Conservation Genet Resour
DOI 10.1007/s12686-012-9611-z

TECHNICAL NOTE

Development and characterization of microsatellite markers for the finetooth shark, *Carcharhinus isodon*

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Received: 20 January 2012 / Accepted: 8 February 2012

Abstract The finetooth shark, *Carcharhinus isodon*, is a small, discontinuously distributed coastal species found in waters of the western Atlantic Ocean from North Carolina in the US through the Gulf of Mexico and in southern Brazil. The species is a component of both commercial and recreational fisheries throughout its range. Here, we report polymerase-chain-reaction primers for 20 polymorphic and 33 monomorphic microsatellites isolated from an enriched genomic library of *C. isodon* DNA, and cross amplification of nine polymorphic and 35 monomorphic microsatellites previously characterized in blacknose shark, *C. acronotus.* All 97 microsatellites were characterized in 31 individuals. The microsatellites will be useful in population studies of finetooth sharks.

Keywords Microsatellites · Finetooth shark · *Carcharhinus isodon* · Cross-amplification

The finetooth shark, *Carcharhinus isodon,* is a small, migratory coastal species with a discontinuous distribution in the western Atlantic Ocean. It has been reported to occur along the continental shelf from North Carolina in the United States (US) to Mexico, in Cuba, and in southern Brazil (Compagno et al. 2005). Although data on population structure of *C. isodon* are limited, differences in life-history characters between finetooth sharks along the eastern coast of the US and those in the Gulf of Mexico are compatible with the hypothesis that there may be separate reproductive units in US waters (Carlson et al. 2003; Drymon et al. 2006; Driggers and Hoffmayer 2009). A recent stock assessment (NMFS 2007) indicated that finetooth sharks in US waters are not currently overfished or experiencing overfishing; however, it was noted that there is less catch and life-history data available for finetooth sharks than for other, small coastal species and that managers should proceed cautiously (NMFS 2007). Here, we describe development and characterization of 52 microsatellites from an enriched genomic library of *C. isodon* DNA and cross-amplification and characterization of an additional 44 microsatellites developed for the blacknose shark, *C. acronotus* (Giresi et al. 2011). The microsatellites will be useful in assessing stock structure of finetooth sharks and thus contribute to better-informed management of the species.

Generation of an enriched genomic library of *C. isodon* DNA followed procedures outlined in Renshaw et al. (2010). A hybridization reaction was performed using 50pmol of a 3′-biotin modified $(CA)_{13}$ oligonucleotide. The hybridization mixture was heated to 95°C for 10 min and then kept at 58°C for 1.25 h. Enriched genomic fragments were ligated into the pCR®2.1-TOPO® vector (Invitrogen) and transformed into *Escherichia coli* (One Shot® TOP10 Chemically Competent Cells, Invitrogen). Positive (white) clones were sent to University of Florida's Interdisciplinary Center for Biotechnology Research (http://www.biotech.ufl.edu/) for sequencing with M13 primers. SEQUENCHER 4.1 (Gene Codes) was utilized to trim vectors and edit sequences. Primer pairs were developed using PRIMER3PLUS (http://www.bioinformatics.nl/cgi-bin/primer3plus/primer3plus.cgi).

Polymerase chain reactions (PCR) for all 97 microsatellites (developed from both *C. isodon* and *C. acronotus)* followed procedures outlined in Boutin-Ganache et al. (2001) and employed three primers. The forward and reverse

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Published online: 22 February 2012

Table 1 Summary data for 29 polymorphic microsatellites characterized in the finetooth shark, *Carcharhinus isodon*

