Table S1. Number of *cytb* haplotypes obtained in each population of *Trachurus picturatus.*

	Mediterranean Sea			Atlantic Ocean			
Haplotype	**AS**	**EM**	**CM**	**CI**	**MA**	**PO**	**AZ**
Hap1	4	0	0	1	1	2	0
Hap2	22	12	11	21	19	66	19
Hap3	1	1	2	3	2	4	1
Hap4	8	1	5	2	2	9	6
Hap5	1	0	0	0	0	0	1
Hap6	1	0	0	0	0	0	0
Hap7	0	2	0	0	0	0	0
Hap8	0	0	1	0	0	0	0
Hap9	0	1	0	0	0	0	0
Hap10	0	0	0	0	0	1	0
Hap11	0	0	0	1	2	0	0
Hap12	0	0	0	1	0	0	0
Hap13	0	0	0	1	0	0	0
Hap14	0	0	0	0	0	0	1
Hap15	0	0	0	0	1	0	0
Hap16	0	0	0	0	1	0	0
Hap17	0	0	0	0	1	0	0
Hap18	0	0	0	0	1	0	0
Hap19	0	0	0	0	1	0	0
Hap20	0	0	0	0	1	0	0
Hap21	0	0	1	0	0	1	0
Hap22	0	0	0	0	0	1	0
Hap23	0	0	0	0	0	1	0
Hap24	0	0	0	0	0	1	0
Hap25	0	0	0	0	0	1	0
Total	37	17	20	30	32	87	28

Table S2. List of *cytb* haplotypes obtained from *Trachurus picturatus* and the sequences that belong to each haplotype. IDs of publicly available sequences have GenBank accession number and the same abbreviation for population used in the study (CM – Central Mediterranean, EM – Eastern Mediterranean, CI – Canary Islands, MA – Madeira, PO – Portugal mainland and AZ – Azores). Only the samples from the Adriatic Sea generated in this study are listed under the same ID that was submitted to GenBank.

Haplotype ID and N of sequences	**Sequence ID (including GenBank accession number and locality for all publicly available sequences)**
Hap1: 8	Tp_1 Tp_21 Tp_130 Tp_156 Tp_MH190972_PO Tp_MH191005_MA Tp_MK047074_CI Tp_MK047124_PO
Hap2: 170	Tp_2 Tp_17 Tp_18 Tp_20 Tp_26 Tp_27 Tp_29 Tp_127 Tp_129 Tp_131 Tp_132 Tp_134 Tp_135 Tp_137 Tp_138 Tp_139 Tp_141 Tp_142 Tp_144 Tp_151 Tp_154 Tp_155 Tp_AF489414_EM Tp_AF489417_EM Tp_AF489418_EM Tp_AF489419_EM Tp_AF489420_EM Tp_AF489421_EM Tp_AF489422_EM Tp_EF392633_CI Tp_EF392634_CI Tp_EF439244_MA Tp_EU246363_EM Tp_EU246364_EM Tp_EU246365_EM Tp_EU246366_EM Tp_EU246368_EM Tp_MH190969_PO Tp_MH190970_PO Tp_MH190971_PO Tp_MH190973_PO Tp_MH190974_PO Tp_MH190975_PO Tp_MH190977_PO Tp_MH190979_AZ Tp_MH190980_AZ Tp_MH190984_AZ Tp_MH190986_AZ Tp_MH190987_AZ Tp_MH190988_PO Tp_MH190989_PO Tp_MH190990_PO Tp_MH190991_PO Tp_MH190992_PO Tp_MH190995_PO Tp_MH190996_PO Tp_MH190997_MA Tp_MH190998_MA Tp_MH190999_MA Tp_MH191000_MA Tp_MH191002_MA Tp_MH191003_MA Tp_MH191004_MA Tp_MH191006_MA Tp_MH191008_CM Tp_MH191009_CM Tp_MH191010_CM Tp_MH191011_CM Tp_MH191012_CM Tp_MH191015_CM Tp_MH191016_CM Tp_MH191020_PO Tp_MH191021_PO Tp_MH191022_PO Tp_MH191023_PO Tp_MH191024_PO Tp_MH191025_PO Tp_MH191026_PO Tp_MH191027_CI Tp_MH191032_CI Tp_MH191033_CI Tp_MK047049_AZ Tp_MK047050_AZ Tp_MK047053_AZ Tp_MK047054_AZ Tp_MK047056_AZ Tp_MK047057_AZ Tp_MK047059_AZ Tp_MK047060_AZ Tp_MK047062_AZ Tp_MK047063_AZ Tp_MK047064_AZ Tp_MK047066_AZ Tp_MK047067_AZ Tp_MK047068_AZ Tp_MK047069_CI Tp_MK047070_CI Tp_MK047071_CI Tp_MK047073_CI Tp_MK047076_CI Tp_MK047077_CI Tp_MK047078_CI Tp_MK047079_CI Tp_MK047080_CI Tp_MK047081_CI Tp_MK047083_CI Tp_MK047084_CI Tp_MK047085_CI Tp_MK047086_CI Tp_MK047087_CI Tp_MK047088_CI Tp_MK047090_MA Tp_MK047093_MA Tp_MK047096_MA Tp_MK047098_MA Tp_MK047100_MA Tp_MK047101_MA Tp_MK047102_MA Tp_MK047104_MA Tp_MK047106_MA Tp_MK047107_MA Tp_MK047109_PO Tp_MK047111_PO Tp_MK047112_PO Tp_MK047113_PO Tp_MK047114_PO Tp_MK047115_PO Tp_MK047117_PO Tp_MK047119_PO Tp_MK047121_PO Tp_MK047122_PO Tp_MK047123_PO Tp_MK047125_PO Tp_MK047126_PO Tp_MK047127_PO Tp_MK047128_PO Tp_MK047129_PO Tp_MK047130_PO Tp_MK047131_PO Tp_MK047132_PO Tp_MK047133_PO Tp_MK047135_PO Tp_MK047136_PO Tp_MK047137_PO Tp_MK047138_PO Tp_MK047139_PO Tp_MK047140_PO Tp_MK047141_PO Tp_MK047142_PO Tp_MK047143_PO Tp_MK047144_PO Tp_MK047145_PO Tp_MK047146_PO Tp_MK047148_PO Tp_MK047150_PO Tp_MK047151_PO Tp_MK047152_PO Tp_MK047155_PO Tp_MK047157_PO Tp_MK047158_PO Tp_MK047162_PO Tp_MK047164_PO

