

Supplementary Information

**Different interspecies demographic history within the same locality. The case study of sea cucumber,
cuttlefish and clam in the Greek waters**

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Table S1. Number of RAD-seq reads per individual for all species and populations. It is indicated the percentage of the reads that have been mapped to the reference genomes. *Holothuria glaberina* was used for *Holothuria tubulosa*, *Mercenaria mercenaria* for *Venus verrucosa* samples and *Sepia pharaonis* for *Sepia officinalis*

Species	Populations	Individuals	Reads	mapped
<i>H. tubulosa</i>	Pagasitikos	H1PA	5853260	4934798 (84.31%)
		H1PS	2447488	2094661 (85.58%)
		H1PW	7732194	6576761(85.06%)
		H4PSP	1443339	1211256(83.92%)
		H5PA	6838597	5796517(84.76%)
		H5PS	5919457	5083709(85.88%)
	Thermaikos	H1T	4932295	4179608(84.74%)
		H2T	5019199	4258828(84.85%)
		H3T	5098605	4330708(84.94%)
		H4T	5011624	4251409(84.83%)
		H5TA	9647325	8252229(85.54%)
<i>S. officinalis</i>	Vistonikos	H1VS	8981207	7709035(84.84%)
		H1VSP	2276218	1952079(85.76%)
		H2VSP	2910654	2427989(83.42%)
		H5VS	4729953	4022013(85.03%)
		H6V	4052188	3455180(85.27%)
	Pagasitikos	S2PA	10176035	2119240(20.83%)
		S2PS	6138668	1275020(20.77%)
		S2PW	2146346	451970(21.6%)
		S3PA	3576183	773617(21.63%)
		S3PSP	2090089	440268(21.06%)
		S3PW	2718176	547462(20.14%)
	Thermaikos	S1TSP	2105240	444158(21.1%)

	S1TW	3000446	629416(20.98%)
	S2TS	2258310	450455(19.95%)
	S4TSP	1906487	410536(21.53%)
	S4TW	2561283	548119(21.4%)
Vistonikos	S2VA	4951637	1046338(21.13%)
	S2VW	2344703	513916(21.92%)
	S3VA	1662960	348552(20.96%)
	S3VS	1588804	334005(21.02%)
	S23VW	2133266	448066(21%)
Pagasitikos	V1PA	6385616	4120243(64.52%)
	V1PS	1804258	1050476(58.22%)
	V1PSP	2301364	1393305(60.54%)
	V5PSP	3140219	2116740(67.41%)
	V5PW	2205105	1346926(61.08%)
<i>V. verrucosa</i> Thermaikos	V1TA	2008451	1283780(63.92%)
	V1TW	2962411	1695602(57.24%)
	V5T	2971680	1780557(59.92%)
	V5TS	4020126	2336170(58.11%)
	V5TSP	2545907	1472597(57.84%)
Vistonikos	V1VA	3953531	2335664(59.08%)
	V1VS	2115597	1183302(55.93%)
	V2VSP	2393752	1413086(59.03%)
	V4V	2992297	1730986(57.85%)
	V5V	2253930	1297470(57.56%)

Table S2. Filtering steps that were carried out to generate the final high-quality SNP dataset starting from the raw SNPs output by the GATK pipeline. The number of retained SNPs after each step is reported. GQ: Genotype quality; DP: Genotype depth of coverage; IGR: Individual genotyping rate; maxDP: Depth of coverage (twice the mean depth of coverage of the raw dataset) greater than 416.24 for *H. tubulosa*, 176.62 for *S. officinalis* and 21.76 for *V. verrucosa*, were removed; MAF: Minimum Allele Frequency; hwe: Hardy-Weinberg equilibrium; ld r2: Linkage Disequilibrium pruning r^2 .

Filtering	<i>H. tubulosa</i>	<i>S. officinalis</i>	<i>V. verrucosa</i>
Raw SNPs	5,274,813	71,171	799,035
Biallelic SNPs	4,450,085	56,460	719,636
GQ > 5	4,450,085	56,460	719,636
DP > 5	4,450,085	56,460	719,636
IGR > 80%	37,030	2,341	5,162
maxDP	37,021	2,320	5,150
MAF > 0.05	16,306	1,228	3,477
Hwe p-value > 0.05	16,306	1,083	3,477
ld r^2 < 0.5	16,142	1,083	3,477

Table S3. Confidence intervals for ABC analysis for *Holothuria tubulosa* populations for both direct and logistic regression of the scenarios comparison.

