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

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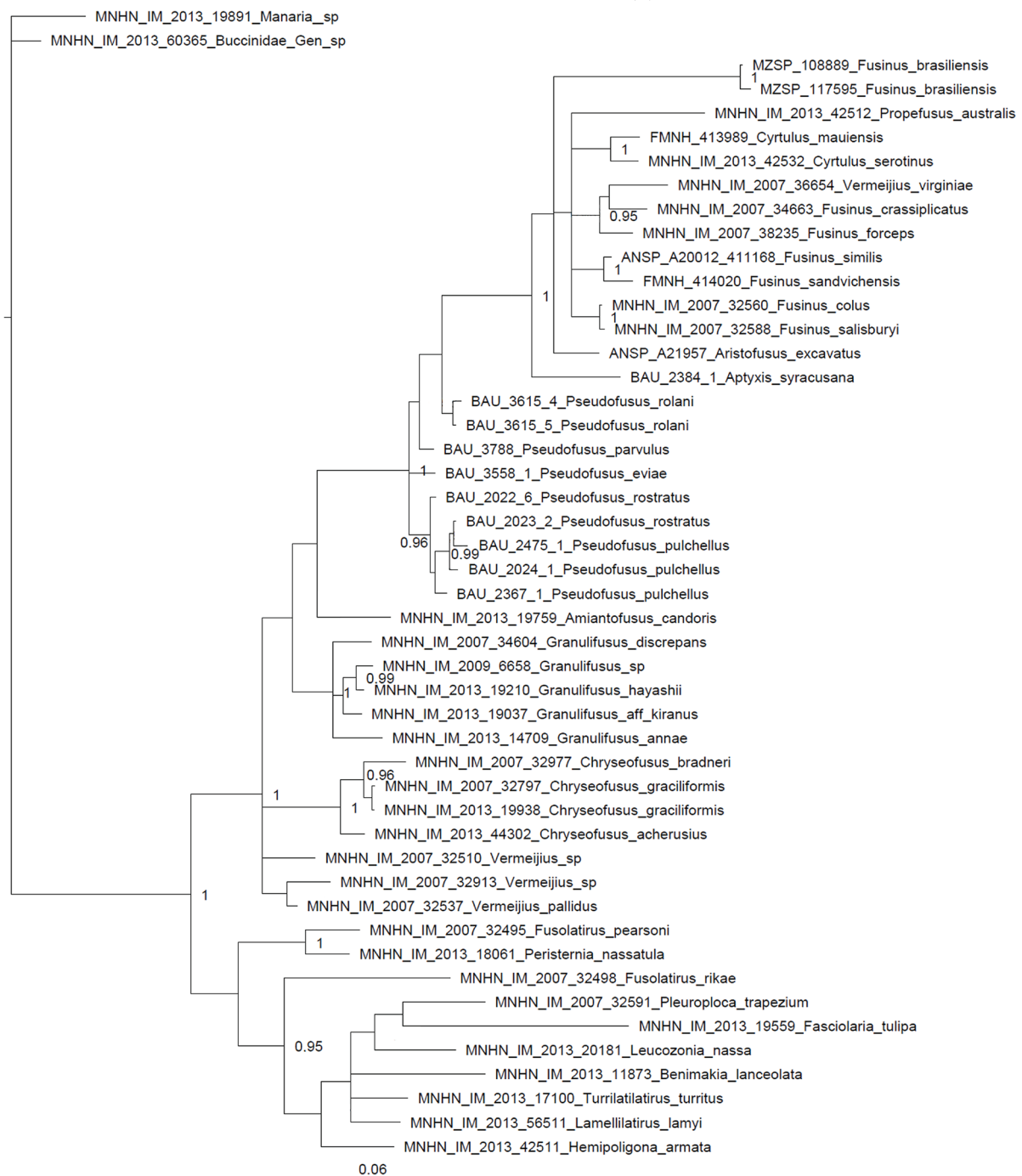


Fig. S1: Phylogenetic relationships among fasciolariaids as illustrated by the **Bayesian** majority consensus tree of the **16S** alignment. The tree is rooted on two buccinoideans (the Eosiphonidae *Manaria* sp., voucher MNHN-IM-013-19891, and an undetermined Buccinidae, voucher MNHN-IM-013-60365).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

