

APPENDIX A

BLAST results of sequences obtained from cloning RAMs primers. Results are shown for *Danio rerio* and other organisms with highly similar sequences. The 1st column shows the RAMs primer used to obtain this sequence alongside the designated name of the clone. The 2nd column identifies the organism that the *C. striata* sequence was compared to along with the query and subject sequences in the 3rd column. Lastly the 4th column shows the predicted function of the query sequence with reference to the compared subject sequence

RA M	Species it was compared to	Sequence	Predicted function	Score	E-value
T113-A5	Bos taurus	Query 241 CAAACAGCAGCTCCACCGTCCGGG 264 Sbjct 2308 CAGACAGCAGCTCCACCGTCAGGG 2285	Bovine elastin a mRNA, complete cds	42.8	0.2
	Danio rerio	Query 241 CAAACAGCAGCTCCACCGTCCGGG 264 Sbjct 2308 CAGACAGCAGCTCCACCGTCAGGG 2285	PREDICTED: Danio rerio similar to a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 15 (LOC100002059), mRNA	35.6	0.6
T113-B1	Rattus norvegicus (Norway rat)	Query 2 ccgcgcgcgcgcgcgcgcgcgTATCCCTGGTGCCGTGCCTGC 41 Sbjct 1101 CCGCCGCCGCCGCCATCTCCCGGGTGCCGTGCCTGC 1140	Rattus norvegicus forkhead box E1 (thyroid transcription factor 2) (Foxe1), mRNA	55.4	6.00E-05
	Danio rerio	Query 38 CTGCTG-TCGATGAAGTACAGGATGTTGTTG 67 Sbjct 561 CTGCTGATTGAGGAAGTACAGGATGTAGTTG 531	PREDICTED: Danio rerio similar to MGC82035 protein (LOC793137), mRNA	35.6	1.2

T113 -B2	Ustilago maydis 521	Query	310	CTCGGGCGCGTTCAGGTTGACCACGTACTCGAGCAG	345	Ustilago maydis 521 hypothetical (UM04864.1) mRNA	42.8	0.31
		Sbjct	1764	CTCGGGCACCTTCATGTTGACCACGTACGAGAGCAG	1729			
	Danio rerio	Query	91	ATGCAGGGCCTGCAGTTGAGTCAG	114	PREDICTED: Danio rerio misc_RNA (LOC100149391), miscRNA	35.6	0.92
		Sbjct	1211	ATGAAGGGCCTGCAGTTGGGTCAG	1234			
T113 -B3	Pan troglodytes (chimpanzee)	Query	382	GCCCGATCTCGTCCGATCTCGGAAGCCAAGTGGAGCCGGGCTGGTTAGTACCTGGTTGG	441	Pan troglodytes transforming growth factor beta regulator 1, transcript variant 3 (TBRG1), mRNA	71.6	6.00 E-10
		Sbjct	7527	GCCCGATCTCGTCTGATCTCGGAAGCTAAGCAGGGTCGGGCCCGGTTAGTACTTGGATGG	7586			
		Query	442	AAGA 445 				
		Sbjct	7587	GAGA 7590				
	Danio rerio	Query	587	GTGAAGAAGAAAGCCAAGCGGCAGCC	612	PREDICTED: Danio rerio hypothetical LOC798935 (LOC798935), mRNA	39.2	0.06 9
		Sbjct	978	GTGAAGAAGAAAGCGAAGCCGCAGCC	1003			
T113 -B6	Salmo salar (Atlantic salmon)	Query	916	GAGCCAAAGCGGCTGCGCACGGGCTACACGCGCCAGCAGGTTCTGGAGCTGGAGAAGGA	975	PREDICTED: Taeniopygia guttata similar to homeobox D4 (LOC100221788), mRNA	84.2	1.00 E-13
		Sbjct	157	GAGCCGAAGCGCTCCCGCACGG-CGTACACGCGCCAGCAGGTGCTGGAGCTGGAGAAGGA	215			
		Query	976	GTTCCACTTCAGCCCGGTAC	995			
		Sbjct	216	GTTCCACTACA-ACCGGTAC	234			
	Danio rerio	Query	918	GCCAAAGCGGCTGCGCACGGGCTACACGCGCCAGCAGGTTCTGGAGCTGGAGAAGGAGT	977	Danio rerio homeo box A4a, mRNA (cDNA clone MGC:154113 IMAGE:8356675), complete cds	59	1e-07
Sbjct		495	GCCCAAGAGGTCTCGCACCG-CCTACACGCGCCAGCAGGCTCTGAGCTTGAAAAAGAGT	553				
Query		978	TCCAATT	984				
Sbjct		554	TCCATTT	560				

T113 -C1	Danio rerio	Query	611	GCACGAATAACAACGGTGAGACCATCCC	638		Danio rerio collagen, type VIII, alpha 1a (col8a1a), mRNA	33.	4.1
		Sbjct	237	GCAAGGATAACAAAGGTGAGACCATTCC	264				
	Rattus norvegicus (Norway rat)	Query	910	TCTCCCTCCTCCGTC-Cgggcggcggcggcggcggcgg	943		Rattus norvegicus similar to PWWP domain containing 2 (LOC683932), mRNA	42.	0.4
		Sbjct	86	TCTCCCTCCTCCGACTCGGGCTGCGGCGGGCGGCGG	52			8	
T113 -C2	Danio rerio	Query	858	GGCTCCGTCCGTGAGCCGTGGCCGCTTCAGGAA	891		PREDICTED: Danio rerio similar to human immunodeficiency virus type I enhancer binding protein 3 (LOC568037), mRNA	35.	1.1
		Sbjct	4775	GGCTCAGTCTGTGAGCCGTGGCCACTTTCAGAAA	4742				
	Ustilago maydis 521	Query	316	CTCGGGCGCGTTCAGGTTGACCACGTA	351		Ustilago maydis hypothetical protein (UM04864.1) partial mRNA	521	0.38
		Sbjct	1764	CTCGGGCACCTTCATGTTGACCACGTACGAGAGCAG	1729			8	
T113 -C6	Danio rerio	Query	90	CGGT-TCTCCGCCGGTCTGTGCTGTTG	114		PREDICTED: Danio rerio similar to transcriptional regulating factor 1 (LOC560284), mRNA	35.	0.32
		Sbjct	2497	CGGTGTCTCCGCTGGTCTGTGCTGTTG	2472				
	Sorghum bicolor (sorghum)	Query	229	GCCGCCGGCGCACGTAGCgggcggcggcggcggcggcgg	264		Sorghum bicolor hypothetical protein (SORBIDRAFT_02g006420) mRNA, complete cds	48.	0.00
		Sbjct	342	GCCGCCGGCGCCGGGGCGGCGGCGGCGGCGGCGGCGG	307			2	3
T113 -C7	Danio rerio	Query	224	TTTGCCGGTGGAGATCAGAGAGTCG	248		PREDICTED: Danio rerio hypothetical LOC559418 (LOC559418), mRNA	37.	0.36
		Sbjct	560	TTTGCCGCTGGAGCTCAGAGAGTCG	536				

