

Supplementary material

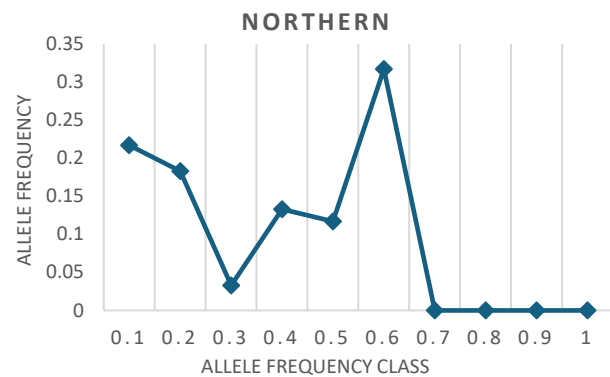
To:

High genetic diversity yet weak population genetic structure in European common terns
by

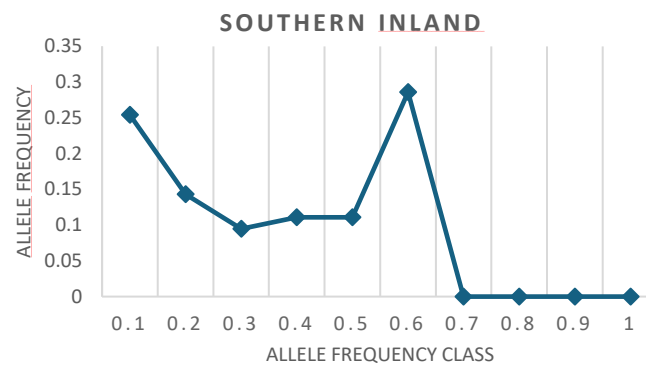
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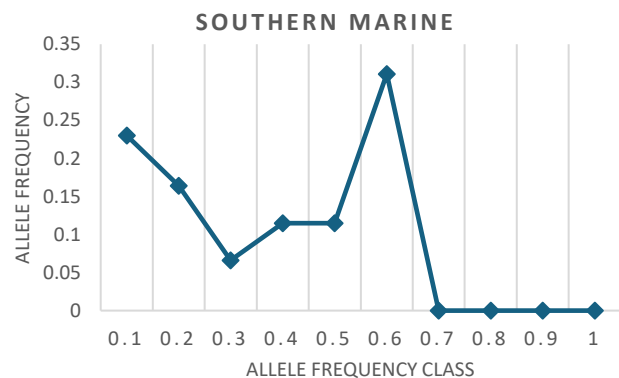
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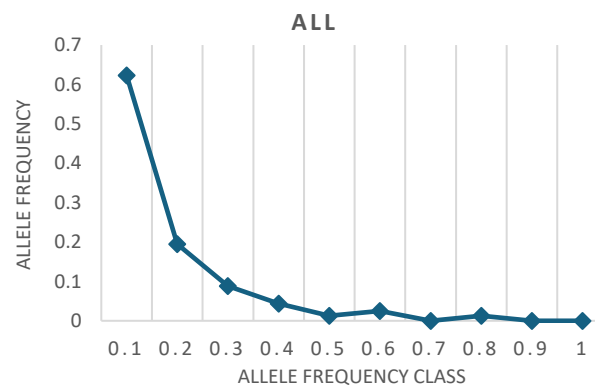
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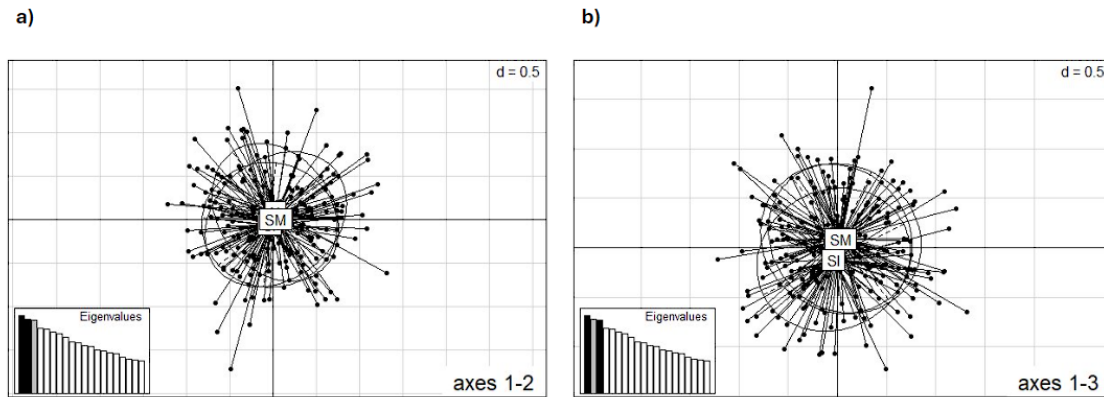
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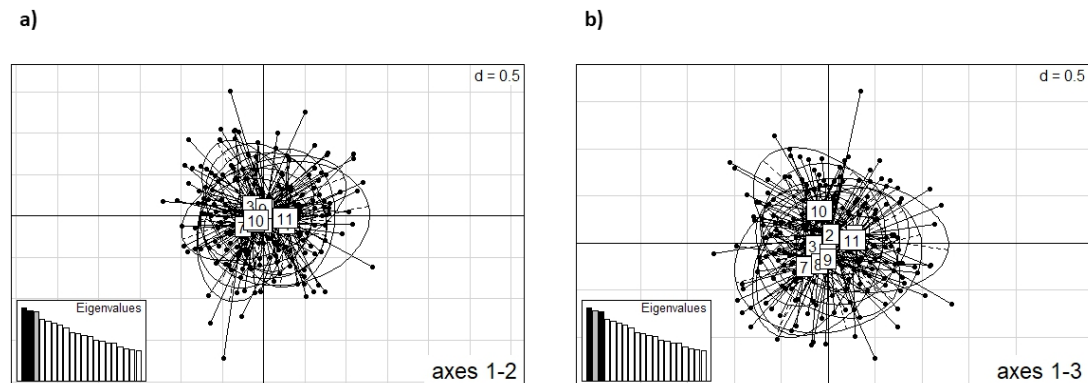
d)