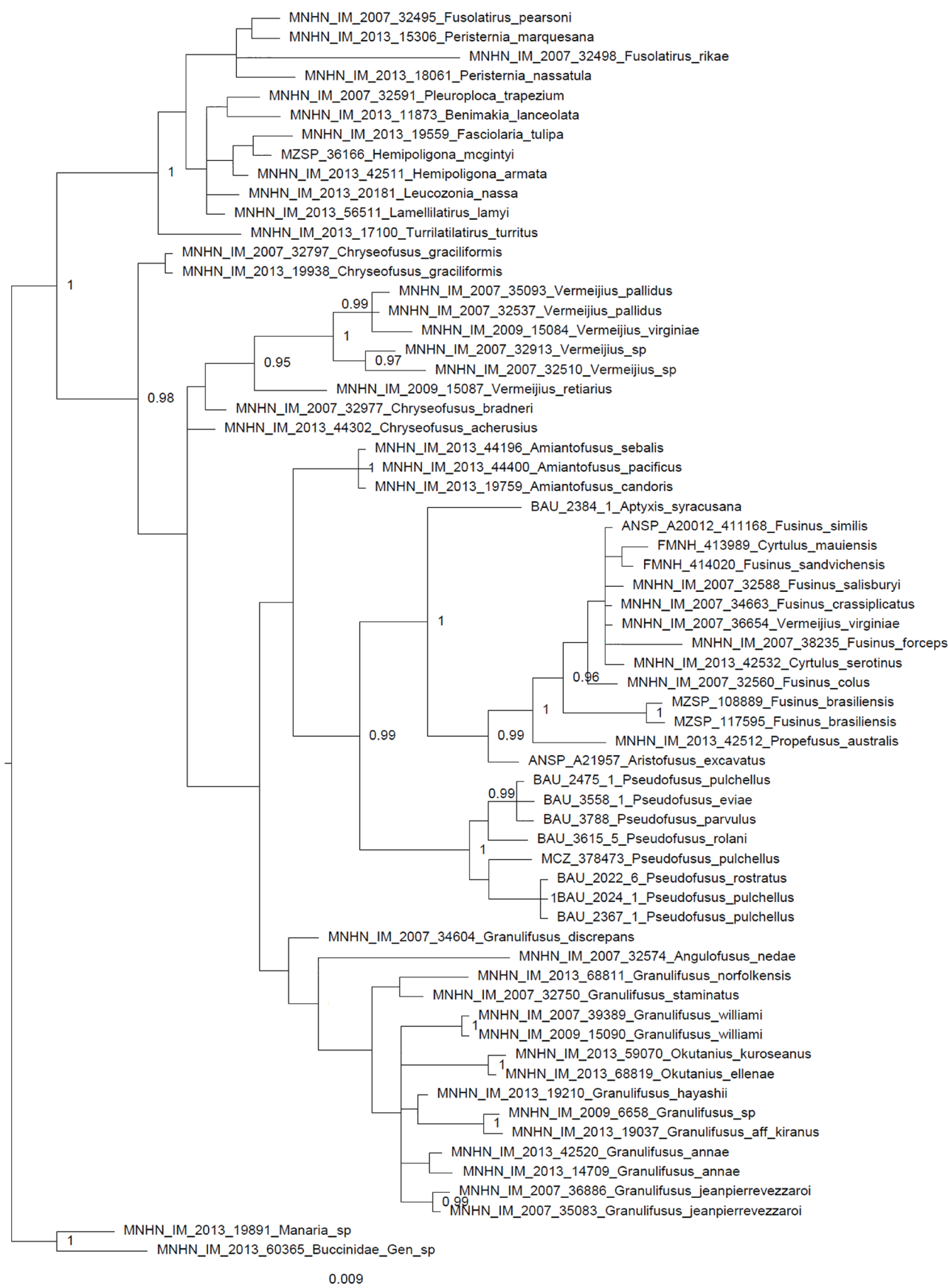


Fig. S2: Phylogenetic relationships among fascioliids as illustrated by the **Bayesian** majority consensus tree of the **28S** alignment. The tree is rooted on two buccinoideans (the Eosiphonidae *Manaria* sp., voucher MNHN-IM-2013-19891, and an undetermined Buccinidae, voucher MNHN-IM-2013-60365).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