Microsat	Primer sequence (5′–3′)[a]	GenBank[b]	Repeat[c]	Clone size[d]	Dye[e]	N/N_A	Range[f]	H_E	H_O	P_{HW}
Primers developed from finetooth shark, *Carcharhinus isodon*										
*Cis*102	ATGCTCTGCAAGGTCAAACC GCGGTTTTGATGTATTGTGC	JQ365946	$(GT)_{16}$	209	FAM	31/3	221–233	0.518	0.516	1.000
*Cis*103	AGACACTTTCTCTCTCACACACAT TGTGGGAATCAGTGAATGGA	JQ365947	$(AC)_{11}$	133	HEX	31/2	152–154	0.032	0.032	1.000
*Cis*107	TCTTCCACTGGCAGGTTAGG GGCATCCACATGATTTTGC	JQ365949	$(CA)_{26}$	275	FAM	31/11	287–311	0.870	0.903	0.766
*Cis*108	ATTGATCAGGGTGGTCAAGC TAGTGCCCTGTGTTGTCTGG	JQ365950	$(CT)_{12}$	255	FAM	31/3	275–283	0.428	0.387	0.753
*Cis*111	TGCCTGTGAGTGTGTGAAAG AATAACTGTGAGGCGCATGG	JQ365952	$(GT)_{15}$	147	HEX	31/3	166–176	0.362	0.387	1.000
*Cis*112	TTCTGACATGCACATTCTTGG TCCCGCTACCATTGTAAACC	JQ365953	$(AC)_{12}$	311	FAM	31/2	325–333	0.032	0.032	1.000
*Cis*113	ACCCCCAGACACACAGAGAC TGTGTTTGTGCATATACATTTGAG	JQ365954	$(AC)_{18}$	93	HEX	31/2	109–111	0.032	0.032	1.000
*Cis*121	GTGGCAGATATTCCCAAACC GGTGTGTGTCTGTGTGATAGAAGC	JQ365959	$(AC)_{16}$	222	HEX	31/8	242–266	0.587	0.613	0.968
*Cis*128	CACAATCCTGAGACAAATCTGC GCTAGCTGGCAGAGAAAACC	JQ365963	$(CA)_7$	236	HEX	31/2	257–273	0.063	0.065	1.000
*Cis*131	GGGAGCTGAGCTAAAAACAGC TTGTTCCCTTTGAGATTTGG	JQ365966	$(CA)_{12}$	293	FAM	31/6	303–317	0.690	0.645	0.930
*Cis*133	CAGGATGATTGACAGGTCAGC TTCAATAGAAGGGGCACACG	JQ365968	$(CA)_8$	308	FAM	31/2	329–333	0.252	0.226	0.487
*Cis*134	TAAAACGACCAGCACTGAGC AGAGGCTGTCGGATGTGG	JQ365969	$(GT)_7$	239	HEX	30/2	263–275	0.499	0.467	1.000
*Cis*139	TTGATGCTACCAATCACAGG ACAACTGAGAGGGGCAAGG	JQ365971	$(TG)_{18}$	206	FAM	31/8	210–236	0.736	0.710	0.089
*Cis*149	ATCACCCCCACCAACACC CTGTTGGATGATTGGGAAGG	JQ365978	$(CA)_{22}$	314	FAM	31/8	331–347	0.702	0.742	0.580
*Cis*157	TTCCTTGGCAGATGTAAATGC CCATGCAACATTGGTCTCC	JQ365982	$(GT)_{20}$	206	NED	31/5	232–242	0.613	0.645	0.119
*Cis*161	ATCTGACTTGGACCCATTGC GAAATGGAGCTGAGTGTCTGG	JQ365986	$(CA)_{25}$	185	HEX	26/8	195–219	0.792	0.731	0.553
*Cis*163	TTTCTTACCCCTGAAGTGTGC CTTCAGAGGCTTACCATGTCG	JQ365988	$(CA)_{22}$	208	NED	31/26	227–307	0.955	0.935	0.449
*Cis*168	AAAGAGTGGGCAGCTCTGG TAGGGCAGGTGCCATAATCC	JQ365992	$(TG)_6$	135	HEX	31/3	158–162	0.466	0.484	1.000
*Cis*170	TGCTGCAACATCATTCTTCC AACCTCTTTATGATTCCCTCAGC	JQ365994	$(TG)_{39}$	214	NED	31/14	221–253	0.865	0.935	0.038
*Cis*175	TCAAATTGCCATTCAAAGAGC TTCCACACTCAAGCATTTGG	JQ365998	$(CA)_{33}$	218	FAM	31/14	219–249	0.846	0.903	0.296
Primers developed from blacknose shark, *Carcharhinus acronotus*										
*Cac*3	ATCGACTCCATGCAGAATCC TGCCCAATGAACAAACAAAA	JN253438	$(CA)_{15}$	232	FAM	31/2	241–249	0.275	0.194	0.152
*Cac*48	TTGAAGGCAAATCATTGTGG AGGTACAAGTGCTGGGATGG	JN253462	$(AC)_{13}$	162	HEX	31/2	177–179	0.063	0.065	1.000
*Cac*50	CATGAGCCCTGGATGTATGC TGCATTGAGACCAACCAAAG	JN253463	$(AC)_9G(CA)_6$	152	NED	31/2	191–193	0.482	0.645	0.079