BP6-B6	Homo sapiens	Query	885	TGTTTGTGTCTGTGCCCGTGCATTCTGTGTCTGTGGCT--TTGTAT-TGAC-GTTTGC	940	PREDICTED: Homo sapiens hypothetical LOC100128366 (LOC100128366), miscRNA	46.	0.03
		Sbjct	66	TGTTTGTGTGTGTGTCTGTGTGCTGTGTGTGTCTGTGTGTGTTGTGTGTGTCTGTGTGT	125		4	4
		Query	941	ATGTGCATGTGTATGTGTGTGTC	963			
		Sbjct	126	TTGTGTGTGTATGTGTGTGTC	148			
	Danio rerio	Query	806	GTGTGTGCTTGTGTACATGAGAAAGGGAGAAAGAGGCTGTGCACAGACTACGTGTCTGCA	865	PREDICTED: Danio rerio hypothetical LOC791614 (LOC791614), mRNA Length=1864	42.	0.00
		Sbjct	1199	GTGTGTGTGTGTGTACA--AGAAAGGGTG-----CTGCCACAGA--ACGTCCC--CA	1153		8	8
		Query	866	TTTGTGAGTGTGGTTATGC-TGTTTGTGTCTGTG	898			
		Sbjct	1152	TGTGTGAGTGTGGATATGCATATTGGTGTGTGTG	1119			
BP6-B7	Arabidopsis thaliana	Query	13	AAGAAGAAGAGGATGTAACAAT	34	Arabidopsis thaliana PHD finger transcription factor, putative (AT2G36720) mRNA, complete cds	41	0.57
		Sbjct	79	AAGAAGAAGAGGATGTAACAAT	58			
	Danio rerio	Query	341	ACTCTTTGCAGCCTTGCAGTTTTGT-TCTGTTGACTTTTC	379	Danio rerio SET domain containing methyltransferase (setd8b), mRNA	35.	0.48
		Sbjct	521	ACTCTTTGCT---TTTCAGTTTCTATCTGTTGACTTTTC	485		6	8b
BP6-B8	Sorghum bicolor	Query	1	ATATTATTATTTAAGAAGAAGAAGA	25	Sorghum hypothetical protein (SORBIDRAFT_01g021910) mRNA, complete cds	41	0.61
		Sbjct	1751	ATATTATAATTTAAGAAGAAGAAGA	1775			
	Danio rerio	Query	13	AAGAAGAAGAAGATGTAACAATTCGTG	39	PREDICTED: Danio rerio similar to pigmentosa RP1 protein (LOC558304), mRNA	35.	0.51
		Sbjct	4442	AAGAAGAAGAAGAAGAAACAATTAGTG	4468		6	

BP6-C3	Aspergillus niger	Query	880	GGTTG-ACAGTTCAGGATTTGTGTTAACAAAATCAGCT-GTGAAGCCTGCCAGTTAT	934	Aspergillus niger CBS 513.88 hypothetical protein (An06g02190)	44.	0.12
		Sbjct	133	GGTTGTACAG--CAGGATTTGGTATAACACTATCAGCTAGAGAATCCTGCCAGTTAT	187			
	Danio rerio	Query	362	TGATAATGTGTGTGTTGTGC	381	PREDICTED: Danio rerio similar to interferon regulatory factor 2	37.	0.35
		Sbjct	1109	TGATAATGTGTGTGTTGTGC	1128			
BP6-C6	Danio rerio	Query	51	GGAGAGTTTGAGGGTGCTCGAGCTTTACAGCGGGATAGGAGGAATGCATTATGCGCTGAG	110	Danio rerio tRNA aspartic acid methyltransferase (trdmt1)	60.	1.00
		Sbjct	77	GGAGCGACTGAGAGTATTTGAAC TATAACAGCGGGATAGGAGGAATGCATTATGC-TTTAA	135			
		Query	111	AGGTGAGCTT	120			
		Sbjct	136	AGGAGAGCTT	145			
	Xenopus laevis (African clawed frog)	Query	59	TGAGGGTGCTCGAGCTTTACAGCGGGATAGGAGGAATGCA	98	Xenopus laevis similar to DNA (cytosine-5-)-methyltransferase (MGC53207), mRNA	50	0.00
		Sbjct	351	TGCGGGTGCTGGAGCTGTACAGCGGGGTCGGAGGAATGCA	390			
BP1 4-A2	Mus musculus (house mouse)	Query	520	AAACA-ACATACTATCTATCTATCTATCTATC	550	PREDICTED: Mus musculus RIKEN C530025M09 gene (C530025M09Rik), mRNA	50	0.00
		Sbjct	2952	AAACACACATACTATCTATCTATCTATCTATC	2921			
	Danio rerio	Query	521	AACAACATACTATCTATCTATCTATCTAT	549	PREDICTED: Danio rerio similar to Neuron-specific protein family member 1 (Brain neuron cytoplasmic protein 1) (LOC558119), mRNA	41	0.01
		Sbjct	1253	AAAAACAT-CTATCTATCTATCTATCTAT	1226			

BP1 4-A4	Danio rerio	Query	8	GATAGATAGATAGATAGATAA	28	PREDICTED: Danio rerio similar to Neuron-specific protein family member 1 (Brain neuron cytoplasmic protein 1) (LOC558119), mRNA	39.	0.07
		Sbjct	1205	GATAGATAGATAGATAGATAA	1225		2	6
	Salmo salar (Atlantic salmon)	Query	629	TCACTGTTGTAA-TGATT-TTACCTTTAGAACTGTTGGTCAATA	670	NCBI Reference Sequence: NM_001140225.1 Salmo salar EBV-induced G-protein coupled receptor 2 (ebi2), mRNA	37.	0.02
		Sbjct	1699	TCACTGTTGTAAGTATTGTTGGCTGCTGAACTGTTGGTCATTA	1656		4	7
BP1 4-A6	Danio rerio	Query	8	GATAGATAGATAGATAGATATGGGAAAGATGT	39	ref[NM_001005923.2] Danio rerio stathmin-like 2a (stmn2a), mRNA	41	0.02
		Sbjct	899	GATAGATAGATAGATAGATTTAAAAAAGATGT	868		1	
	Salmo salar (Atlantic salmon)	Query	5	AGCGATAGATAGATAGATAGATA-TGGGAAAGATGTGCAACA	45	ref[NM_001140278.1] Salmo salar HBS1-like protein (hbs1l), mRNA	37.	0.02
		Sbjct	2399	AGGGATGGATAGATAGATAGATAGAGGGATGGATGTG-AACA	2359		4	6
BP1 4-A8	Danio rerio	Query	606	TTTATGGTTTAAATGGTGTAAACATGCTTTTT	637	ref[XM_679676.2] PREDICTED: Danio rerio similar to butyrophilin, subfamily 2, member A2 (LOC556776), mRNA	41	0.02
		Sbjct	954	TTTATCATTATGGTGTAAACAATGCTTTTT	985		9	
	Salmo salar	Query	564	GACTGAGGGAAGGAACCAGAATGTTGT	590	ref[NM_001139555.1] Salmo salar homeobox protein HoxD1aa (hoxd1aa), mRNA	31.	1.5
		Sbjct	1259	GACTGAGGGAAGTTCCAAAATGTTGT	1285		9	

