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[Technical Note]

Characterization of Red Drum Microsatellite Markers in Spotted Seatrout

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Abstract.—Polymerase chain reaction primers for a total of 132 nuclear-encoded microsatellites originally developed from genomic libraries for red drum *Sciaenops ocellatus* produced reliable and consistent amplifications in the closely related spotted seatrout *Cynoscion nebulosus*. Thirty-three of the primers amplified microsatellites that were monomorphic among a sample of 30 individuals, while 12 of the remaining 99 polymorphic loci exhibited possible null alleles. This provides a set of 87 microsatellite loci that will be highly useful in future genetic studies related to the stock enhancement and culture of spotted seatrout. Spotted seatrout comprise an important recreational fishery in the bays and estuaries in U.S. waters of the Gulf of Mexico and western Atlantic Ocean, and stock enhancement via supplementation with hatchery-reared individuals is ongoing, planned, or under consideration in several southern states.

Spotted seatrout *Cynoscion nebulosus* comprise an important recreational fishery in the bays and estuaries in U.S. waters of the Gulf of Mexico and western Atlantic Ocean (Vanderkooy and Muller 2003). One management strategy to protect this fishery is stock enhancement via artificial hatchery spawning and the subsequent release of offspring (Blankenship and Leber 1995). Presently, approximately 3.5 million spotted seatrout fingerlings from two hatcheries are supplemented in Texas bays and estuaries by the Texas Parks and Wildlife Department (TPWD; D. Abrego and R. Vega, personal communication); similar programs are either planned or under consideration in other southern states (T. Bert, Florida Fish and Wildlife Conservation Commission, personal communication; W. Hawkins, University of Southern Mississippi, personal communication). Assessment of genetic diversity within both the hatchery broodstock and recipient populations and unequivocal identification of hatchery-raised fish in the wild are critical to the successful implementation of stock enhancement (Ward et al. 2006; Bert et al. 2007).

Nuclear-encoded microsatellites (abundant short stretches of DNA composed of di-, tri-, or tetranucleotide arrays embedded in unique DNA; Weber and May 1989; Weber 1990) are ideal genetic tools for assessing these issues because of their generally high level of polymorphism and codominant Mendelian inheritance (Liu and Cordes 2004). In addition, microsatellites are useful in estimating the genetic parameters for traits such as growth rate, thermal tolerance, and disease resistance that are important to fish culture. To date, microsatellites have been used successfully to provide critical data relative to the TPWD stock enhancement program for red drum *Sciaenops ocellatus* (Gold et al. 2008; Karlsson et al. 2008c) and to assess the heritability of juvenile growth traits and thermal tolerance (Ma et al. 2007; Saillant et al. 2007).

A certain number of microsatellites generally are necessary for (1) unequivocal identification of hatchery-raised fish in the wild (Renshaw et al. 2006; Karlsson et al. 2008c), and (2) determination of the pedigree of offspring and estimation of genetic parameters when multiple families are generated via spontaneous group spawning (Saillant et al. 2007). Recently, a summary of 269 microsatellite PCR primers, developed in our laboratory from genomic libraries of red drum, was made available (Karlsson et al. 2008a). Red drum and spotted seatrout are both members of the family Sciaenidae, and microsatellite polymerase chain reaction (PCR) primers often amplify across members of the same family (Renshaw et al. 2007). The goal of this study was to identify PCR primers for red drum microsatellites that would reliably amplify microsatellites in spotted seatrout and be useful in spotted seatrout stock enhancement and culture.