Supplementary Figure S1. Distribution of microsatellite allele frequencies for separate groups: a) Northern, b) Southern Inland, c) Southern Marine group, and d) all 219 samples, calculated using the mode shift test in Bottleneck software.



Supplementary Figure S2. Results of Principal Components Analysis from ADEGENET with samples in the Northern (N), Southern Inland (SI), and Southern Marine (SM) group showing: a) first and second axes with corresponding eigenvalues in the lower left corner; b) first and third axes with corresponding eigenvalues in the lower left corner.



Supplementary Figure S3. Results of Principal Components Analysis from ADEGENET with samples grouped by sampling locations showing: a) first and second axes with corresponding eigenvalues in the lower left corner; b) first and third axes with corresponding eigenvalues in the lower left corner. Numbers correspond to the sampling locations (see Fig. 1)

Supplementary Table S1. List of sampling locations from each group with coordinates and numbers of samples used for microsatellite and mitochondrial DNA analyses.

Group	Country	Location	Location abbreviation	Sample type	Coordinates	Number of samples					
						Microsatellites		Mitochondrial DNA			
						This study	Total per group	This study	Svetličić et al. (2019)	Total per location	Total per group
Northern	Germany	1. Riether Werder	RW	Feather	53° 42' 22" N, 14° 16' 07" E	/	65	25	/	25	85
		2. Lieps	LIEPS	Feather	53°27' 15" N, 13° 08' 43" E	65		60	/	60	
Southern Inland	Hungary	3. Varpalota	VAR	Blood	47° 11' 40" N, 18° 11' 25" E	14	95	13	/	13	153
		4. Irmapuszta	IRMA	Blood	46° 45' 59" N, 17° 44' 46" E	17		14	/	14	
	Slovenia	5. Ptuj	PTUJ	Blood	46° 24' 7" N, 15° 53' 10" E	21		/	23	23	
	Croatia	6. Šoderica	SOD	Blood	46° 14' 28" N, 16° 54' 45" E	/		17	/	17	
		7. Rakitje	RAK	Blood	45° 47' 49" N, 15° 50' 24" E	15		45	4	49	
		8. Siromaja	SIR	Blood	45° 45' 42" N, 16° 11' 4" E	28		14	23	37	
Southern Marine	Slovenia	9. Sečovelje	SEC	Feather	45° 29' 12" N, 13° 35' 53" E	19	59	11	9	20	81
	Italy	10. Rovigo	ROV	Blood	45° 1' 31" N, 12° 13' 31" E	24		23	/	23	
		11. Ravenna	RAV	Blood	44 ° 30' 14" N, 12°15' 15" E	16		15	/	15	
	Croatia	12. Školjić	SKO	Blood	43° 58' 24" N, 15° 21' 9" E	/		23	/	23	
Total						219	219	260	59	319	319

Supplementary Table S2. Microsatellite diversity indices with the number of alleles (Na), the number of private alleles (Pa), allelic richness (AR), observed (Ho) and expected (He) heterozygosity, and p-values for HWE test before the multiple-test correction (pHWE). After correction, none of the p-values remained significant. Mean values and standard deviation (S.D.) are provided where applicable.