Species	Population		Scenario1	Scenario2	Scenario3	Scenario4
<i>H. tubulosa</i>	Pagasitikos	Regression value	0	0.580	0	0.420
		Direct				
		95% CI low	0	0.147	0	0
		95% CI high	0	1	0	0.853
		Regression value	0.014	0.523	0.008	0.455
	Thermaikos	Logistic				
		Regression	0.009	0.518	0.004	0.449
		95% CI low	0.018	0.528	0.013	0.460
		95% CI high				
		Regression value	0	0.616	0	0.384
Vistonikos	Direct	Regression	0	0.189	0	0
		95% CI low	0	1	0	0.810
		95% CI high	0			
		Regression	0	0.796	0	0.203
		value				
	Logistic	Regression	0	0.739	0	0.146
		95% CI low	0	0.854	0	0.261
		95% CI high	0			
		Regression	0	0.552	0	0.448
		value				

Table S4. Confidence intervals for ABC analysis for *Sepia officinalis* populations for both direct and logistic regression of the scenarios comparison.

Species	Population		Scenario1	Scenario2	Scenario3	Scenario4
S. officinalis	Pagasitikos	Regression value	0.006	0.018	0.924	0.052
		Direct Regression	95% CI low	0	0	0.692
		95% CI high	0.074	0.135	1	0.247
	Thermaikos	Regression value	0	0.025	0.917	0.056
		Logistic Regression	95% CI low	0	0.025	0.911
		95% CI high	0	0.025	0.922	0.061
	Vistonikos	Regression value	0.014	0.306	0.456	0.224
		Direct Regression	95% CI low	0	0	0.019
		95% CI high	0.117	0.709	0.893	0.589
		Regression value	0.016	0.263	0.462	0.259
		Logistic Regression	95% CI low	0.013	0.258	0.456
		95% CI high	0.019	0.268	0.467	0.263
	Vistonikos	Regression value	0	0.078	0.844	0.078
		Direct Regression	95% CI low	0	0	0.526
		95% CI high	0	0.313	1	0.313
		Regression value	0.004	0.034	0.922	0.039
		Logistic Regression	95% CI low	0.002	0.031	0.917
		95% CI high	0.007	0.037	0.927	0.043

Table S5. Confidence intervals for ABC analysis for *Venus verrucosa* populations for both direct and logistic regression of the scenarios comparison.

Species	Population		Scenario1	Scenario2	Scenario3	Scenario4
<i>V. verrucosa</i>	Pagasitikos	Regression value	0.900	0.02	0	0.080
		Direct Regression	95% CI low	0.637	0	0
		95% CI high	1	0.142	0	0.318
	Thermaikos	Regression value	0.921	0.024	0.025	0.029
		Logistic Regression	95% CI low	0.913	0.021	0.025
		95% CI high	0.928	0.027	0.025	0.038
Vistonikos	Thermaikos	Regression value	0.520	0.020	0.260	0.200
		Direct Regression	95% CI low	0.082	0	0
		95% CI high	0.958	0.143	0.645	0.551
	Vistonikos	Regression value	0.956	0.024	0.016	0.003
		Logistic Regression	95% CI low	0.934	0	0
		95% CI high	0.979	0.521	0.539	0.511
Vistonikos	Vistonikos	Regression value	0.880	0	0.08	0.04
		Direct Regression	95% CI low	0.595	0	0
		95% CI high	1	0	0.318	0.212
	Vistonikos	Regression value	0.905	0.003	0.043	0.048
		Logistic Regression	95% CI low	0.898	0.001	0.039
		95% CI high	0.912	0.005	0.048	0.054

Table S6. Mean values of temperature, salinity and oxygen recorded during seasonal samplings.

