

Isolation and characterization of twenty-six microsatellite loci for the tetraploid fish Dabry's sturgeon (*Acipenser dabryanus*)

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Abstract To evaluate the population genetic diversity as a means of devising conservation strategies, we constructed (CA)_n and (CT)_n enriched genomic libraries for *Acipenser dabryanus*, a narrowly endemic and endangered species in China. Twenty-six polymorphic microsatellite markers were developed using the fast isolation by AFLP of sequences containing repeats (FIASCO) protocol. Between 3 and 13 alleles per locus were observed. Mean expected heterozygosities (H_E) and Shannon-Wiener Diversity Indices (H') per locus ranged from 0.303 to 0.806, and from 0.480 to 1.893, respectively. The microsatellite markers described here are valuable tools for the population genetics research of *A. dabryanus*.

Keywords Genetic diversity · Microsatellites · *Acipenser dabryanus* · China

The tetraploid fish Dabry's sturgeon (*Acipenser dabryanus* Dumeril, 1868) in the genus *Acipenser* had been an important commercially fish, which is mainly distributed in the mainstem of the upper Yangtze River and its tributaries (Zen 1990; Zhuang et al. 1997). The natural population has been declined drastically in the last two decades due to

overfishing, damming, pollution and habitat alteration and destruction (Zhuang et al. 1997). Since 1982, only tens of specimens have been captured incidentally in the upper reaches of Yangtze River, and now the species rarely occurs in reaches below the Gezhouba Dam, which was built in 1981 across the Yangtze River at Yichang, Hubei Province (Zhuang et al. 1997; Chen 2007). Consequently, the species was listed as a First Class Protected Animal by the China Government in 1989 (Wei et al. 1997). It was also characterized as a Critical Endangered species in the International Union for Conservation of Nature and Natural Resources (IUCN) Red List (IUCN 2010), and protected animal in the Appendix II of CITES. The need for rehabilitation of Dabry's sturgeon has been recognized, several efforts have been undertaken to support the recovery of this endangered species, including establishing a national nature reserve, controlled reproduction and re-stocking of cultured juveniles (Zhang et al. 2011). To better address the conservation status of endangered species in the Yangtze River, a management programme based on genetics is being devised to define the efficiency of these conservation measures (Zhu et al. 2005). Despite the increasing demand for preservation and management plans, no suitable high-resolution genetic data have been available for this tetraploid species.

Microsatellites or simple sequence repeats have been used widely and efficiently as molecular markers in studying population genetics, parentage and kinship analyses because of their high level of polymorphism, co-dominant Mendelian inheritance and rapid detection protocols (O'Connell and Wright 1997; Chistiakov et al. 2006). In this study, we report a set of polymorphic microsatellite loci for *A. dabryanus* that can serve as effective genetic markers for conducting further assessments of quantifying genetic diversity within and among this endangered species.

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Table 1 Primer sequences and characteristics of 26 microsatellite loci in *Acipenser dabryanus*