Locus	Northern (N=65)						Southern Inland (N=95)						Southern Marine (N=59)						All samples (N=219)				
	Na	Pa	AR	Ho	He	pHWE	Na	Pa	AR	Ho	He	pHWE	Na	Pa	AR	Ho	He	pHWE	Na	AR	Ho	He	pHWE
RBG29	9	1	8.723	0.769	0.796	0.143	8	0	7.518	0.695	0.751	0.627	8	0	7.898	0.780	0.726	0.936	9	7.815	0.740	0.758	0.189
RBG18	8	2	7.843	0.692	0.753	0.510	6	0	5.931	0.716	0.738	0.493	6	0	5.949	0.746	0.728	0.191	8	6.657	0.717	0.739	0.959
RBG28	8	1	7.859	0.723	0.789	0.648	7	0	6.972	0.842	0.777	0.270	7	0	6.998	0.780	0.732	0.844	8	7.208	0.790	0.768	0.822
RBG27	9	0	8.625	0.734	0.699	0.152	10	1	9.541	0.737	0.766	0.020	7	0	6.931	0.552	0.574	0.376	10	8.947	0.687	0.702	0.031
RBG13	6	0	6.000	0.781	0.764	0.797	6	0	6.000	0.811	0.792	0.732	6	0	6.000	0.702	0.758	0.561	6	6.000	0.773	0.780	0.861
K32	3	0	3.000	0.393	0.348	0.880	3	0	2.999	0.316	0.380	0.110	4	1	3.949	0.339	0.337	0.339	4	3.260	0.344	0.359	0.474
MsSh23	9	1	8.548	0.754	0.749	0.001	12	2	10.766	0.747	0.761	0.909	9	1	8.949	0.864	0.845	0.513	14	10.635	0.781	0.795	0.129
MsSh21	9	1	8.979	0.846	0.790	0.493	8	0	7.531	0.777	0.765	0.425	7	0	7.000	0.627	0.737	0.220	9	8.201	0.757	0.765	0.225
MsSh07	6	0	5.981	0.692	0.656	0.016	7	0	6.558	0.737	0.654	0.420	7	0	6.896	0.593	0.644	0.362	7	6.615	0.685	0.654	0.763
MsSh10	5	0	4.982	0.508	0.556	0.235	5	0	4.998	0.600	0.609	0.379	5	0	4.996	0.525	0.568	0.846	5	4.962	0.553	0.585	0.305
MsSh31	4	0	3.862	0.523	0.613	0.134	4	0	3.989	0.642	0.686	0.463	4	0	4.000	0.763	0.660	0.167	4	3.950	0.639	0.670	0.798
MsSh20	13	1	12.584	0.831	0.877	0.196	13	0	12.326	0.853	0.877	0.468	13	0	12.792	0.695	0.839	0.053	14	12.236	0.804	0.871	0.100
MsSh09	8	0	7.995	0.738	0.821	0.375	10	1	9.520	0.863	0.839	0.871	8	0	7.965	0.793	0.813	0.451	10	9.110	0.807	0.834	0.185
MsSh18	13	3	12.788	0.846	0.858	0.121	13	1	12.266	0.758	0.819	0.635	11	1	10.945	0.712	0.816	0.406	17	13.426	0.772	0.834	0.078
MsSh08	10	2	9.721	0.800	0.819	0.022	8	0	7.562	0.737	0.806	0.096	8	1	7.896	0.729	0.724	0.540	11	8.805	0.753	0.792	0.048
MsSh48	10	0	9.982	0.938	0.884	0.182	10	0	9.911	0.853	0.856	0.174	10	0	9.949	0.831	0.876	0.568	10	9.979	0.872	0.874	0.155
MsSh03	5	0	5.000	0.646	0.676	0.763	6	1	5.932	0.600	0.657	0.192	5	0	4.949	0.610	0.584	0.976	6	5.588	0.616	0.646	0.177
MsSh37	7	0	6.993	0.475	0.421	0.935	7	0	6.474	0.489	0.461	0.428	5	0	5.000	0.446	0.429	0.200	7	6.427	0.473	0.441	0.632
Mean	7.89		7.748	0.705	0.715		7.94		7.600	0.709	0.722		7.22		7.170	0.671	0.688		8.83	7.768	0.698	0.715	
S.D.	2.76			0.145	0.150		2.90			0.140	0.132		2.42			0.139	0.145		3.55		0.132	0.140	
Sum	142	12	139.47				143	6	136.79				130	4	129.06				159	139.82			

Supplementary Table S3. Pairwise F_{ST} values between sampling sites based on microsatellite data with lines dividing them into their respective groups. Significant values ($p < 0.05$) are marked in bold, while darker shades depict higher significant F_{ST} values according to the legend in the lower right corner.

