

Population genetic structure of the perlemoen *Haliotis midae* in South Africa: evidence of range expansion and founder events

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Appendix 1. *Haliotis midae*. Allozyme genetic summary statistics for the 5 polymorphic loci at each locality. N = number of individuals analysed, H_o = observed heterozygosity, H_e = expected heterozygosity

Locus/allele	Paternoster	Hangklip	Mossel Bay	Cape Recife	Wavecrest
<i>dia-1</i>					
106	0.045	0.010	0.012	0.010	0.010
104	0.352	0.323	0.373	0.286	0.268
100	0.568	0.656	0.618	0.612	0.646
97	0.023	0.010	0.000	0.031	0.049
85	0.011	0.000	0.000	0.061	0.024
N	44	48	51	49	41
H_o	0.432	0.458	0.529	0.469	0.463
H_e	0.557	0.470	0.484	0.544	0.513
<i>gpi-1</i>					
127	0.000	0.010	0.010	0.010	0.010
114	0.125	0.260	0.186	0.230	0.180
100	0.830	0.680	0.765	0.730	0.780
80	0.045	0.040	0.010	0.020	0.030
77	0.000	0.010	0.029	0.010	0.000
N	44	50	51	50	50
H_o	0.298	0.460	0.412	0.400	0.380
H_e	0.273	0.473	0.383	0.418	0.362
<i>mdh-1</i>					
105	0.011	0.000	0.000	0.000	0.000
100	0.886	0.898	0.912	0.920	0.987
84	0.045	0.034	0.039	0.060	0.038
68	0.057	0.068	0.049	0.020	0.064
N	44	44	50	50	50
H_o	0.192	0.192	0.176	0.120	0.179
H_e	0.211	0.190	0.166	0.151	0.191
<i>mpi-1</i>					
116	0.443	0.580	0.529	0.515	0.698
100	0.523	0.390	0.412	0.324	0.219
95	0.000	0.010	0.039	0.074	0.010
75	0.034	0.020	0.020	0.074	0.052
65	0.000	0.000	0.000	0.015	0.021
N	44	50	48	50	50
H_o	0.500	0.500	0.544	0.412	0.548
H_e	0.535	0.516	0.569	0.629	0.467
<i>pgm-1</i>					
117	0.000	0.010	0.000	0.000	0.000
112	0.307	0.330	0.324	0.357	0.344
100	0.614	0.530	0.598	0.582	0.552
88	0.068	0.110	0.049	0.051	0.083
79	0.011	0.020	0.029	0.010	0.021
N	44	50	51	49	48
H_o	0.531	0.540	0.540	0.449	0.521
H_e	0.477	0.604	0.588	0.537	0.576

Appendix 2. *Haliotis midae*. Allele frequencies for 3 microsatellite loci from 6 locations in South Africa. Number of individuals in parentheses. For locality name abbreviations see Fig. 1. bp: base pairs

Alleles (bp)	Da (29)	Ri. (29)	Kl (50)	Ms (50)	St (26)	Cr (51)
<i>CmrHr 2.15</i>						
243	–	–	0.031	–	–	0.020
249	–	0.058	–	0.017	–	–
251	–	–	–	–	–	0.010
253	–	0.019	0.010	0.017	–	0.020
257	–	0.019	0.010	–	–	–
261	–	0.038	0.052	–	–	–
263	–	0.058	–	–	–	–
265	0.024	–	0.052	–	–	–
267	0.286	0.308	0.365	0.103	0.229	0.176
269	0.071	0.038	–	–	–	–
271	–	–	0.010	–	–	–
273	0.048	–	0.010	–	–	0.039
275	0.071	–	0.010	–	–	0.020
276	0.024	–	–	–	–	–
277	0.452	0.385	0.333	0.690	0.625	0.569
279	–	0.019	0.031	0.086	0.021	0.069
281	0.024	0.038	0.063	0.069	0.063	0.069
283	–	–	0.021	0.017	0.063	0.010
293	–	0.019	–	–	–	–
<i>CmrHr 2.23</i>						
243	0.917	0.904	0.878	0.897	0.808	0.843
253	0.083	0.096	0.122	0.103	0.192	0.157
<i>CmrHr 2.29</i>						
426	0.354	0.212	0.214	0.310	0.558	0.314
428	–	–	0.010	0.034	–	0.010
430	–	–	0.010	–	–	–
442	–	–	0.010	–	–	–
444	–	–	0.010	–	–	–
446	–	–	0.010	–	–	–
448	0.063	0.096	0.071	–	0.038	0.069
450	–	–	0.010	–	–	0.010
452	–	–	0.020	–	–	–
454	0.021	–	0.010	–	–	–
456	–	–	0.020	–	–	–
458	0.021	–	0.010	0.086	–	0.029
460	–	–	0.031	0.069	–	–
462	0.438	0.615	0.500	0.345	0.365	0.451
464	0.021	–	0.020	–	–	0.010
466	–	–	0.020	0.017	–	–
468	0.083	0.077	0.020	0.138	0.038	0.108