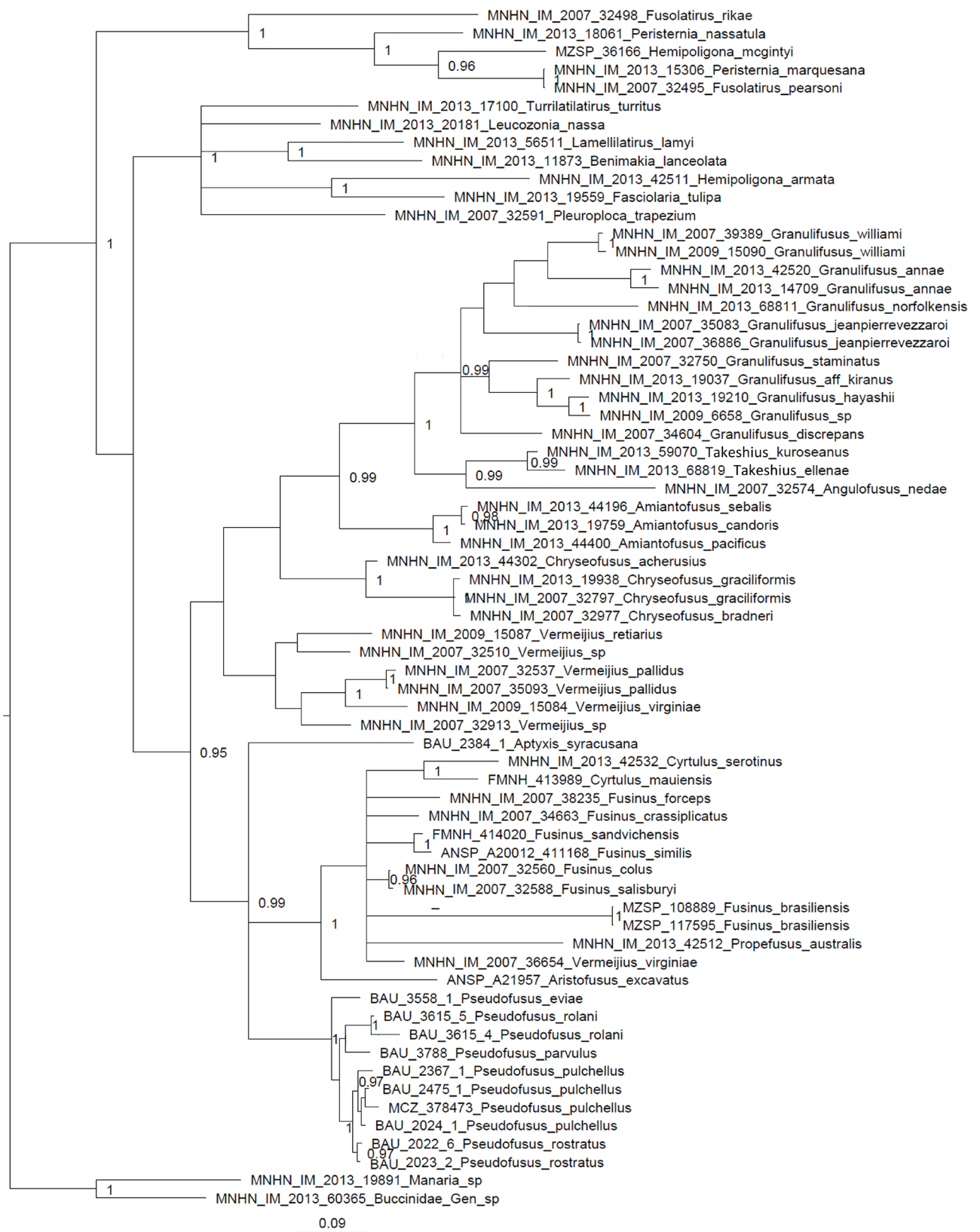


Fig. S3: Phylogenetic relationships among fascioliariids as illustrated by the **Bayesian** majority consensus tree of the **COI** alignment. The tree is rooted on two buccinoideans (the Eosiphonidae *Manaria* sp., voucher MNHN-IM-2013-19891, and an undetermined Buccinidae, voucher MNHN-IM-2013-60365).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