Group	Northern		Southern Inland					Southern Marine		
	Sampling location	Lieps	Varpalota	Irmapuszta	Ptuj	Rakitje	Siromaja	Sečovlje	Rovigo	Ravenna
Northern	Lieps	-								
Southern Inland	Varpalota	0.0090	-							
	Irmapuszta	0.0087	0.0074	-						
	Ptuj	0.0046	0.0072	0.0012	-					
	Rakitje	0.0182	0.0142	0.0289	0.0060	-				
	Siromaja	0.0076	0.0082	0.0173	0.0052	0.0040	-			
Southern Marine	Sečovlje	0.0153	0.0212	0.0322	0.0163	0.0329	0.0169	-		
	Rovigo	0.0141	0.0131	0.0222	0.0181	0.0356	0.0149	0.0180	-	
	Ravenna	0.0159	0.0124	0.0109	0.0095	0.0323	0.0178	0.0178	0.0155	-

F_{ST} stat. significant

>0.03

>0.02<0.03

>0.01<0.02

<0.01

Supplementary Table S4. Variable sites for all haplotypes with the order number in the first row and nucleotide position in the second row. Dots represent nucleotides identical to the first sequence.

Haplotype ID	1 5	2 18	3 22	4 39	5 43	6 76	7 88	8 93	9 96	10 99	11 130	12 224	13 265	14 270	15 283	16 390	17 399	18 439	19 474	20 479	21 482	22 709	23 710
Stehi01	A	T	A	-	C	A	A	C	C	A	G	T	A	G	A	T	T	A	C	G	G	T	G
Stehi02	G	.	.	-	.	.	.	.	T	.	.	.	.	.	.	.	.	.	.	.	.	.	.
Stehi03	.	.	.	-	.	.	.	.	T	.	.	.	.	.	.	.	.	.	.	.	.	.	.
Stehi04	.	.	.	-	.	.	.	.	.	.	A	.	.	.	.	.	.	.	.	.	.	.	.
Stehi05	G	.	.	-	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
Stehi06	.	.	.	-	.	.	.	T	T	.	.	.	.	.	.	.	.	.	.	.	.	.	.
Stehi07	.	.	.	-	.	.	.	.	T	.	.	.	.	.	.	.	.	G	.	.	.	.	.
Stehi08	.	C	.	-	.	.	.	.	T	.	A	.	.	.	.	.	.	.	.	.	.	.	.
Stehi09	.	.	.	-	.	.	.	.	.	.	.	.	.	A	.	.	.	.	.	.	.	.	.
Stehi10	G	.	.	-	.	.	.	.	T	.	.	.	.	.	.	.	.	.	T	.	.	.	.
Stehi11	.	.	.	-	.	.	.	.	T	.	.	.	.	.	.	.	.	.	T	.	.	.	.
Stehi12	.	.	.	-	.	.	.	.	T	.	A	.	.	.	.	.	.	.	.	.	.	.	.
Stehi13	.	.	.	-	.	G	.	.	T	.	.	.	.	.	.	.	.	.	.	.	.	.	.
Stehi14	.	.	.	-	.	.	.	T	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
Stehi15	.	.	.	-	T	.	.	.	T	.	A	.	.	.	.	.	.	.	.	.	.	.	.
Stehi16	G	.	.	-	.	.	.	.	T	.	A	.	.	.	.	.	.	.	.	.	.	.	.
Stehi17	.	.	.	-	.	.	.	T	.	.	A	.	.	.	.	.	.	.	.	.	.	.	.
Stehi18	.	.	.	-	.	.	.	.	T	G	A	.	.	.	.	.	.	.	.	.	.	.	.
Stehi19	.	.	.	-	.	.	.	.	T	.	A	.	.	G	.	.	.	.	.	.	.	.	.
Stehi20	G	.	.	-	.	.	.	T	T	.	.	.	.	.	.	.	.	.	.	.	.	.	.
Stehi21	.	.	.	-	T	.	.	T	T	.	.	.	.	.	.	.	.	.	.	.	.	.	.
Stehi22	.	C	.	-	.	.	.	.	T	.	.	.	.	.	.	.	.	.	.	.	.	.	.
Stehi23	G	.	.	-	.	G	.	.	T	.	.	A	.	.	.	.	.	.	.	.	.	.	.
Stehi24	.	.	.	-	.	.	.	.	T	.	A	.	.	.	.	.	.	.	.	.	A	.	.
Stehi25	.	.	.	-	.	.	.	.	T	.	.	G	.	.	.	.	.	.	.	.	.	.	.
Stehi26	.	.	.	-	.	.	.	.	T	G	.	.	.	.	.	.	.	.	.	.	.	.	.
Stehi27	G	.	.	T	.	G	.	.	T	.	.	.	.	.	.	.	.	.	.	.	.	.	.
Stehi28	.	.	.	T	.	.	.	.	T	.	A	.	.	.	.	.	.	.	.	.	.	.	.
Stehi29	G	.	.	-	.	.	.	T	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
Stehi30	.	.	G	-	.	.	.	.	T	.	.	.	.	.	.	.	.	.	.	.	.	.	.
Stehi31	.	.	.	-	.	.	.	.	T	.	.	.	.	.	.	.	.	.	T	A	.	.	.
Stehi32	.	.	.	-	.	.	.	.	T	G	.	.	.	.	.	.	G	.	.	.	.	.	.
Stehi33	.	.	.	-	.	.	G	.	T	.	.	.	.	.	.	.	.	.	.	.	.	.	.
Stehi34	.	.	.	-	.	.	.	.	.	.	A	.	.	.	.	C	.	.	.	.	.	.	.
Stehi35	.	.	.	T	.	.	.	.	T	.	.	.	.	.	.	.	.	.	.	.	.	.	.
Stehi36	G	.	.	-	.	.	.	.	T	.	.	.	.	.	.	.	.	.	.	.	.	G	T
Stehi37	.	.	.	-	.	.	.	.	T	.	.	.	.	.	.	.	.	.	.	.	.	G	T
Stehi38	.	.	.	-	.	.	.	.	T	.	A	.	.	.	.	.	.	.	.	.	.	G	T
Stehi39	G	.	.	-	.	.	.	.	T	G	.	.	.	.	.	.	.	.	.	.	.	.	.
Stehi40	.	.	.	-	.	.	.	.	T	.	.	.	.	.	G	.	.	.	.	.	.	.	.