BP1 4-B1	Danio rerio	Query	260	GTCTCTCACTCACAAAGACTCTCACACACTCTCACACT 	297	>ref[NM_200015.1]	46.	3.00
		Sbjct	1541	GTCTCTCACTCACACACACTCTCACACACTCACACT 	1504	Danio rerio trk-fused gene (tfg), mRNA	4	E-04
	Salmo salar	Query	260	GTCTCTCACTCACAAAGACTCTCACACACTCTCACACT 	297	ref[NM_001140278.1]	35.	0.04
		Sbjct	1541	GTCTCTCACTCACACACACTCTCACACACTCACACT 	1504	Salmo salar HBS1-like protein (hbs11), mRNA	6	6
BP1 4-B2	Danio rerio	Query	260	GTCTCTCACTCACAAAGACTCTCACACACTCTCACACT 	297	>ref[NM_200015.1]	46.	3.00
		Sbjct	1541	GTCTCTCACTCACACACACTCTCACACACTCACACT 	1504	Danio rerio trk-fused gene (tfg), mRNA	4	E-04
	Salmo salar	Query	385	TCTATCTATCTATCTATCC 403 		ref[NM_001140278.1]	35.	0.04
		Sbjct	2375	TCTATCTATCTATCTATCC 2393		Salmo salar HBS1-like protein (hbs11), mRNA	6	6
BP1 4-B3	Danio rerio	Query	8	GATAGATAGATAGATAGATAGG 29 		>ref[NM_212827.2]	41	0.01
		Sbjct	2760	GATAGATAGATAGATAGATAGG 2781		Danio rerio monoamine oxidase (mao), mRNA		
	Salmo salar	Query	5	AGCGATAGATAGATAGATAGATAG 28 		>ref[NM_001140278.1]	35.	0.04
		Sbjct	2399	AGGGATGGATAGATAGATAGATAG 2376		Salmo salar HBS1-like protein (hbs11), mRNA	6	5
BP1 4-B5	Danio rerio	Query	246	GGGCTGGAAGGCTATTATAAT 266 		>ref[XM_689347.3]	33.	1.1
		Sbjct	2403	GGCCTGGAAGGCTATTATAAT 2383		PREDICTED: Danio rerio similar to myosin, heavy polypeptide 11, smooth muscle (LOC566080), mRNA	7	
	Salmo salar	Query	5	AGCGATAGATAGATAGATAGATAG 28 		ref[NM_001140278.1]	35.	0.04
		Sbjct	2399	AGGGATGGATAGATAGATAGATAG 2376		Salmo salar HBS1-like protein (hbs11), mRNA	6	5
						gb BT045574.1 Salmo salar clone ssal-rgf-525-	bits	

						146 HBS1-like protein putative mRNA, complete cds		
BP1 4-A2	Danio rerio	Query	86	CAACACCCACAACAACAACAAGCGACAACCACAGCAA	122	ref XM_001345821.2 PREDICTED: Danio rerio similar to novel immune type receptor protein (LOC100007383), mRNA	41	0.02
		Sbjct	506	 CAACACCAACAACAACAACA-CAACAACAACAACA	541		8	
	Oncorhynchus mykiss (rainbow trout)	Query	290	ACAAACTACTACTACTACTCT	310	ref NM_001160638.1 Oncorhynchus mykiss Bola-like protein 3 (bola3), mRNA	33.	0.42
		Sbjct	1032	 ACAAACTACTACTACTACT	1012		7	
BP1 4-A4	Danio rerio	Query	468	GCTTCTTTGGAGGaaaaaaaaaacaacaaacaaaa	503	>ref NM_194393.1 Danio rerio guanylate cyclase activator 1C (guca1c), mRNA	44.	0.00
		Sbjct	1792	 GCTTCTTTGGA--AAAAAAAAAAAAAAAAAAAAA	1825		6	2
	Salmo salar	Query	335	CTGTTTCATGTAGTCACA	352	ref NM_001140151.1 Salmo salar Brain protein I3 (bri3), mRNA	33.	0.42
		Sbjct	2525	 CTGTTTCATGTAGTCACA	2542		7	
BP1 3-A1	Danio rerio	Query	761	ACGGAAAATAAAAAATAACAATAGC	784	ref XM_001336004.2 PREDICTED: Danio rerio similar to ATPase family AAA domain-containing protein 2B (LOC795783), mRNA	39.	0.08
		Sbjct	2468	 ACGGAAAATAAAAAAGAACAATAGC	2445		2	9

	Salmo salar	Query	469	TGTGGGAAAGCTGTTGCTTGGGG	491		ref NM_001139732.1	33.	0.38
		Sbjct	992	TGTGGTAGAGCTGTTGCTTGGGG	1014		Salmo salar proteasome	7	
							(prosome, macropain)		
							26S subunit, non		
							ATPase, 3-2		
							(LOC100194647), mRNA		
BP1	Danio rerio	Query	107	AAAAGACAGCAGAGGAGAGGAATGAGA	133		ref XM_001338002.2	35.	0.69
3-A2		Sbjct	1319	AAAACCCAGCAGAGGAGAGGAAAGAGA	1293		PREDICTED: Danio rerio	6	
							similar to POU domain,		
							class 2, transcription		
							factor 2		
							(LOC100002311), mRNA		
	Salmo salar	Query	508	ACACAAATGCCCTGAGTGA	526		ref NM_001160484.1	35.	0.06
		Sbjct	251	ACACAAATGCCCTGAGTGA	269		Oncorhynchus mykiss	6	9
							BMP and activin		
							membrane-bound		
							inhibitor		
							(LOC100301651), mRNA		
BP1	Danio rerio	Query	115	AATCAGACATTTGGTAAAGTCA	136		ref NM_200083.1 Danio	35.	0.93
3-A3		Sbjct	1118	AATCAGACATTTGGTAAAGACA	1139		rerio proenkephalin-like	6	
							(penkl), mRNA		
	Oncorhynchus mykiss (rainbow trout)	Query	595	ctgcacctcctgctctctctctctctctctctctctctctctctcCTGTCCCATTTTGTCTAT	654		>ref NM_001124218.1	39.	0.00
		Sbjct	187	CTGCAACTCTGTCTGTCTGTCTCTCTCTCTATCTCTC-TGTC-----TTTCTAT	138		Oncorhynchus mykiss 11-	2	8
							beta-hydroxysteroid		
							dehydrogenase		
							(LOC100135822),		
							mRNA		
BP1	Danio rerio	Query	676	TGACTTTACCAAATGTCTGATT	697		ref NM_200083.1 Danio	35.	0.93
3-A4		Sbjct	1139	TGTCTTTACCAAATGTCTGATT	1118		rerio proenkephalin-like	6	
							(penkl), mRNA		

	Oncorhynchus mykiss (rainbow trout)	Query	150	AGAGATAGAAACAAAATGGGGACAG-gagagagagagagagagagagagagagagag	205		ref[NM_001124218.1]	41	0.00
		Sbjct	134	AGAGATAGAAA-----GACAGAGAGATAGAGAGAGAGACAGACAGACAGAG	181		Oncorhynchus mykiss 11-beta-hydroxysteroid dehydrogenase (LOC100135822), mRNA		2
BP1 3-A5	Danio rerio	Query	771	GCTCTGCTGAAGCCAGTT	788		ref[NM_001045117.2]	33.	4.3
		Sbjct	1264	GCTCTGCTGAAGCCAGTT	1247		Danio rerio fibronectin type III and SPRY domain containing 1 (fsd1), mRNA	7	
	Salmo salar	Query	492	GTGGCGCTTTTCTCATAGCTCACGCTGTAG	520		>ref[NM_001141001.1]	35.	0.12
		Sbjct	586	GTGGCGCTTTTCTCATCGGTCACGGTGGAG	614		Salmo salar COMM domain-containing protein 9 (comd9), mRNA	6	
BP1 3-A7	Danio rerio	Query	123	AAAGGAGAAAATAATGAGTGTGGCATCA	150		ref[XM_001922428.1]	33.	1.1
		Sbjct	658	AAAGGAGAAAATAAGAAGTTTGGGATCA	685		PREDICTED: Danio rerio similar to Transmembrane protein 16F (LOC100149606), mRNA	7	
	Salmo salar	Query	113	GGAGAGAGATAAAGGA	128		>ref[NM_001140252.1]	30.	1.4
		Sbjct	1362	GGAGAGAGATAAAGGA	1377		Salmo salar RNA 3-terminal phosphate cyclase (rtc1), mRNA	1	
BP1 3-A8	Danio rerio	Query	260	TCTGAGT-TTTATATATCAATCACCAATATTGATT	293		>ref[XM_001918483.1]	37.	0.3
		Sbjct	1501	TCTCAGTGTTTACATATCAATCACCTATATTATT	1535		PREDICTED: Danio rerio hypothetical protein LOC100149989 (LOC100149989), mRNA	4	

