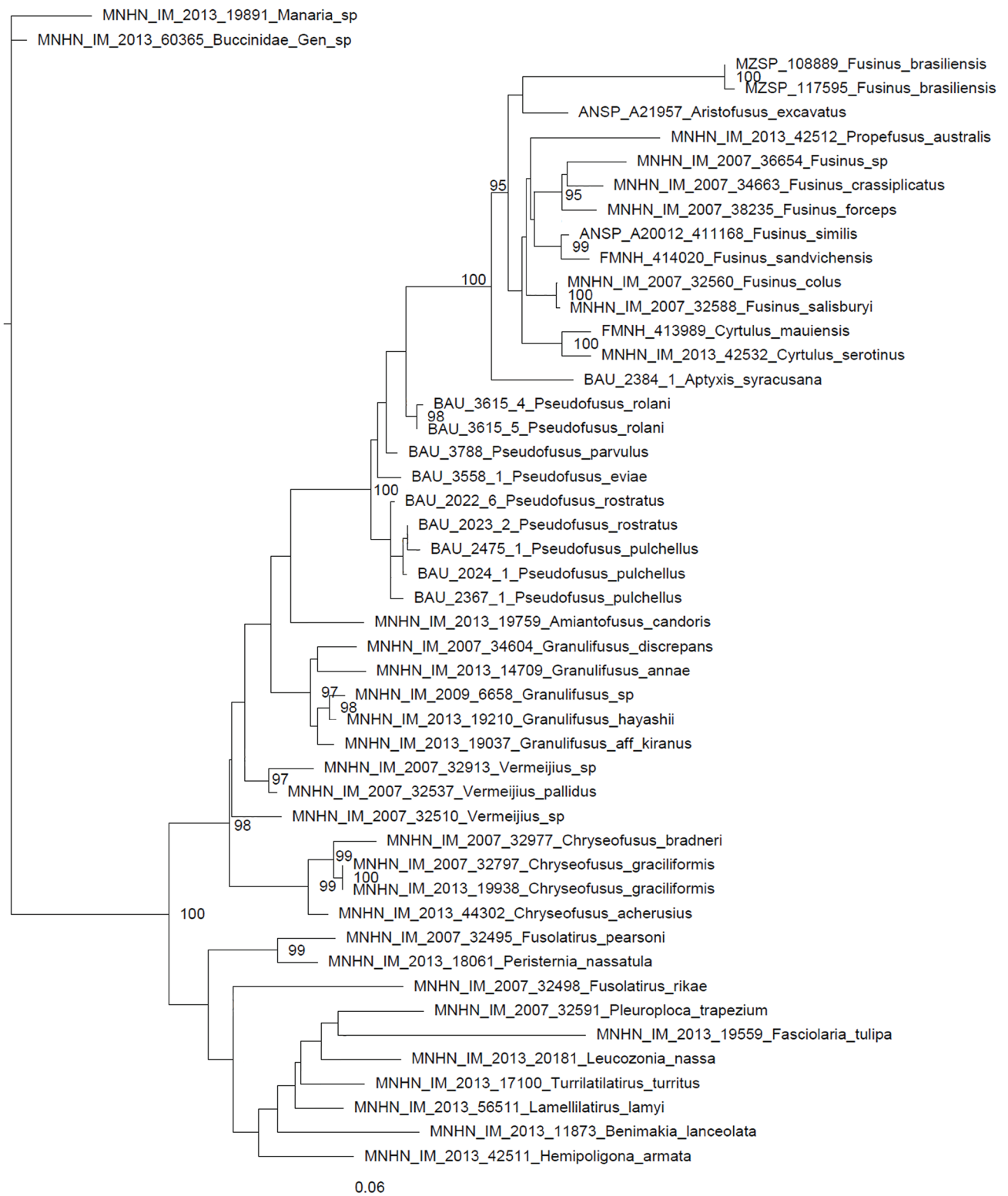


**Fig. S3:** Phylogenetic relationships among fascioliariids as illustrated by the **Bayesian** majority consensus tree of the **COI** alignment. The tree is rooted on two buccinoideans (the Eosiphonidae *Manaria* sp., voucher MNHN-IM-2013-19891, and an undetermined Buccinidae, voucher MNHN-IM-2013-60365). Support values are given as posterior probabilities for the Bayesian analysis based on 107 generations, 25% burnin (only values  $\geq 0.95$  are shown).

