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MICROSATELLITE RECORDS

Microsatellite records for volume 12, issue 2

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Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
Pelochelys cantorii	Pc_01[a]	F:TGAGCAGATTGAAGGAGCCATCTC R:CTTAAAGAGATCTGGCTCCACTCATC	$(GTA)_{12}$	230–245	33	4	0.818 (0.682)
Pelochelys cantorii	Pc_02[a]	F:TCAACCATTGCCCAGTATGTGTCC R:CCATTCCTGTGAAATGGGAACAGC	$(GT)_9$	292–312	33	4	0.909 (0.601)
Pelochelys cantorii	Pc_03[a]	F:GGTATTGTAACTACCAAGCTG R:GTGTAGTTAAGCACTGGAATAGGAATCT	$(TATC)_6$	175–179	32	2	0.594 (0.502)
Pelochelys cantorii	Pc_04[a]	F:GTCAAGAGGAACTGAACACCAG R:CTGAAGGCAACAGAATGGAAACCG	$(ATC)_6$	243–258	35	2	0.086 (0.083)
Pelochelys cantorii	Pc_05[a]	F:AGCAATTCACAGCAGGGCCTTATT R:GCATTGTATTTTGGGTGTCCT	$(TG)_{12}$	304–316	33	6	0.758 (0.695)

Electronic supplementary material The online version of this article (https://doi.org/10.1007/s12686-020-01148-6) contains supplementary material, which is available to authorized users.

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
Pelochelys cantorii	Pc_06 [a]	F:AGCTGTTGGCTGTGATGTCTT R:GTCCCCCTTCCTAGTCTCTTA	$(TCC)_{12}$	200–215	35	3	0.314 (0.281)
Pelochelys cantorii	Pc_07[a]	F:CCATGCGGGTCTTACAAGG R:CAGAGTAGTATCCAGGTCCATC	$(AC)_{19}$	186–198	35	4	0.429* (0.554)
Pelochelys cantorii	Pc_08[a]	F:CACTGCACATGTCTCTGAAT R:CCGATAGATCCCTGTAGTGTAG	$(AAT)_4$	139–148	35	2	0.429 (0.342)
Pelochelys cantorii	Pc_09[a]	F:TGTTCCCAGTGTCCCTAAGC R:GCAAAGTGCGCTCATGGT	$(AGC)_4$	269–272	33	2	0.394 (0.321)
Pelochelys cantorii	Pc_010[a]	F:CCATATTCTTTTGCAGTGATACTT R:TCACCTCAGTACGTGTATGC	$(TG)_{18}$	254–256	31	2	0.258 (0.228)
Pelochelys cantorii	Pc_011[a]	F:ATCTTCCAACTGACCGATTCT R:GCATTTTGATGCCGGAGTAT	$(CA)_8$	191–197	33	3	0.576 (0.439)
Pelochelys cantorii	Pc_012[a]	F:GATTCGTGGGAGAATCAGGA R:CGTTTCTGGGCATCACATTACC	$(AGC)_4$	130–139	35	2	0.429 (0.342)
Pelochelys cantorii	Pc_013[a]	F:GTGGCTCAACAGTCATTTCA R:GCACACACACTCAACCTAGAC	$(TG)_{10}$	315–323	35	4	0.600 (0.617)
Pelochelys cantorii	Pc_014[a]	F:GTGGTGCTTGTATCTGGTGGTTGA R:CACCTGTGTGATTAGCGTCA	$(ACGCGC)_5$	138–150	35	3	0.171 (0.210)
Pelochelys cantorii	Pc_015[a]	F:AAACAGTAGAAGAACGTGCC R:GGGGATCGTGTTACAGTATGG	$(CT)_{16}$	278–298	35	7	0.914 (0.781)
Pelochelys cantorii	Pc_016[a]	F:CACAGGAGACAATAGCCTTGGTATG R:CTGGCATCGTCAACATACTT	$(TAA)_7$	147–150	33	2	0.455 (0.508)
Pelochelys cantorii	Pc_017[a]	F:CGGAGCATGACTTCGGTTTC R:AGAGGGTGAAGGGAATAGC	$(TC)_{13}$	307–319	33	5	0.515* (0.717)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
Pelochelys cantorii	Pc_018[a]	F:ACATCCCTTCTTACGCATGTA R:GGAGGAAATCTGTGGCTACG	$(\mathrm{GT})_{11}$	199–207	33	5	0.879 (0.756)
Pelochelys cantorii	Pc_019[a]	F:GAAAGGGAGGTGACTCGCTTATTG R:TGAGAGGTCATCTAGTCCAGTCCT	$(\mathrm{AG})_{16}$	177–183	35	3	0.543 (0.513)