	Salmo salar	Query	113	GGAGAGAGATAAAGGA	128		ref NM_001140252.1	30.	1.4
							Salmo salar RNA 3-	1	
		Sbjct	1362	GGAGAGAGATAAAGGA	1377		terminal phosphate		
							cyclase (rtc1), mRNA		
BP1	Salmo salar	Query	77	CCTTACACCTTGTGTGTCTGCAT	101		ref NM_001141870.1	37.	0.01
3-B1							Salmo salar	4	9
		Sbjct	347	CCATACACCTTGTGTGTTTCTGCAT	323		Retinoblastoma-binding		
							protein 9 (rbbp9), mRNA		
	Danio rerio	Query	539	CACAATGGAGAGACTGATCATAAAGGgagagagagagaga	578		ref XM_691174.2	37.	0.19
							PREDICTED: Danio rerio	4	
		Sbjct	130	CATAACGGAGAGACTGAGAAGAGTGAGAGAGAGAGAGAGA	91		leprecan-like 2 (leprel2),		
							mRNA		
BP1	Danio rerio	Query	483	TTTTTATGTTTAGGTTTTTA	502		ref NM_200582.1 Danio	37.	0.29
3-B4							rerio thyroid hormone	4	
		Sbjct	1598	TTTTTATGTTTAGGTTTTTA	1617		receptor interactor 13		
							(trip13),		
							mRNA		
	Salmo salar	Query	17	tctctTTGTTTCTGTTGTTGTA	38		>ref NM_001140778.1	31.	1.2
							Salmo salar Sperm	9	
		Sbjct	507	TCTCTTGGTTCCTGTTGTTGTA	486		flagellar protein 1 (spef1),		
							mRNA		

APPENDIX B

Microsatellite primers designed. The appendix shows the microsatellite primers designed after cloning inserts were sequenced. Also the microsatellite repeat motif, GenBank accession number, and product size in basepairs are shown.

RAM	locus name	GenBank accession No.	Primer number	Microsats	F. primer	R. Primer	product size (bp)
T113	SYSC-T113-1	GU323270	T113-1	(CCG) ₆	TTCCAAGCTTGTAGAGGAAC	GACTTTGACGTCGAGTTTTTC	236
T113				(CGCGT) ₂	TTCCAAGCTTGTAGAGGAAC	GACTTTGACGTCGAGTTTTTC	236
T113				(CGAC) ₂	TTCCAAGCTTGTAGAGGAAC	GACTTTGACGTCGAGTTTTTC	236
T113			T113-2	(AGGCGC) ₂	AAAGTTGGAGTGAAACGAGA	CTTAAAGCAGCCATTTTCTG	166
T113	SYSC-T113-2	GU323271	T113-3	(GGTC) ₂	GAGCGGAACATTTAATACGA	GTTTCAGGTTGACCACGTACT	271
T113			T113-4	(CCGA) ₂	GTGTTCAACGGAAAGAAGAG	GAATCCCAAGAATCTGGAAC	182
T113				(CGG) ₆	GTGTTCAACGGAAAGAAGAG	GAATCCCAAGAATCTGGAAC	182
T113	SYSC-T113-3	GU323272	T113-5	(CGAC) ₂	GTTTCAGGTTGACCACGTACT	GAGCGGAACATTTAATACGA	271
T113	SYSC-T113-4	GU323273	T113-6	(GGGC) ₂	CTTGAAGGACAATTCAATGC	TAAGCTATGGCTGGCTCTAC	210
T113				(GCT) ₃	CTTGAAGGACAATTCAATGC	TAAGCTATGGCTGGCTCTAC	210
T113			T113-7	(GCCA) ₂	GCAAAATGTAAGTCTACGA	GAAAAGGCTTACATCACCTG	206
T113			T113-8	(GAA) ₃	CAGGTGATGTAAGCCTTTTC	GGCTACACTTTTCAATCCAC	250
T113	SYSC-T113-5	GU323274	T113-9	(CAGA) ₃	CACCAAGGTGAACCCTTC	ACAGAGATGTGCGTCCTTAC	219
T113			T113-10	(ATTTC) ₂	GTAAGGACGCACATCTCTGT	CACACACACATTCACATTCA	272
T113			T113-11	(TCACT) ₂	CCCTGTATTTCAATTTCTCCA	ACCAAACTGCAATCTCTCT	296
T113				(CTTT) ₃	CCCTGTATTTCAATTTCTCCA	ACCAAACTGCAATCTCTCT	296
T113			T113-12	(TTG) ₃	CCCCTTTCTTTCTTTTCAGT	TCAGCTGCAGAGTTACACAC	241
T113				(TTAT) ₂	CCCCTTTCTTTCTTTTCAGT	TCAGCTGCAGAGTTACACAC	241

