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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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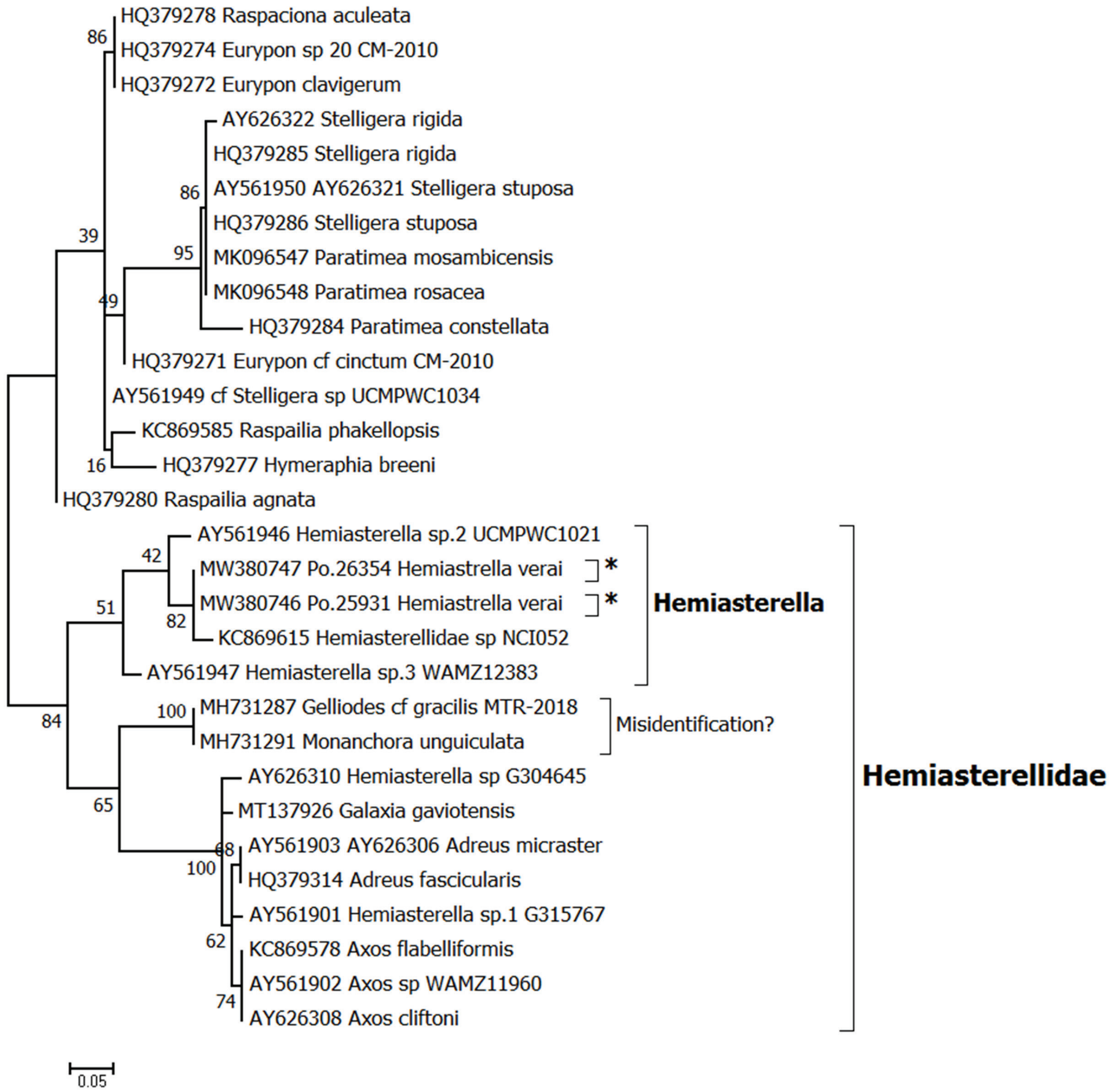

Fig. S1: Phylogenetic tree used to support the morphological identification *Hemiasterella verae* sp. nov. (marked by '*'). The maximum likelihood tree was reconstructed with PhyML 3.0 (Guindon *et al*., 2010) based on 28S rDNA sequences, using the GTR model of sequence evolution. Bootstrap supports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