Supplementary Table S5. Relative frequencies of mtDNA control region haplotypes by groups and for all samples. Absolute frequencies of haplotypes are shown in brackets.

Haplotype ID	Northern (N=85)	Southern Inland (N=153)	Southern Marine (N=81)	All samples (N=319)
Stehi01	0.0588 (5)	0.098 (15)	0.1358 (11)	0.0972 (31)
Stehi02	0.0118 (1)	0.0392 (6)	0.0864 (7)	0.0439 (14)
Stehi03	0.4941 (42)	0.3333 (51)	0.4321 (35)	0.4013 (128)
Stehi04	0.0353 (3)	0.0784 (12)	0.0247 (2)	0.0533 (17)
Stehi05	0.0353 (3)	0.0458 (7)		0.0313 (10)
Stehi06	0.0706 (6)	0.0327 (5)	0.0864 (7)	0.0564 (18)
Stehi07		0.0588 (9)		0.0282 (9)
Stehi08		0.0065 (1)		0.0031 (1)
Stehi09		0.0065 (1)		0.0031 (1)
Stehi10		0.0065 (1)		0.0031 (1)
Stehi11	0.0235 (2)	0.0065 (1)		0.0094 (3)
Stehi12	0.1059 (9)	0.0719 (11)	0.037 (3)	0.0721 (23)
Stehi13		0.0065 (1)		0.0031 (1)
Stehi14	0.0118 (1)	0.0131 (2)	0.0988 (8)	0.0345 (11)
Stehi15		0.0261 (4)		0.0125 (4)
Stehi16	0.0118 (1)	0.0131 (2)		0.0094 (3)
Stehi17		0.0065 (1)		0.0031 (1)
Stehi18	0.0235 (2)		0.037 (3)	0.0157 (5)
Stehi19		0.0131 (2)		0.0063 (2)
Stehi20		0.0131 (2)		0.0063 (2)
Stehi21		0.0065 (1)		0.0031 (1)
Stehi22	0.0118 (1)		0.0617 (5)	0.0188 (6)
Stehi23		0.0392 (6)		0.0188 (6)
Stehi24	0.0353 (3)			0.0094 (3)
Stehi25	0.0235 (2)			0.0063 (2)
Stehi26		0.0131 (2)		0.0063 (2)
Stehi27	0.0118 (1)			0.0031 (1)
Stehi28	0.0118 (1)			0.0031 (1)
Stehi29	0.0118 (1)			0.0031 (1)
Stehi30	0.0118 (1)			0.0031 (1)
Stehi31		0.0065 (1)		0.0031 (1)
Stehi32		0.0065 (1)		0.0031 (1)
Stehi33		0.0065 (1)		0.0031 (1)
Stehi34		0.0065 (1)		0.0031 (1)
Stehi35		0.0065 (1)		0.0031 (1)
Stehi36		0.0065 (1)		0.0031 (1)
Stehi37		0.0065 (1)		0.0031 (1)
Stehi38		0.0065 (1)		0.0031 (1)
Stehi39		0.0065 (1)		0.0031 (1)
Stehi40		0.0065 (1)		0.0031 (1)

