

The following supplement accompanies the article

Microsatellites from sponge genomes: the number necessary for detecting genetic structure in *Hemimycale columella* populations

Janina González-Ramos, Gemma Agell, Maria J. Uriz*

*Corresponding author: iosune@ceab.csic.es

Aquatic Biology 24: 25–34 (2015)

Supplement.

Table S1. Microsatellite loci isolated from *Hemimycale columella*.

Locus	Genbank accession number	F and R (Primer sequence [5'-3'])	Repeat motif	T ^a (°C)	Size range	Allele no.
Hemi_2	KP212688	F:GCCTCTTCAACTGCACTGAC R:GTTGAGCGAATGAAGGAAGC	(CT) ₅	52°C	104-208	5
Hemi_3	KP212689	F:GCAAATAGAGCAACCAGCCA R:ACAGATCATGCCACCACAGA	(AG) ₅	54°C	239-308	4
Hemi_4	KP212690	F:CAGAAGCGAGGAAGAAATGG R:TGCAATCTGACTCTGGCATC	(CA) ₅	55°C	248-338	8
Hemi_5	KP212691	F:TGAGTGCAACAAGGCAAGTC R:GCTGTGTCATATGCTGAGGC	(AC) ₉	54°C	165-173	4
Hemi_7	KP212692	F:TAGATCACTGCAAACCGCTG R:AGAATGGCTCGTCCTGAATG	(TG) ₆	54°C	211-223	6
Hemi_9	KP212693	F:TTTCATTATTCGAGCGGAGC R:ACATAGCATGACGTGACCGA	(ATGT) ₈	55°C	124-142	5
Hemi_10	KP212694	F:GCCTCTGAAGACTTGCTGCT R:CTGCAGATTTGCAAGATGGA	(TA) ₂ C (CCA) ₇	53°C	229-265	11
Hemi_11	KP212695	F:AAGAGTAAGGAAGCACCGCA R:GGCTGACTTCTGTGACTCCA	(TGTA) ₂ T (TTA) ₃ (TGTA) ₈	53°C	148-158	6
Hemi_12	KP212696	F:TGTGGCATTGAGCTGAACTT R:CCGGTCTGCTGAACACAAT	(AG) ₅ C (AG) ₂	55°C	276-286	2
Hemi_13	KP212697	F:ATGCAGGTCAGTCAAAGCCT R:GACCAGGCTGTTTGGAAATATC	(TC) (TCC) ₂ TC (TG) ₈	55°C	147-157	3
Hemi_14	KP212698	F:CGGATTAACAGCGTTTGGAT R:TTCCTGACCACTCCACATGA	(CT) ₂ (GT) ₆	55°C	154-175	8
Hemi_15	KP212699	F:AAATGAAGCTGCTGGTTGCT R:AACCACCTCCATGATGCTC	(CT) ₂ C(CA) ₉ T(TA) ₃ (CA) (CAAG) ₅ CA	55°C	142-177	7
Hemi_16	KP212700	F:AAGTATGGTGGTCCAGACGG R:TTGGTCCTTGTAAGATCGGTG	AG (AGG) ₅ AGA (AGG) ₂	55°C	168-184	6
Hemi_17	KP212701	F:AATCTGAGCTGGACTCGGAC R:CTCTGCATCCGACTCTGACA	(CAC) ₅	55°C	139-148	4

Table S2. Allele frequency for each locus and population corrected for downward bias resulting from the presence of null alleles (MicroChecker).

