

Supplementary material

Marine Biodiversity

The bigfin reef squid (*Sepioteuthis lessoniana* Férussac, 1831) species complex in the Mediterranean Sea: genetic evidence for multiple Red Sea lineages in a Lessepsian migrant

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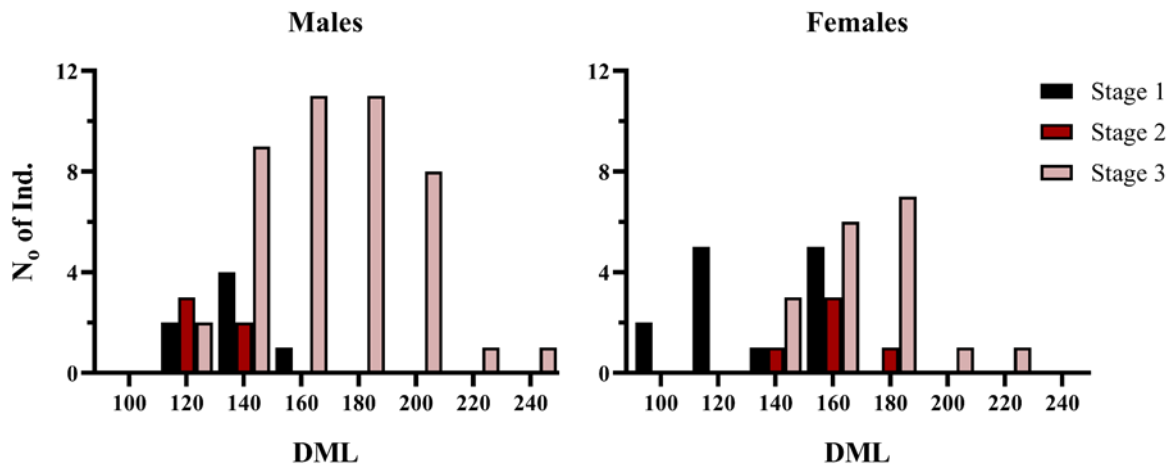


Fig. S1 Bar plot depicting dorsal mantle length (DML) of female (right) and male (left) individuals according to the maturity stage