Pelochelys cantorii	Pc_020[a]	F:TCAGGCAGCTGCACTTCATTGG R:AGTGAAGTCCTTGTCCGTGA	$(\mathrm{AGCAG})_{4}$	122–132	35	3	0.657 (0.520)
Pelochelys cantorii	Pc_021[a]	F:ATGACAAACATCCTTCCAGT R:ATTGCAGGTAAGCAGGAGTA	$(\mathrm{GGA})_{5}$	244–247	33	2	0.606 (0.496)
Pelochelys cantorii	Pc_022[a]	F:TGGAGCCAAACACTAAAGAGCCAA R:ATCCATCTTCGGGGCTC	$(\mathrm{CTTT})_{5}$	175–179	35	2	0.486 (0.448)
Pelochelys cantorii	Pc_023[a]	F:CTCACACTGCTACCCTCTGAA R:TGACAGCACAGTTAAACAGGCAGT	$(\mathrm{CCAGC})_{4}$	301–306	35	2	0.200* (0.373)
Pelochelys cantorii	Pc_024[a]	F:TGCTGGGTACGACTGCAC R:GCAAGCTCATACTGCCCTG	$(\mathrm{TG})_{12}$	228–234	35	3	0.714 (0.519)
Tridacna crocea	TC2–1[b]	F:TGCCCGGCAATCCGCACA R:GCTTGGCTGGAGCAGATGTT	$(\mathrm{GCT})_{4}$	308–317	30	3	0.700 (0.501)
Tridacna crocea	TC2–2[b]	F:ATCGCAATGTCCGGGTTT R:CATAATGCACCTCGCACCC	$(\mathrm{AATAC})_{4}$	204–243	30	8	0.667 (0.721)
Tridacna crocea	TC2–3[b]	F:TTCTTTACACGGGTTCTC R:ATTGCCGCAGTTTTAGTG	$(\mathrm{GT})_{15}$	105–127	30	2	0.300 (0.508)
Tridacna crocea	TC2–4[b]	F:ATAGCCTGTAACAAGCAG R:GCATGAGGTCATGGGTCA	$(\mathrm{TTG})_{6}$	210–232	30	7	0.700 (0.749)
Tridacna crocea	TC2–5[b]	F:GGTGCTGAAACGCTATAC R:CAGACTCTGAGATTGGAC	$(\mathrm{AT})_{5}$	350–371	30	5	0.533 (0.628)
Tridacna crocea	TC2–6[b]	F:TCATCGCTGGATTCACTAG R:TTCATGCCCAAGAAGGAC	$(\mathrm{AGA})_{5}$	125–143	30	8	0.667 (0.784)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
Tridacna crocea	TC2–7[b]	F:AATGAGACCGGGTATGAG R:GTGGTGGTGATGCTTGTA	$(ATG)_5$	215–240	30	7	0.724 (0.814)
Tridacna crocea	TC2–8[b]	F:CAATGTTTGACCCAAGAG R:ACGAGTGTACGCATAGAA	$(GT)_7$	514–538	30	7	0.600 (0.823)
Tridacna crocea	TC2–9[b]	F:TGTCTGGTCCACGAGTTA R:AGGAAAGTGACGACGAAG	$(TTC)_5$	520–541	30	6	0.433* (0.824)
Tridacna crocea	TC2–10[b]	F:AAGCCGTTTTCCATAGGT R:ACATTCGTAGATGCACTG	$(AG)_7$	351–368	30	6	0.357* (0.790)
Tridacna crocea	TC2–11[b]	F:GTTGGGTAACGGGTAAAT R:CAAAGGCATTGGACATTC	$(CAAT)_5$	363–420	30	8	0.360* (0.825)
Tridacna crocea	TC2–12[b]	F:CTCGGTGAAACTGAACTT R:TAGCACATGGAGGATTGT	$(CT)_6$	253–277	30	2	0.267 (0.506)
Tridacna crocea	TC2–13[b]	F:AAAGTAGCACCAATCCAC R:ATGCTTACCATGAAACCC	$(TG)_8$	340–355	30	7	0.433* (0.683)
Tridacna crocea	TC2–14[b]	F:GCCACAGAACGGAGGAGTT R:TCAGCAGCCGCTACCAAT	$(AGC)_5$	302–320	30	2	0.033 (0.097)
Tridacna crocea	TC2–15[b]	F:ACCAGTGGCTGTAGATTG R:TACATCATCATCCCCTCC	$(TGA)_6$	160–225	30	5	0.500 (0.509)
Tridacna crocea	TC2–16[b]	F:GCAGTTGCCTTTCCCAATA R:CAGCAGCAAAGAGTGTAGAGC	$(AT)_7$	173–218	30	8	0.767 (0.763)
Tridacna crocea	TC2–17[b]	F:CGAAATCTTGTCTTGTGG R:TGTCCTGGCAAACTATCT	$(TG)_8$	302–345	30	6	0.733 (0.819)
Tridacna crocea	TC2–18[b]	F:CTGCCCTGAAGTGATTGG R:CGCTATGTTTGCTACCCT	$(AT)_7$	250–290	30	7	0.767 (0.799)