	Tp_MK047165_PO Tp_MK047166_PO Tp_MK047167_PO Tp_MK047168_PO Tp_MK047169_CM Tp_MK047171_CM Tp_MK047173_CM Tp_MK047174_CM
Hap3: 14	Tp_3 Tp_AY526547_CM Tp_EF439245_MA Tp_EU246367_EM Tp_MH191007_CM Tp_MH191017_PO Tp_MH191019_PO Tp_MH191029_CI Tp_MH191034_CI Tp_MK047051_AZ Tp_MK047072_CI Tp_MK047099_MA Tp_MK047149_PO Tp_MK047153_PO
Hap4: 33	Tp_22 Tp_23 Tp_145 Tp_146 Tp_147 Tp_148 Tp_150 Tp_153 Tp_AF489423_CM Tp_AF489424_CM Tp_EU246362_EM Tp_MH190981_AZ Tp_MH190982_AZ Tp_MH190983_AZ Tp_MH190985_AZ Tp_MH190993_PO Tp_MH190994_PO Tp_MH191013_CM Tp_MH191014_CM Tp_MH191018_PO Tp_MH191028_CI Tp_MK047058_AZ Tp_MK047061_AZ Tp_MK047075_CI Tp_MK047091_MA Tp_MK047108_MA Tp_MK047110_PO Tp_MK047116_PO Tp_MK047120_PO Tp_MK047156_PO Tp_MK047159_PO Tp_MK047161_PO Tp_MK047172_CM
Hap5: 2	Tp_140 Tp_MH190978_AZ
Hap6: 1	Tp_143
Hap7: 2	Tp_AF489415_EM Tp_AF489416_EM
Hap8: 1	Tp_AY526546_CM
Hap9: 1	Tp_EU246361_EM
Hap10: 1	Tp_MH190976_PO
Hap11: 3	Tp_MH191001_MA Tp_MK047082_CI Tp_MK047089_MA
Hap_12: 1	Tp_MH191030_CI
Hap13: 1	Tp_MH191035_CI
Hap14: 1	Tp_MK047065_AZ
Hap15: 1	Tp_MK047092_MA
Hap16: 1	Tp_MK047094_MA
Hap17: 1	Tp_MK047095_MA
Hap18: 1	Tp_MK047097_MA
Hap19: 1	Tp_MK047103_MA
Hap20: 1	Tp_MK047105_MA
Hap21: 2	Tp_MK047118_PO Tp_MK047170_CM
Hap22: 1	Tp_MK047134_PO
Hap23: 1	Tp_MK047154_PO

Hap24: 1	Tp_MK047160_PO
Hap25: 1	Tp_MK047163_PO

Table S3. Hierarchical analysis of molecular variation (AMOVA) for *Trachurus picturatus* populations, based on *cytb* sequences data. Variation was partitioned among and within groups (Mediterranean Sea and Atlantic Ocean) and populations (Adriatic Sea, Central and Eastern Mediterranean Sea, mainland Portugal, Madeira, Canary Islands and Azores). Calculations shown are: degrees of freedom (d.f.); sums of squares; variance components (Va, Vb, and Vc); percentage of variation; fixation indices (F_{CT}, F_{SC}, F_{ST}); and significance levels (p-value).

Source of variation	**d.f.**	**Sum of squares**	**Variance components**	**Percentage of variation (%)**	**Fixation indices**	**p-value**
Among groups	1	0.381	0.00003 (Va)	0.01	**F_{CT}:** 0.0001	0.23
Among populations within groups	5	1.870	0.00119 (Vb)	0.36	**F_{SC}:** 0.0036	0.33
Within populations	244	81.630	0.33455 (Vc)	99.64	**F_{ST}:** 0.0036	0.29
Total	250	83.880	0.33577			