Temperature (°C)		Chl- α (mg m $^{-3}$)		Salinity (psu)	
	Pagasetikos		Pagasetikos		Pagasetikos
Apr	14	Apr	0.889	Apr	37.97
Jun	21	Jun	0.451	Jun	35.86
Nov	18	Nov	1.205	Nov	37.36
Jan	14	Jan	1.081	Jan	38.55
	Thermaikos		Thermaikos		Thermaikos
Apr	14	Apr	1.871	Apr	37.92
Jun	21	Jun	1.021	Jun	35.39
Nov	18	Nov	1.346	Nov	37.44
Jan	13	Jan	1.467	Jan	38.35
	Vistonikos		Vistonikos		Vistonikos
Apr	12	Apr	0.324	Apr	38.06
Jun	19	Jun	0.223	Jun	35.96
Nov	17	Nov	0.496	Nov	37.55
Jan	11	Jan	0.581	Jan	38.39

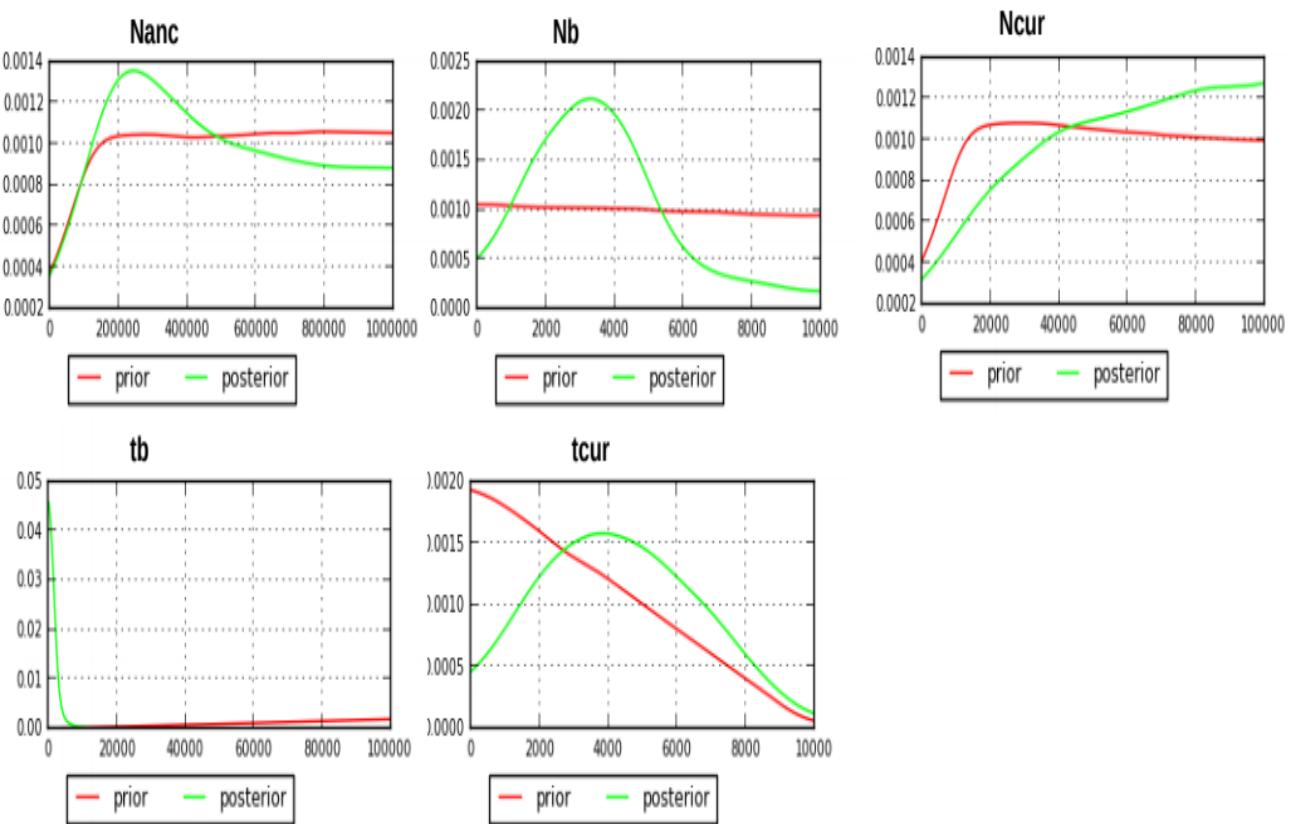


Figure S1. Posterior (green line) and prior (red line) distribution plots of ABC analysis based on 4×10^6 simulated data sets of historical effective population sizes and time of historical events based on scenario 2 of *H. tubulosa* for Pagasitikos population; Nanc: Ancestral population, Nb: bottlenecked population, Ncur: recovered population, tb: time of bottleneck event, tcur: time of recovery