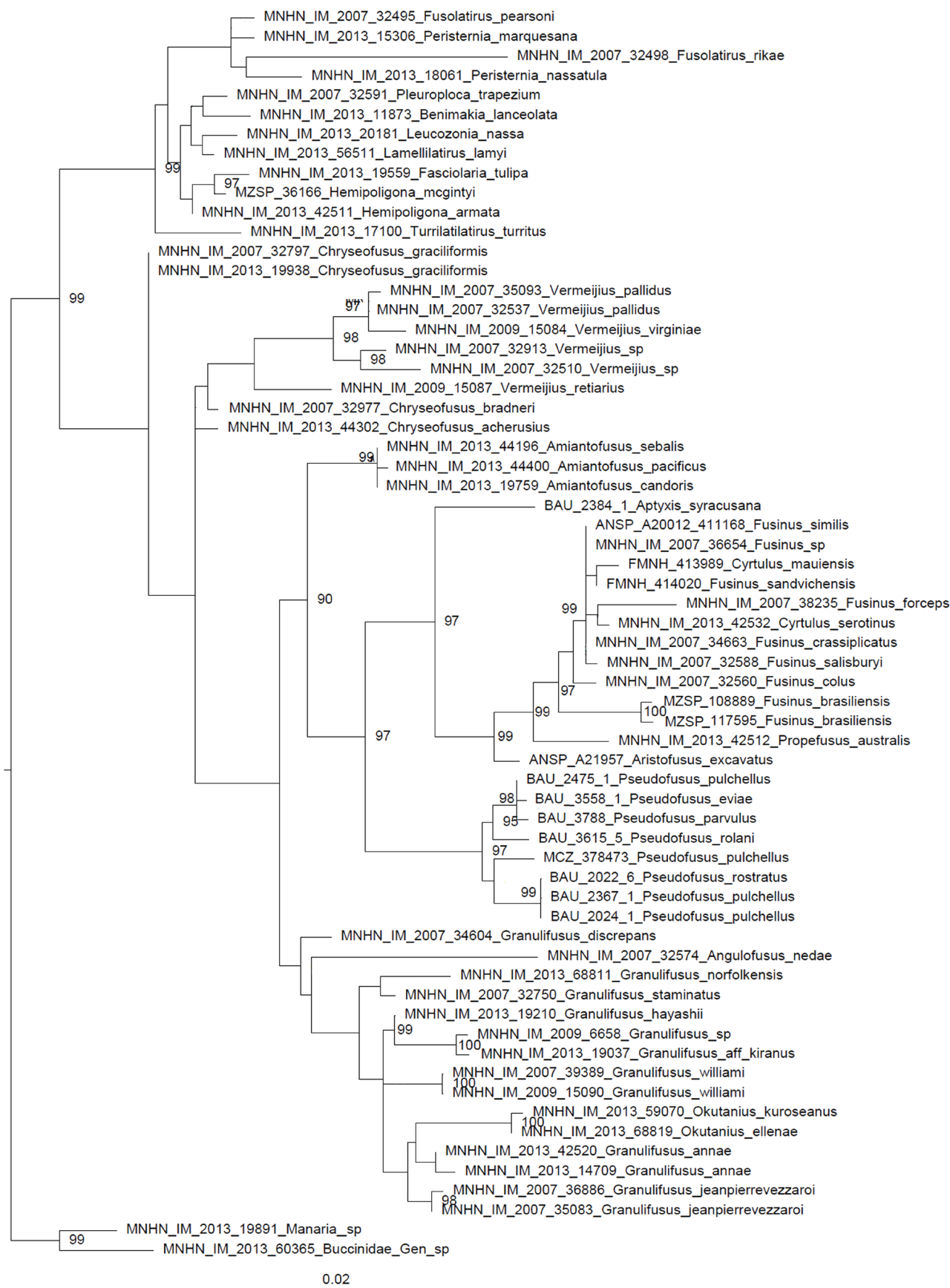




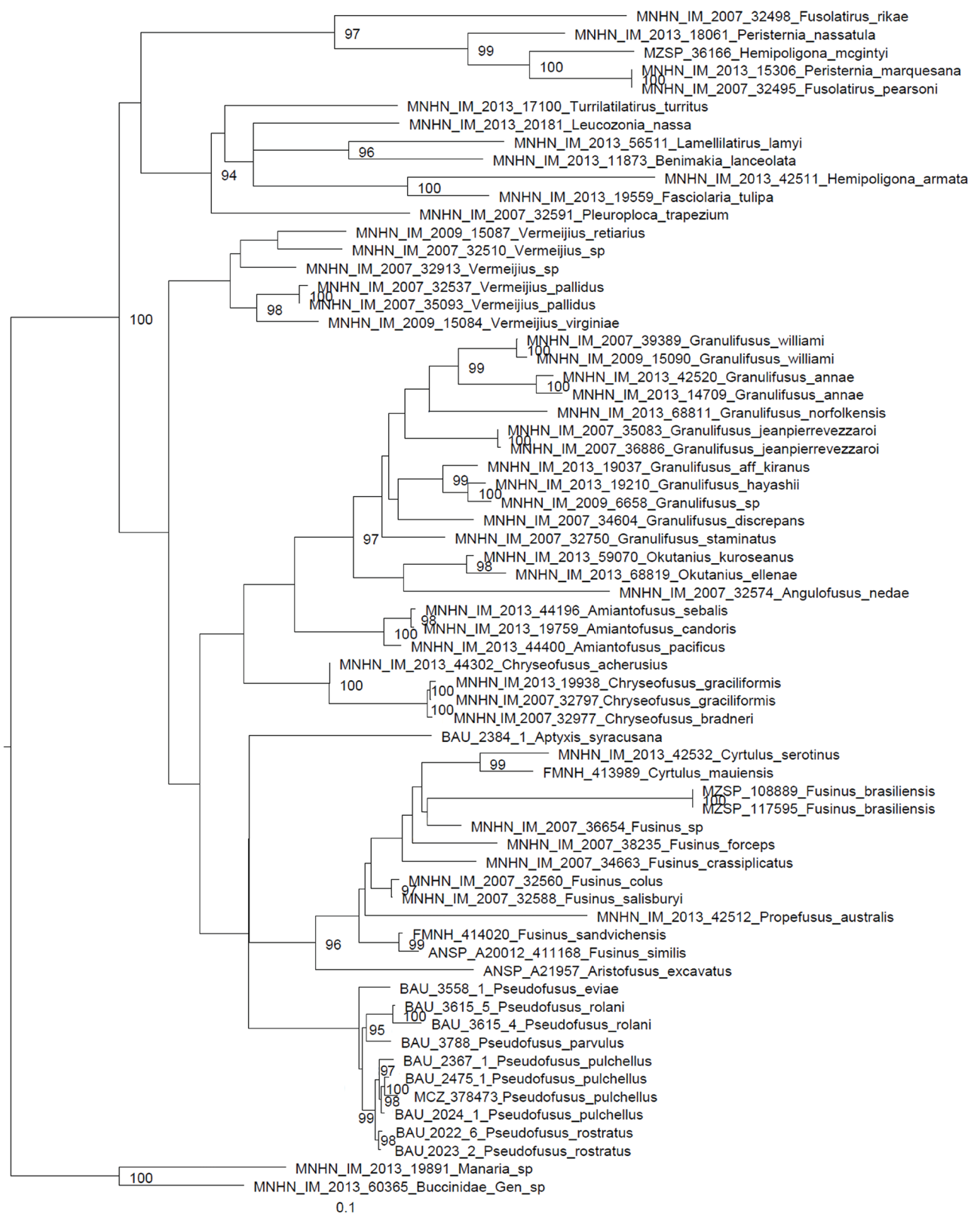
**Fig. S4:** Phylogenetic relationships among fascioliariids as illustrated by the Bayesian majority consensus tree of the H3 alignment. The tree is rooted on two buccinoideans (the Eosiphonidae *Manaria* sp., voucher MNHN-IM-2013-19891, and an undetermined Buccinidae, voucher MNHN-IM-2013-60365). Support values are given as posterior probabilities for the Bayesian analysis based on 107 generations, 25% burnin (only values  $\geq 0.95$  are shown).