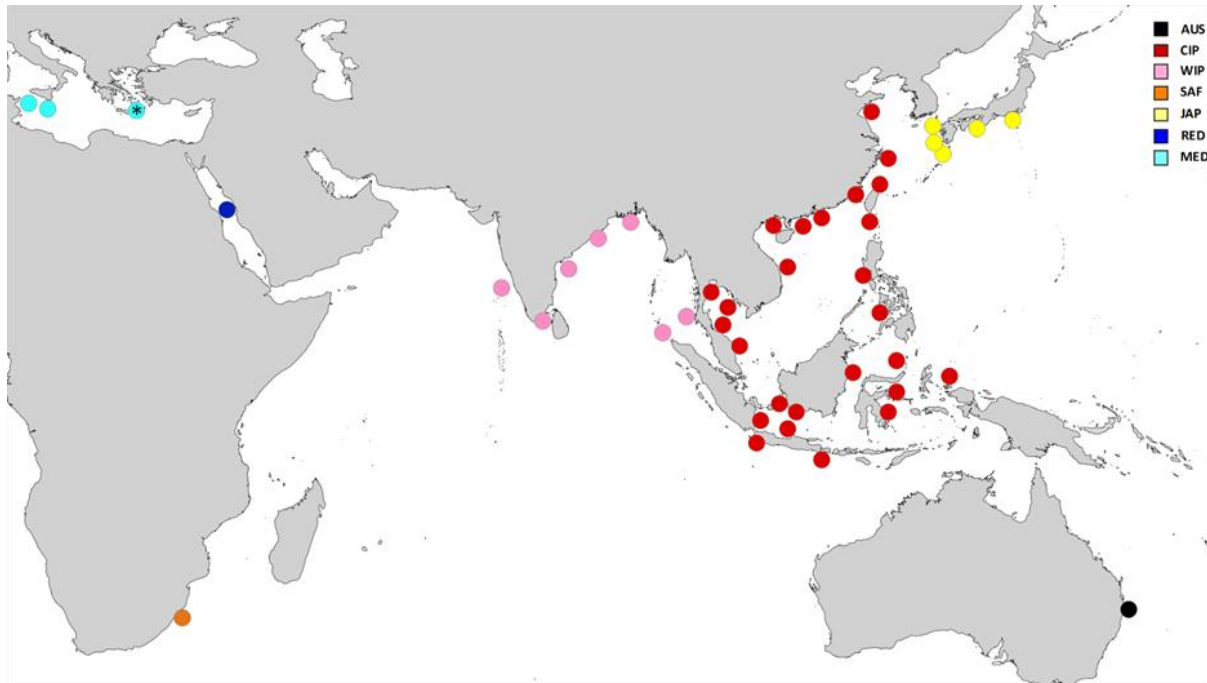


Fig. S2 Map of the approximate origin of the sequences analyzed in the present study. Colors of sampling locations correspond to the color of geographic regions (based on the biogeographic realms in Spalding et al., 2007) that were used in the haplotype networks (Fig. 3, Fig. S3). MED: Mediterranean Sea, RED: Red Sea, SAF: South Africa, WIP: Western Indo-Pacific region, CIP: Central Indo-Pacific region, JAP: Japan and AUS: Australia. The sampling location of the individuals used in the present study is indicated with a black asterisk

