

SM 4. AMOVA

Table S4.1. Results of AMOVA for COI, and NADH2 datasets for the *T. marmorata* Sardinian sequences. *** = P-values < 0.001; ** = P-value <0.01; * = P-value <0.05. Between parentheses are the locations as shown in Figure 1. S= south, SW = southwestern, N = north, NW = northwestern, E = east, NE = northeast, W = west.

<i>T. marmorata</i> COI (Sardinia)			
Source of variation	Percentage of variation	Fixation Index	P-value
One group			
Among populations	14.90	$\Phi_{ST} = 0.149$	**
Within populations	85.10		
Two groups (N+SW+NW+W / S+E+NE)			
Among groups	-15.66	$\Phi_{CT} = -0.15658$	ns
Among populations	26.83	$\Phi_{SC} = 0.23196$	**
Within populations	88.83	$\Phi_{ST} = 0.11170$	**
Three groups (N+NE+NW / W+SW/S+E)			
Among groups	-0.71	$\Phi_{CT} = 0.007$	ns
Among populations	20.39	$\Phi_{SC} = 0.202$	***
Within populations	80.32	$\Phi_{ST} = 0.197$	***
<i>T. marmorata</i> NADH2 (Sardinia)			
One group			
Among populations	13.08	$\Phi_{ST} = 0.131$	**
Within populations	86.92		
Two groups (N+SW+NW+W / S+E+NE)			
Among groups	-8.98	$\Phi_{CT} = -0.089$	ns
Among populations	19.79	$\Phi_{SC} = 0.181$	**
Within populations	89.19	$\Phi_{ST} = 0.108$	**
Three groups (N+NE+NW / W+SW/S+E)			
Among groups	0.33	$\Phi_{CT} = 0.003$	ns
Among populations	4.38	$\Phi_{SC} = 0.047$	ns
Within populations	95.3	$\Phi_{ST} = 0.047$	*

Table S4.2. Results of AMOVA for COI, and NADH2 datasets for the *T. torpedo* Sardinian sequences. *** = P-values < 0.001; ** = P-value <0.01; * = P-value <0.05. Between parentheses are the locations as shown in Figure 1. S= south, N = north, NE = northeast, W = west.

<i>T. torpedo</i> COI (Sardinia)			
Source of variation	Percentage of variation	Fixation Index	P-value
One group			
Among populations	18.86	$\Phi_{ST} = 0.188$	*
Within populations	81.14		
Two groups (N+W / NE+S)			
Among groups	-45.14	$\Phi_{CT} = -0.451$	ns
Among populations	58.72	$\Phi_{SC} = 0.404$	ns
Within populations	86.42	$\Phi_{ST} = 0.136$	*
Three groups (N+NE / W/S)			
Among groups	-197.15	$\Phi_{CT} = -1.971$	ns
Among populations	215.65	$\Phi_{SC} = 0.725$	ns
Within populations	81.5	$\Phi_{ST} = 0.185$	*
<i>T. torpedo</i> NADH2 (Sardinia)			
One group			
Among populations	-3.82	$\Phi_{ST} = -0.038$	ns
Within populations	103.82		
Two groups (N+NW+W / NE+S)			
Among groups	21.73	$\Phi_{CT} = 0.217$	ns
Among populations	-21.41	$\Phi_{SC} = -0.273$	ns
Within populations	99.69	$\Phi_{ST} = 0.003$	ns
Three groups (N+NE+NW / W / S)			
Among groups	14.54	$\Phi_{CT} = 0.145$	ns
Among populations	-9.31	$\Phi_{SC} = -0.109$	ns
Within populations	94.77	$\Phi_{ST} = 0.052$	ns

Table S4.3. Results of AMOVA for COI, and NADH2 datasets for the *T. nobiliana* Sardinian sequences. *** = P-values < 0.001; ** = P-value <0.01; * = P-value <0.05.

<i>T. nobiliana</i> COI (Sardinia)			
Source of variation	Percentage of variation	Fixation Index	P-value
One group			
Among populations	-90.38	$\Phi_{ST} = -0.904$	ns
Within populations	190.38		
<i>T. nobiliana</i> NADH2 (Sardinia)			
One group			
Among populations	46.58	$\Phi_{ST} = 0.466$	ns
Within populations	53.42		

Table S4.4 Results of AMOVA tested on the base of BAPS results for COI and NADH2 datasets for *T. marmorata*. Between parentheses are the Sardinian locations as shown in Figure 1 (S= south, SW = southwestern, N = north, NW = northwestern, E = east, NE = northeast, W = west), as well as other locations of sequences retrieved in public repositories: Atlantic Ocean (PT = Portugal, Se = Senegal) - Western Mediterranean (TY = Tyrrhenian Sea, Sp = Spain, Al = Algeria) - Central Mediterranean (Ma= Malta, SiC = Sicily, Nad =North Adriatic Sea, Sad = South Adriatic Sea) - Eastern Mediterranean (IS = Israel CY = Cyprus, Tk= Turkey, GR = Greece).