Locus	Repeat motif	Primer (5'–3')	T _a (°C)	Size (bp)	N _a	H _E	H'	GenBank Accession no.
Ada1-24	(GT)23	F: CCACTACAGCTTTGAATAAAAACAG R: AGCAGCTGTGGATTTTTCGTG	58	188	4	0.664 (0.012)	1.164 (0.024)	JX897686
Ada2-57	(TG)46	F: GGGAGGTGGCTGATTGCAGC R: CATCCCTGCCAACCTTACATTC	58	210	3	0.570 (0.010)	0.918 (0.021)	JX897687
Ada3-76	(CA)25	F: CAGGCACACACAAAACAGAAACA R: GCACTACATCACAAGCTATACAGCA	56	194	7	0.759 (0.008)	1.579 (0.023)	JX897688
Ada4-123	(AC)54	F: GGCCCTCGTCCCTGATAGTATTCT R: TACTGCGCATGGGCAATTGGAG	58	241	13	0.785 (0.013)	1.893 (0.042)	JX897689
Ada5-236	(GT)43	F: GGACTTCAAAACAAAGACTGTACCC R: GCCAGGGGTGGATTATAACTGTTT	58	302	5	0.722 (0.004)	1.363 (0.017)	JX897690
Ada6-418	(GT)17	F: GGGGCTAAAAGAACCCGAGGT R: CCAACTGACGCAAATGATTTGTAT	58	164	5	0.678 (0.006)	1.202 (0.017)	JX897691
Ada7-450	(TG)19	F: GGAGAAGGCTTTCAGGGCAGGC R: CCAACCCCTGACAGTTTTTCCTG	58	215	4	0.690 (0.007)	1.226 (0.020)	JX897692
Ada8-468	(CA)21	F: TCACACACACCTCATATTCCC R: CGTGTGTGCAGGGTTTGCATT	58	218	7	0.791 (0.006)	1.697 (0.021)	JX897693
Ada9-477	(TG)50	F: GCATACTGCGCATGGGCAATTGG R: GGCCCTCGTCCCTGACAGTAAGCT	58	231	4	0.670 (0.014)	1.198 (0.029)	JX897694
Ada10-215	(GA)69	F: CCACTGGACCACACAGCCTCC R: GGTA AAAAGCTGTGAAAATTAGCC	58	249	4	0.744 (0.004)	1.375 (0.007)	JX897695
Ada11-217	(GA)70	F: GGTGAAGAATCAAAGTAGTGCTTTG R: TGTGGAACTGGGTTTATTTCATTAG	56	247	7	0.736 (0.014)	1.543 (0.028)	JX897696
Ada12-229	(CT)46	F: CGGCAGCTCTGTGATACTGAGAGTG R: CCCCTTAGCCCTTCATCTGTAATG	58	378	5	0.747 (0.008)	1.431 (0.025)	JX897697
Ada13-247	(CA)66	F: GGGAGATATACAAAATGTGTGAAAAG R: CGAGAGTACAACACCCGTACACGGGT	58	248	5	0.786 (0.007)	1.620 (0.022)	JX897698
Ada14-265	(TG)43	F: GGAGGCGCCGGAATGTG R: ACAGAGCAATAAAAATGGGCAGATTT	58	183	6	0.780 (0.006)	1.604 (0.020)	JX897699
Ada15-269	(CA)29	F: AGCACGTCTACACTCCTTGGGCAAC R: GGTTCAAAGGGAGGGAGAGAGATGG	56	361	5	0.771 (0.000)	1.547 (0.001)	JX897700
Ada16-273	(CA)23	F: CCCCATCCCTGCCAACCTTACATT R: CAGACTGTGGAGCCATGGATCCC	58	220	5	0.785 (0.005)	1.575 (0.010)	JX897701
Ada17-295	(GT)51	F: GACGCCCTTCTAAACGCCAAC R: GGGCAAGGTGCAGGCACAC	58	244	5	0.686 (0.018)	1.362 (0.033)	JX897702
Ada18-307	(GT)15	F: GGGCTGGGTTGCAGGTTTTAT R: TGTAATGTGCAGTTCTGAC	58	191	3	0.630 (0.010)	1.040 (0.016)	JX897703
Ada19-255	(CA)25	F: GTTACAGGTGTTATTACCAGCGCC R: ATTGAAGCGCGCAGAATAGGCTATA	56	232	3	0.303 (0.032)	0.480 (0.037)	JX897704
Ada20-202	(TG)18	F: TGGGTACCAGTGTGGTCTCTGTG R: AATGAGGAGCGAAGAAAAGTGTGT	58	295	4	0.692 (0.010)	1.290 (0.020)	JX897705
Ada21-396	(AC)19	F: CGCACCCAGCATCATGAAAC R: GGATAAGTGAGTCATAAAAACCGC	58	217	5	0.722 (0.007)	1.40 (0.020)	JX897706
Ada22-331	(TG)36	F: ACTTTTATAACGGGTATCCTTTTGTG R: CCCAATTACACCCGAGTAC	58	180	6	0.648 (0.006)	1.266 (0.014)	JX897707
Ada23-364	(TG)36	F: TTCTGTGTATTGTGAGGGTACGGGG R: GTTTGGGCCGGGGTTTACG	58	181	3	0.510 (0.007)	0.752 (0.018)	JX897708
Ada24-209	(TG)16	F: AGCCAATCACTAATTTGCCTGTTTT R: TGTGGTCAGGGACTGGGCGG	58	191	3	0.500 (0.005)	0.731 (0.008)	JX897709