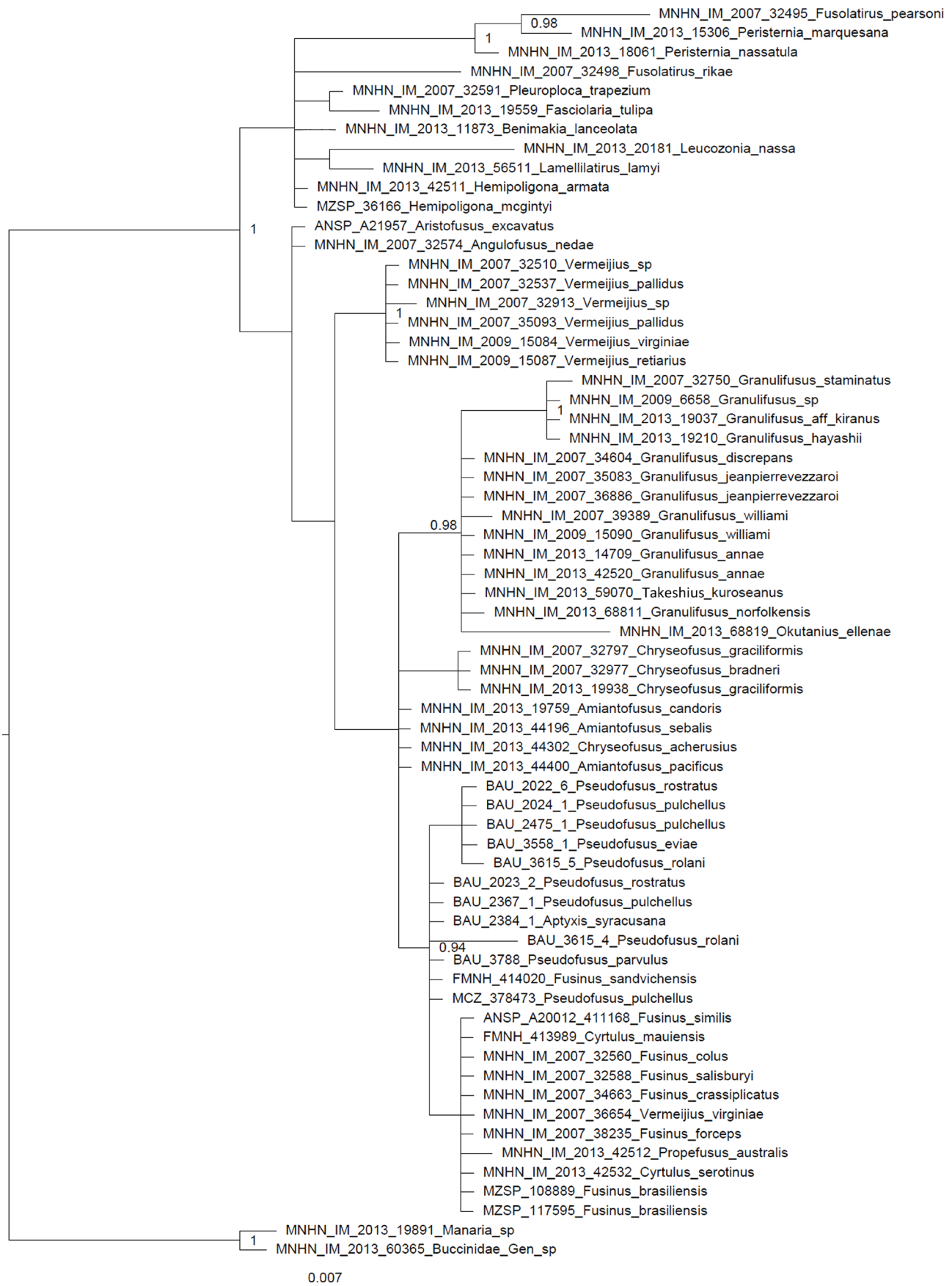


Fig. S4: Phylogenetic relationships among fascioliariids as illustrated by the **Bayesian** majority consensus tree of the **H3** alignment. The tree is rooted on two buccinoideans (the Eosiphonidae *Manaria* sp., voucher MNHN-IM-2013-19891, and an undetermined Buccinidae, voucher MNHN-IM-2013-60365).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