Methods

Thirty spotted seatrout from the Lower Laguna Madre, Texas were provided by TPWD personnel. Genomic DNA from each individual was extracted using a standard phenol–chloroform protocol (Sambrook et al. 1989). A total of 132 of the PCR primers available for red drum microsatellites provided reliable and consistent amplifications of spotted seatrout DNA. The PCR protocols followed those outlined by Saillant et al. (2004) for red drum microsatellites *Soc9* to *Soc445* and those outlined by Karlsson et al. (2008b) for microsatellites *Soc500* to

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TABLE 1.—Summary data for red drum microsatellites characterized for spotted seatrout. The fluorescently labeled primer is in bold text with the appropriate label signified by one (6-Fam), two (Hex), or three (Ned) plus signs. Information taken from earlier descriptions of these microsatellites (Saillant et al. [2004] for *Soc9–Soc445* and Karlsson et al. [2008a] for *Soc508–Soc738*) is indicated by asterisks.

Microsatellite	Primer sequence (5′–3′)[a]*	GenBank accession number[b]*	Repeat sequence*	T_A[c]	N/N_A[d]	Size range[e]	H_E/H_O[f]	P_{HW}[g]
Soc9	**AACATTTCCATCACGTATTTATCT**$^{++}$ TCCACATGAACACCAGTGCAGTTC		$(AT)_{27}$	51	14/2	248–252	0.138/0.143	1.000
Soc11	**GCCGAGTCACGAAGGAACAGAGAA**$^{+}$ TGTCGTCTCATCTATCTCCATCTC	AF73258	$(GA)_{11}$	62	21/4	216–242	0.331/0.238	0.138
Soc44	GAGGGTGACGCTAACAGTTGA **CACAGCTCCACTCTGATATG**$^{++}$	AF73264	$(CA)_{22}(GT)_5$	62	25/2	202–204	0.040/0.040	1.000
Soc50	**CCCGTGATTTTAGGCTCAGATA**$^{++}$ CCTTTAGAGTGCAGTAAGTGATTT	AF73266	$(GT)_7$	58	25/5	183–197	0.586/0.520	0.788
Soc83	TGCTGTAATTGAAAAGCAGTGTAC **AGCGGAACTAGAATTGGTTTTATA**$^{++}$	AF73269	$(TG)_{19}$	56	12/2	113–115	0.391/0.167	0.093
Soc99	**CACCCACTGACACACACATACAC**$^{+++}$ GGAACCAATATGTCTGCCATGAT	AF73272	$(CA)_{29}$	62	28/9	151–169	0.771/0.750	0.052
Soc133	CATTTGGACCATCGCTACTGCTG **CTTGGCATTTCCAGACATCACTG**$^{+}$	AF73276	$(TGC)_{10}$	56	27/4	193–202	0.592/0.741	0.457
Soc140	GGTGCAAACACAGCCATACAGT **GCAAAATCGAAGACCGAGTTTAG**$^{+++}$	AF73277	$(CTGT)_8$	56	29/2	130–134	0.034/0.034	1.000
Soc243	GACGGGGATGCCATCTGC **AATGCGAAAAAGACGAAACAGT**$^{+}$	AF73283	$(CCT)_9$	56	29/4	101–110	0.533/0.483	0.705
Soc402	**CATATTTAACGAGCGACATAGC**$^{++}$ AAACAGATGAAGCACCTGGACT	AY161012	$(CA)_{20}$	52	29/5	126–134	0.618/0.690	0.924
Soc407	**AAAGTCTGCCTCTTACAGCTTC**$^{+}$ GAGTTAAAGCGTGTGCTAGTCC	AY161016	$(CA)_{13}$	56	30/2	130–132	0.033/0.033	1.000