T113			(TG)10	CCCCTTTCTTTCTTTTCAGT	TCAGCTGCAGAGTTACACAC	241	
T113			(TGAATG)2	CCCCTTTCTTTCTTTTCAGT	TCAGCTGCAGAGTTACACAC	241	
T113		T113-13	(TAATC)2	TCTTGGATCTTTTCCCAGTA	AAGGGAGAAAGTCAGAGTCC	263	
T113		T113-14	(CTGGAG)2	AGCACATGCCTTTGTAAAAC	GGCTGAAGTGGAACCTCT	201	
T113	SYSC-T113-6	GU323275	T113-15	(TCAG)2	CTGCTGGATACCTTGGATAG	GTCATTTTCGCAGAGAGAAC	224
T113		T113-16	(ACTGTT)2	GTTCTCTCTGCGAAAATGAC	TCCTTGAAGTAAACCGAGAA	287	
T113			(ACCC)2	GTTCTCTCTGCGAAAATGAC	TCCTTGAAGTAAACCGAGAA	287	
T113			(TGCG)2	GTTCTCTCTGCGAAAATGAC	TCCTTGAAGTAAACCGAGAA	287	
T113			(AAAT)2	GTTCTCTCTGCGAAAATGAC	TCCTTGAAGTAAACCGAGAA	287	
T113		T113-17	(CTC)3	ATAACAACGGTGAGACCATC	TACACTGCACAGAAATACCG	174	
T113		T113-18	(GTCG)2	CGGTATTTCTGTGCAGTGTA	GAACTCTAGAGGGGATCCAG	208	
T113			(CTCC)2	CGGTATTTCTGTGCAGTGTA	GAACTCTAGAGGGGATCCAG	208	
T113			(CGG)6	CGGTATTTCTGTGCAGTGTA	GAACTCTAGAGGGGATCCAG	208	
T113		T113-19	(GGCA)2	CGGTATTTCTGTGCAGTGTA	TAACGCCACAAGCCTTGAA	242	
T113	SYSC-T113-7	GU323276	T113-20	(CGAC)2	GTTCAGGTTGACCACGTACT	GAGCGGAACATTTAATACGA	271
T113		T113-21	(TCCG)2	CAACCGTTAAGGTGTGACAT	CAGATCCAGCCTTTTTCC	219	
T113	SYSC-T113-8	GU323277	T113-22	(CGG)6	GCCGAGAAGGTAAAGAAAA	GATCCAGATCTTAATCCGAGT	242
T113	SYSC-T113-9	GU323278	T113-23	(GTGCC)2	AAGGCTTGGACGCTGAGT	TTCGACTCTCTGATCTCCAC	237
T113			(GCC)5	AAGGCTTGGACGCTGAGT	TTCGACTCTCTGATCTCCAC	237	
T113		T113-24	(GGTC)2	GAGCGGAACATTTAATACGA	G TTCAGGTTGACCACGTACT	271	
T113		T113-25	(GGCC)2	GTGTTCAACGAAAAGAAGA	GTGTCGGATACTGCTAAGGA	217	
T113			(CGG)3	GTGTTCAACGAAAAGAAGA	GTGTCGGATACTGCTAAGGA	217	
BP6	SYSC-BP6-1	GU323262	BP6-1	(GTAA)2	TAGGCAACTTTTAGGACTCG	AGCGACTGAGATTAGGTCAA	286
BP6	SYSC-BP6-2	GU323263	BP6-2	(AGAGG)2	AGAAGAAGAAGAAGCCGAGT	GAAAAACAGAGCAGGAACAC	223
BP6				(AGTC)2	AGAAGAAGAAGAAGCCGAGT	GAAAAACAGAGCAGGAACAC	223
BP6		BP6-3	(GT)13	AGAAGAAGAAGAAGCCGAGT	GTACATTAGCACGCACACAC	282	
BP6		BP6-4	(GT)16	TCGAGCTGTGTTAAGTGTG	GTTCTGTGTTTTCATCT	288	

BP6			(GCTT)2	TCGAGCTGTGTTTAAGTGTG	GTTTCGTGTTGTTTTCCATCT	288	
BP6			BP6-5	(ATTT)2	AGATGGAAAACAACACGAAC	GAAACACAGTCGGTTCAGAT	265
BP6			BP6-6	(GTGTGC)2	CGTGGAGGTGAATCATTAT	CACTGTATTTTTGCCTCTCC	296
BP6	SYSC-BP6-3	GU323264	BP6-7	(GAAG)2	TTGAAATGTGTTTCAGCAGTG	CACAAGTGAACAGACACAGG	159
BP6			BP6-8	(CTGG)2	GCTCCTGTGCTGTTCACTT	CAGATTAATGAGCAGCTGAA	216
BP6	SYSC-BP6-4	GU323265	BP6-9	(CAGT)2	GTTTTTGTTCCTTCCTCTC	ATTTACCTTAGCGAGGGTTT	290
BP6				(ATGT)2	GTTTTTGTTCCTTCCTCTC	ATTTACCTTAGCGAGGGTTT	290
BP6			BP6-10	(GAAA)2	TGCCAATGTATGTGTTCACT	ATTTACCTTAGCGAGGGTTT	261
BP6				(GTTG)2	TGCCAATGTATGTGTTCACT	ATTTACCTTAGCGAGGGTTT	261
BP6			BP6-11	(TAATG)2	GTCCACATGTACCTGACACA	CACTGTGGTGGTCTGTTGTA	293
BP6			BP6-12	(TGCATG)2	TGTGGTTATGCTGTTTGTGT	GTGATGAACATTTGACCACA	170
BP6	SYSC-BP6-5	GU323266	BP6-13	(GTAA)2	TCCAAATTCCTCGTACCTA	CAACAGAACAAAACCTGCAAG	291
BP6	SYSC-BP6-6	GU323267	BP6-14	(CTT)4	GTTACAAGGGTGAGAAACCA	AGGGGATCCAGATCTAACAT	167
BP6	SYSC-BP6-7	GU323268	BP6-15	(TACA)2	TCTGCGTGTTATGTCAGTGT	GAGCCTTCATGCTTCAATAC	218
BP6				(CCAG)2	TCTGCGTGTTATGTCAGTGT	GAGCCTTCATGCTTCAATAC	218
BP6			BP6-16	(TGTT)2	GTTGCGGTTAATGATATGGT	AGAGCATTCTCACACACACA	189
BP6			BP6-17	(GT)7	GAAGCTGCCTGAAAAACTAA	GAGTACGGAAGCAGAAACAC	284
BP6				(ATTT)2	GAAGCTGCCTGAAAAACTAA	GAGTACGGAAGCAGAAACAC	284
BP6				(TTAAAT)6	GAAGCTGCCTGAAAAACTAA	GAGTACGGAAGCAGAAACAC	284
BP6				(TCTT)2	GAAGCTGCCTGAAAAACTAA	GAGTACGGAAGCAGAAACAC	284
BP6	SYSC-BP6-8	GU323269	BP6-18	(GTT)3	GCTTTTTGTGCGAGTTAGAT	AAAAGCACTCAGGATAAACC	226
BP14	SYSC-BP14-1	GQ853134	BP14-1	(CTGT)2	ATTACAGCTGTGTGGGTTTC	CAATGTCTGAAGGTTGTAGGT	212
BP14			BP14-2	(TAA)3	TCAAGTGAGACAGCATTTTG	TGTCATCACTTCACCATTG	162
BP14				(TTAG)2	TCAAGTGAGACAGCATTTTG	TGTCATCACTTCACCATTG	162
BP14	SYSC-BP14-2	GQ853135	BP14-3	(AAAG)2	ACAAAACCGAGATAAACACG	GCACACACATACAAGTGGAG	213
BP14	SYSC-BP14-3	GQ853136	BP14-4	(TGAGG)2	ATATGGGAAAGATGTGCAAC	CAGGTACGTCAGGTACAGGT	269
BP14			BP14-5	(GTACCT)2	GAGTTGGTGAATGAGGAAAA	CCCCATCACACTGAACTATT	287