Tridacna crocea	TC2–19[b]	F:AGGAAAGGCGGGAGAAGA R:TAAGCGGACGGCGTAGAT	$(TTG)_5$	360–438	30	6	0.600 (0.789)
Tridacna crocea	TC2–20[b]	F:CCGAGGCTTGTAGCTTCTCC R:CGTTGCCATCATCCTGGTC	$(CGT)_7$	303–340	30	6	0.400* (0.618)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
Tridacna crocea	TC2–21[b]	F:TTTCTGCCTTTGACTGGA R:TTGCCTCTATGATTGTAAGC	$(TA)_7$	380–445	30	7	0.933 (0.770)
Tridacna crocea	TC2–22[b]	F:ACGAGTGGCTTCAAGTGC R:GGATTCGTAAGCTACAGCAC	$(TCA)_5$	200–228	30	2	0.100 (0.097)
Tridacna crocea	TC2–23[b]	F:ACATGACCACGATTCTTC R:TGATCTATTCCGTCCACT	$(TTG)_6$	265–320	30	6	0.567* (0.805)
Tridacna crocea	TC2–24[b]	F:TACCTTGACAGCTTCTGA R:TCTTGAGTTAACCCCTCT	$(TG)_6$	154–208	30	10	0.462 (0.767)
Tridacna crocea	TC2–25[b]	F:CACAGAAGGATTGAGGGAT R:CAGGGACAGGTGTATTGGAT	$(CAT)_5$	125–186	30	3	0.333 (0.288)
Tridacna crocea	TC2–26[b]	F:TTCCTTGCGCTGTGAGTC R:ACGTAGAGGGACGGGATA	(AT)6	461–483	30	4	0.267 (0.348)
Tridacna crocea	TC2–27[b]	F:AGCCTTCTCCAGCCAACA R:TGCGCTGTAACCTTCTTTG	(TC)6	248–269	30	5	0.467 (0.560)
Tridacna crocea	TC2–28[b]	F:CAGGGCATGGCTCTTGTA R:TCGTGTCCGGCTTAGTGA	(AT)6	307–340	30	5	0.367 (0.563)
Tridacna crocea	TC2–29[b]	F:ATGTTCTGACACGGGCTTCG R:AAGGACCACAGGGTCAAACG	(GC)6	145–196	30	6	0.433 (0.382)
Montipora digitata	Md01[c]	F:CCCAATTTCAGTTGTCTCCAT R:GCATGTAAGCTTCCACTTCCT	$(AC)_{15}$	161–189	52	13	0.712 (0.775)
Montipora digitata	Md02[c]	F:GCCAGTTCGATAATGACCAGA R:CCCTCTAAGTTAGTTGCCCGA	$(AG)_{12}$	170–200	51	15	0.738 (0.784)
Montipora digitata	Md03[c]	F:TTGAAGACCCGTTCTAGCCA R:GATTGCTGTGCTCCTCGAAT	$(AAC)_8$	309–324	52	5	0.502 (0.553)
Montipora digitata	Md04[c]	F:TCATGGATTCGACACCGC R:GGCCATAACTTGACAGAGAACG	$(AAC)_9$	291–314	52	10	0.642 (0.712)
Montipora digitata	Md05[c]	F:TTCCTCTCGGTTGCAAGAAT R:GGCCAAACGGGAAATGTTAT	$(AAC)_{11}$	157–178	44	6	0.223* (0.734)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
Montipora digitata	Md06[c]	F:CAGCTGACCTTGATGAGCCT R:GTTGCAAATAGACCAGATCACC	$(AAC)_{11}$	277–310	52	6	0.619 (0.674)
Montipora digitata	Md07[c]	F:CTGAAACCAAGCCCAGGTAA R:TGATATCTTTGCTCCACCCAG	$(AAC)_{12}$	231–303	51	10	0.657 (0.704)
Montipora digitata	Md08[c]	F:CACAGGTGGCAAGAACATACAT R:TGGCTAATGCACGTTTCAAG	$(AAT)_{10}$	175–223	52	15	0.585 (0.626)
Montipora digitata	Md09[c]	F:TACATGTATGTGCGCCGTTC R:AGTTCGTGGCTATCATGTCG	$(AAT)_{13}$	168–204	52	10	0.750 (0.756)
Montipora digitata	Md10[c]	F:CAACGCATGTAAACCTCGATT R:GCATTTGTAAAGTTTCACGTTTG	$(AAT)_{14}$	220–295	52	9	0.573 (0.653)
Montipora digitata	Md11[c]	F:TGGAGGAGGGATATTGTTGC R:GCCCATAGCACTTTAAGGGA	$(ATC)_{8}$	125–140	52	5	0.388 (0.420)
Montipora digitata	Md12[c]	F:GGTGGATACCAAACTGAAGCA R:GGCCCAAACAAGCACCTAT	$(ATC)_{8}$	181–190	52	4	0.423 (0.427)
Montipora digitata	Md13[c]	F:AATATTGCTGCCAAAGTGGG R:TTGCGAAAGCGTACTTTGAA	$(ATC)_{9}$	219–231	51	5	0.735 (0.770)
