Supplementary Information 2

Genomic resources for the spotted ragged-tooth shark *Carcharias taurus*

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Microsatellite-marker amplification

Selected microsatellite primers were modified by adding an M13 sequence (TGTAAAACGACGGCCAGT) to the forward primer for amplification, using the three-primer amplification protocol of Schuelke (2000), and by adding a PIG-tail (GTTT; Brownstein et al. 1996) to the reverse primer. Each 10-µl PCR reaction contained 5 µl of KAPA2G Fast Multiplex Mix (containing KAPA2G Fast HotStart DNA Polymerase, PCR Buffer, 3 mM $MgCl_2$, and 200 µM of each dNTP), 2 µl of H_2O, 0.5 µl of forward primer (1 pmol/µl), 1 µl of reverse primer (2 pmol/µl), 1 µl of fluorescently labelled (NED/VIC/FAM/PET) M13 primer (2 pmol/µl), and 0.5 µl of template DNA (50 ng/µl).

Thermocycling conditions

Protocol 1: Ctaur3, Ctaur4, Ctaur10, Ctaur11, Ctaur21 and Ctaur22
94 °C for 3 min, five 3-step cycles at 94 °C for 30 sec, 60 °C to 52 °C for 20 sec in 2 °C steps per cycle, 72 °C for 30 sec, followed by 35 3-step cycles at 94 °C for 30 sec, 52 °C for 20 sec, 72 °C for 30 sec, and a final extension at 72 °C for 10 min.

Ctaur2: Same as Protocol 1 (above) except annealing and extension time were increased to 30 sec and 45 sec, respectively.

Protocol 2: Ctaur20 and Ctaur24
94 °C for 3 min, four 3-step cycles at 94 °C for 30 sec, 60 °C to 52 °C for 20 sec in 2 °C steps per cycle, 72 °C for 10 sec, followed by 25 3-step cycles at 94 °C for 30 sec, 55 °C for 20 sec, 72 °C for 10 sec, and a final extension at 72 °C for 5 min.

Ctaur26: Same as Protocol 2 (above) except final extension time was increased to 45 min.

Protocol 3: Ctaur19
94 °C for 3 min, four 3-step cycles at 94 °C for 20 sec, 60 °C to 52 °C for 15 sec in 2 °C steps per cycle, 72 °C for 10 sec, followed by 25 3-step cycles at 94 °C for 30 sec, 57 °C for 20 sec, 72 °C for 15 sec, and a final extension at 72 °C for 15 min.

Mitogenome assembly

An initial assembly was performed using Mira 4.9.6 (Chevreux et al. 2004) and MITOBIM 1.8 (Hahn et al. 2013) with the previously published mitogenome (GenBank Accession number: KF569943.1; Chang et al. 2015) of the species as the initial bait template. The sequence was annotated with the web-based tool MitoAnnotator (Iwasaki et al. 2013).

Table S1: Single nucleotide polymorphisms (SNPs) found in 16 gene regions of the mitogenome of spotted ragged-tooth shark *Carcharias taurus* specimens from South Africa, Australia and the United Arab Emirates. ATP = adenosine triphosphate; CO = cytochrome *c* oxidase subunit; cytb = cytochrome *b*; NADH = nicotinamide adenine dehydrogenase subunit; rRNA = ribosomal ribonucleic acid

Gene	Length (bp)	SNPs	Relative variation (%)
CO1	1 553	8	0.515
CO2	690	2	0.290
CO3	785	1	0.127
NADH1	974	7	0.719
NADH2	1 042	9	0.864
NADH3	348	2	0.575
NADH4L	296	2	0.676
NADH4	1 380	11	0.797
NADH5	1 829	15	0.820
NADH6	521	5	0.960
Cytb	1 144	11	0.962
12S rRNA	949	2	0.211
16S rRNA	1 669	8	0.479
ATP6	683	4	0.586
ATP8	171	1	0.585
Control region	1 058	7	0.662

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