Soc409	**TTTATCTGCTCTGTGTGGAAGT**$^{++}$ ATCTATTTGTCGGTTTCTCTGC	AY161017	$(TG)_{11}$	52	26/6	283–297	0.526/0.423	0.104
Soc410	**GTACCAAGTCAGCCAGTGTCAG**$^{+}$ TCTCTGTGTCCCTCTGTGTTTG	AY161017	$(TG)_{17}$	56	27/3	290–298	0.073/0.074	1.000
Soc412	**CACAGAAACTCAGCTCGAGACC**$^{++}$ AGGAAGAATGTACAAGGTGTTC	AY161019	$(AC)_{13}$	49	30/6	121–131	0.382/0.400	0.628
Soc415	CTCAGCACCCTCAGACATATGG **CACAAGTTAAGTGGTATCGAGT**$^{++}$	AY161020	$(TG)_{15}$	52	30/16	186–246	0.911/0.867	0.007
Soc416	**CTCGATACCACTTAACTTGT**$^{+++}$ ATCGACATAATCTGGCACCA	AY161020	$(GA)_{38}$	49	30/17	139–191	0.909/0.833	0.082
Soc417	**CTTACGTGATAAAGTGTGGGTGA**$^{+}$ ATATGCCAGTAATCCACCGAAG	AY161020	$(AC)_{24}$	47	15/6	86–96	0.713/0.667	0.808
Soc418	GTTTTTCTGGCATTTATGGATG **TGAGGTTATCAAACACCTGCCCACT**$^{+}$	AY161021	$(TG)_{24}$	52	29/2	253–255	0.267/0.310	1.000
Soc419	**ATTTAGCCAACTGCTCCGCTCA**$^{+}$ GAGTGCGTGGTGTAGGGGGGTA	AY161022	$(AC)_{20}$	56	26/12	237–269	0.858/0.846	0.603
Soc423	**GTCACCGCACCATGATGGAGAT**$^{+}$ TACCACTTACACTCAGCAGGTG	AY161025	$(CA)_{26}$	51	30/7	183–223	0.420/0.433	0.178
Soc426	**GAGAGGACGTGAGCTGCTGA**$^{+}$ TGAGAAACAGAAACAGAAGGT	AY161028	$(CA)_{11}$	52	30/14	121–159	0.876/0.767	0.042
Soc431	**GACACGCTGTGGTAGATGAAAACG**$^{++}$ TGTATATTAGTTGGCAAGGCAGAG	AY161032	$(TG)_{29}$	53	30/11	125–155	0.648/0.667	0.602
Soc432	**TTTAGGCTACGTCTGGAGGCACA**$^{++}$ GTGTGTTTGAGGGTCAGCGTAC	AY161033	$(AC)_{16}$	52	29/12	90–118	0.727/0.690	0.165
Soc434	**GACACTCCCAGATATGCTGA**$^{++}$ TCCTTGTTTATCTTGGTGCTGT	AY161034	$(CA)_{23}$	52	28/9	127–183	0.695/0.750	0.124
Soc439	**ACTCTCGTCCCACTTACCACA**$^{++}$ TATGTTTGCATATAAGCTCA	AY161037	$(TG)_{17}$	49	30/4	87–101	0.437/0.467	0.701
Soc508	GCAGCACATTTCAGCACAC TAATGCCCCTGTTATCTATCTA	EF609022	$(GATA)_{18}$		15/17	242–230	0.943/0.933	0.651
Soc510	AGATGCCAACACCTCTAAAACT ACAGACCACTCCGACTCAAA	EF609024	$(GATA)_8$		18/6	264–316	0.470/0.389	0.232
Soc516	GCAGACACAAAATGTTCAAAGCA GGAAGACTCACGGAGCAGGTT	EF609027	$(CA)_{11}$		23/2	178–182	0.507/0.478	1.000
Soc522	CTAGTGGATCTGCTTGATGCTTT GCACACGTCTGAGGAGTGAA	EF609029	$(CA)_{13}$		29/6	125–141	0.572/0.482	0.111
Soc525	CACTGTGGGGACATTTAGAGG GGGTGTGACAAACTCAGGGAC	EF609032	$(CA)_{14}$		30/2	111–113	0.033/0.033	1.000
Soc527	CCAAATGTCAAGCCTGCTC GCTGTGAAAATCTCACCACACTT	EF609034	$(TG)_{16}$		27/2	195–203	0.140/0.148	1.000
Soc532	GAGTGCTCACAAAGTGCCAG GTGCCAGATAGATGCTGACG	EF609037	$(CA)_{14}$		22/11	134–166	0.867/0.864	0.873

TABLE 1.—Continued.