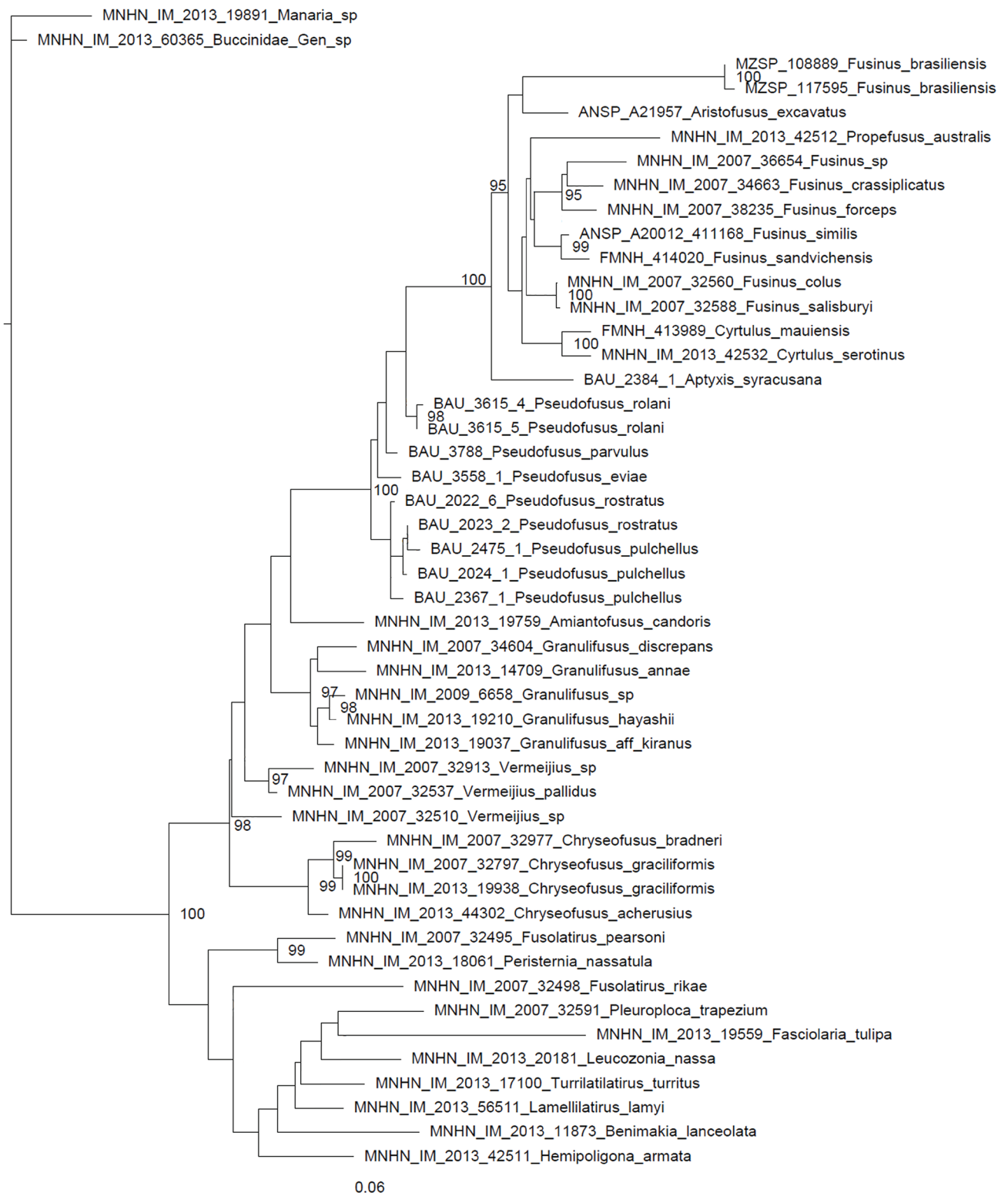


Fig. S5: Phylogenetic relationships among conoideans as illustrated by the **ML** majority consensus tree of the **16S** alignment. The tree is rooted on two buccinoideans (the Eosiphonidae *Manaria* sp., voucher MNHN-IM-2013-19891, and an undetermined Buccinidae, voucher MNHN-IM-2013-60365). Support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