<i>T. marmorata</i> COI (all sequences)			
Source of variation	Percentage of variation	Fixation Index	P-value
One group			
Among populations	53.31	$\Phi_{ST} = 0.533$	***
Within populations	46.69		
Two groups (PT+Nad+SiC+N+SW+NW+W+S+E+NE+TY+Sp+Al / IS+CY+TK+GR+Sad+MA)			
Among groups	57.58	$\Phi_{CT} = 0.575$	***
Among populations	11.27	$\Phi_{SC} = 0.265$	***
Within populations	31.15	$\Phi_{ST} = 0.688$	***
<i>T. marmorata</i> NADH2 (all sequences)			
One group			
Among populations	30.95	$\Phi_{ST} = 0.309$	***
Within populations	69.05		
Three groups (Se / Sp+N+SW+NW+W+S+E+NE / GR+MA)			
Among groups	55.46	$\Phi_{CT} = 0.555$	*
Among populations	6.07	$\Phi_{SC} = 0.136$	**
Within populations	38.47	$\Phi_{ST} = 0.615$	***

Table S4.5. Results of AMOVA tested on the base of BAPS results for COI and NADH2 datasets for *T. torpedo*. Between parentheses are the Sardinian locations as shown in Figure 1 (S= south, N = north, NE = northeast, W = west), as well as other locations of sequences retrieved in public repositories: Atlantic Ocean (PT = Portugal, Se = Senegal) - Western Mediterranean (TY = Tyrrhenian Sea, AI = Algeria) - Central Mediterranean (SiC = Sicily, Sad = South Adriatic Sea) - Eastern Mediterranean (IS = Israel).

<i>T. torpedo</i> COI (all sequences)			
Source of variation	Percentage of variation	Fixation Index	P-value
One group			
Among populations	22.73	$\Phi_{ST} = 0.227$	*
Within populations	77.27		
Two groups (PT+TY+AI+N+NE+W+S / IS+Sad+SiC)			
Among groups	12.36	$\Phi_{CT} = 0.123$	*
Among populations	16.34	$\Phi_{SC} = 0.186$	ns
Within populations	71.30	$\Phi_{ST} = 0.287$	*
Two groups (PT+TY+AI+N+NE+W+S+Sad+SiC / IS)			
Among groups	22.78	$\Phi_{CT} = 0.228$	ns
Among populations	13.01	$\Phi_{SC} = 0.168$	ns
Within populations	64.21	$\Phi_{ST} = 0.358$	*
Three groups (PT+TY+AI+N+NE+W+S / IS / Sad+SiC)			
Among groups	26.87	$\Phi_{CT} = 0.269$	*
Among populations	8.43	$\Phi_{SC} = 0.115$	ns
Within populations	64.70	$\Phi_{ST} = 0.353$	*
<i>T. torpedo</i> NADH2 (all sequences)			
One group			
Among populations	80.23	$\Phi_{ST} = 0.802$	ns
Within populations	19.77		
Two groups (Se / N+NW+W+NE+S)			
Among groups	51.02	$\Phi_{CT} = 0.510$	ns
Among populations	2.79	$\Phi_{SC} = 0.057$	ns
Within populations	46.20	$\Phi_{ST} = 0.538$	ns

Table S4.6. Results of AMOVA tested on the base of BAPS results for COI and NADH2 datasets for *T. nobiliana*. Between parentheses are the Sardinian locations as shown in Figure 1 (S= south, E = east, W = west), as well as other locations of sequences retrieved in public repositories: Atlantic Ocean (CA = Canada, PT = Portugal, USA) - Western Mediterranean (TY = Tyrrhenian Sea) - Central Mediterranean (SiC = Sicily) - Saf = South Africa - AUS = Australia, NZ = New Zealand, Tas = Tasman Sea - Na = not available.

<i>T. nobiliana</i> COI (all sequences)			
Source of variation	Percentage of variation	Fixation Index	P-value
One group			
Among populations	63.36	$\Phi_{ST} = 0.633$	***
Within populations	36.64		
Two groups (Na+Saf+AUS+NZ+PT+SiC+TY+E+S+W / CA)			
Among groups	91.53	$\Phi_{CT} = 0.915$	ns
Among populations	3.05	$\Phi_{SC} = 0.359$	**
Within populations	5.42	$\Phi_{ST} = 0.946$	***
<i>T. nobiliana</i> NADH2 (all sequences)			
One group			
Among populations	83.95	$\Phi_{ST} = 0.839$	***
Within populations	16.05		
Two groups (Na+Tas+Saf+E+S+W / USA)			
Among groups	79.60	$\Phi_{CT} = 0.796$	ns
Among populations	14.66	$\Phi_{SC} = 0.718$	**
Within populations	5.75	$\Phi_{ST} = 0.942$	***