Microsatellite	Primer sequence (5′–3′)[a]*	GenBank accession number[b]*	Repeat sequence*	T_A[c]	N/N_A[d]	Size range[e]	H_E/H_O[f]	P_{HW}[g]
Soc538	CCAGCATATTTTGAGCAGC TGAAGGTTTTCCCCGTAGT	EF609041	$(CA)_{17}$		15/6	208–222	0.694/0.733	0.753
Soc548	CGCACACACAAAAACAGTGAG CCATCGGTCCAGTATGAAGTC	EF609048	$(CA)_{13}$		25/7	166–188	0.500/0.400	0.230
Soc550	CGCAGACAGACAGCCTCTAT CATCCTCTCCTCAGTGTAGCC	EF609050	$(CA)_{26}$		16/9	217–255	0.782/0.813	0.344
Soc551	TCAACCACACTCAGGTCCAG GCAACACAAAGCACTCACAAA	EF609051	$(CA)_{10}$		27/7	257–277	0.576/0.444	0.110
Soc558	CAGTGAACAGGAACGACTTTTAGA GACCCATCAACCTCCAGCA	EF609058	$(CA)_{18}$		28/11	185–223	0.805/0.714	0.617
Soc559	TGTGGGACAAGATGTGAAAT TTACCTTGGAAACGGTGTGA	EF609059	$(CA)_{31}$		22/3	201–209	0.251/0.272	1.000
Soc564	TGCCAGCATCCGTCTACTCA AAGAGCCGACCAATCAGAGAG	EF609063	$(CA)_{15}$		28/14	172–210	0.879/0.786	0.512
Soc566	GGACAAGAGAAGCAGCAGACG TCATCACGTCCAAAGCTACG	EF609065	$(GA)_{13}$		30/4	171–179	0.555/0.433	0.166
Soc567	ACACACACTCCCACAGATGAAT CGCTGCCCCAAAATAGAAT	EF609066	$(CA)_{31}$		17/3	236–240	0.469/0.353	0.225
Soc571	CGTGAACTGAGCGGAGACA GGGAGTGTGTGAGAATGTGGA	EF609070	$(CA)_{20}$		28/9	234–252	0.851/0.821	0.580
Soc575	GGACGCACCATCTCTCCATCT AGGCTTTGCTCTTTTCAGACG	EF609074	$(CA)_{11}$		19/10	246–276	0.809/0.895	0.103
Soc580	CTGAGCCTGAACGCACATCAT GAACAAACAACTGTCACCTGCTG	EF609079	$(CA)_{25}$		15/2	301–309	0.331/0.400	1.000
Soc586	GGGAAATGGACACAAAAGAAT CACCTGGGACCTTAGTCACTT	EF609082	$(CA)_{35}$		25/6	151–161	0.740/0.800	0.348
Soc588	TGAATGACTTGCTTTGCTGAA AATAACCCCCACCTCTCCCT	EF609084	$(GA)_{22}$		30/13	180–212	0.875/0.900	0.224
Soc590	CAATGGACAGTTTGAGAGTTC GAAACCCACACCAATCACT	EF609086	$(CA)_{18}$		28/4	187–193	0.733/0.821	0.656
Soc592	AGAAGGAGGTCAGGAGGCATT TCCCATTCACAAACACAAGCA	EF609087	$(CA)_{13}$		28/5	125–133	0.631/0.607	0.144
