

Figure S1. *Cox1* haplotype network

built using Median Joining algorithm in Network for the octopus' haplotypes found in the 93 samples analyzed. Circles represent different haplotypes and size is proportional to its frequency. Colors indicate each population.

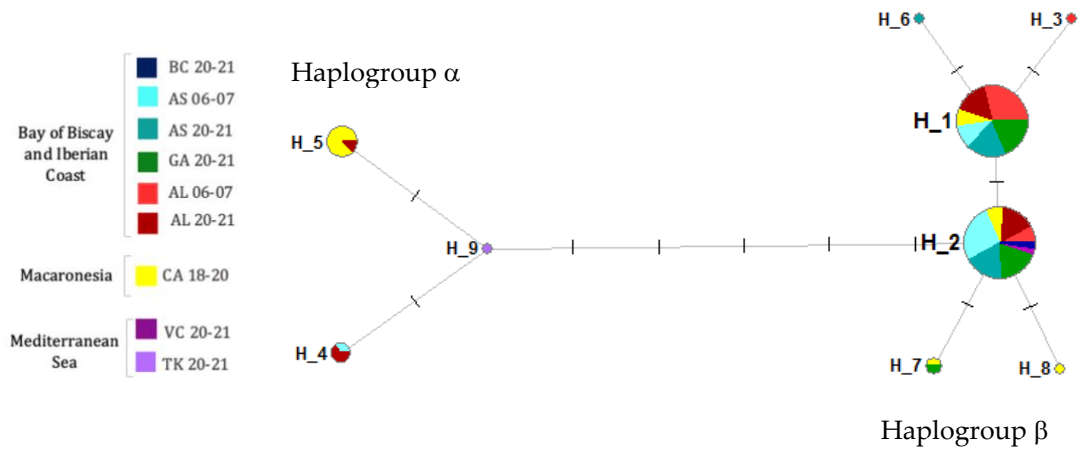


Table S1. Summary of the sequence differences between haplotypes from the concatenated dataset.

The numbers made referent to the position of the variable site within the concatenated sequence. In blue the variable sites from *cox1* sequence and in black the variable sites from the CR sequence. The name of the haplotypes belonging to α haplogroup is depicted in black. The frequency of each haplotype (freq.) is also included in the table.

Variable sites and position within the concatenated sequence		
	1133344456666666777777777788888889911111111111111	
	114947943444588011246788901257770700000000011112	
	036728324168408916377119036970472302456688800355	
Haplotype		Freq.
H_1	CTTTCTTACCCCTCTGTTTATCCTACCACCGTTAGACTTCTGCGCTCT	24
H_2	CTTTCTTACCCCTCTGTTTATCTTACCACCGTTAGACTTCTGCGCTCT	10
H_3	CTTTCTTACCCTCCTCGTTTATCCTACAACCGTTAGACTTCTGCGCTCT	26
H_4	CTTTCTTACCCCTCATTTATCCTACCACCGTTAGACTTCTGCGCTCT	1
H_5	CTTTTCTACCCCTCTGTTTATCCTACCACCGTTAGACTTCTGCGCTCT	1
H_6	CTTTCTTACCCTCCTCGTTTATCCTACCACCGTTAGACTTCTGCGCTCT	4
H_7	CTTTCTTACCCTCCTCGTTTATCCTACCACCGATAGACTTCTGCGCTCT	2
H_8	CTTTCTTACCCCTCTGTTTACCTTACCACCGTTAGACTTCTGCGCTCT	1
H_9	TCATCCTATTCTCACCGCCTGTTCTGTAGTCATCAAACCCTCATTTTCCT	3
H_10	CTTTCTTACCCTCCTCGTTTATCCTACCGCCGTTAGACTTCTGCGCTCT	2
H_11	CTTTCTTACCCTCCTCGTTTATCCTACCACCGTTGGGCTTCTGCGCTCT	1
H_12	TCATCCTATCTTCCCTACCCGTTCTGCAGTCGTCAAAGCCCCATTTTCCT	7
H_13	CTTTCTTACCCTCCTCGTTTATCCTACAACGTTAGACTTCTGCGCTCT	1
H_14	CTTTCTTACCCTCCTCGTTTATCCTACCACCGTCAGACTTCTGCGCTCT	1
H_15	CTTTCTTGCCCCCTCTGTTTATCCTACCACCGTTAGACTTCTGCGCTCT	1
H_16	CTTACTTACCCTTCTCGTTTATCCCACCACCGTTAGACTTCTGCGCTCT	1
H_17	TCATCCTATCTTCCCTACCCGTTCTGCAGTCGTCAAAGCCCCATTTCCC	1
H_18	CTTTCTCACCCCTCCTCGTTTATCCTACAACCGTTAGACTTCTGCGCTCT	1
H_19	CTTTCTTACCCCTCTGTTTATCCTACCACCATAGACTTCTGCGCTCT	2
H_20	CTTTCTTACCCTCCTCGTTTATCCTACCGCCGTTAGACTTCTGCGCCCT	1
H_21	CTTACTTACCCTCCTCGTTTATCCTACAACCGTTAGACTTCTGCGCTTT	1
H_22	TCATCCTATCCTCACCGCCTGTTCTGTAGTCATCAAACCCTCATTTTCCT	1