Appendix 3. *Haliotis midae*. Genetic diversity estimates for South African populations. N: sample size; N_{allele} : number of alleles, Mean N_{allele} : mean number of alleles per population; H_o : observed heterozygosity; H_e : expected heterozygosity; D : Selander's index of heterozygote deficiency, negative values indicates an excess of homozygotes. p: probability of deviation from Hardy-Weinberg equilibrium. **Significant departure from Hardy-Weinberg equilibrium after sequential Bonferroni correction for multiple tests across loci. 'All loci' provides mean values, with the exception of N_{allele} , which is the sum of alleles across loci. All loci p-value calculated by combining probabilities across loci, and significance determined by comparison to critical values of chi-squared in Sokal & Rohlf (1981). For locality name abbreviations see Fig. 1

Group	Population		<i>CmrHr</i> 2.15	<i>CmrHr</i> 2.23	<i>CmrHr</i> 2.29	All loci	
All	Total	N	199	205	205	203	
		N_{allele}	19	2	17	38	
		Mean N_{allele}	9	2	7.8	12.7	
		H_o	0.429	0.188	0.554	0.390	
		H_e	0.669	0.243	0.674	0.529	
		p	<0.001**	0.993	0.006**	<0.001**	
	West	Da	N	21	24	24	23.0
			N_{allele}	8	2	7	17
			H_o	0.333	0.167	0.500	0.333
			H_e	0.742	0.194	0.703	0.546
			p	0.003**	1.000	0.031	<0.010**
			D	-0.551	-0.139	-0.289	-0.326
		Ri	N	26	26	26	26.0
			N_{allele}	11	2	4	17
			H_o	0.462	0.192	0.462	0.372
H_e			0.776	0.212	0.596	0.528	
p			0.001**	1.000	0.026	<0.010**	
D			-0.405	-0.094	-0.225	-0.241	
Kl		N	48	49	49	48.7	
		N_{allele}	13	2	17	32	
		H_o	0.396	0.245	0.612	0.418	
		H_e	0.781	0.217	0.702	0.567	
		p	<0.001**	1.000	0.280	<0.001**	
		D	-0.493	0.129	-0.128	-0.164	
East	Ms	N	29	29	29	29.0	
		N_{allele}	7	2	7	16	
		H_o	0.414	0.207	0.621	0.414	
		H_e	0.512	0.220	0.766	0.499	
		p	0.215	1.000	0.030	>0.100	
		D	-0.191	-0.059	-0.189	-0.147	
	St	N	24	26	26	25.3	
		N_{allele}	5	2	4	11	
		H_o	0.458	0.231	0.500	0.396	
		H_e	0.560	0.348	0.563	0.490	
		p	0.069	0.201	0.927	>0.100	
		D	-0.182	-0.336	-0.112	-0.210	
	Cr	N	51	51	51	51.0	
		N_{allele}	10	2	8	20	
		H_o	0.510	0.275	0.627	0.471	
		H_e	0.641	0.267	0.712	0.540	
		p	0.004	1.000	0.135	<0.025**	
		D	-0.204	0.030	-0.119	-0.098	