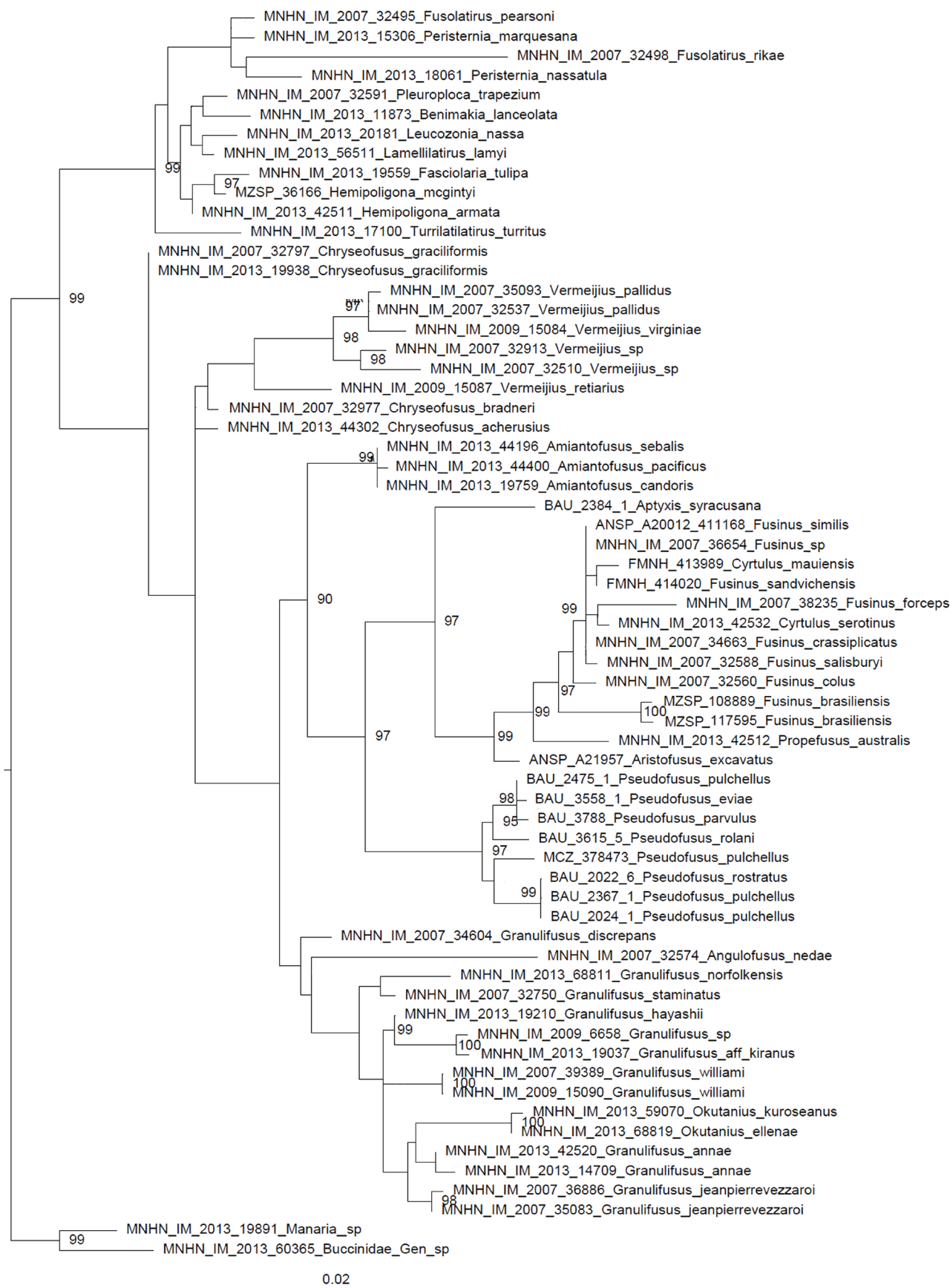


Fig. S6: Phylogenetic relationships among conoideans as illustrated by the **ML** majority consensus tree of the **28S** alignment. The tree is rooted on two buccinoideans (the Eosiphonidae *Manaria* sp., voucher MNHN-IM-2013-19891, and an undetermined Buccinidae, voucher MNHN-IM-2013-60365). Support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