Table S2. Population pairwise ϕ_{ST} values from *cox1* in octopus' samples.

ϕ_{ST} values, using pairwise comparisons as distance method, are located below diagonal and above diagonal their correspondent p-values (italics). Significance (* $p < 0.05$). Significance after Bonferroni correction (cut off value $p < 0.0033$) in bold.

	Asturias 2006-2007	Asturias 2020-2021	Galicia 2020-2021	Algarve 2006-2007	Algarve 2020-2021	Canary Islands 2018-2021
Asturias 2006-2007			<i>0.25978</i>	<i>0.44431</i>	<i>0.00861</i>	<i>0.35531</i>
Asturias 2020-2021	0.04300		<i>0.99990</i>	<i>0.24017</i>	<i>0.17167</i>	<i>0.00119</i>
Galicia 2020-2021	0.00933	-0.04895		<i>0.13226</i>	<i>0.24037</i>	<i>0.00307</i>
Algarve 2006-2007	0.24908*	0.06832	0.12536		<i>0.02465</i>	<i>0.00020</i>
Algarve 2020-2021	0.00784	0.07626	0.06926	0.15537*		<i>0.06019</i>
Canary Islands 2018-2021	0.27538*	0.36418*	0.35522*	0.41770*	0.10293	

Table S3. Population pairwise ϕ_{ST} values from CR in octopus' samples.

ϕ_{ST} values, using pairwise comparisons as distance method, are located below diagonal and above diagonal their correspondent p-values (italics). Significance (* $p < 0.05$). Significance after Bonferroni correction (cut off value $p < 0.0033$) in bold.

	Asturias 2006-2007	Asturias 2020-2021	Galicia 2020-2021	Algarve 2006-2007	Algarve 2020-2021	Canary Islands 2018-2021
Asturias 2006-2007			<i>0.25730</i>	<i>0.34185</i>	<i>0.00822</i>	<i>0.45203</i>
Asturias 2020-2021	0.01058		<i>0.99990</i>	<i>0.21077</i>	<i>0.11712</i>	<i>0.00149</i>
Galicia 2020-2021	0.00270	-0.04978		<i>0.10187</i>	<i>0.10544</i>	<i>0.00149</i>
Algarve 2006-2007	0.10147*	0.03509	0.07656		<i>0.01346</i>	<i>0.00020</i>
Algarve 2020-2021	-0.00279	0.09650	0.09608	0.13592*		<i>0.05396</i>
Canary Islands 2018-2021	0.28215*	0.38766*	0.38857*	0.41558*	0.11231	