



Supplementary Material

Short Communication: Development and Characterization of Twenty-Three Novel Polymorphic Microsatellite Markers for Mussel *Mytilus coruscus*

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Table I.- Characterization of 23 polymorphic microsatellite loci isolated from *Mytilus coruscus*. The table shows the locus name code, primer sequences (5'-3'), repeat motif, annealing temperature (Ta), allele size range, test population sample size, number of alleles (N_a), observed heterozygosity (H_o), expected heterozygosity (H_e), P-value of Hardy-Weinberg Equilibrium (HWE) test, polymorphism information content (PIC).

Locus/ Accession No.	Primer sequences (5'-3')	Repeat motif	Ta (°C)	Size (bp)	Samples	N_a	H_o	H_e	HWE	PIC
MC08/ KX423595	F:TCACATGACTCTATAACAACCCCTTT R:TATCCAGCCACAACGGACTTA	(ATTT)3	60	204-270	35	13	0.686	0.840	0.065	0.822
MC18/ KX423596	F:CACGGATCTCGGGTATTCTCTG R:CAGTCGGATGTTGTTTATTGATGTG	(TA)7	60	177-187	34	6	0.971	0.774	0.052	0.740
MC22*/ KX423597	F:CTTTGGCAGCAGAATATCACAG R:ACAGGATCGGAAGTGAATGAGT	(TA)7	60	335-389	33	19	0.485	0.909	0.000	0.902
MC27*/ KX423598	F:GCAACATTTACCGATGAAGACA R:CGGACATTCCAGAAGAAACATA	(AT)6	60	319-337	35	8	0.371	0.807	0.000	0.780
MC31/ KX423599	F:TGTACTGCACCTTCTTTTCTTGGC R:TGCAAGCTGACTCTTACAATAACC	(AT)9	60	342-424	35	15	1.000	0.895	0.146	0.885
MC34/ KX423600	F:GGCAGAGGGTCATAGTTTTTCAC R:CCCTTTCTGTGATTTCCCTCAAC	(TA)7	59	240-252	35	7	0.400	0.617	0.152	0.563
MC36/ KX423601	F:GCTTTTGTGATTACTGTGAAGACG R:CATGATATGGCAACATTGGACT	(TA)7	60	161-187	35	8	0.971	0.688	0.307	0.661
MC43*/ KX423602	F:TACTGTCCTTTCCAGAGCAGAC R:CCAAAACGCACCATACATTAAC	(TGA)6	58	386-442	35	11	0.143	0.794	0.000	0.771
MC44/ KX423603	F:TCCCTTTGTCTCTTGTTCAT R:TGAATGGCGTTTACCCTCTTAT	(CA)6	59	182-208	35	8	0.257	0.351	0.061	0.340
MC47/ KX423604	F:GATAGAGTTGGGAAAAGCAACG R:CATACAAATCAAACATGACGGG	(AT)7	60	249-329	34	19	0.676	0.824	0.507	0.812
MC49*/ KX423605	F:GCGCAGAAGGTATTGATTGTT R:GAAGAAGTGGCAGAAAACAGG	(GCT)6	60	253-333	32	16	0.625	0.908	0.000	0.902
MC54/ KX423606	F:TATTTTGACGAAGTGCTACCCC R:AAAGTAAGTGGACGAAGGTGGA	(AC)7	60	228-306	35	21	0.514	0.847	0.190	0.832

Locus/ Accession No.	Primer sequences (5'-3')	Repeat motif	Ta (°C)	Size (bp)	Samples	N_a	H_o	H_e	HWE	PIC
MC57/ KX423607	F:TGTCAGAGGCCAATAAAACAAC R:TTCGGGTTCCCTAAACATTAACC	(ACAA)5	59	239-333	31	21	0.742	0.888	0.125	0.879
MC62/ KX423608	F:AATTCTCTTTCCATCAGGTCCA R:GTGTTTCTAGGGGTGATCTTGC	(TTC)6	59	253-315	35	13	0.571	0.809	0.417	0.784
MC63/ KX423609	F:CTGAGACGGTAATAGAAATGAATGG R:GGCCTCATCAAGGAACATAAAA	(TG)10	60	253-299	35	8	1.000	0.757	0.053	0.724
MC66/ KX423610	F:TGTTTACCCATTGCTGGTGA R:GACCATTGTGCTGACATTTCTT	(TA)7	59	242-264	35	7	0.314	0.518	0.166	0.489
MC68/ KX423611	F:GCTGAAGTCTGCGATAAAACCT R:ATGAAAGACACACTGGTTGTGG	(GA)8	59	195-299	35	11	0.857	0.691	0.244	0.666
MC74/ KX423612	F:CATGTCAGCCAATGTAAAAGC R:AGCTGGGTCTATGTTATCGCTC	(AT)8	59	287-305	35	10	0.486	0.726	0.147	0.696
MC76/ KX423613	F:GAAAATCGCTGAATTGGTTATC R:GCATTTGAGAAAATAAGGGACG	(AT)7	60	260-318	35	15	1.000	0.894	0.518	0.885
MC90/ KX423614	F:GCACACACATCATACTTGCACA R:CAGAGGGTCCAAACCAAAATAC	(AC)6	60	257-303	35	11	0.514	0.804	0.119	0.779
MC99/ KX423615	F:ACAACCTAGAAAACAGGGGCAA R:GCTGTAGGTAGTATTTGGCATGAA	(AC)9	60	388-470	35	21	0.743	0.903	0.633	0.896
MC101*/ KX423616	F:CAAAGAATGGGAAGCAGTTTG R:ATTTGGTCAGTTGCGTTCATC	(TA)8	59	217-351	31	19	0.323	0.926	0.000	0.921
MC104/ KX423617	F:ATTACGCGCATGTGTCTATCAC R:TTACCGAAACTGCATGTCAACT	(TTAT)5	60	237-301	34	10	0.471	0.558	0.796	0.538

*Significant deviating from HWE ($P < 0.001$).