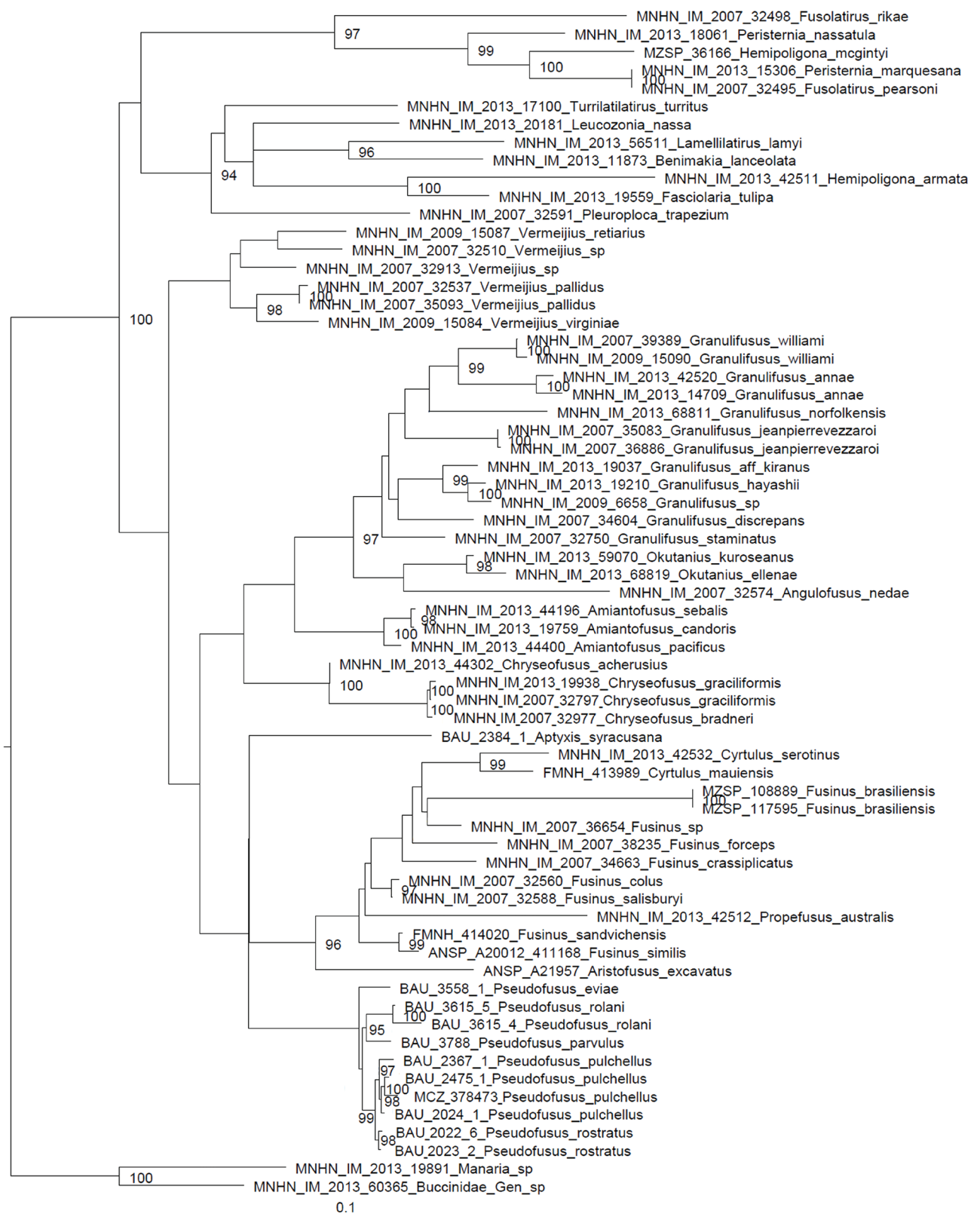


Fig. S7: Phylogenetic relationships among conoideans as illustrated by the ML majority consensus tree of the COI alignment. The tree is rooted on two buccinoideans (the Eosiphonidae *Manaria* sp., voucher MNHN-IM-2013-19891, and an undetermined Buccinidae, voucher MNHN-IM-2013-60365). Support values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