BP14			BP14-6	(GCAG)2	TGACGTACCTGATGACAGAA	TCTAACCCATAGAGCAGAGC	283
BP14				(AAAGG)2	TGACGTACCTGATGACAGAA	TCTAACCCATAGAGCAGAGC	283
BP14			BP14-7	(GCTCT)2	GTGTGGAAAAGAGGTGAAGA	TGATGAGCTCGTTCCTTATT	263
BP14	SYSC-BP14-4	GQ853137	BP14-8	(TCCT)2	AATATTCCCAATCCTCTTC	CAAAGGGAACAAAGCATAAC	276
BP14				(GAAT)2	AATATTCCCAATCCTCTTC	CAAAGGGAACAAAGCATAAC	276
BP14			BP14-9	(TGAA)2	GTCTGGTTATGCTTTGTTCC	ACATGCAAGGAAGACTATGC	154
BP14			BP14-10	(GGAA)2	GTCTTCCTTGCATGTCTTTG	TCAGGCCTGCAGTATAAGTT	297
BP14				(TTCA)2	GTCTTCCTTGCATGTCTTTG	TCAGGCCTGCAGTATAAGTT	297
BP14				(TGTTT)2	GTCTTCCTTGCATGTCTTTG	TCAGGCCTGCAGTATAAGTT	297
BP14	SYSC-BP14-5	GQ853138	BP14-11	(ACTG)2	AGACAAAGAACAGGTGTGGA	GACAGGTGAAACGAGAAAAG	157
BP14			BP14-12	(TTTC)2	ACAAAGAACAGGTGTGGAAC	AGACAGGTGAAACGAGAAAA	156
BP14			BP14-13	(CTCA)2	ACAAAGAACAGGTGTGGAAC	AAACGAGGGAACATAACCTC	299
BP14				(GTTT)2	ACAAAGAACAGGTGTGGAAC	AAACGAGGGAACATAACCTC	299
BP14	SYSC-BP14-6	GQ853139	BP14-14	(ATGTAC)2	GTCAGAGGGATGTTTAATGG	AGCAGTTTTTGTTCACATC	268
BP14	SYSC-BP14-7	GQ853140	BP14-15	(GTCAC)2	GGGCATTTTGTTCATGCTA	TTCTGAAGAGTGTCCACCACA	207
BP14			BP14-16	(ACCAAG)2	GTTAACACTGTGCCACTCCT	TTTGGCTTAATCTCACCTA	235
BP14	SYSC-BP14-8	GQ853141	BP14-17	(CTGG)2	GATTGGGCTGTAAGTGTTTC	CCGTTGGCGTTATTCATTAT	199
PCT6	SYSC-PCT6-1	GQ853142	PCT6-1	(ACA)4	GTGGGGAAATTCTTGAACAT	GATTTCAAGGCTGACAAAAG	165
PCT6			PCT6-2	(ACT)5	CTTTTGTGAGCCTTCAAATC	GTTAGCTGGTGTGAGAGAGG	205
PCT6			PCT6-3	(AGAGC)2	TGATGAGCTCGTTCCTTATT	CAAGACTCAAAGGAAAGGTG	174
PCT6			PCT6-4	(CCTTT)2	TCTAACCCATAGAGCAGAGC	TGACGTACCTGATGACAGAA	283
PCT6			PCT6-5	(CCTG)2	CACCTTTCCTTTGAGTCTTG	TGACGTACCTGATGACAGAA	242
PCT6			PCT6-6	(CAGGTA)2	CACCTTTCCTTTGAGTCTTG	GAAAAGGATGAAGAGCAGAA	293
PCT6	SYSC-PCT6-2	GQ853143	PCT6-7	(ATTC)2	TGGACGGGATAGATAGATA	CATCTGAGACCTGGAGTAGC	173
PCT6				(AAG)3	TGGACGGGATAGATAGATA	CATCTGAGACCTGGAGTAGC	173
PCT6			PCT6-8	(TTAT)2	GGGGGATTCATTCAAGAAG	ATCGCTACAACGCTATGATT	224
PCT6			PCT6-9	(CGGAC)2	GCTGCAGCTGGAATATTAAC	TTTGTTCGAAACGGTTATAC	271

PCT6			PCT6-10	(TTTA)2	GACTTACCCTCTCTCCTCGT	TATTAGCTTAACGTCGCACA	277
PCT6			PCT6-11	(AAGTT)2	ACACAGTTTTGTCCCATTTC	CTGCTGTGAAAAACAATCTC	289
PCT6			PCT6-12	(ACAT)2	TGTGCGACGTTAAGCTAATA	GTTTGTGTATGCTTCTGTGTG	153
PCT6			PCT6-13	(TATC)4	TGTGCGACGTTAAGCTAATA	CCAGATCTTTTAGCGATAG	193
BP13	SYSC-BP13-1	GQ853144	BP13-1	(CAGG)2	GAAAATCAAAGAGGCACATC	CCAAATCAGGAGTCTGAGAG	246
BP13			BP13-2	(AATG)2	CTCTCAGACTCCTGATTTGG	TTCAAACCTCTGGAGAGAAA	250
BP13			BP13-3	(GGAA)2	TTTCTCTCCAGGAGTTTGAA	TGTCACGTCTCATTGTCAGT	275
BP13			BP13-4	(AAAATA)2	TATCGAAAAGACTGGAAGGA	CAAAGACGTATCGGTTTCTC	157
BP13	SYSC-BP13-2	GQ853145	BP13-5	(AC)6	TCTCTCTCTCTCTCTCTCTC	ATTCACCTCCTGTTACACC	239
BP13			BP13-6	(CA)10	CTCTCTCTAACACACACACACC	ATTCACCTCCTGTTACACC	224
BP13			BP13-7	(AGAGG)2	GACAAACGCAGAGAAAAGAC	ATTCACCTCCTGTTACACC	154
BP13			BP13-8	(CAGC)2	GGTGTGAACAGGAAGTGAAT	CATTTGTGTGGTGTGTCATT	289
BP13			BP13-9	(CACAC)2	TATTACCCCGTTCAACCTTA	GACATTTCTTGGCCAGTTC	261
BP13	SYSC-BP13-3	GQ853146	BP13-10	(TACA)2	CCAATGTCTGAAAGCAAAGT	TGAAGAGAATCGACTGAACC	264
BP13			BP13-11	(TCACTT)2	CCAATGTCTGAAAGCAAAGT	TGAAGAGAATCGACTGAACC	264
BP13			BP13-12	(TACTG)2	GCTGCTATGTGTGCTCTGTA	TTATCTCGCTCTTTCAAACC	299
BP13				(GTTT)2	GCTGCTATGTGTGCTCTGTA	TTATCTCGCTCTTTCAAACC	299
BP13				(TGTT)2	GCTGCTATGTGTGCTCTGTA	TTATCTCGCTCTTTCAAACC	299
BP13			BP13-13	(ACCCAT)2	TTTGAAAGAGCGAGATAAGG	AGAGAGAGAGAGCAGGAGGT	183
BP13				(CTTT)2	TTTGAAAGAGCGAGATAAGG	AGAGAGAGAGAGCAGGAGGT	183
BP13			BP13-14	(CT)13	TTTGAAAGAGCGAGATAAGG	TAGAAACAAAATGGGGACAG	218
BP13	SYSC-BP13-4	GQ853147	BP13-15	(GA)15	TAGAAACAAAATGGGGACAG	TTTGAAAGAGCGAGATAAGG	222
BP13			BP13-16	(GAAA)2	AGAGAGAGAGAGCAGGAGGT	TTTGAAAGAGCGAGATAAGG	183
BP13				(ATGGGT)2	AGAGAGAGAGAGCAGGAGGT	TTTGAAAGAGCGAGATAAGG	183
BP13				(CCAC)2	AGAGAGAGAGAGCAGGAGGT	TTTGAAAGAGCGAGATAAGG	183
BP13			BP13-17	(AAAC)2	TTATCTCGCTCTTTCAAACC	GCTGCTATGTGTGCTCTGTA	299
BP13				(CAAAC)2	TTATCTCGCTCTTTCAAACC	GCTGCTATGTGTGCTCTGTA	299