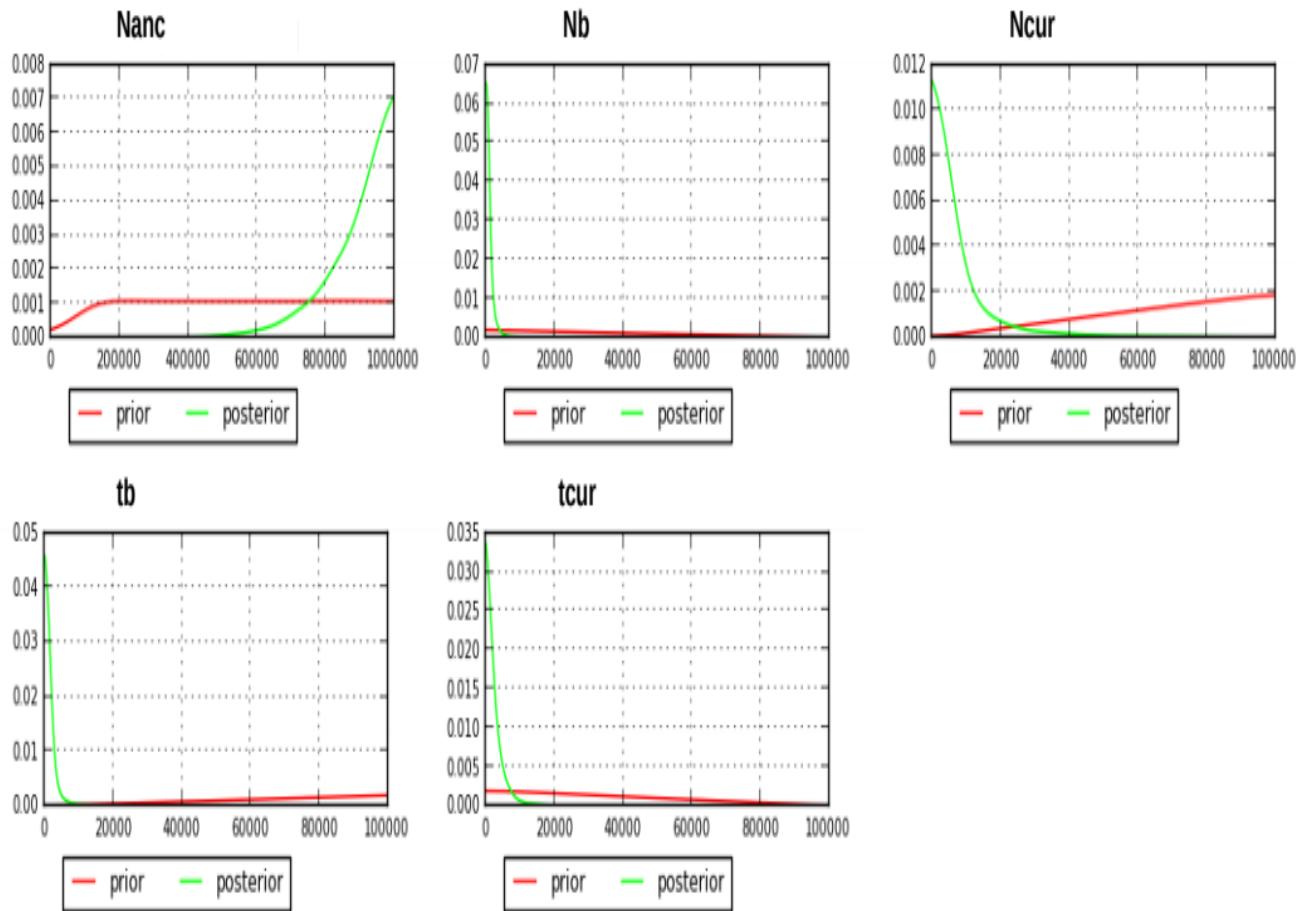


Figure S2. Posterior (green line) and prior (red line) distribution plots of ABC analysis based on 4×10^6 simulated data sets of historical effective population sizes and time of historical events based on scenario 2 of *H. tubulosa* for Thermaikos population; N_{anc}: Ancestral population, N_b: bottlenecked population, N_{cur}: recovered population, t_b: time of bottleneck event, t_{cur}: time of recovery