Table 1 continued

Microsat	Primer sequence (5′–3′)[a]	GenBank[b]	Repeat[c]	Clone size[d]	Dye[e]	N/N_A	Range[f]	H_E	H_O	P_{HW}
*Cac*59	TTCTGGATGCTTCCAATTCC TTGTGGGAATTGCTCATGG	JN253469	$(GA)_{13}$	237	FAM	31/2	256–258	0.151	0.161	1.000
*Cac*67	GTAACCCATGCCTGCAGTTC CTGTCAAATTGCCGATAGGG	JN253474	$(AC)_{31}$	174	FAM	31/22	195–253	0.955	0.968	0.638
*Cac*B4	AAATTGCCTACTCCTGCACA AGTGCATGCGTGACTGAGAG	JN253477	$(TC)_{10}$	231	HEX	31/2	248–252	0.032	0.032	1.000
*Cac*B12	AGCTCTGCCCCGAGATAAAT AACGTGATGGGACAAATGGT	JN253482	$(CA)_9$	170	FAM	31/2	189–191	0.032	0.032	1.000
*Cac*B14	GCACCCTATCCTTCCCTTCT GTGCCTGTCCCAACAAGTTT	JN253484	$(AC)_{14}$	263	FAM	31/2	284–286	0.032	0.032	1.000
*Cac*B20	ATACACCCAAGCATGCACAC CAATCTGCCATGCCATAAAA	JN253487	$(CA)_{10}$	94	HEX	31/2	114–116	0.123	0.129	1.000

N number of individuals assayed, N_A number of alleles detected, H_E expected heterozygosity, H_O observed heterozygosity, P_{HW} probability of deviation from the expectations of Hardy–Weinberg equilibrium

[a] Primer sequences are forward (top) and reverse (bottom)

[b] Genbank accession number

[c] Repeat indicates repeat motif

[d] Clone size is the size (in base pairs) of the allele in the sequenced clone

[e] Dye utilized to fluoresce microsatellites

[f] Range refers to size range in base pairs of alleles

Table 2 Summary data for 66 monomorphic microsatellites characterized in the finetooth shark, *Carcharhinus isodon*