BP13				(TACAG) ²	TTATCTCGCTCTTTCAAACC	GCTGCTATGTGTGCTCTGTA	299
BP13			BP13-18	(AAAGTG) ²	TGAAGAGAATCGACTGAACC	CCAATGTCTGAAAGCAAAGT	264
BP13				(TGTA) ²	TGAAGAGAATCGACTGAACC	CCAATGTCTGAAAGCAAAGT	264
BP13	SYSC-BP13-6	GQ853148	BP13-21	(ACACAT) ²	GTCTCTCTCTCTTTTCG	TTTTCTCTCCCTCTTTTCCT	239
BP13			BP13-22	(GCTG) ²	CTCTCTTTCGCACACACATA	CTTTTCTCTCCCTCTTTTCC	232
BP13				(GGAGA) ²	CTCTCTTTCGCACACACATA	CTTTTCTCTCCCTCTTTTCC	232
BP13			BP13-23	(GAGGA) ²	CTCTCTTTCGCACACACATA	TCCCTCTCTTTTTCTCTCC	241
BP13			BP13-24	(GAGG) ²	CTCTCTTTCGCACACACATA	CATTTTACCTCCTCCCATC	262
BP13	SYSC-BP13-7	GQ853149	BP13-25	(AC) ⁷	CACAGACTTTCGAACACCTT	TTATAAAGCTGCTTCCCATC	211
BP13				(TTTA) ²	CACAGACTTTCGAACACCTT	TTATAAAGCTGCTTCCCATC	211
BP13			BP13-26	(ATCA) ²	GGTTTTGTCCACTGTAAAGG	AATTCACGTGAGTCAGTTC	240
BP13				(AGTAA) ²	GGTTTTGTCCACTGTAAAGG	AATTCACGTGAGTCAGTTC	240
BP13				(ACAT) ²	GGTTTTGTCCACTGTAAAGG	AATTCACGTGAGTCAGTTC	240
BP13				(GTGA) ²	GGTTTTGTCCACTGTAAAGG	AATTCACGTGAGTCAGTTC	240
BP13			BP13-27	(TTAA) ²	TAGTTCCTTTGCTTCTGGTT	TTCCTGACCAGTTGAGAAAC	224
BP13			BP13-28	(TTAA) ²	AATCTCTGACCAAAAACAGC	TCTTCACTTTCCTCATCC	266
BP13			BP13-29	(GGAC) ²	CAACAGTGGAGAGGAAAAAC	CTGTCTCTGTCCTCAGGTGT	197
BP13	SYSC-BP13-8	GQ853150	BP13-30	(CACT) ²	TCTCTGTCTGTTTCCCTGTC	TGCTCCTGTGTGGTATATGA	233
BP13			BP13-31	(TACA) ²	GTGGGAATAGGAGATGTTGA	TCTCCATTGTGTCTCACTCA	275
BP13				(ATCC) ²	GTGGGAATAGGAGATGTTGA	TCTCCATTGTGTCTCACTCA	275
BP13				(CTCA) ²	GTGGGAATAGGAGATGTTGA	TCTCCATTGTGTCTCACTCA	275
BP13				(CCTTG) ²	GTGGGAATAGGAGATGTTGA	TCTCCATTGTGTCTCACTCA	275
BP13			BP13-32	(TGAG) ²	GTGGGAATAGGAGATGTTGA	TGATCAGTCTCTCCATTGTG	284
BP13	SYSC-BP13-9	GQ853151	BP13-33	(TGT) ³	TGTGTCTCTCTCTCTTTGTT	TTGTGCCACAGTGTATCTA	194
BP13			BP13-34	(AGGT) ²	CTGTTGTTGTACCTGTGTCTG	TTGTGCCACAGTGTATCTA	171
BP13				(ACAG) ²	CTGTTGTTGTACCTGTGTCTG	TTGTGCCACAGTGTATCTA	171
BP13			BP13-35	(TATT) ²	CTGTTGTTGTACCTGTGTCTG	CTGGACCACCACGATATACT	271

BP13	BP13-36	(TTTAAA)2	CATTTGAAACGTGTTGTGTC	CTATCCGTGATGGTAGGTGT	299
BP13		(CGCTG)2	CATTTGAAACGTGTTGTGTC	CTATCCGTGATGGTAGGTGT	299
BP13	BP13-37	(AAAG)2	CACCTTCAAGTGGGTCTTAG	GACTTCTTTACACCCAGACG	239

APPENDIX C

Allele frequencies of all microsatellite loci isolated from *C. striata*.

Locus	Allele#	Size	Johore	Kedah	Negeri Sembilan	Pahang	Penang	Selangor	Terengganu	Overall
T79113-7	1	196	0.3667	0.3500	0.3500	0.3667	0.4167	0.4600	0.4286	0.3892
T79113-7	2	200	0.0000	0.0000	0.0000	0.0167	0.0000	0.0000	0.0357	0.0074
T79113-7	3	204	0.6333	0.6500	0.6500	0.6167	0.5833	0.5400	0.5000	0.5985
T79113-7	4	208	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0357	0.0049
PIC= 0.490242										
T79113-11	1	291	0.1667	0.4833	0.0500	0.2000	0.4423	0.5000	0.2381	0.2927
T79113-11	2	295	0.7833	0.4667	0.0500	0.5333	0.5192	0.4808	0.6905	0.4948
T79113-11	3	299	0.0500	0.0500	0.9000	0.2667	0.0385	0.0192	0.0714	0.2124
PIC= 0.624386										
BP6-2	1	213	0.3000	0.3833	0.0500	0.7000	0.8333	0.8462	0.3667	0.4903
BP6-2	2	218	0.2333	0.1833	0.4167	0.0667	0.0000	0.0000	0.1167	0.1481
BP6-2	3	223	0.4667	0.4333	0.5333	0.2333	0.1667	0.1538	0.5167	0.3617
PIC= 0.606845										
BP6-4	1	256	0.0167	0.0000	0.0000	0.0167	0.0000	0.0192	0.0000	0.0073
BP6-4	2	262	0.0167	0.0000	0.0000	0.0000	0.0167	0.0000	0.0000	0.0049
BP6-4	3	264	0.0667	0.3667	0.0667	0.2000	0.3833	0.7115	0.1167	0.2646
BP6-4	4	266	0.0167	0.0167	0.0167	0.0000	0.0000	0.0000	0.0000	0.0097
BP6-4	5	268	0.0167	0.0000	0.0167	0.0167	0.0000	0.0192	0.0000	0.0097
BP6-4	6	270	0.0000	0.0000	0.0167	0.0000	0.0333	0.0000	0.0000	0.0073
BP6-4	7	272	0.0000	0.0000	0.0000	0.0333	0.0000	0.0000	0.0667	0.0146

