

Mediterranean Marine Science

Vol 22, No 2 (2021)

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doi: [10.12681/mms.25837](https://doi.org/10.12681/mms.25837)

To cite this article:

IDAN, T., SHEFER, S., FELDSTEIN, T., & ILAN, M. (2021). New discoveries in Eastern Mediterranean mesophotic sponge grounds: updated checklist and description of three novel sponge species. *Mediterranean Marine Science*, 22(2), 270–284. <https://doi.org/10.12681/mms.25837>

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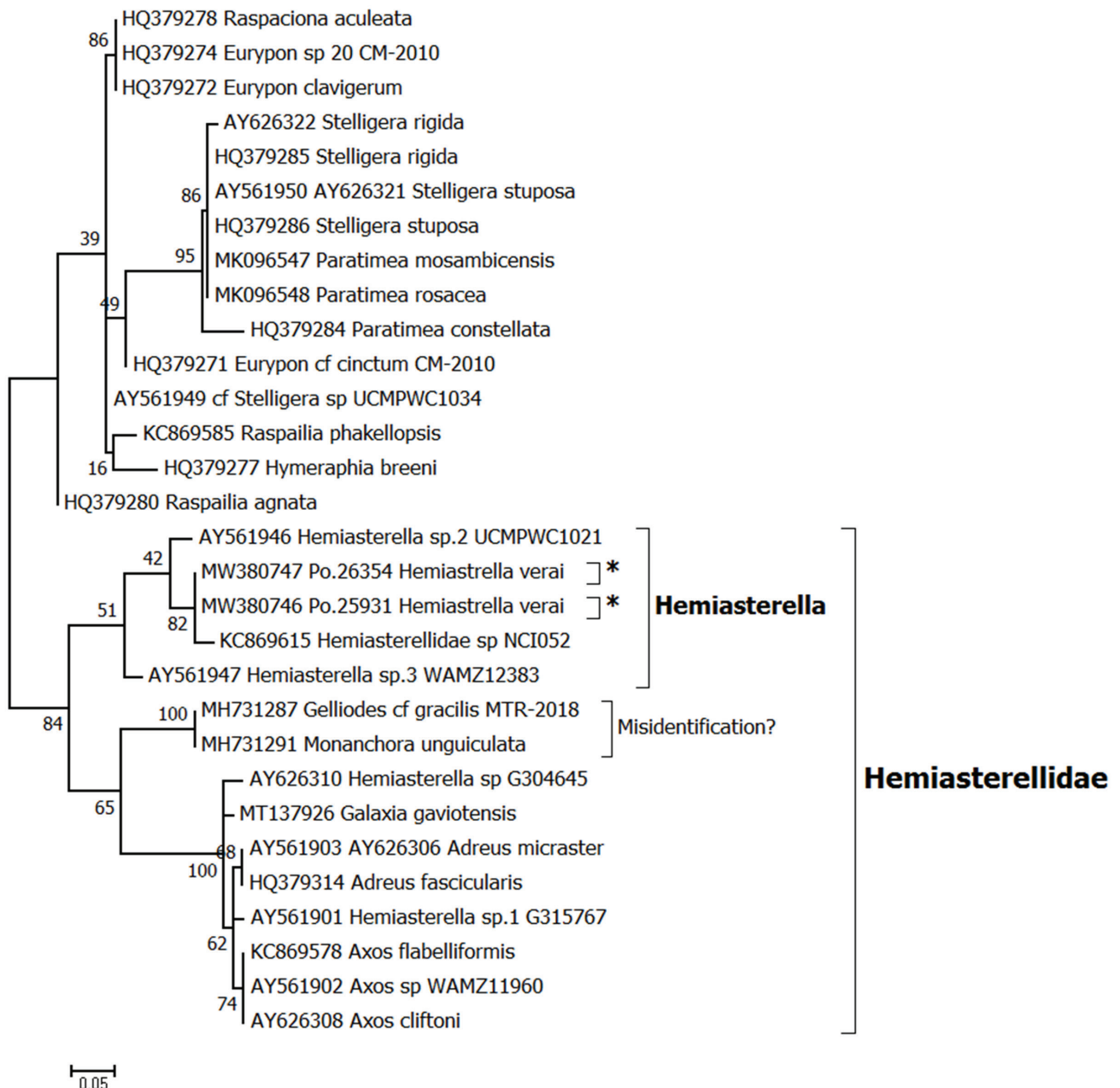