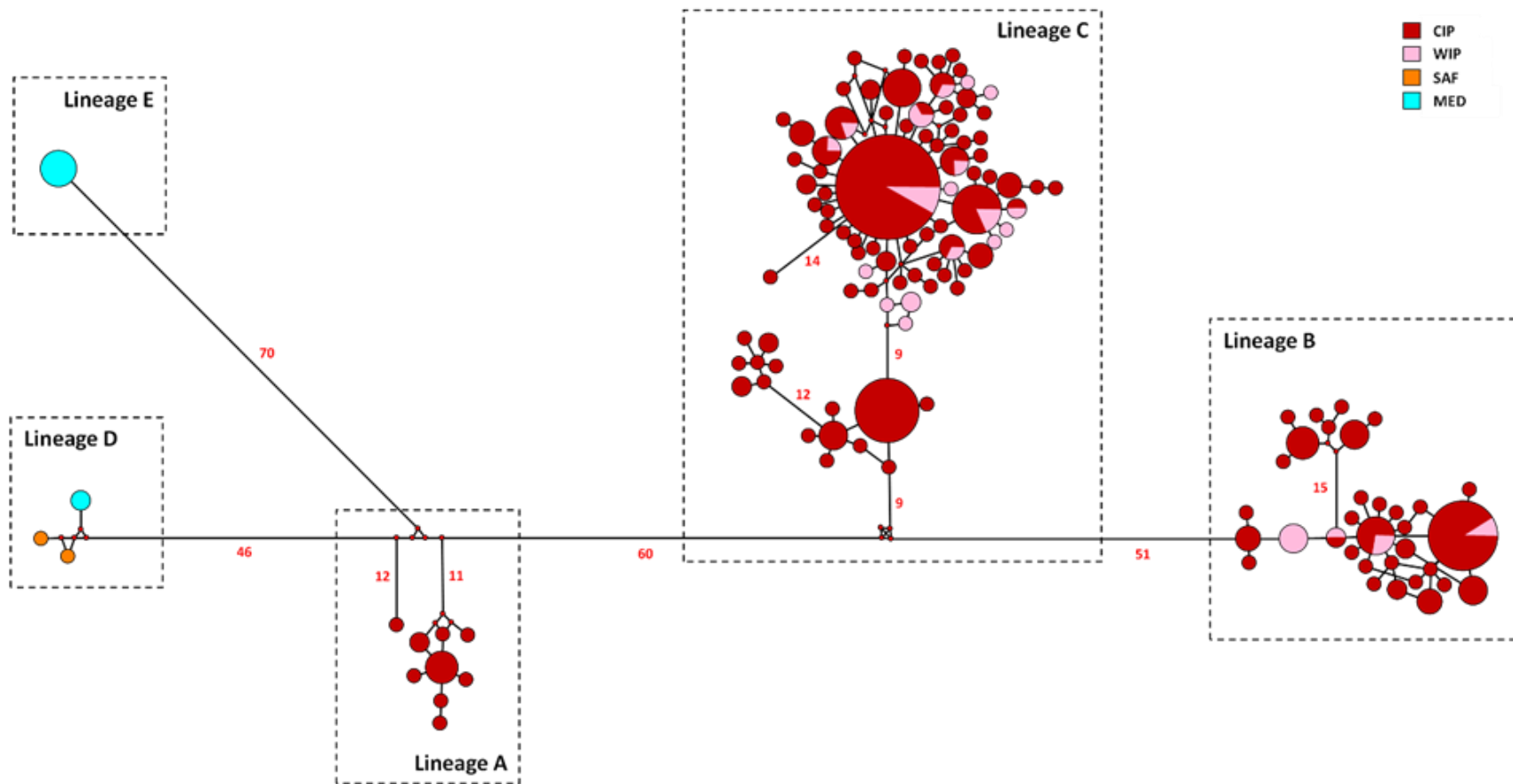


Fig. S3 Median-joining haplotype network depicting haplotypes of the concatenated dataset (COI + 16S). Each circle represents a haplotype and its size is proportional to its relative frequency. Each color corresponds to a different sampling region (CIP: Central Indo-Pacific region, WIP: Western Indo-Pacific region, SAF: South Africa, MED: Mediterranean Sea). Red nodes represent possible median vectors while numbers indicate nucleotide differences between haplotypes (differences less than five nucleotides are not shown)