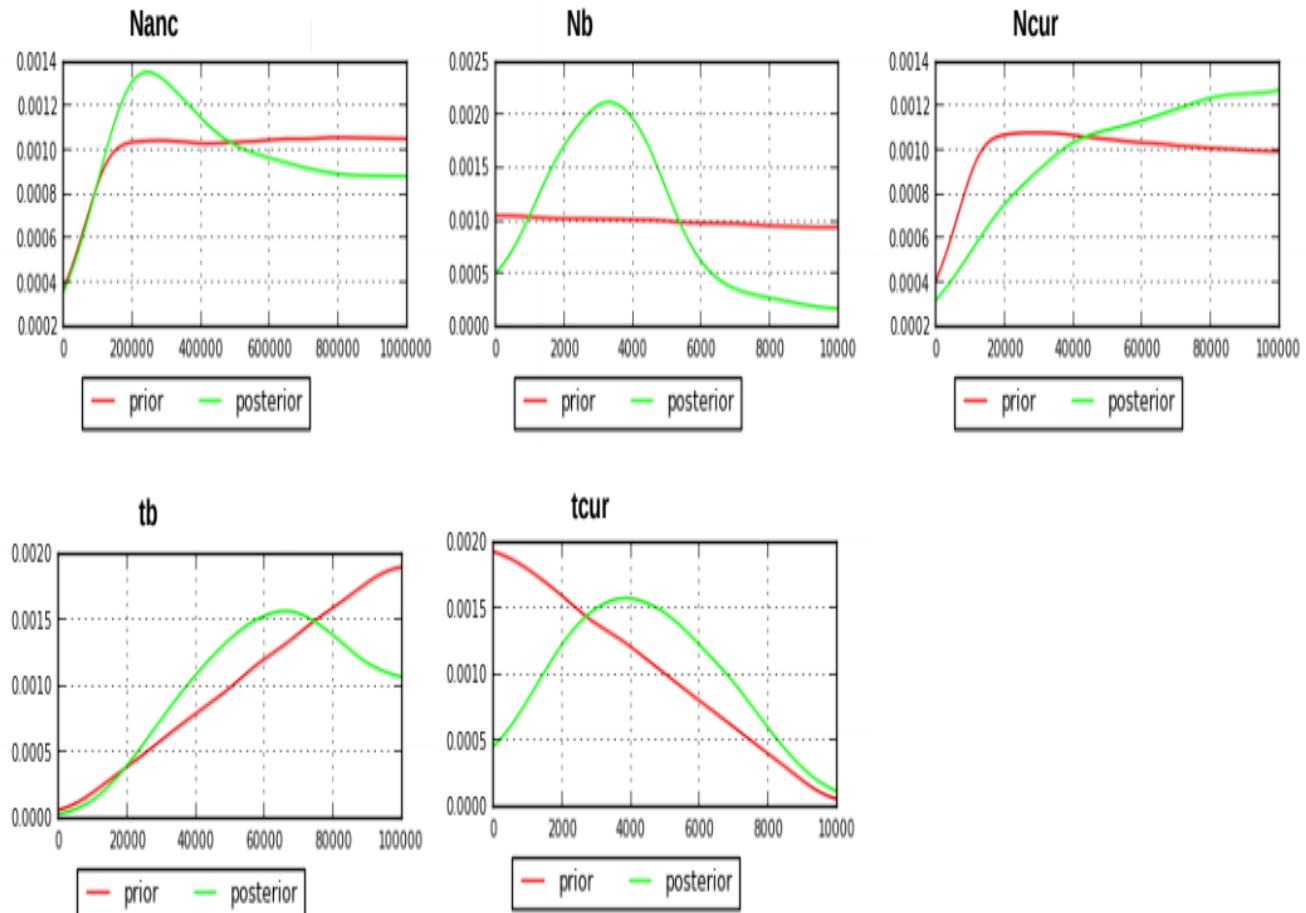


Figure S3. Posterior (green line) and prior (red line) distribution plots of ABC analysis based on 4×10^6 simulated data sets of historical effective population sizes and time of historical events based on scenario 2 of *H. tubulosa* for Vistonikos population; N_{anc}: Ancestral population, N_b: bottlenecked population, N_{cur}: recovered population, t_b: time of bottleneck event, t_{cur}: time of recovery