Fig. S1: Phylogenetic tree used to support the morphological identification *Hemiasterella verae* sp. nov. (marked by '*'). The maximum likelihood tree was reconstructed with PhyML 3.0 (Guindon *et al.*, 2010) based on 28S rDNA sequences, using the GTR model of sequence evolution. Bootstrap supports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

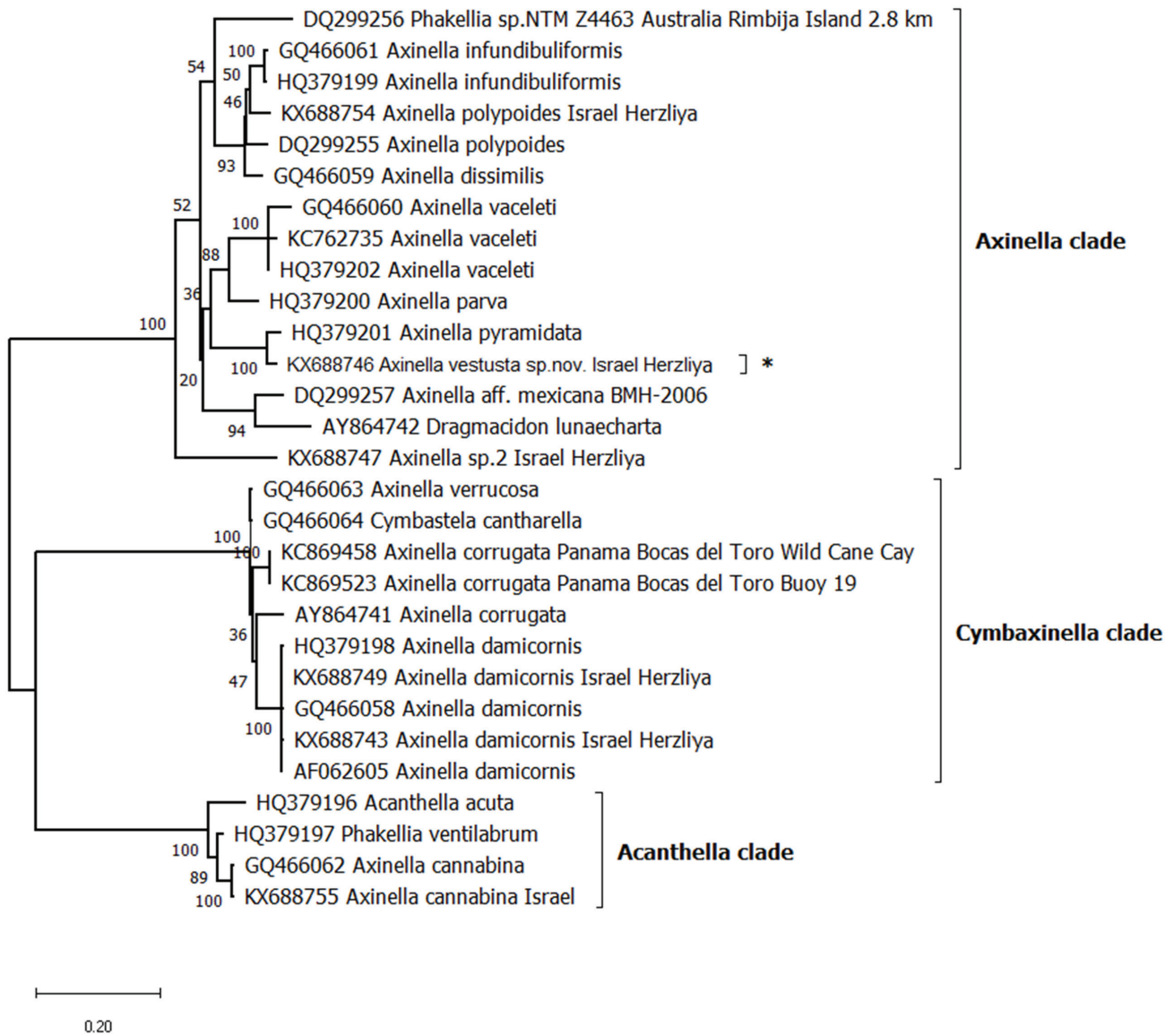


Fig. S2: Phylogenetic tree based on 28S rDNA sequences, used to support the morphological identification of *Axinella venusta* sp. nov. (marked by ‘*’). The maximum likelihood tree was reconstructed with PhyML 3.0 (Guindon *et al.*, 2010), using the GTR model of sequence evolution. Bootstrap supports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