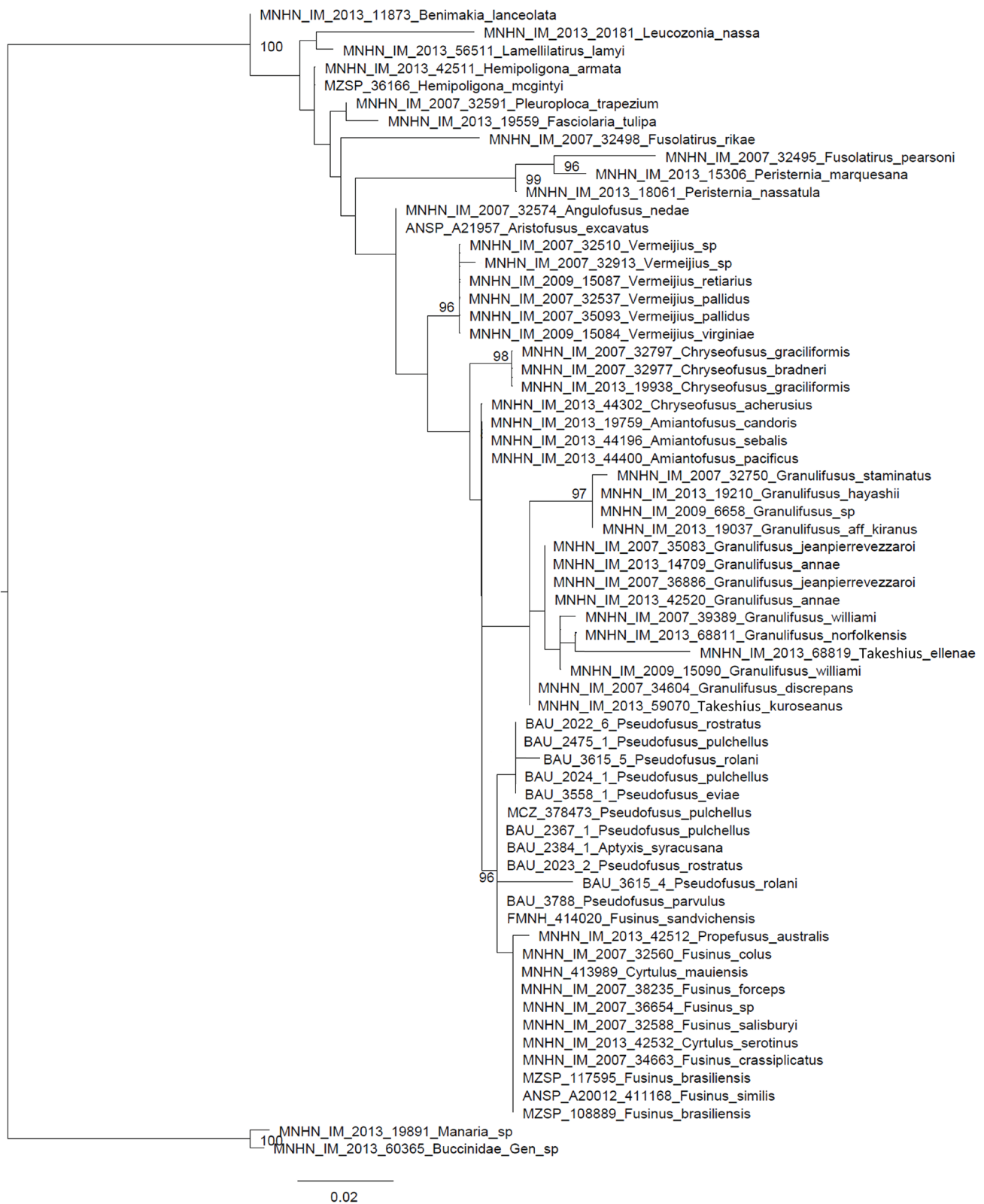
**Fig. S5:** Phylogenetic relationships among conoideans as illustrated by the **ML** majority consensus tree of the **16S** alignment. The tree is rooted on two buccinoideans (the Eosiphonidae *Manaria* sp., voucher MNHN-IM-2013-19891, and an undetermined Buccinidae, voucher MNHN-IM-2013-60365). Support values are given as ultrafast bootstrap support after ML analysis of 1000 pseudoreplicates (only values  $\geq 95\%$  are shown).



**Fig. S6:** Phylogenetic relationships among conoideans as illustrated by the ML majority consensus tree of the 28S alignment. The tree is rooted on two buccinoideans (the Eosiphonidae *Manaria* sp., voucher MNHN-IM-2013-19891, and an undetermined Buccinidae, voucher MNHN-IM-2013-60365). Support values are given as ultrafast bootstrap support after ML analysis of 1000 pseudoreplicates (only values  $\geq 95\%$  are shown).



**Fig. S7:** Phylogenetic relationships among conoideans as illustrated by the ML majority consensus tree of the COI alignment. The tree is rooted on two buccinoideans (the Eosiphonidae *Manaria* sp., voucher MNHN-IM-2013-19891, and an undetermined Buccinidae, voucher MNHN-IM-2013-60365). Support values are given as ultrafast bootstrap support after ML analysis of 1000 pseudoreplicates (only values  $\geq 95\%$  are shown).



**Fig. S8:** Phylogenetic relationships among conoideans as illustrated by the ML majority consensus tree of the H3 alignment. The tree is rooted on two buccinoideans (the Eosiphonidae *Manaria* sp., voucher MNHN-IM-2013-19891, and an undetermined Buccinidae, voucher MNHN-IM-2013-60365). Support values are given as ultrafast bootstrap support after ML analysis of 1000 pseudoreplicates (only values  $\geq 95\%$  are shown).