Table 1 continued

Locus	Repeat motif	Primer (5′–3′)	Ta (°C)	Size (bp)	Na	H _E	H′	GenBank Accession no.
Ada25-249	(AC) ₄₆	F: GGCCCTCGTCCCTGACAGTAAG R: CATGGGCAATTGCAGACAGGTG	56	213	10	0.806 (0.008)	1.818 (0.031)	JX897710
Ada26-245	(TC) ₈ (TG) ₃₅	F: TGCAGTATTAAGAAGCGCGCAGATT R: CATGTTACAGGTGTTGTTACCAGC	56	262	4	0.410 (0.004)	0.651 (0.017)	JX897711

Ta annealing temperature, Na observed number of alleles, H_E mean expected heterozygosity H′ Shannon-Wiener Diversity Indices

We collected the fins of 24 individuals from the Institute of Rare Hydrobiology in Yibin City, Sichuan province, China. The total genomic DNA was extracted by a universal and rapid salt-extraction method (Salah and Iciar 1997). Microsatellite-enriched genomic library for the repeat motif (CA)_n and (CT)_n was constructed essentially following the fast isolation by AFLP of sequences containing repeats (FIASCO) protocol (Zane et al. 2002) with the following modifications: (1) 400 ng DNA from pre-amplification step was mixed with 1 μM of a 5-biotinylated oligonucleotide probe in a total volume of 100 μL (6×SSC, 0.1 % SDS) at 55 °C for 30 min. (2) DNA is separated from the beads-probe complex by three times washes with 50 μL of TE buffer (Tris-HCl 10 mM, EDTA 1 mM, pH 8.0). Enriched fragments were ligated into pMD18-T vector (TaKaRa) and propagated in the DH5α strain of *Escherichia coli* (TaKaRa). After polymerase chain reaction (PCR) confirmation, 400 positive clones with insertion of 200–600 bp were sequenced with ABI PRISM 3,700. The repeat regions were analysed using software Tandem Repeats Finder (Benson 1999), and 67 primer sets were designed based on flanks of putative microsatellite sequences. The polymorphism of these microsatellite loci was examined with 24 individuals collected. The PCR amplification was carried out in a mixture of 25 μL volume on a PTC-100 thermocycler (Biorad, USA), containing 1×PCR buffer (TaKaRa), 50–100 ng genomic DNA, 0.25 μM for each primer, 150 μM dNTPs, 1.5 mM MgCl₂ and 0.25 U Taq DNA polymerase (TaKaRa). Thermal cycle was conducted with an initial denaturation at 94 °C for 5 min, followed 35 cycles including a denaturation at 94 °C for 40 s, an annealing at the proper temperature (Table 1) for 40 s and an extension at 72 °C for 40 s, and a final extension at 72 °C for 10 min. PCR products were visualized on 8 % polyacrylamide gel stained with silver staining. A 50 bp DNA ladder molecular marker (TaKaRa) was used as standard to identify size of alleles. The analyses of polymorphism, including number of alleles (Na), expected heterozygosity (H_E), and Shannon–Wiener Diversity Indices (H′) were performed using ATetra 1.2 (Van Puyvelde et al. 2010), which was developed for analyzing tetraploid microsatellite

data. In this study, we constructed (CA)_n and (CT)_n enriched genomic libraries for *A. dabryanus*. 42 pairs of primer were proved to have specific amplification products, but only 26 primer sets were polymorphic in the population of 24 Dabry’s sturgeon individuals (Table 1). The number of alleles per locus ranged from 3 to 13 with an average of 5.2, and mean expected heterozygosities (H_E) and shannon-Wiener Diversity Indices (H′) per locus ranged from 0.303 to 0.806, and from 0.480 to 1.893, respectively (Table 1). These identified microsatellite markers can be employed effectively to examine fine-scale population structure and genetic diversity to allow parentage analysis for Re-stocking management of *A. dabryanus*.

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