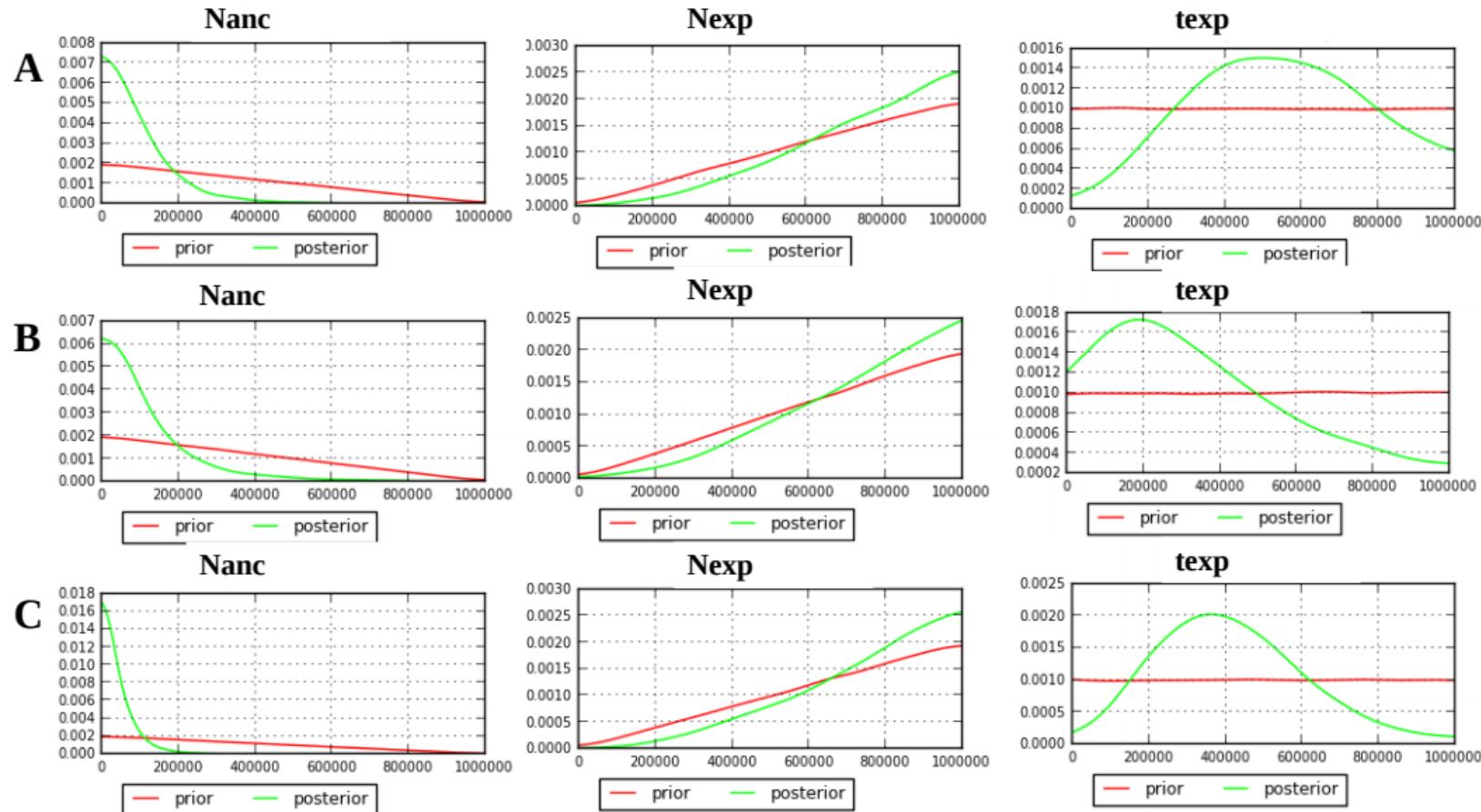


Figure S4. Posterior (green line) and prior (red line) distribution plots of ABC analysis based on 4×10^6 simulated data sets of historical effective population sizes and time of historical events based on scenario 3 of *S. officinalis* for Pagasitikos (A), Thermaikos (B) and Vistonikos (C) population; N_{anc}: Ancestral population, N_{exp}: expanded population, t_{exp}: time of expansion