Supplementary Table S6. Supplementary Table S6. Mitochondrial DNA pairwise F_{ST} (below diagonal) and Φ_{ST} values (above diagonal) between groups. N – Northern group, SI – Southern Inland group (whole sample size), SI subsample – Southern Inland group subsample (81 samples), SM – Southern Marine group. Significant values marked in bold ($p < 0.05$).

Group	N	SI / SI subsample	SM
N		0.0079 / 0.0374	0.0211
SI / SI subsample	0.0168 / 0.0348		0.0212 / 0.0350
SM	0.0110	0.0157 / 0.0278	

Supplementary Table S7. Pairwise F_{ST} values (below diagonal) and pairwise Φ_{ST} values (above diagonal) between sampling sites based on mtDNA with lines dividing them into their respective groups. Significant values ($p < 0.05$) are marked in bold, while darker shades depict higher significant F_{ST}/Φ_{ST} values. Abbreviations of sampling locations are specified in Suppl. Table 1.

Group		Northern		Southern Inland						Southern Marine			
	Location	RW	LIEPS	VAR	IRMA	PTUJ	SOD	RAK	SIR	SEC	ROV	RAV	SKO
Northern	RW		0.0013	-0.0484	0.0278	-0.0012	0.0065	0.0497	0.0155	0.0197	0.0238	0.0278	-0.0079
	LIEPS	0.0419		-0.0186	0.0691	0.0425	0.1095	0.0408	0.0149	0.0159	0.0876	0.1044	-0.0212
Southern Inland	VAR	-0.0173	0.0602		-0.0082	-0.0315	0.0024	-0.0005	-0.0241	0.0012	0.0376	0.0468	-0.0174
	IRMA	-0.0140	0.0918	-0.0461		0.0154	0.0487	0.0423	0.0337	0.0514	0.0937	0.0905	0.0539
	PTUJ	-0.0079	0.0599	-0.0074	-0.0120		0.0247	0.0090	-0.0126	0.0129	0.0394	0.0474	0.0346
	SOD	0.0079	0.0758	-0.0006	-0.0039	-0.0117		0.1369	0.0997	0.1108	0.0419	0.0375	0.0905
	RAK	-0.0024	0.0253	-0.0075	0.0055	-0.0069	0.0132		-0.0132	0.0284	0.1363	0.1518	0.0469
	SIR	0.0094	0.0175	0.0210	0.0299	0.0124	0.0329	-0.0058		-0.0103	0.0760	0.0890	0.0098
Southern Marine	SEC	0.0122	0.0204	0.0365	0.0478	0.0322	0.0723	0.0099	0.0028		0.0268	0.0370	-0.0174
	ROV	-0.0081	0.0464	-0.0047	-0.0054	0.0053	0.0152	0.0031	0.0016	-0.0141		-0.0569	0.0455
	RAV	0.0214	0.0843	0.0030	-0.0001	0.0227	0.0388	0.0360	0.0313	0.0578	-0.0077		0.0609
	SKO	0.0482	0.0083	0.0680	0.0919	0.0581	0.0971	0.0285	0.0296	0.0087	0.0434	0.0849	

F_{ST} stat.
significant

>0.09

>0.06<0.09

>0.03<0.06

<0.03

Φ_{ST}
stat.significant

>0.015

>0.1<0.15

>0.05<0.1

<0.05