Microsat	Primer sequence (5′–3′)[a]	GenBank[b]	Repeat[c]	Clone Size[d]	Dye[e]	N/N_A	Allele size[f]
Primers developed from finetooth shark, *Carcharhinus isodon*							
*Cis*104	CCAAAGGATACTCCCAGTGC TGTTCTTTGTGTCTGGATGACC	JQ365948	$(TG)_8$	190	FAM	31/1	212
*Cis*109	CTTTGAGGGGGCTGATAACC TTCTATTTAACCGGCTTCTGC	JQ365951	$(TC)_{10}$	216	HEX	31/1	237
*Cis*114	TAAGGAGCAGTTTGGCAAGG GGTGGGGATATGATCAGTGC	JQ365955	$(GT)_{14}$	286	FAM	31/1	308
*Cis*116	CCCAGCAATATTCATTCACC AATCGAATCTGCCTCATTGC	JQ365956	$(TG)_7$	135	HEX	31/1	157
*Cis*118	AACCCACATGGAGAAAGTGC AGGGTGGCATAGTGGTTAGC	JQ365957	$(CA)_{16}$	133	HEX	31/1	129
*Cis*119	GGAGCATCAGTTCCATACCG GAACGATGGAAGTTGGTTCC	JQ365958	$(CA)_5$	286	FAM	31/1	307
*Cis*122	ATTGTCACTTTGGGCTCTGC AGCCACAAGTCCAGAGAACC	JQ365960	$(AC)_6$	294	FAM	31/1	316
*Cis*124	TCCCCTTTACCAACACTTCC CACTGGGTAAGGGTGAAAGC	JQ365961	$(CA)_5$	119	HEX	31/1	139
*Cis*126	CGTGTGTGCATGTGTGCAT TGAGAAGCAGAAATCATGAGAAA	JQ365962	$(TG)_6$	88	HEX	31/1	108
*Cis*129	ACGGAACCCTTTTAATCAGC AGGTGACAGCATGAGTTTGC	JQ365964	$(CA)_8$	289	FAM	31/1	313
*Cis*130	CCTTTGCAGTCCATCTCTCC	JQ365965	$(CA)_6$	157	NED	31/1	177

