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Table S1. 16S rRNA and COI gene sequence accession numbers.

Sample	Location	16S accession no.	COI accession no.
Nms1-IL Nahsholim South	32.61422° N, 34.91535° E	OR127150	
Nms2-IL Nahsholim South	32.61421° N, 34.91537° E	OR127183	OR185512
Nmn1-IL Nahsholim North	32.61559° N, 34.91573° E	OR127149	OR185513
Nmn2-IL Nahsholim North	32.61609° N, 34.91531° E	OR127184	
Nmn3-IL Nahsholim North	32.61669° N, 34.91530° E	OR127185	OR185555
Nmn4-IL Nahsholim North	32.61775° N, 34.91605° E	OR127186	
Tnn1-IL Tel Nami North	32.66082° N, 34.92508° E	OR127187	
Tnn2-IL Tel Nami North	32.66090° N, 34.92519° E	OR127188	
Bmn1-IL Habonim Nature reserve North	32.64674° N, 34.92229° E	OR127189	
Tnn3a-IL Tel Nami North Mega cluster	32.66090° N, 34.92550° E	OR127190	

Fig. S1: Nine clusters (out of 44) of *D. anguliferum* which were documented and photographed in "M" area (in Habonim nature reserve).

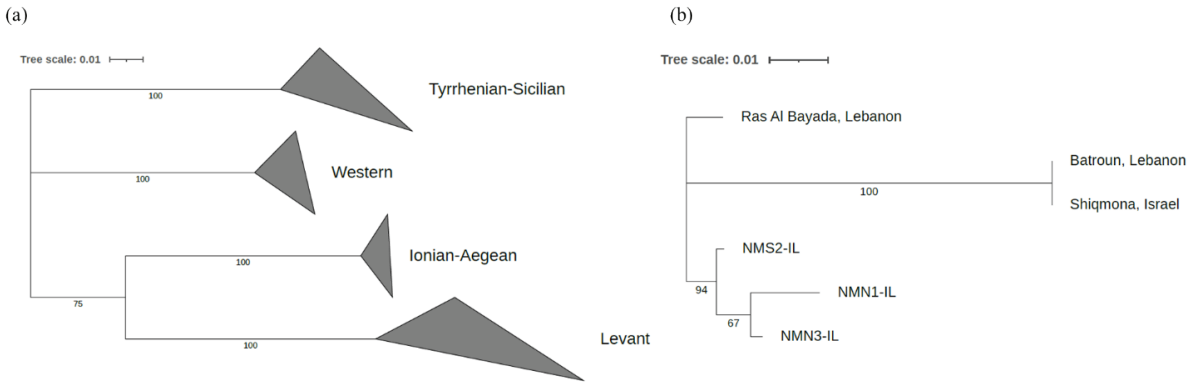

Fig. S2: Unrooted phylogenetic trees of the mitochondrial cytochrome oxidase subunit I (COI) gene sequences using maximum likelihood analysis. Numbers at the branch represent bootstrap values, indicating the statistical support for the branching pattern. (a) Phylogenetic tree of the samples from the current study and related reference sequences obtained from NCBI GenBank that originate from all Mediterranean Sea sample points obtained during the study of Calvo *et al.*, 2015. The triangles combine all the sequences of the same group within them. (b) Levantine sea lineage tree of the samples from the current study and reference sequences from NCBI GenBank that originate from Calvo *et al.*, 2015.