Soc594	TCGTGCTCTGTCTCCGTTC TGACTATTTTTGCTTTTTACTTC	EF609089	$(CA)_{13}$		16/2	206–208	0.417/0.563	0.250
Soc601	CTTTGGGACAACAGAAATGC TCCAGCAAGCAGACAACAAT	EF609094	$(GA)_{22}$		25/4	166–172	0.626/0.560	0.535
Soc602	AGCAACCATTCTTCCCACAC CCATCACACACCAGGGTTAA	EF609095	$(CA)_{12}CG(CA)_5$		28/11	153–189	0.728/0.821	0.762
Soc609	CCCGCATTAGACAGAAAAC ATGGGTATGTGTGGCTTACAG	EF609099	$(CA)_{23}$		26/8	269–285	0.762/0.846	0.579
Soc616	TTCCTCTCTCCGTGTTTGTGTT ACTGGGCAGGTTTCTTCTGAC	EF609104	$(CA)_{32}$		26/7	307–329	0.434/0.385	0.387
Soc618	ACCCGATAAGGAAACAAGCAGA CATCACCGTCCAACCAGAGAA	EF609106	$(GA)_{17}$		27/2	118–120	0.107/0.111	1.000
Soc619	GCGTTCTCTCTCTCGTGACAA GCTCTCCTGCGTCTCGTCTT	EF609107	$(CA)_{19}$		23/3	171–183	0.357/0.261	0.337
Soc620	CGTGTCAGCCACAATCTCCA AGCCCAGCCTAAACCTCTCA	EF609108	$(CA)_{13}$		15/4	149–165	0.628/0.733	0.351
Soc623	CACTTTCACTTTCTGCCCTCA TCTGGTTTCTGGCTTTCATACA	EF609111	$(CA)_{14}$		21/9	127–147	0.757/0.810	0.770
Soc624	CACGCTGGTCTTTTTCTCAA CTGGGGTTATTTGTGTGTGC	EF609112	$(CA)_{28}AA(CA)_7$		15/8	125–151	0.802/0.667	0.192
Soc625	TACCCTCAGAAATGGTCGCTT GAGAGTGTTTACCCCGTGTGC	EF609113	$(CA)_{12}$		27/2	115–117	0.037/0.037	1.000
Soc626	ACTTTGAGCCAATGCTTTCC GTGAGCTGTGTATCCCTGTGC	EF609114	$(CT)_6(CA)_9$		29/5	184–194	0.655/0.759	0.877
Soc635	CATCAGCACGGTTATTTTCTTG CCTCTCTCTTTTCTTCCCTCG	EU015887	$(CA)_{23}$		25/14	239–269	0.918/0.920	0.697
Soc640	AGGACATTTGGAGTGGAAGAGTA ATGGGGACAGGAGGTTTTCTA	EU015892	$(CA)_{14}$		23/7	163–181	0.670/0.565	0.219
Soc645	GAGTTGGTCAATAGCCACAGG ATCTGAAGGGCAGGTGTTTG	EU015896	$(CA)_{20}$		29/3	150–154	0.163/0.172	1.000
Soc646	GGGAAAGTAGATAGGGGCACA AGAGGTCAGGGTTGAGCAGAGT	EU015897	$(CA)_{16}$		19/7	120–140	0.657/0.579	0.241
Soc654	CTCCGCTGCCAAACTGAC TGTGCTCTACATCCTCCTCCT	EU015905	$(CA)_{13}$		14/4	162–178	0.558/0.500	0.555
Soc657	GGAAAGCAAAGCAAAAGAAACT AGCCGAATGAGACAGAGGAAA	EU015908	$(CA)_{34}$		30/2	195–201	0.127/0.133	1.000