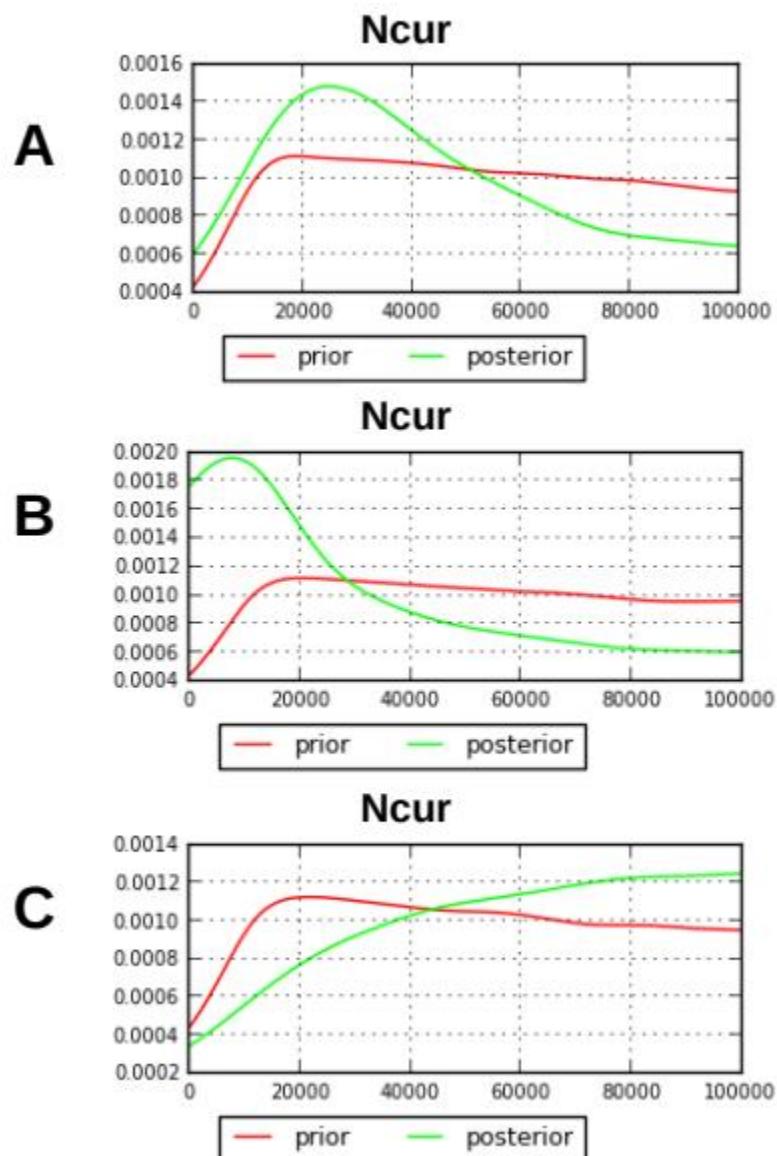


Figure S5. Posterior (green line) and prior (red line) distribution plots of ABC analysis based on 4×10^6 simulated data sets of historical effective population sizes and time of historical events based on scenario 1 of *V. verrucosa* for Pagasitikos (A), Thermaikos (B) and Vistonikos (C) population; N_{cur} : constant population effective size