BP6-4	8	274	0.0500	0.0000	0.0000	0.0000	0.0167	0.0000	0.0000	0.0097
BP6-4	9	276	0.0500	0.0000	0.0000	0.2833	0.3000	0.0385	0.2500	0.1335
BP6-4	10	278	0.2000	0.0000	0.0000	0.1333	0.1167	0.0577	0.0000	0.0728
BP6-4	11	280	0.0333	0.0333	0.0000	0.0333	0.0000	0.0000	0.0000	0.0146
BP6-4	12	284	0.0000	0.0167	0.0167	0.0333	0.0167	0.0000	0.0167	0.0146
BP6-4	13	286	0.0333	0.4833	0.0000	0.0000	0.0833	0.0192	0.1000	0.1044
BP6-4	14	288	0.4333	0.0167	0.0333	0.1500	0.0000	0.0192	0.0000	0.0947
BP6-4	15	290	0.0500	0.0000	0.8167	0.0500	0.0333	0.0000	0.0000	0.1383
BP6-4	16	294	0.0000	0.0500	0.0000	0.0000	0.0000	0.0962	0.1000	0.0340
BP6-4	17	296	0.0167	0.0167	0.0167	0.0333	0.0000	0.0192	0.3500	0.0655
										PIC= 0.929815
BP14-1	1	204	0.0500	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0074
BP14-1	2	208	0.0333	0.0000	0.0000	0.0333	0.0000	0.0000	0.0000	0.0098
BP14-1	3	212	0.7667	0.0000	0.6833	0.4833	0.5333	0.5192	0.5000	0.5025
BP14-1	4	216	0.1500	0.8393	0.3167	0.4500	0.4667	0.4808	0.5000	0.4534
BP14-1	5	220	0.0000	0.1607	0.0000	0.0333	0.0000	0.0000	0.0000	0.0270
										PIC= 0.541771
BP14-5	1	274	0.0172	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0025
BP14-5	2	280	0.7241	0.7000	0.6500	0.5333	0.6207	0.7115	0.8667	0.6863
BP14-5	3	286	0.2586	0.3000	0.3500	0.4667	0.3793	0.2885	0.1333	0.3113
										PIC= 0.432078
BP14-14	1	254	0.1034	0.2167	0.3167	0.3167	0.2667	0.1731	0.1833	0.2268
BP14-14	2	266	0.8966	0.7833	0.6833	0.6833	0.7333	0.8269	0.8167	0.7732
										PIC= 0.350724

APPENDIX D

Genotype frequencies of the 7 microsatellite loci in the 7 populations of *Channa striata*.

Locus	Genotype						
Population	Johore	Kedah	Negeri Sembilan	Pahang	Penang	Selangor	Terengganu
T79113-7	196/204 (22)	196/204 (21)	196/204 (21)	196/204 (22)	196/204 (25)	196/204 (23)	196/204 (24)
	204/204 (8)	204/204 (9)	204/204 (9)	200/204 (1) 204/204 (7)	204/204 (5)	204/204 (2)	200/208 (2) 204/204 (2)
T79113-11	291/295 (10)	291/291 (9)	291/295 (3)	291/291 (3)	291/291 (10)	291/291 (9)	291/291 (2)
	295/295 (18)	295/295 (9)	299/299 (27)	291/295 (3)	291/295 (3)	291/295 (7)	291/295 (6)
	295/299 (1)	295/299 (9)		291/299 (3)	295/295 (12)	291/299 (1)	295/295 (11)
	299/299 (1)	291/299 (2)		295/295 (12)	299/299 (1)	295/295 (9)	295/299 (1)
		295/299 (1)		295/299 (5) 299/299 (4)			299/299 (1)
BP6-2	213/213 (3)	213/213 (6)	213/223 (3)	213/213 (16)	213/213 (20)	213/213 (18)	213/213 (1)
	213/218 (2)	213/223 (11)	218/223 (25)	213/223 (10)	213/223 (10)	213/223 (8)	213/223 (20)
	218/218 (2)	218/223(11)	223/223 (2)	223/218 (4)			223/218 (7)
	223/213 (10)						223/223 (2)
	223/218 (8)						
	223/223 (5)						
BP6-4	256/278 (1)	264/264 (6)	264/290 (4)	256/276 (1)	262/274 (1)	264/264 (13)	264/272 (1)
	262/288(1)	264/284 (1)	266/290 (1)	264/264 (3)	264/264 (5)	256/268 (1)	264/276 (3)
	264/264 (1)	264/286 (9)	268/290 (1)	264/272 (1)	264/276 (4)	264/276 (2)	264/296 (3)
	264/288 (2)	266/288 (1)	270/290 (1)	264/276 (1)	264/278 (5)	264/278 (2)	272/286 (1)
	266/276 (1)	280/280 (1)	284/290 (1)	264/278 (2)	264/284 (1)	264/286 (1)	272/296 (2)

	274/278 (1)	286/288 (8)	288/290 (1)	264/288 (2)	264/286 (2)	264/288 (1)	276/286 (3)
	274/288 (2)	286/294 (3)	288/296 (1)	266/276 (1)	264/290 (1)	264/294 (4)	276/296 (9)
	276/286 (1)	286/296 (1)	290/290 (20)	268/284 (1)	270/270 (1)	264/296 (1)	284/296 (1)
	276/296 (1)			272/284 (1)	276/276 (5)	278/294 (1)	286/296 (2)
	278/278 (1)			276/276 (5)	276/286 (3)		294/294 (3)
	278/280 (1)			276/288 (4)	276/290 (1)		296/296 (2)
	278/288 (7)			278/278 (2)	278/278 (1)		
	280/ 288 (1)			278/288 (1)			
	286/ 288 (1)			278/290 (1)			
	288/288 (5)			280/280 (1)			
	288/290 (2)			288/288 (1)			
				290/290 (1)			
				296/296 (1)			
BP14-1	204/212 (3)	216/216 (19)	212/212 (11)	208/208 (1)	212/212 (2)	212/212 (2)	212/216 (30)
	208/208 (1)	216/220 (9)	212/216 (19)	212/212 (1)	212/216 (28)	212/216 (23)	
	212/212 (17)			212/216 (27)		216/216 (1)	
	212/216 (9)			220/220 (1)			
BP14-5	274/280 (1)	280/280 (12)	280/280 (9)	280/280 (2)	280/280 (7)	280/280 (11)	280/280 (22)
	280/280 (14)	280/286 (18)	280/286 (21)	280/286 (28)	280/286 (22)	280/286 (15)	280/286 (8)
	280/286 (13)						
	286/286 (1)						
BP14-14	254/266 (6)	254/266 (13)	254/254 (1)	254/266 (19)	254/254 (1)	254/266 (9)	254/266 (11)
	266/266 (23)	266/266 (17)	254/266 (17)	266/266 (11)	254/266 (14)	266/266 (17)	266/266 (19)
			266/266 (12)		266/266 (15)		

APPENDIX E

Linkage disequilibrium P-values for each locus pair across all populations. Disequilibrium values were compared between all pairs of loci in this study. In the table cells of locus 1 and its adjacent cell locus 2 is evaluated.

Locus 1	Locus 2	χ^2	df	P-value
T79113-7	T79113-11	17.548749	14	0.228112
T79113-7	BP6-2	12.818405	14	0.540870
T79113-11	BP6-2	28.164490	14	0.013529
T79113-7	BP6-4	12.211426	14	0.589328
T79113-11	BP6-4	17.900198	14	0.211364
BP6-2	BP6-4	Infinity	14	Highly sign.
T79113-7	BP14-1	5.017687	12	0.957386
T79113-11	BP14-1	17.390959	12	0.135473
BP6-2	BP14-1	9.784631	12	0.634848
BP6-4	BP14-1	10.984315	12	0.530263
T79113-7	BP14-5	12.613864	14	0.557128
T79113-11	BP14-5	12.241525	14	0.586913
BP6-2	BP14-5	11.316097	14	0.661045
BP6-4	BP14-5	13.533682	14	0.484997
BP14-1	BP14-5	4.389479	12	0.975340
T79113-7	BP14-14	5.801600	14	0.971247
T79113-11	BP14-14	7.194186	14	0.926966
BP6-2	BP14-14	19.583150	14	0.143841
BP6-4	BP14-14	19.722423	14	0.139138
BP14-1	BP14-14	9.278950	12	0.678938
BP14-5	BP14-14	10.694707	14	0.709835

χ^2 : chi-square value; df: degree of freedom; P-value: probability value of significance (P<0.05)