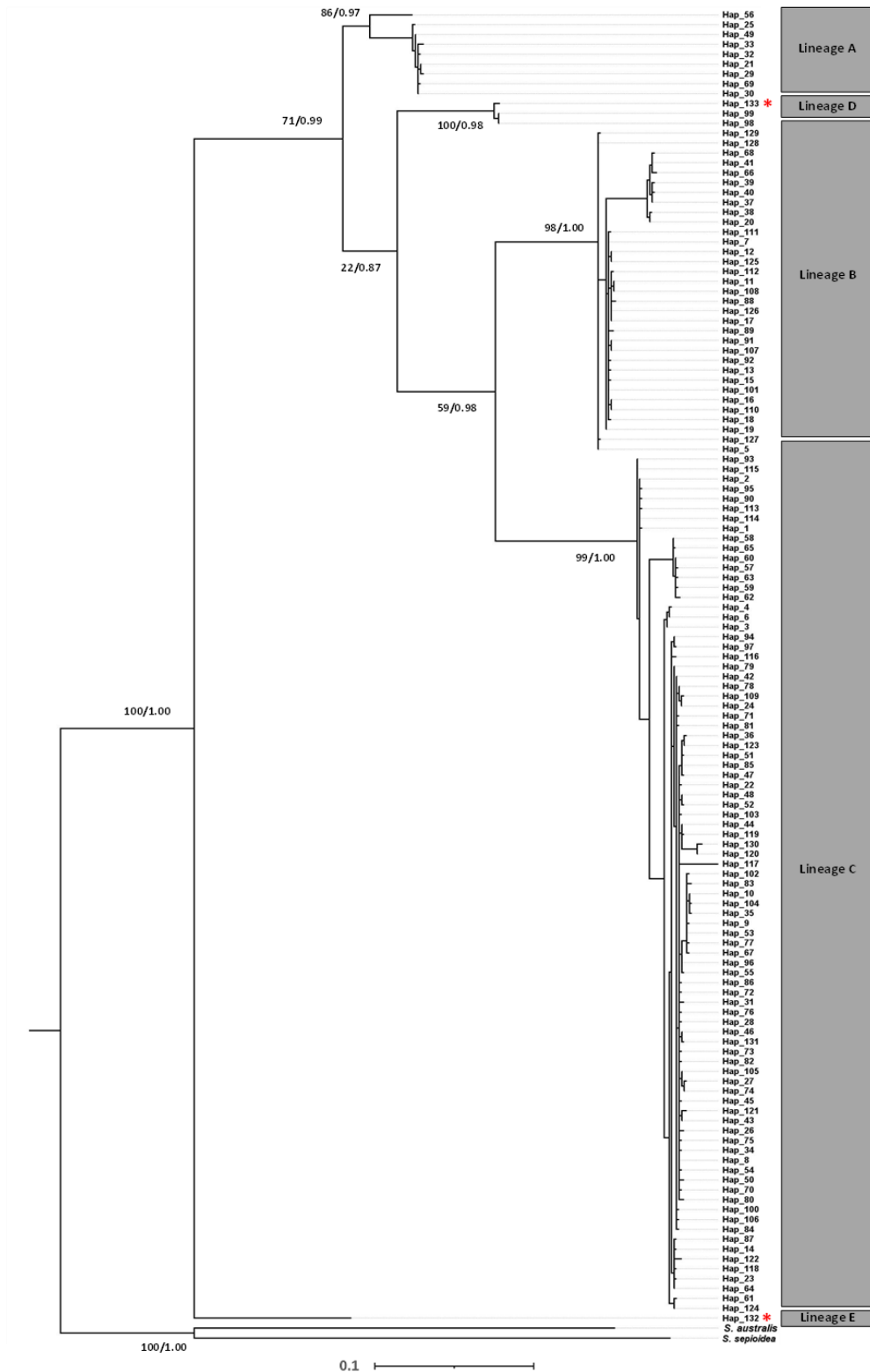


Fig. S4 Maximum likelihood tree based on the concatenated dataset. Only support values for the main clades are shown. The integer numbers indicate bootstrap values, while decimal numbers indicate posterior probabilities derived from the MrBayes analysis (Bayesian inference). Haplotypes found in the Mediterranean Sea are indicated with a red asterisk. Hap prefix corresponds to Con haplotypes in Table S3

Table S1 Range of values or means of selected indices for *S. lessoniana* in Mediterranean areas of distribution. The indices values are compared to the ones estimated for *S. cf. lessoniana* of Crete

Indices	Rhodes	Syria	Egypt	Malta-Lampedusa	Crete
MWI	<40%	34-36%	43%	28-39%	30-40%
FLI	87-97%	91-98%	>90%	87-92%	82-95%
FWI	66-70%	-	≥73%	68-72%	47-86%
CLI	38-52%	-	-	-	30-50%
TST	-	-	17-22	-	15-33
AST	-	-	20-25	-	16-29
CL/TEN	33%	-	-	-	29%
BLS	No	-	Yes	-	0-5
HCL/AL	25%	-	-	-	25%
GW/GL	17%	-	-	-	18%
N	2	2	2	2	93
DML	196-244	155-179	195-200	163-260	91-227
Reference	Lefkaditou <i>et al.</i> , 2009	Ammar & Maarooof, 2019	Emam & Ali, 2010; Riad, 2020	Marrone <i>et al.</i> , 2025	This study

***MWI**: Mantle width to Dorsal Mantle Length (DML) ratio, **FLI**: Fin length to DML ratio, **FWI**: Fin width to DML ratio, **CLI**: Tentacle club length to DML ratio, **TST** και **AST**: number of tentacle and arm sucker teeth, respectively, **CL/TEN**: Tentacle club to tentacle length ratio, **BLS**: number of suckers on buccal lappets, **HCL/AL**: Hectocotylus length to ventral arm length ratio, **GW/GL**: Gladius width to Gladius length ratio, **N**: Sample size, **DML**: Dorsal mantle length.

Table S2 Interspecific and intraspecific mean p-distances (%) between lineages estimated for the COI dataset B

	A	B	C	D	E
A	1.2				
B	12.2	1.7			
C	12.3	11.7	1.3		
D	8.7	11.5	12.9	0.3	
E	11.8	15.1	14.4	13.8	0.3

Table S3 Detailed metadata of the sequences used in the present study (excel file ESM 2)