TABLE 1.—Continued.

Microsatellite	Primer sequence (5′–3′)[a]*	GenBank accession number[b]*	Repeat sequence*	T_A[c]	N/N_A[d]	Size range[e]	H_E/H_O[f]	P_{HW}[g]
Soc658	AATCTCCCAGTGCCTTTGA CTGCTTTTTCCCTCTATTTCTC	EU015909	$(GA)_{14}$		28/10	165–191	0.800/0.821	0.461
Soc660	TTGCCAATGTTCTTTCTCTCT ATTCCTACTCCTGCCAAGAT	EU015911	$(CA)_{12}CT(CA)_2AA(CA)_5$		30/18	115–167	0.902/0.867	0.193
Soc661	ACCGCCTCAAAACAACACA AGGAGATTGGGAGTGGAGATA	EU015912	$(CA)_{13}$		30/6	155–165	0.749/0.800	0.761
Soc662	CGTCTTTAGGAAGGTGTGGC CCTGTCTGGAGGGGAAAAC	EU015913	$(CA)_{20}CC(CA)_{16}AA(CA)_3$		30/6	89–121	0.641/0.700	0.779
Soc666	TAATCTCTGTGTGTGTCCAGGTG GACGCAAGGCTGAGGCATA	EU015917	$(CA)_4CG(CA)_{21}$		25/6	194–208	0.416/0.400	0.286
Soc667	TAACGCTCTGTCCATCACTG CATCTACGAATGCCCAACA	EU015918	$(CA)_{14}CCTA(CA)_5$		27/11	219–249	0.851/0.778	0.169
Soc670	TTCGTCCCGTCACAGCACA CAAAGAGAGATGAATAAACCCAAAG	EU015921	$(CA)_{30}$		29/3	220–224	0.132/0.138	1.000
Soc671	CGCCTCTCTTCCTCAGATGT ACAGTGGGCAAATCCATACA	EU015922	$(CA)_{30}TACG(CA)_4$		30/5	187–199	0.499/0.433	0.126
Soc672	CGTATGGTGAGTGTTGGCA TGTCGTCTCTGAATGTGTCCT	EU015923	$(CA)_{22}$		14/2	139–141	0.254/0.286	1.000
Soc675	TGTCCCCATAAAGAACAAGG ACACAACGTCTACAGGAAGGC	EU015925	$(CAGA)_4CAGG(CAGA)_2CAGG(CAGA)_2$		30/2	92–96	0.097/0.100	1.000
Soc683	TTCGCACACATACATAACTAAACT AGCGTCATAATCCAACTGTCA	EU015932	$(CA)_6CTGA(CA)_7$		29/3	185–195	0.132/0.138	1.000
Soc685	TCAAACAGGGTCATTGGTGA AGGAGAAACGCAGGGAAGA	EU015934	$(CA)_{14}$		29/3	220–226	0.605/0.517	0.666
Soc692	TGCTGCCATTGAGAAGAGA TTTGTATGTTAGGGGTTGTGT	EU015941	$(CA)_{10}$		28/3	121–131	0.137/0.143	1.000
Soc694	CTCGCTCCCATCGTGACT TCCTGAAAGTTGTGCTTGTCC	EU015943	$(CA)_{11}$		15/9	175–193	0.857/1.000	0.717
Soc695	TCTGGAGGGATGATGTGTTT CCTGTTTCACTGCTACTCGC	EU015944	$(CA)_{21}CT(CA)_5$		16/3	129–133	0.123/0.125	1.000
Soc696	GAAAATGGTGAAAACCCTGA CAAAATGGAGAAGCCTGAAG	EU015945	$(CA)_{31}$		15/3	185–193	0.191/0.200	1.000
Soc706	ACTCTGTTGCTCCACTACCCA GCTCTTCTCCTGTTTGTGTGA	EU015954	$(CA)_5AA(CA)_8$		14/4	162–170	0.267/0.214	0.206
Soc708	TTCCCACTAGAGCTGTGATTGA TCTGACTTCCTCTGCCCATT	EU015956	$(CA)_{17}$		15/10	148–174	0.823/0.800	0.766
Soc713	AATAGTTTCCTCTGGATTGACG TGGCTTAGACAAGTGGTGCT	EU015961	$(CA)_{18}$		15/3	184–188	0.591/0.533	0.712
Soc730	GCACAGGGAGATAAACACAG CTGAAGAAAAGCCAGAGTGAA	EU015974	$(CA)_{14}$		29/2	101–130	0.034/0.034	1.000
Soc738	TGTAACAGCAGAGACTGAAGC CTGGGTGAAAGGCAGAGTA	EU015981	$(CA)_{28}$		28/3	94–98	0.105/0.107	1.000