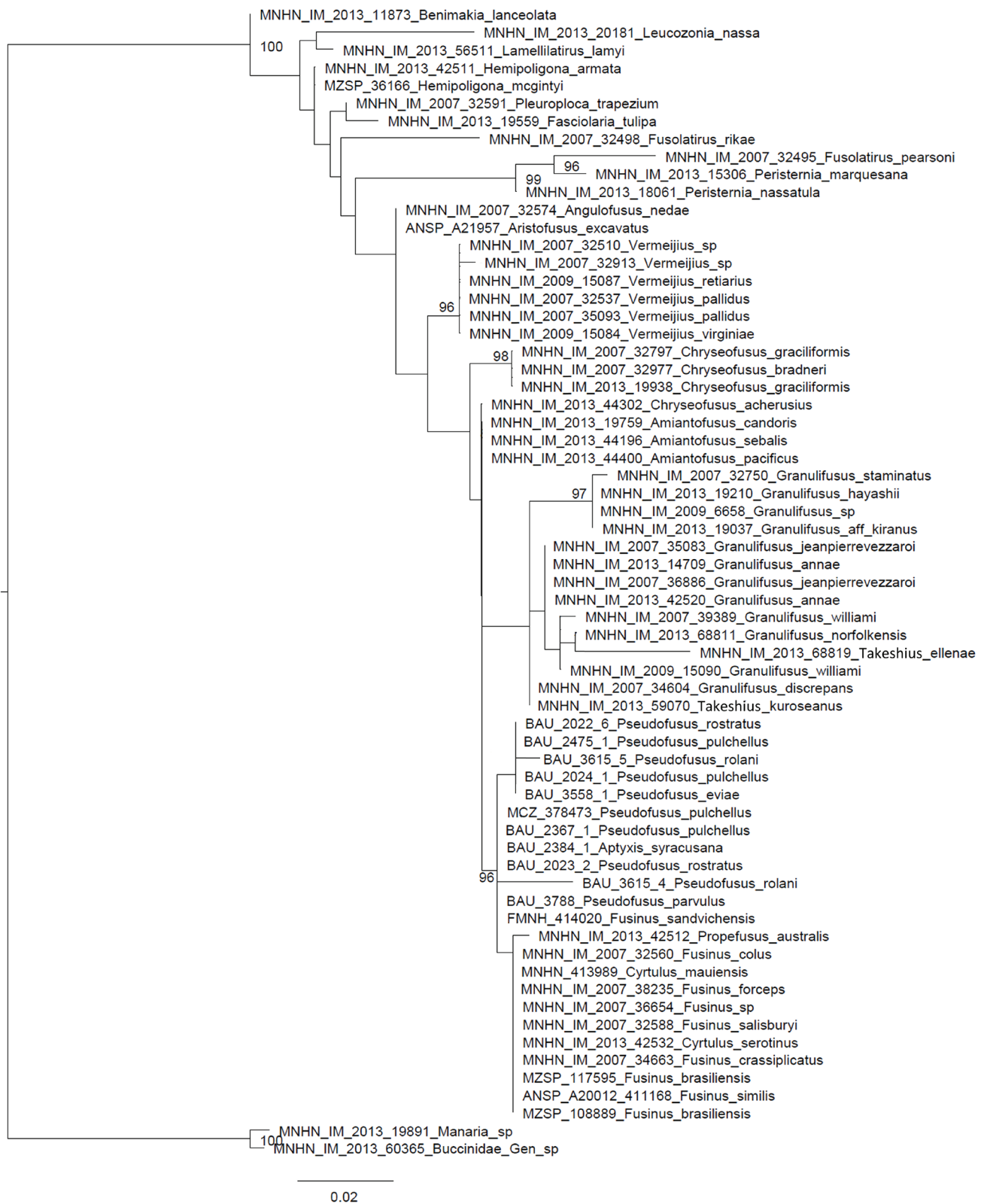


Fig. S8: Phylogenetic relationships among conoideans as illustrated by the ML majority consensus tree of the H3 alignment. The tree is rooted on two buccinoideans (the Eosiphonidae *Manaria* sp., voucher MNHN-IM-2013-19891, and an undetermined Buccinidae, voucher MNHN-IM-2013-60365). Support values are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