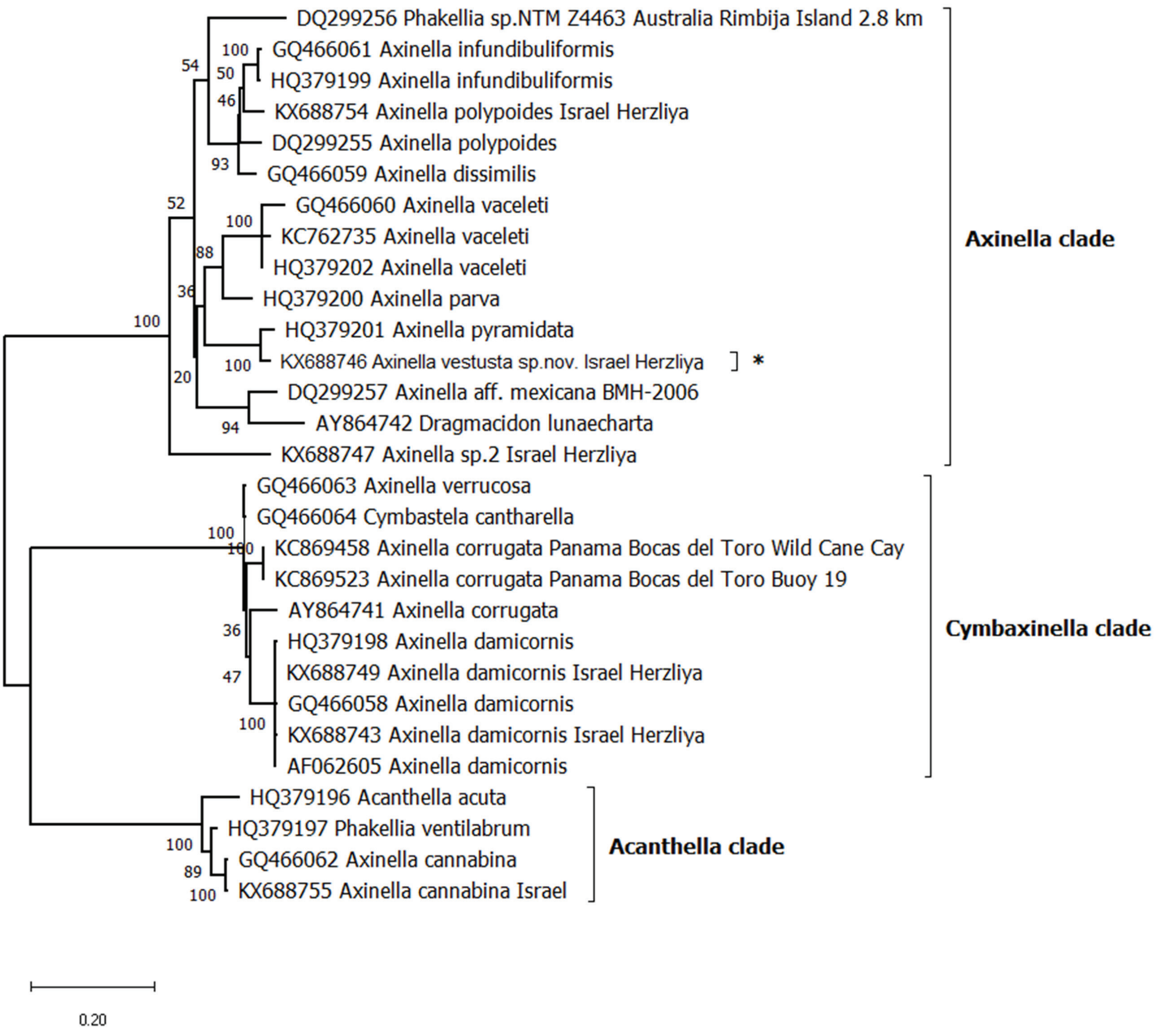

Fig. S2: Phylogenetic tree based on 28S rDNA sequences, used to support the morphological identification of *Axinella venusta* sp. nov. (marked by '*'). The maximum likelihood tree was reconstructed with PhyML 3.0 (Guindon *et al*., 2010), using the GTR model of sequence evolution. Bootstrap supports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