Montipora digitata	Md14[c]	F:TTGAGGAGTTAAATTAGAGATGCTATT R:CAGAGGAAACCAGTTTGGAAC	$(ATC)_{15}$	160–196	52	7	0.473 (0.502)
Montipora digitata	Md15[c]	F:AAAGGTCAGACTAAACCTCTCCA R:AGAGATCTTACCACTGCGCC	$(ATC)_{16}$	177–216	52	12	0.762 (0.832)
Montipora digitata	Md16[c]	F:CAGGTATAGCGGGTCCACAT R:CATACACGTGGCGACTTCTG	$(AAAC)_{7}$	119–139	52	5	0.481 (0.540)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
Montipora digitata	Md17[c]	F:CTGCGCTCATTAATGGTCAA R:TATGGCTGAACAAATTGGCA	$(AAAC)_8$	242–258	52	4	0.642 (0.691)
Montipora digitata	Md18[c]	F:GCGTTCATAACTGCGAGGAT R:TCAATTACATCCGGCTGAGG	$(AAAT)_7$	229–245	51	4	0.490 (0.523)
Montipora digitata	Md19[c]	F:AGAGCCACTCTGTGGAAACG R:GTGGCAAGCTTAAACAAGCA	$(AAGT)_{15}$	144–184	52	8	0.677 (0.706)
Montipora digitata	Md20[c]	F:CGTTGAAGTCACCTACCGTG R:TGACTGCTTCTACCATTGTATTGA	$(AATC)_9$	224–248	52	5	0.607 (0.631)
Montipora digitata	Md21[c]	F:TGTTCGAATTCTGGCACAAA R:TGAAGAATCGACCGTGGATAA	$(AGAT)_9$	151–211	52	8	0.592 (0.670)
Psammocora contigua	Pc01[d]	F:CCATGTTAGCCGTATGGGTT R:GGCAATGGATTAGTCTGCGT	$(AAC)_7$	154–175	32	7	0.755 (0.778)
Psammocora contigua	Pc02[d]	F:CTTCCAGTGTACGAGCTCCA R:GGTGCTTATTCAAGAAATTCCG	$(AAC)_9$	103–160	32	11	0.688 (0.822)
Psammocora contigua	Pc03[d]	F:AGTGAATTGCCAAGTCGAGG R:TGGCAGTCGAATTGAAGACA	$(AAC)_{10}$	136–170	32	10	0.813 (0.846)
Psammocora contigua	Pc04[d]	F:AAACATGATGATTTATGCAAACAAG R:GAATGCCGCCTTTGTAACAT	$(AAC)_{11}$	183–219	32	10	0.756 (0.809)
Psammocora contigua	Pc05[d]	F:AAACTCAACGGCTCTCCGA R:AGCACTTGCACAAGCGACAG	$(AAC)_{13}$	189–213	30	4	0.623 (0.664)
Psammocora contigua	Pc06[d]	F:GCCCAAAGGTATTTGGATTG R:TTAAAGCGTCTGCGATGATG	$(AAG)_{12}$	208–238	32	10	0.800 (0.822)
Psammocora contigua	Pc07[d]	F:GAGGTAGCTTCATCGCTTCG R:GGTCCTTAATCAACGCCAAA	$(AAT)_8$	129–162	30	8	0.750 (0.799)
Psammocora contigua	Pc08[d]	F:CGAGCTTCATACGAGCTGTC R:GCCGATTGTTTGTAACACCA	$(AAT)_{13}$	114–159	31	11	0.790 (0.838)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
Psammocora contigua	Pc09[d]	F:AAACGGTTTGCCTTGTCTGA R:CGGCCATGGTGAGAAGTAAT	$(AAT)_{13}$	135–177	32	8	0.438 (0.494)
Psammocora contigua	Pc10[d]	F:GGCACCGTCTGTTTCCTC R:TGAAGAAATTAGGCGTAAACATCA	$(AAT)_{14}$	118–157	31	10	0.759 (0.865)
Psammocora contigua	Pc11[d]	F:TTTAGTGTCCTTAATTCGCACAG R: CACCCTAATTCACGTGTAAGAAC	$(ATC)_{8}$	232–268	30	12	0.684 (0.774)
Psammocora contigua	Pc12[d]	F:AAATTTCAACTGCAAACTGGC R:TGCTAGACGCGACTGTAGTCAT	$(ATC)_{9}$	121–154	32	8	0.731 (0.794)
Psammocora contigua	Pc13[d]	F:CATCTGCGTCAGAAGACTGG R:CTGGACGCCTCCTGTAAATG	$(ATC)_{9}$	252–270	32	4	0.557 (0.678)
Psammocora contigua	Pc14[d]	F:CAGAACCCGACGTTTCTTGT R:CGACCATTCACTCCATTCAG	$(ATC)_{11}$	264–330	30	14	0.776 (0.895)
Psammocora contigua	Pc15[d]	F:TGGTCAATAACTATATGCAATCAGG R:GGATTTATGATCATGCTACAAATGAA	$(AAAC)_{7}$	207–248	31	11	0.797 (0.876)
