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Last Interglacial dispersal and genetic diversification, from eastern Mediterranean penultimate glacial refugia, and pre-LGM demographic expansion drive genetic panmixia within the hermit crab *Clibanarius erythropus* (Decapoda: Anomura: Diogenidae) across the East Atlantic and Mediterranean Sea

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Table S1. Genetic diversity estimates for the examined hermit crab *Clibanarius erythropus* populations, based on the analysis of 316 base pairs of the mitochondrial Cox1 gene. Values reported for each population as well as for the total dataset are: sample size (*N*), number of polymorphic sites (*N*ps), number of haplotypes (*N*h), haplotype diversity (*h*), nucleotide diversity (π), and mean number of nucleotide differences (K).

Population	*N*	*N*ps	*N*h	*h*	π	K
Portugal	11	1	2	0.182	0.0006	0.182
Cádiz	23	9	8	0.526	0.0025	0.783
Alicante	17	6	7	0.662	0.0026	0.809
Ibiza	10	0	1	0.000	0.0000	0.000
Girona	10	3	4	0.533	0.0019	0.600
Elba	13	2	3	0.295	0.0010	0.308
Messina	10	4	5	0.667	0.0025	0.800
Pula	10	3	4	0.644	0.0024	0.756
Igoumenitsa	10	1	2	0.200	0.0006	0.200
Chalkidiki	10	0	1	0.000	0.0000	0.000
Çeşme	6	3	3	0.600	0.0032	1.000
Girne	18	9	8	0.641	0.0032	1.000
Total	148	23	28	0.447	0.0018	0.575

The population of Portugal was defined by the combination of specimens of *Clibanarius erythropus* from the two locations of Vila Nova de Milfontes and Praia da Luz. The population of Cádiz was defined by the combination of specimens of the studied hermit crab species from the two locations of Corrales de Rota and La Caleta.

Table S2. Geographic distribution of the 47 haplotypes of *Clibanarius erythropus* recorded at the 11 populations from the East Atlantic Ocean and Mediterranean Sea, based on the analysis of 700 base pairs of the mitochondrial Cox1 gene.

Population	Haplotypes																																														
	H 1	H 2	H 3	H 4	H 5	H 6	H 7	H 8	H 9	H 10	H 11	H 12	H 13	H 14	H 15	H 16	H 17	H 18	H 19	H 20	H 21	H 22	H 23	H 24	H 25	H 26	H 27	H 28	H 29	H 30	H 31	H 32	H 33	H 34	H 35	H 36	H 37	H 38	H 39	H 40	H 41	H 42	H 43	H 44	H 45	H 46	H 47
Cádiz	1	11	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Alicante	0	9	0	0	0	2	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ibiza	0	8	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Girona	0	7	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Elba	0	9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Messina	0	5	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pula	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Igoumenitsa	0	8	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chalkidiki	0	8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Çeşme	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0
Girne	0	7	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1

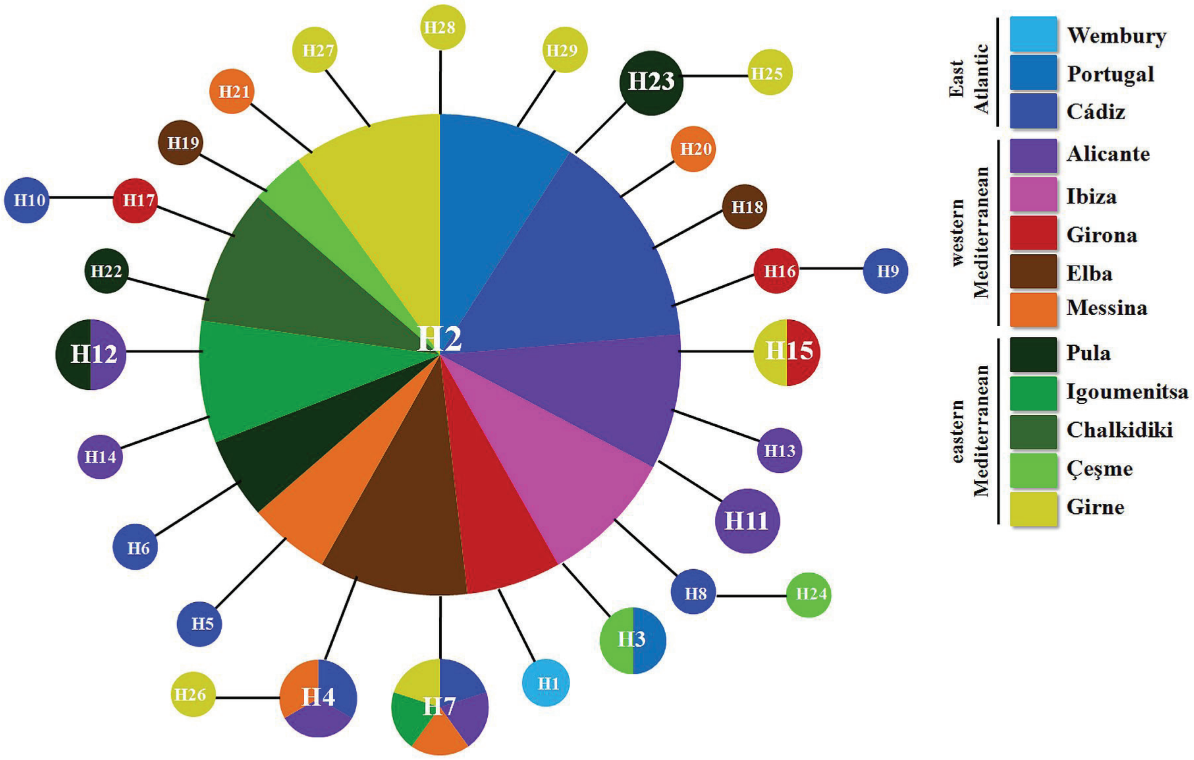

Fig. S1: TCS parsimony network of *Clibanarius erythropus*, based on the alignment of 316 bp of the mitochondrial Cox1 gene, showing the evolutionary relationships among the recorded 29 haplotypes (obtained from the comparison of a total dataset of 149 Cox1 sequences). Each connecting line indicates one mutational step between haplotypes. Circle sizes depict proportions of haplotypes; the smallest corresponds to 1 and the largest to 110 individuals.