Table 2 continued

Microsat	Primer sequence (5′–3′)[a]	GenBank[b]	Repeat[c]	Clone Size[d]	Dye[e]	N/N_A	Allele size[f]
	TCTGGTTCTTTGTCTGTGTTCC						
*Cis*132	GATGGCTAATGTTCCCTTGG	JQ365967	$(GT)_9$	91	HEX	31/1	113
	CGATAAGGGAATGAGGTTCC						
*Cis*138	GGGATTGGATAGACACATTATGG	JQ365970	$(TG)_{12}$	116	NED	28/1	138
	TGCTGTCGATGTCTTCAAGC						
*Cis*140	TGGGCACATTGTAGGAATGC	JQ365972	$(CA)_{10}$	313	FAM	31/1	334
	TGTTTGTAACAGGATGGTCTATGC						
*Cis*142	CAACACCAAAATATCCAAAGAGG	JQ365973	$(GT)_5$	259	NED	31/1	280
	TTGAACAGTGGGCCATTAGG						
*Cis*144	ACATGTTCACCCAACTGACC	JQ365974	$(CA)_{10}$	265	NED	31/1	285
	TCATTGGGATCTGAGTGTCG						
*Cis*145	TGAACTCACTGCATCCATCG	JQ365975	$(CA)_8$	279	FAM	31/1	299
	GATGGCATAGCGTTAAATTGG						
*Cis*147	CGGGGCAAATGTTACAAAGC	JQ365976	$(TG)_7$	255	NED	31/1	278
	ACCCTGTCACAAGCATAGCC						
*Cis*148	GGTTGCTGTTTAGGGCTGTT	JQ365977	$(TC)_{10}$	124	FAM	31/1	145
	CCAGTTAGCAAACAGCACAGG						
*Cis*151	TGCGCATCATACATTTTAAGC	JQ365979	$(AC)_7$	264	FAM	31/1	284
	CCCTGACATTCAGACTTACACG						
*Cis*154	GCCAAGACCACTGAAATAATCC	JQ365980	$(CA)_{10}$	130	HEX	31/1	150
	TCTCAGCACCTCACACAACC						
*Cis*156	ACCCATGCTTATCCTTCTGC	JQ365981	$(AC)_6$	275	NED	31/1	296
	GGCATGTCTGGTAAGTGTGC						
*Cis*158	AGGAATTGCATGACCAGAGC	JQ365983	$(GT)_{15}$	310	FAM	31/1	334
	CTCACAAGAAACAACACTGTATCC						
*Cis*159	TTGCAAACAGATGATGTCTGG	JQ365984	$(GT)_5$	262	NED	31/1	286
	ACAATGCAAGATTGGGAAGC						
*Cis*160	GATGAACAATAATGGATGAGTTGG	JQ365985	$(TG)_8$	161	HEX	31/1	184
	AACCCCGGTGAAAATCTAGG						
*Cis*162	CCTCCTTAGTTTGGCTGAGG	JQ365987	$(AC)_6$	269	FAM	31/1	290
	ACGTGTGCCTGTGATAATGC						
*Cis*165	TGTCTGTTCTGGAGAGACTTGC	JQ365989	$(AC)_9$	270	FAM	31/1	290
	TTTCAGGTGTTTTGGCAACC						
*Cis*166	CAGTCTGTCGATTCCACTGC	JQ365990	$(GT)_7$	208	NED	31/1	230
	GTCCAAAGGCTGGAATAACG						
*Cis*167	TCAGACCTGCTGAGATTTTCC	JQ365991	$(TG)_8$	89	HEX	31/1	110
	TCTAAATCGCAAGACCAACC						
*Cis*169	TTTCCCTATATCTGGCAAAGC	JQ365993	$(CA)_{15}$	275	FAM	31/1	295
	ACACTTGTTGCGTTTGATCG						
*Cis*171	CAGGGAGACACACAATCTCTC	JQ365995	$(CA)_{10}$	158	HEX	31/1	178
	TTATAGCTGGGGGCAGTGAG						
*Cis*172	TTCTCCTCGCTGTGAATGG	JQ365996	$(GT)_6$	143	HEX	31/1	149
	ATCGGTGTGACTGGAAAAGC						
*Cis*174	TTTGCGTAGCTCTGTGATGG	JQ365997	$(TG)_5$	96	HEX	31/1	117
	GATGCTGGGAGTCTCTGAGG						
Primers developed from blacknose shark, *Carcharhinus acronotus*							
*Cac*7	TGCACATTGAAAATGCCCTA	JN253439	$(CAA)_4$	206	NED	31/1	243
	TGCTCCTGTGAAGCATCTTG						

