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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 28 S 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.