Table S7. Genetic indices per species and population. No: Number of alleles; Ea: Effective alleles; H_{OBS} : observed heterozygosity; H_{EXP} : expected heterozygosity, F_{IS} : fixation inbreeding index

Holothuria	Pop_ID	No	Ea	HoBS	HExp	Fis
	Pagasanikos	29946	1.295	0.120 +/- 0.001	0.228 +/- 0.001	0.362 +/- 0.002
	Vistonida	14344	1.229	0.158 +/- 0.001	0.186 +/- 0.001	0.124 +/- 0.002
	Thermaikos	1817	1.223	0.338 +/- 0.002	0.183 +/- 0.001	-0.234 +/- 0.002
Sepia	Pop_ID	No	Ea	HoBS	HExp	Fis
	Pagasanikos	212	1.515	0.531 +/- 0.011	0.340 +/- 0.005	-0.016 +/- 0.035
	Thermaikos	195	1.494	0.486 +/- 0.013	0.331 +/- 0.006	0.047 +/- 0.043
	Vistonida	114	1.414	0.476 +/- 0.013	0.293 +/- 0.006	-0.010 +/- 0.033
Venus	Pop_ID	No	Ea	HoBS	HExp	Fis
	Pagasanikos	450	1.285	0.296 +/- 0.005	0.222 +/- 0.003	-0.095 +/- 0.009
	Thermaikos	388	1.285	0.309 +/- 0.005	0.222 +/- 0.003	-0.121 +/- 0.010
	Vistonida	393	1.295	0.321 +/- 0.006	0.228 +/- 0.003	-0.135 +/- 0.008

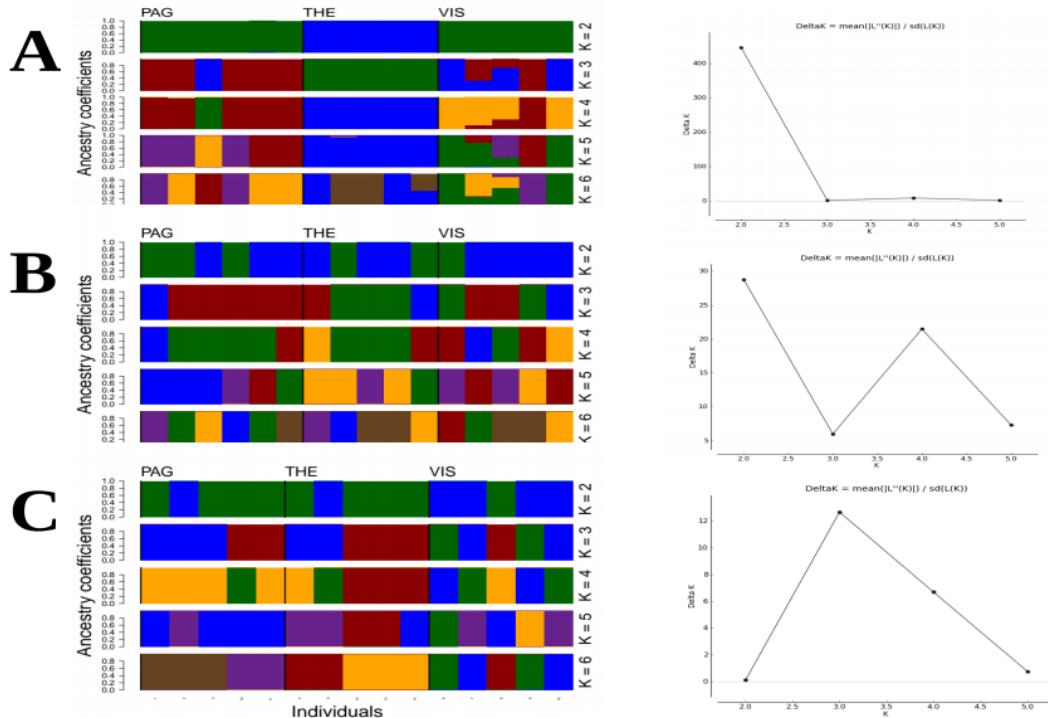


Figure S6. Structure plots and Delta-K against K for Structure run given the reduction of Ln from K = 2 for all populations made using HARVESTER. A: Holothuria; B: Sepia; C: Venus