Table 2 continued

Microsat	Primer sequence (5′–3′)[a]	GenBank[b]	Repeat[c]	Clone Size[d]	Dye[e]	N/N_A	Allele size[f]
*Cac*8	GTGCAGATATACATACATCACACACT GTATTGCTTGGTGCGAGGTT	JN253440	$(CA)_7$	119	HEX	31/1	127
*Cac*13	TGTCTTTCTGGGCAGCAGTA TTGCCACCACTGCAGTAAAC	JN253441	$(TG)_7$	100	HEX	31/1	121
*Cac*15	TGTCCGCTAAGCTTTCGTTT ACAACCCTGATTTTGCGAAG	JN253443	$(CA)_{10}$	194	NED	31/1	212
*Cac*16	TCGGAGGAACACCTCAAAAC AGTCCATCCGAAATGACAGC	JN253444	$(GT)_6$	116	HEX	31/1	138
*Cac*17	GCAATATTCTGCCCAAAGGA CTTGTCTGACACTGGCCTGA	JN253445	$(CT)_6$	214	NED	31/1	237
*Cac*18	GGGATTCGAGGAATGCTACA GCTGTCAGGTAAGGCCAAAT	JN253446	$(CA)_7$	141	HEX	31/1	166
*Cac*20	GCCATTGCTGCTGTTGATAA CATTTTGTTGTGTGGCCAAG	JN253447	$(GT)_6$	255	FAM	31/1	277
*Cac*35	TCCTTTGAAGTGCCTTGTGA GGAGGTTTGCGCAACAAATG	JN253452	$(GTT)_5$	148	HEX	31/1	171
*Cac*36	CAGCACTGACCTGTTGTCGT CAATAACGTATCCCCGGTGT	JN253453	$(GTT)_6$	156	HEX	31/1	177
*Cac*37	TAACCGAAAGAGGTGGTGCT ATTTCATCGTGAAGGTGGTG	JN253454	$(GA)_5$	230	NED	31/1	243
*Cac*38	GCGACATCACAGTGAAAGGA TGCACATGTACGCACTCTGA	JN253455	$(GT)_6$	269	NED	31/1	290
*Cac*42	CACACATGTACCCATGCACA AAACCTTCTTCCCTGCCACT	JN253457	$(CA)_{11}$	261	FAM	31/1	294
*Cac*43	GGGTGCAGTGCCAGAATAAG ATGTGAGGTCTGCGTCAGTG	JN253458	$(CA)_5$	204	NED	31/1	232
*Cac*44	GGGGAGAGCTTAGGAGATGG TTCATCATGCTCTGCCAATC	JN253459	$(TG)_5$	158	NED	31/1	180
*Cac*45	GGGTAAATTGGAGAGGTCAGG TCACTTGTCCTGCCAGTGTC	JN253460	$(CA)_{13}$	250	NED	31/1	306
*Cac*46	TGCACATGCTCACACATACC AAAGGGTTTGAGCTGGAAGG	JN253461	$(CA)_{11}$	222	FAM	31/1	242
*Cac*56	ACCGAGATGCAAAGAGAAGG GTCTTTGGGCAAGCTGTGAG	JN253466	$(GA)_{11}$	230	FAM	31/1	244
*Cac*57	TTTATCGTCCAAAATAATGCTGAG TGGAAACATAGCGCAGTGAG	JN253467	$(TG)_{27}$	228	NED	31/1	212
*Cac*58	TGCTTGGTACCAGTCAGCTC AGCACCCAGACACAAGTGC	JN253468	$(GT)_{18}$	184	NED	31/1	112
*Cac*60	AGGAATGGAGCAGGGTTTTC GATGGGAGTGTGTGCATGAG	JN253470	$(CT)_5$	250	FAM	31/1	269
*Cac*63	ACGCATGAACATTCACTTGG GCTTGGCAACTGTTTCTTGG	JN253471	$(GT)_6$	236	NED	31/1	258
*Cac*66	CCAACACAAATTCACATGCAC CCTCCTTGAGGAAGGAAACC	JN253473	$(CA)_{14}$	219	HEX	31/1	232
*Cac*68	TGCTGAGAACGGTCAGAGTG CACACACTCCACACCCAAAG	JN253475	$(TG)_7$	152	Hex	31/1	185
*Cac*B3	CCAAGACAGGAGGTGAGAGC AATCGCTCATGCAACACAAC	JN253476	$(CA)_7$	328	FAM	31/1	350

