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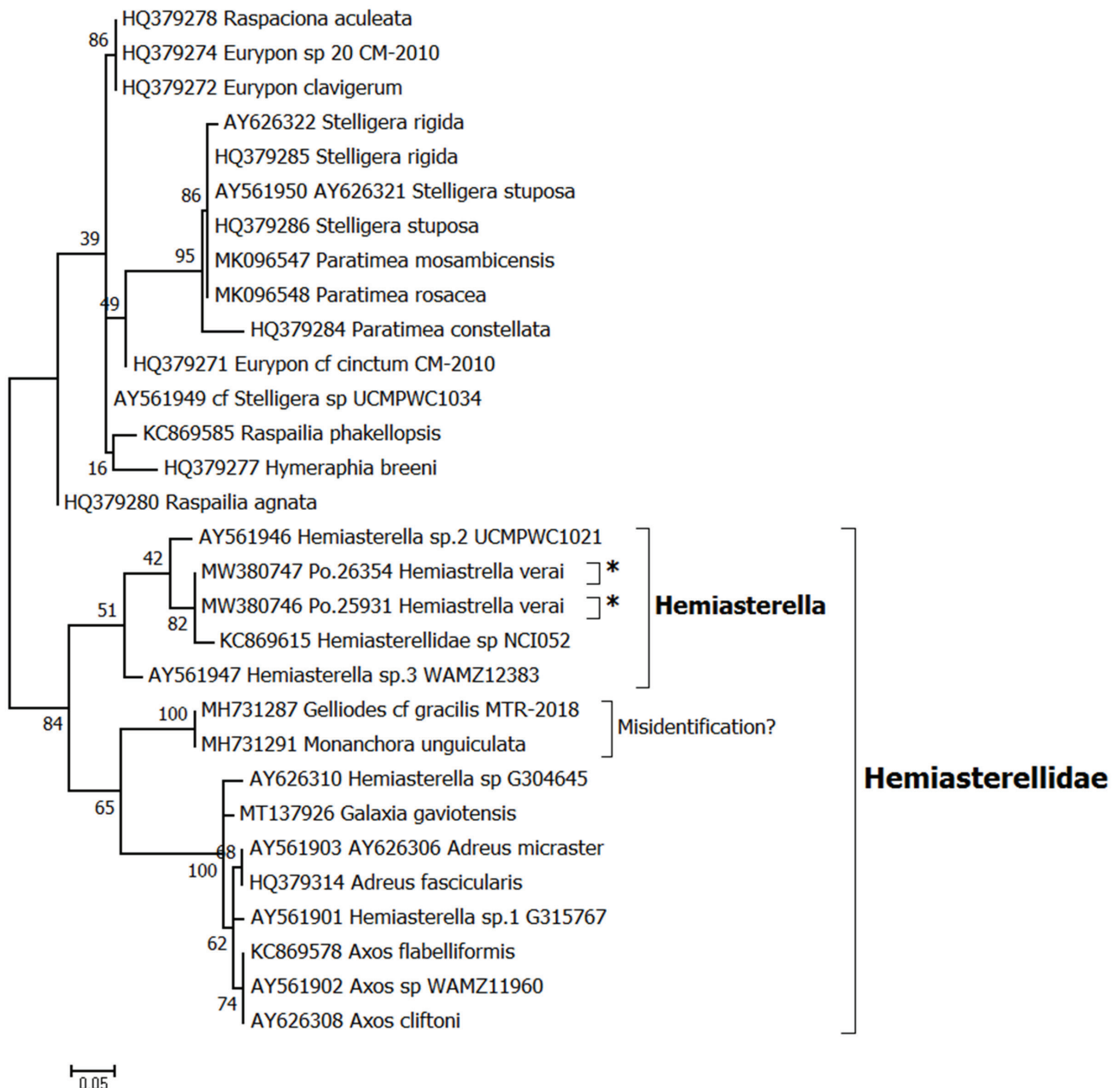
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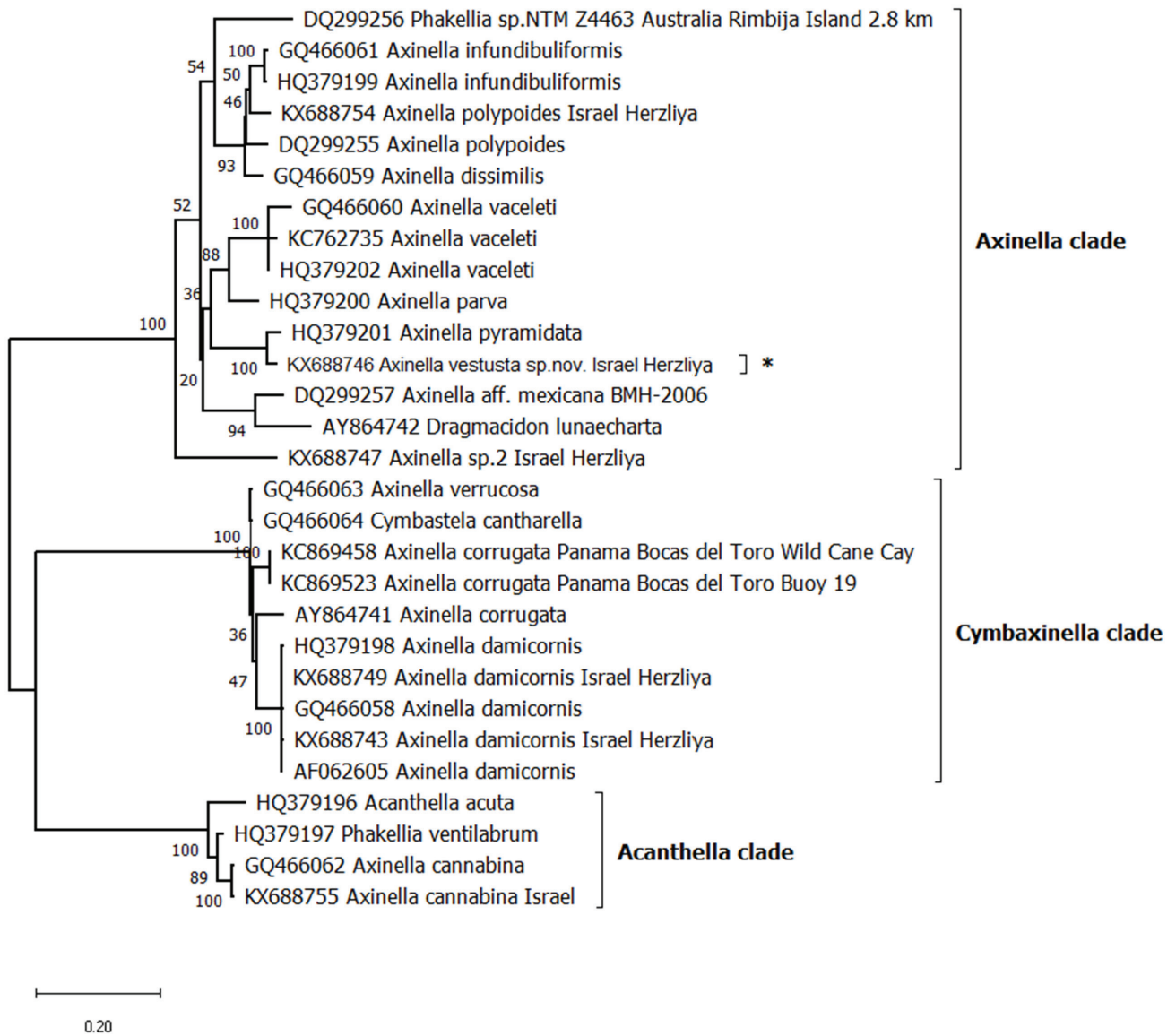
## New discoveries in Eastern Mediterranean mesophotic sponge grounds: updated checklist and description of three novel sponge species

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**Fig. S1:** Phylogenetic tree used to support the morphological identification *Hemiasterella verae* sp. nov. (marked by “\*\*”). The maximum likelihood tree was reconstructed with PhyML 3.0 (Guindon *et al.*, 2010) based on 28S rDNA sequences, using the GTR model of sequence evolution. Bootstrap supports are given near the corresponding nodes.



**Fig. S2:** Phylogenetic tree based on 28S rDNA sequences, used to support the morphological identification of *Axinella venusta* sp. nov. (marked by ‘\*’). The maximum likelihood tree was reconstructed with PhyML 3.0 (Guindon *et al.*, 2010), using the GTR model of sequence evolution. Bootstrap supports (100 replicates) given near the corresponding nodes.