Psammocora contigua	Pc16[d]	F:TTCGTGAAGGTAGAACGCCT R:GCACAATATAGTTTAAGTGAAACGGA	$(AAAG)_{13}$	136–194	32	13	0.803 (0.902)
Psammocora contigua	Pc17[d]	F:TTTACTTAGTTATTCACCGACCGTT R:TGTGTAAACTACCCACTAGGTCAA	$(AATC)_{7}$	119–183	31	11	0.723 (0.832)
Psammocora contigua	Pc18[d]	F:TGCTTTCAGTGATCCCTTCC R:TGTCCGTTTAAACCAGTGGA	$(AATC)_{8}$	110–158	32	9	0.713 (0.785)
Psammocora contigua	Pc19[d]	F:CTGGGCTTTAACTTGCTGGT R:TTCAAGGTAATCCCACGTCA	$(AATC)_{10}$	192–220	32	7	0.631 (0.784)
Psammocora contigua	Pc20[d]	F:CGAAAGGTAATCTCAAACATTGC R:AGGGCATACGGTTTGATAGC	$(AATT)_{7}$	130–134	32	2	0.313 (0.461)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
Psammocora contigua	Pc21[d]	F:TACACATGCCCAACCGACT R:CCCAGCCAGTCTGTTACGTT	$(ACCG)_7$	148–204	32	7	0.685 (0.744)
Psammocora contigua	Pc22[d]	F:TCGAACTGATACCTCCTTAAACAA R:GAGTTGGCCCGGAATCTAGT	$(AGCC)_8$	200–244	32	9	0.781 (0.870)
Pteropus dasymallus	Ks24[e]	F:TGGTGCACATGCTCTGTTCC R:GCTACATGTCACAGCTACTTTGG	AAG	171–198	24	10	0.917 (0.839)
Pteropus dasymallus	Ks38[e]	F:CAGACCTAGAGAGTCACACATGG R:GGTTTTGTGTTGACCTTTTGCC	GAAA	121–169	24	13	0.875 (0.877)
Pteropus dasymallus	Ks41[e]	F:AGAAAGGAAGAAAGAGAAAGAGGG R:CTTCCATGCTTCAAATTCACTTCC	GAAA	111–187	24	13	0.917 (0.874)
Pteropus dasymallus	Ks47[e]	F:AAAACCTTCCTCTTCCCCCG R:AGGGAATGGAGATTCTTCCTTCC	AAAG	146–218	24	13	0.864 (0.881)
Pteropus dasymallus	Ks48[e]	F:AGTCCAGCTTAGTAAATAGGGTCC R:ACCTTATAAAACAAGTATGCTGTGTGG	AAAG	148–224	24	14	0.958 (0.891)
Pteropus dasymallus	Ks50[e]	F:AGAACATCAAAACTGCAAGATGC R:GCAAAACTACAAGGCTATGGGC	AGAA	182–246	24	12	0.833* (0.878)
Pteropus dasymallus	Ks51[e]	F:AGTGTACAATTCAACCGTATGGC R:ACAAAGTTGCCTCACTTTTGATCC	CTAT	152–164	24	4	0.348 (0.419)
Pteropus dasymallus	Ks52[e]	F:CAACCAAAAGCAATCAGTTGATCC R:GGTAGGTAGATAGGTAGGTAGGTAGG	ATCT	129–153	24	7	0.708 (0.774)
Pteropus dasymallus	Ks54[e]	F:AAAGCAAAGGCAACAAAGGC R:TTCCTTTGCTGTGCAGAAGC	AAAT	98–122	24	5	0.750 (0.635)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
Pteropus dasymallus	Ks55[e]	F:AGAAGGCAAGATCCTTGGCC R:AACAGAGGCTGAGACCAAGC	ATGG	146–158	24	4	0.542 (0.577)
Pteropus dasymallus	Ks56[e]	F:TTCCAGGGTTCACAAATGCG R:AGTGTGAACAGAAGGCAGGG	CATC	99–107	24	3	0.583 (0.510)
Pteropus dasymallus	Ks59[e]	F:TCGAAAATGAGATTCTCAGGTCC R:AAATCACATGGATAATTCGAATCCG	TAGA	143–163	24	6	0.750 (0.747)
Pteropus dasymallus	Ks60[e]	F:ACATAAACGGAAAAGAAAGCTCTGG R:AAGCAAAACTCACCACCTCC	TATC	113–149	24	7	0.579* (0.789)
Pteropus dasymallus	Ks64[e]	F:TCTTCTATCATCTGTCTGTCTGCC R:TCACGTTACCATCTGTGTGAGG	TCTA	173–185	24	4	0.542 (0.602)
Pteropus dasymallus	Ks65[e]	F:ACTTGAGGGCTCATGATCACC R:TCCAAATACAAGACAGAAGCACG	TAAA	157–165	24	3	0.435 (0.510)
Pteropus dasymallus	Ks67[e]	F:AGGGTAATCCTTGCACAGCC R:GGTCATGGTTGTGCTTGTCC	TGTT	159–187	24	8	0.792 (0.817)