Micro	HA	HC	Micro	HA	HC	Micro	HA	HC
<u>Hemi_2</u>			<u>Hemi_9</u>			<u>Hemi_14</u>		
194	0.154	0.217	120		0.043	154	0.083	0.056
198	0.212	0.170	124		0.239	160	0.208	0.222
202	0.212	0.150	128	0.179	0.261	162	0.042	0.037
206	0.019		132	0.357	0.326	164		0.019
208	0.404	0.470	137	0.036		168	0.021	
<u>Hemi_3*</u>			142	0.429	0.130	169	0.583	0.574
135		0.167	<u>Hemi_10*</u>			171	0.042	0.074
147	0.040	0.017	229	0.240	0.357	175	0.021	0.019
153	0.880	0.767	230	0.160		<u>Hemi_15*</u>		
161		0.033	233		0.048	141	0.232	0.250
175	0.080	0.017	245	0.060	0.048	148	0.250	0.147
<u>Hemi_4</u>			248		0.024	163	0.232	0.074
239	0.080		250	0.060	0.024	165	0.179	0.338
241	0.040	0.018	252	0.060	0.071	168	0.054	0.015
243		0.018	255	0.060	0.238	170	0.036	0.176
248	0.680	0.714	257		0.095	177	0.018	
251		0.250	259	0.320		<u>Hemi_16*</u>		
253	0.140		261	0.020	0.095	167	0.096	0.161
259	0.020		265	0.020		169		0.129
308	0.040		<u>Hemi_11</u>			174	0.288	0.468
<u>Hemi_5</u>			148	0.045	0.018	177	0.500	0.129
165		0.031	150	0.432	0.143	181	0.096	0.065
168	0.500	0.360	152	0.023	0.054	184	0.019	0.048
170	0.397	0.531	154	0.227	0.429			
172	0.103	0.078	156	0.250	0.321	<u>Hemi_17*</u>		
<u>Hemi_6*</u>			158	0.023	0.036	139	0.019	0.040
230	0.107		<u>Hemi_12</u>			141	0.167	0.120
255	0.250		275	0.167	0.063	145	0.204	0.420
257	0.375	0.597	286	0.839	0.983	148	0.611	0.340
268	0.268	0.403	<u>Hemi_13</u>			154		0.080
<u>Hemi_7*</u>			141		0.054			
211	0.048	0.087	147	0.179	0.036			
213	0.024		150	0.161	0.125			
217	0.143	0.130	157	0.661	0.786			
219	0.405	0.609						
221	0.286	0.152						
223	0.095	0.022						

Private alleles for each population are in bold. Compound loci are underlined. *Indicates presence of null alleles

Table S3. Results from hierarchical analysis of molecular variance (AMOVA) between populations using the several sets of microsatellites.

	Source of variation	Sum of squares	Variance components	Percentage variation	p-value
Group of 6 (45 Alleles)	Among populations	9.07	0.12	5.62	p < 0.001
	Among individuals within populations	135.5	0.56	26.97	p < 0.001
	Within individuals	78.5	14.7	67.39	p < 0.001
	Total	223	21.8		
Group of 9(62 Alleles)	Among populations	13	0.18	5.63	p < 0.001
	Among individuals within populations	185.1	0.74	22.73	p < 0.001
	Within individuals	116	23.3	71.63	p < 0.001
	Total	313.9	32.6		
Group of 12(78 Alleles)	Among populations	14.3	0.19	4.77	p < 0.01
	Among individuals within populations	227.9	0.72	17.55	p < 0.001
	Within individuals	165	3.17	77.68	p < 0.001
	Total	407.2	4.08		
Group of 15(88 Alleles)	Among populations	17.2	0.23	4.89	p < 0.001
	Among individuals within populations	269.4	0.84	17.63	p < 0.001
	Within individuals	194	36.72	77.47	p < 0.001
	Total	480.6	4.74		
Group of Comp.(51 Alleles)	Among populations	10.07	0.14	5.35	p < 0.001
	Among individuals within populations	155.4	0.62	23.30	p < 0.001
	Within individuals	96	1.89	71.34	p < 0.001
	Total	261.4	26.50		
Group of Perfect(37Alleles)	Among populations	7.15	0.09	4.33	p < 0.01
	Among individuals within populations	114	0.22	10.44	p < 0.001
	Within individuals	98	1.78	85.23	p < 0.001
	Total	219.2	2.09		