Table 2 continued

Microsat	Primer sequence (5′–3′)[a]	GenBank[b]	Repeat[c]	Clone Size[d]	Dye[e]	N/N_A	Allele size[f]
*Cac*B8	GGCTGATTTTGATGTGGTGA CCCTGGAAGTTGGTATTGGA	JN253480	$(AG)_6$	241	FAM	31/1	263
*Cac*B11	AACTGTGGCTTTGCTTGCTT TCCCAGACTGTGGACATCAT	JN253481	$(GA)_{11}$	259	FAM	31/1	280
*Cac*B13	GGGATAGGACTGGGGACATT ACAAGAGGCCAGAAACTGGA	JN253483	$(TG)_6$	243	NED	31/1	266
*Cac*B19	AGGAACTTAGGGACGCCTGT ATGCACTGTCCATACCAGCA	JN253486	$(GT)_6$	183	NED	31/1	205
*Cac*B22	GACAGGGAGGAGAGATTGAGA TCCTGCAGTATCCCACTAGTCA	JN253488	$(GA)_6$	142	HEX	31/1	94
*Cac*B23	CAAGGTTAACCCAACGCAAT GTAGCACGCGAGAAACAATG	JN253489	$(TTGAT)_5$	282	FAM	31/1	303
*Cac*B25	GGCCATAGGGCTGACTACAA CATCCAGCATTATCCAAGCA	JN253490	$(AAC)_4$	203	NED	31/1	225
*Cac*B28	GACATGCACATTCACAAGCA TGAGTGTGTGGCTGTGGGTA	JN253492	$(CA)_7$	110	HEX	31/1	129
*Cac*B42	ACGCTTGATAGCGCATTTTT AGCTTCACAGGCAGGAAGAG	JN253496	$(GTT)_5$	194	HEX	31/1	150
*Cac*B44	AAAGGGCAGCAATTTGTGAG ACACCTGCCAAAAGACGTG	JN253497	$(TG)_6$	173	FAM	31/1	333

N number of individuals assayed, N_A number of alleles detected

[a] Primer sequences are forward (top) and reverse (bottom)

[b] Genbank accession number

[c] Repeat indicates repeat motif

[d] Clone size is size (in base pairs) of the allele in the sequenced clone

[e] Dye utilized to fluoresce microsatellites

[f] Allele size refers to size in base pairs of allele

primers were purchased from Integrated DNA Technologies (IDT). The forward primer included an additional 21-bp sequence (5′-GCCTCGTTTATCAGATGTGGA-3′). The third primer, the 21-bp tail sequence, was labeled with either 6-FAM, HEX or NED (Dye Set D, Applied Biosystems) enabling amplicons to be fluorescently labeled. Primer sets yielding clean amplifications were run on 31 individuals obtained off the coast of South Carolina. Amplicons were electrophoresed on an ABI 377 automated sequencer with a 400HD (Rox) Size Standard (Applied Biosystems). Allele sizing and calling were performed using GENESCAN® version 3.1.2 and GENOTYPER® version 2.5 software (Applied Biosystems).

Genetic variability for each microsatellite assayed was measured as number of alleles, gene diversity (expected heterozygosity), and observed heterozygosity, as calculated in GDA (Lewis and Zaykin 2001). A Fisher's exact test, as implemented in GDA, was used to test for significant departures from the expectations of Hardy–Weinberg equilibrium at each microsatellite. MICROCHECKER version 2.2.3 (Van Oosterhout et al. 2004) was utilized to assess for the presence of null alleles, large-allele dropout, and/or stuttering at each microsatellite.

Summary data for all polymorphic microsatellites are presented in Table 1; summary data for monomorphic microsatellites are presented in Table 2. For polymorphic microsatellites, the number of alleles detected ranged from two (14 loci) to 26 (*Cis*163); expected heterozygosity ranged from 0.032 (six loci) to 0.955 (*Cac*67 and *Cis*163), while observed heterozygosity ranged from 0.032 (six loci) to 0.968 (*Cac*67). No evidence of null alleles, large allele dropout, or stuttering at any microsatellite locus was detected with MICROCHECKER. No microsatellite loci deviated significantly from the expectations of Hardy–Weinberg equilibrium after sequential Bonferroni correction (Rice 1989). The microsatellites described here will prove useful for population genetic studies of *C. isodon* and potentially for other carcharhinid species.

Acknowledgments We thank B. Frazier of South Carolina's Department of Natural Resources for providing tissue samples. Work was supported by the Cooperative Research Program (CRP) of the National Marine Fisheries Service (NOAA, Department of Commerce)

under Grant NA10NMF4540109. This paper is number 85 in the series 'Genetic Studies in Marine Fishes' and Contribution No. 210 of the Center for Biosystematics and Biodiversity at Texas A&M University.

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