Pteropus dasymallus	Ks68[e]	F:TGATTGTCTTTGAGCTGGAGGG R:TGTCAAGCCTCAGGTACAGG	TTAT	110–134	24	6	0.650 (0.748)
Pteropus dasymallus	Ks69[e]	F:GGATAGAAGTCTCCAAAGGGGG R:CATCCGTCTGTCCATCGTCC	GATG	120–136	24	5	0.391* (0.522)
Pteropus dasymallus	Ks70[e]	F:GGAAGACCAGGTGCTGTAGG R:AGCTACAAGAGAGTCTGGAAAGG	TAC	103–115	24	5	0.542 (0.655)
Pteropus dasymallus	Ks71[e]	F:AGGTTCTAATTTCTCCAATTCTTCACC R:TCAGATAACACCGCACACCC	TAT	102–120	24	5	0.652 (0.720)
Pteropus dasymallus	Ks73[e]	F:GTTTCTACTCCCTGCCAGAGG R:TTCCTGCAAGACAAAGGGGG	ATT	103–112	24	4	0.500 (0.510)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
Pteropus dasymallus	Ks74[e]	F:AGCCTCTTCTCTGTTATTATCATTGC R:TTGACGAAGCAGTAACTCAGC	ATC	87–96	24	4	0.750 (0.629)
Pteropus dasymallus	Ks75[e]	F:AGCCAGGTCTAAAGTGCAGG R:CTCCACAACAAGTTTACAGGGG	CAG	132–150	24	4	0.708 (0.687)
Pteropus dasymallus	Ks76[e]	F:TCAGATAACACCGCACACCC R:TGTTTTCCATAGTGGCTGTACC	ATA	151–159	24	5	0.667 (0.733)
Pteropus dasymallus	Ks77[e]	F:ACATGACCTAACTCACTTCTCTGG R:GTCGCTTAGCATAGTTTCCAGC	CAT	97–103	24	3	0.500 (0.461)
Pteropus dasymallus	Ks78[e]	F:ACTGGGAACTCCATCAACGC R:CAAAGGCTGAGTCTGACTTTGC	TAA	137–155	24	7	0.739 (0.733)
Pteropus dasymallus	Ks79[e]	F:TATGAACCCCAGTGTTGGCC R:TGCCACAGTCATTTCTAGATGC	TTG	95–101	24	3	0.500 (0.508)
Pteropus dasymallus	Ks81[e]	F:AAACACATCTTTTGATACCTGAACC R:AATACTGCCAACACTTCCAGG	ATG	114–135	24	4	0.292* (0.592)
Pteropus dasymallus	Ks84[e]	F:AAGGGGAAAATGCCAGGTGG R:CCTTTGTTTCCTAAAAGCCTGGG	AAC	136–148	24	5	0.350* (0.668)
Pteropus dasymallus	Ks86[e]	F:AATCCCTTGCCAGTCTGAGC R:AGAGGTATGTTGGCCTACAGC	AAT	120–135	24	6	0.542 (0.647)
Pteropus dasymallus	Ks87[e]	F:ATTTCCAGGAGGGGGATTGC R:TGTTGATTGTTCTTTGTTGCTGC	TAG	158–170	24	5	0.696 (0.765)
Pteropus dasymallus	Ks88[e]	F:GCCAAGAGGAAAGATCTATGTGC R:GCCATAAGCATATTCATCACTTCC	GAT	155–158	24	2	0.417 (0.375)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
Pteropus dasymallus	Ks89[e]	F:ACCCCTTAGAATCTGCAGTTAGC R:CTTTACAGAGCACGTAGTAGTGG	TTA	95–113	24	6	0.583 (0.667)
Pteropus dasymallus	Ks90[e]	F:CCACCTAGGTGCTGTAGGC R:AGAACTGCATCTTTTTCATAAGGC	AAG	113–146	24	9	0.375* (0.838)
Actinopyga echinites	Ae01[f]	F:GGCTGAGTGTCACCTCCTTC R:TATCAGACAGCGGCATCGTC	$(AT)_5$	187–209	32	5	0.374 (0.403)
Actinopyga echinites	Ae02[f]	F:GATCTACAGTGTGCGAACCG R:ACAAAGTGACGCCAGTAGGG	$(AT)_5$	227–249	32	6	0.492 (0.517)
Actinopyga echinites	Ae03[f]	F:GCCTATAGACAATGGCACCC R:GGACCTGAGATGAAGCCGTC	$(AG)_5$	116–124	32	5	0.426 (0.464)
Actinopyga echinites	Ae04[f]	F:TGTCTTCTCAAGGGCTGGTG R:GCATGTTTCTGATTGCCTTGC	$(AC)_5$	251–281	32	8	0.792 (0.822)
Actinopyga echinites	Ae05[f]	F:TCACAACAGCTCACTCCAGC R:GCCGGGCCGTTATTGAAGAA	$(AG)_5$	169–181	30	6	0.710 (0.795)
Actinopyga echinites	Ae06[f]	F:AGTGTGGAATGATCTACCCTGG R:ACATTAGCTATGGCAAGGATAATTGG	$(AC)_5$	311–327	31	4	0.347 (0.385)