[a] Primer sequences are forward (top) and reverse (bottom).
[b] Sequence for *Soc9* is not available in GenBank.
[c] Annealing temperature in °C.
[d] N is the number of samples that were scored, and N_A the number of alleles detected.
[e] Refers to alleles thus far uncovered; for *Soc508* to *Soc738*, size includes the 21-base-pair 5′ tail sequence primer used for PCR amplification (Karlsson et al. 2008c).
[f] H_E and H_O are expected and observed heterozygosities, respectively.
[g] Probability of deviation from Hardy–Weinberg expectations.

Soc739. For the first group of markers (*Soc9*–*Soc445*), one of three fluorescent labels (6-Fam, Hex, or Ned) was attached to one of the primers in each pair (Table 1). For the second set of markers (*Soc500*–*Soc739*), the 5′ tail sequence primer as described in Karlsson et al. (2008b) and the 6-Fam fluorescent label were used for each amplification. The amplified PCR products were run on an ABI-377 automated sequencer, and the alleles were sized using the Genescan-500 Rox size standard (Applied Biosystems); allele sizing and calling were performed with Genescan 3.1.2 and Genotyper 2.5 software, respectively. The genetic variability of each microsatellite was measured by the number of alleles, gene diversity (expected heterozygosity), and observed heterozygosity. Wright's F_{IS}, estimated as Weir and Cockerham's f in the software program GDA (Lewis and Zaykin 2001), was used to measure the departure of genotype proportions from Hardy–Weinberg expectations at each microsatellite. Fisher's exact test, as performed in GDA, was used to

test the significance of departures from Hardy–Weinberg equilibrium (genotype) expectations at each microsatellite and for departure from genotypic equilibrium at pairs of microsatellites. The effect of Hardy–Weinberg departures (within-locus disequilibrium) on the significance of between-locus linkage disequilibrium tests was removed by preserving genotypes in GDA (Lewis and Zaykin 2001). Evidence for the occurrences of null alleles, large-allele dropout, or both, was explored with Microchecker (Van Oosterhout et al. 2004).

Results and Discussion

Thirty-five of the PCR primers in the first set of markers (*Soc9–Soc445*) and 97 in the second set (*Soc500–Soc739*) generated microsatellite bands that could be scored easily. Summary data for all 132 microsatellites may be found at http://wfsc.tamu.edu/doc, under the file name Appendix 1, which is under the heading North American Journal of Aquaculture (2009). Of these, 33 of the PCR primers appeared to amplify monomorphic microsatellites, while 12 of the remaining 99 polymorphic microsatellites exhibited possible null alleles upon further evaluation with Microchecker: *Soc442*, *Soc445*, *Soc535*, *Soc589*, *Soc622*, *Soc628*, *Soc638*, *Soc642*, *Soc668*, *Soc715*, *Soc721*, and *Soc737*. Genotypes at two of these microsatellites, *Soc445* and *Soc628*, deviated significantly from Hardy–Weinberg expectations after Bonferroni correction (Rice 1989). Summary data for the remaining 87 microsatellite loci are presented in Table 1; the number of alleles detected per microsatellite ranged from 2 (17 loci) to 18 (*Soc660*). Expected heterozygosity ranged from 0.033 (*Soc407* and *Soc525*) to 0.943 (*Soc508*), while observed heterozygosity ranged from 0.033 (*Soc407* and *Soc525*) to 0.933 (*Soc508*). All pairwise comparisons of microsatellites did not deviate significantly from genotypic equilibrium after Bonferroni correction (Rice 1989). The microsatellites characterized in this study will prove highly useful for future genetic studies related to the stock enhancement and culture of spotted seatrout.

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