Actinopyga echinites	Ae07[f]	F:GCACAAGTTCAGCACGACAA R:TGCTCCTGTTATCATGCAAGGA	$(AC)_6$	157–183	31	7	0.474 (0.510)
Actinopyga echinites	Ae08[f]	F:TGCTACTCGAACAGCTGTAGT R:AGGCTGTACGTACGTGTTGG	$(AT)_7$	164–180	32	6	0.681 (0.757)
Actinopyga echinites	Ae09[f]	F:CCCTGCAATGCGATGAAAGA R:ACTAGTTACGTTACAGCAAAGGT	$(AG)_8$	139–157	32	7	0.729 (0.795)
Actinopyga echinites	Ae10[f]	F:GGAAGATCAGGGTGGTGCAA R:TCTCTGGCCACATATAACTTGCA	$(AC)_8$	204–234	30	6	0.500 (0.526)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
Actinopyga echinites	Ae11[f]	F:CCCTCTTCCTAAAGCTGCCA R:TCAGCATCCACTTGTGAAGT	$(AC)_9$	170–176	30	4	0.531 (0.587)
Actinopyga echinites	Ae12[f]	F:GAGACCACCCACATCGCAC R:GCGGCATTTCAATAACATGTGG	$(AT)_{10}$	142–154	30	6	0.629 (0.695)
Actinopyga echinites	Ae13[f]	F:GGCAGGGATCTTGGATACCA R:AGACAAGGCACAAGAATGAGAGT	$(AC)_{14}$	180–236	32	13	0.862 (0.894)
Actinopyga echinites	Ae14[f]	F:TCTATTATTTACTTCCACTCAGCGTGA R:AGCATATCTCAAAGATGAAGTTGATGG	$(AAAC)_5$	249–303	31	12	0.762 (0.860)
Actinopyga echinites	Ae15[f]	F:TGGGCAACAGTACAATTCGGT R:TGAGCTTGCCTCTCCATGTG	$(AT)_5$	220–244	30	4	0.611 (0.667)
Actinopyga echinites	Ae16[f]	F:AGTCTTCTCGCTTTCTCTTGTGT R:CGGACCTCTAAAGAGTAATCTGCT	$(AT)_5$	178–182	30	3	0.543 (0.600)
Actinopyga echinites	Ae17[f]	F:AGTGTTGTGTTGATTGTGCGT R:CAAGAGGCAAGTTGTACGCC	$(AC)_5$	129–163	32	6	0.733 (0.783)
Actinopyga echinites	Ae18[f]	F:CAAACAGAAAGGCAGCGGTG R:ACTGATAACCAATAGAGCACGAGA	$(AT)_6$	296–348	30	10	0.931 (0.942)
Actinopyga echinites	Ae19[f]	F:GCACTTAGCTCATGGGACCA R:TGCTCGAGAGGCATTCCATG	$(AC)_8$	124–148	32	10	0.729 (0.751)
Actinopyga echinites	Ae20[f]	F:ACACCCTGCGTGAATGAAGA R:CCGACACCAGTGCAGAATTC	$(AAC)_5$	293–305	31	5	0.457 (0.481)
Pseudopungtungia nigra	PN4[g]	F:TCGGTGGATGCGAGGAATAC R:TTCCGCCTGTCAGTCAAGAC	$(AC)_6$	194–202	30	4	0.700 (0.585)
Pseudopungtungia nigra	PN23[g]	F:GGCACTCAAGGATAATCTGAAC R:TGTATCCGGCCTCTGTGTAG	$(GT)_{10}$	200–212	30	5	0.567 (0.565)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
Pseudopungtungia nigra	PN28[g]	F:CTCTCCAAATATAGTGCCATCCA R:ATCCTCCTTTCACCCTCCGT	$(AC)_{10}$	237–247	30	5	0.600 (0.575)
Pseudopungtungia nigra	PN64[g]	F:TCAACACAACGGACAGATTCG R:CTATAAGTACTGCCCCGTGCT	$(AC)_{8}$	249–255	30	3	0.500 (0.603)
Pseudopungtungia nigra	PN70[g]	F:GTCGCCAACAGCTCATCTTG R:GCTGAGAGCTTGAGTCATCAC	$(GT)_{9}$	268–278	30	6	0.700 (0.724)
Pseudopungtungia nigra	PN71[g]	F:TCCACACCGCACCACAATG R:CGCATCACACACACCGTAAC	$(TG)_{9}$	214–226	30	7	0.800 (0.789)
Pseudopungtungia nigra	PN75[g]	F:CCTGCATCCATGCCGTATAG R:GCTGTTATAGCGCTGATGATAG	$(AC)_{9}$	199–217	30	8	0.867 (0.813)
Pseudopungtungia nigra	PN88[g]	F:CAACAGGCTCCACGATTGC R:CTGCCCTCGGAAATAAGATGG	$(AC)_{7}$	176–186	30	6	0.633 (0.676)
Pseudopungtungia nigra	PN92[g]	F:CCGTGCTCATATACAGTCCTC R:CCGCATTGTTCCTCCGATTG	$(CA)_{10}$	258–266	30	5	0.600 (0.710)
Pseudopungtungia nigra	PN94[g]	F:CAGCACTTCCTGTTGGAGGT R:GGAGTATGTAAGGGGTCCAGA	$(CT)_{8}$	100–104	30	3	0.467 (0.493)
Pseudopungtungia nigra	PN98[g]	F:CAGGATGAGTCCATCGTCTC R:GCTCAGAAGTGACCGACAGA	$(GT)_{10}$	281–301	30	9	0.900 (0.866)
Pseudopungtungia nigra	PN99[g]	F:AGAGGAGGTCAGATGCTATGC R:GCCAATAATCCGTGCCGATAG	$(TC)_{8}$	225–245	30	5	0.667 (0.679)
Pseudopungtungia nigra	PN123[g]	F:GGGACACACTTAGCAAGCCT R:GCCAGTGAGATTGAAAGACCA	$(GT)_{10}$	213–223	30	6	0.700 (0.742)
Pseudopungtungia nigra	PN124[g]	F:GAGACGCACGACTGATGAAG R:GGCTAACAGGGCGATTGATTG	$(AC)_{10}$	246–258	30	6	0.733 (0.728)

Species	Locus	Primer sequence (5′–3′)	Repeat motif	Size range (bp)	Sample size (N)	Number of alleles (N_A)	H_o (H_e)
Pseudopungtungia nigra	PN125[g]	F:CTGCACTCACTTCCATAGACG R:AACAGTGACTCAGTGGACAGG	$(TG)_9$	166–184	30	6	0.600 (0.611)
Pseudopungtungia nigra	PN126[g]	F:CCACACTACTGAGACTAAACTG R:TGACAGACCATCTTGCATTCTG	$(GT)_9$	180–186	30	4	0.767 (0.706)
Pseudopungtungia nigra	PN133[g]	F:AGACAGCTCAGGACCAATCC R:CCACTAACTGACGTGCAGAAT	$(AC)_9$	226–234	30	4	0.467 (0.541)
Pseudopungtungia nigra	PN139[g]	F: GTGCGAGTGAACGACTGATG R: ACTTGTGCCTGCTGCTAGAG	$(TG)_9$	208–218	58	4	0.567 (0.607)
Pseudopungtungia nigra	PN147[g]	F: GGCTTATGTGGCTTCGGATAC R: AGGTGAGCCTGAGAGAGAAG	$(AC)_9$	122–128	58	4	0.633 (0.729)
Pseudopungtungia nigra	PN154[g]	F: CCCACCAGATTGTATCGGGAT R: TCTGTGTTAACGGTGCAGGAA	$(TC)_{10}$	161–169	0.767	5	0.767 (0.703)

*Indicates significant deviations from Hardy–Weinberg expectations after Bonferroni corrections

[a] Chen C et al. Identification of 24 novel microsatellite loci for the endangered Asian giant soft-shelled turtle *Pelochelys cantorii* (Trionychidae) (ESM 1)

[b] Ma H et al. Development of microsatellite markers for the boring giant clam (*Tridacna crocea*) (ESM 2)

[c] D'Alexis Q et al. Isolation and characterization of 21 microsatellite loci from the finger coral *Montipora digitata* (Scleractinia, Acroporidae) and cross-amplification tests of *Montipora capitata* microsatellite loci (ESM 3)

[d] Bruggemann F et al. Isolation and characterization of 22 microsatellite loci from the Indo-Pacific coral *Psammocora contigua* (Scleractinia, Psammocoridae) (ESM 4)

[e] Taki et al. Development of 34 microsatellite markers for the Ryuku flying fox (*Pteropus dasymallus*) (ESM 5)

[f] Pierrat J et al. Isolation and characterization of 20 microsatellite loci from a commercial tropical sea cucumber, *Actinopyga echinites* (Echinodermata, Holothuroidea) (ESM 6)

[g] Kim K-R et al. Development of 20 novel microsatellite markers for the black shinner (*Pseudopungtungia nigra*) using next generation sequencing (ESM 7)