New record of the rare ragged-tooth shark, *Odontaspis ferox* (Chondrichthyes: Odontaspidae) from the south-west Atlantic identified using DNA bar coding

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An unidentified shark carcass (minus head, fins and entrails) was landed in Fortaleza, Brazil following its commercial fishery capture off Ceará State in north-eastern Brazil. The absence of key morphological characters precluded traditional identification, necessitating the employment of DNA bar coding techniques. The obtained 639 nts COI sequence fragment perfectly matched six of seven Odontaspis ferox sequences available on the Barcode of Life Data (BOLD) system database, and was 99.2% similar to the seventh.

Keywords: elasmobranch, vulnerable species, fisheries landings, occurrence record, Odontaspis ferox

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INTRODUCTION

The plight of sharks and rays (the elasmobranchs) is now welldocumented but there are still serious gaps in our knowledge of elasmobranch distribution, abundance, movement and life history that significantly detract from enlightened management (Musick et al., 2000; Fowler et al., 2005). Many shark species are apex marine predators that are valued in artisanal and large-scale fisheries because they represent large sources of protein and ready income owing to the value of their fins. Because of handling and seafood quality considerations, sharks are frequently eviscerated, beheaded and finned at sea, producing a more compact carcass that is more readily stored prior to landing and the fins are also stored due to their high economic value. Such carcasses lack critical morphological characters needed to make accurate species identification and thus have proven problematic to fishery biologists seeking species-specific catch and landing data needed for fishery management (Morgan & Burgess, 2005). Such species-level data are the starting point of any fishery management initiative (Wong et al., 2009). In addition, the presence of rare species may be under-reported, which can have serious conservation and management implications since many shark species are conservation-dependent.

The ragged-tooth shark *Odontaspis ferox* is globally distributed in warm-temperate and tropical waters. Despite its wide

Corresponding author: J. Santander-Neto Email: jonessn@gmail.com geographical range, it occurs only infrequently as by-catch in Mediterranean commercial fisheries and is more rarely encountered in other parts of the world (Fergusson *et al.*, 2008). In the western Atlantic, *O. ferox* has been recorded from off North Carolina (Sheehan, 1998), South Carolina and the east coast of Florida (Ross & Quattrini, 2007), the Gulf of Mexico (Bonfil, 1995; Sulak *et al.*, 2007), Cuba (Claro & Parenti, 2001), and off Natal and Fernando de Noronha Archipelago in north-eastern Brazil (Menni *et al.*, 1995; Garla & Garcia-Júnior, 2006). Due to its natural rarity, low fecundity, and the increasing fishing pressure in parts of its range, *O. ferox* is listed as vulnerable in the *IUCN Red List of Threatened Species* (Pollard *et al.*, 2007) and stated as declining by Compagno (2001).

Recently Holmes *et al.* (2009) applied the Barcode of Life Data (BOLD) system search engine as well as a phylogenetic approach (tree match) to identify shark species from fins confiscated in Australia. Some studies concluded that BOLD was precise in species identification, especially in cases of perfect sequence matches (Ward *et al.*, 2005, 2008; Holmes *et al.*, 2009; Wong *et al.*, 2009) even when compared to tree match.

MATERIALS AND METHODS

During a regular sampling of shark landings in Ceará State (CE), north-eastern Brazil, a singular carcass caught the attention of the first author. The relative positions and base widths of dorsal, pectoral, pelvic, and anal fins suggested it was a lamniform shark. Although species-level identification was not possible, it was clear that it was not any of the species known to occur in the region (Jucá-Queiroz *et al.*, 2008).

Additional collection data for this distributional record are as follows: the unsexed (gonads and pelvic fins missing) specimen was caught by handline off Fortaleza, CE, Brazil (03°13'S 38°29'W). The fishing gear was operating at an approximate 50-m depth. The carcass was landed in Mucuripe Inlet, Fortaleza, CE, Brazil, on 3 May 2008.

With the goal of identifying the shark carcass genetically, a tissue sample was retained for analysis using DNA bar coding techniques.

Total cell DNA was extracted using the QIAGEN DNeasy kit, according to the manufacturer's instructions (QIAGEN Inc., Valencia, CA, USA). A set of universal primers (Fish F2-t1 and Fish R2-t1; Ward et al., 2005) was used for sequencing a region of the mitochondrial gene cytochrome c oxidase 1 gene (COI). The 25-µl amplification reactions consisted of 1X buffer, two units of IMMOLASE DNA polymerase (Bioline Inc., Boston, MA, USA), o.4 mM dNTPs, 4.0 mM MgCl₂, 0.3 µM of each primer, 0.1 µg/µl bovine serum albumen, and 20-50 ng of total cell DNA. Cycling conditions were 95°C for 7 minutes, 30 cycles of 94°C for 30 seconds, 50°C for 90 seconds, and 72°C for 45 seconds with a final extension at 72°C for 3 minutes. Amplicons were purified with QIAquick kit (QIAGEN Inc., Valencia, CA, USA) following manufacturer's instruction. Both strands were sequenced and run on a MEGABACE 1000 (G.E. Healthcare). The COI sequence was submitted to the BOLD search engine. Species match was based on genetic distance analyses under a Kimura 2 Parameter model. Percentage similarities with each of the top 99 matching specimens were obtained.

RESULTS

The 639 nts (non-transcribed spacer) obtained sequence fully matched (100% similarity) six of seven *Odontaspis ferox* (Risso, 1810) (Lamniformes: Odontaspididae) sequences available in the BOLD database (FMVIC 655-08; ESHKD 133-07; PHANT 428-08; PHANT 932-08; AMS 019-06; PHANT 425-08). The remaining *O. ferox* specimen was 99.21% similar (AMS 021-06). The close match to *O. ferox* sequences coupled with available morphological evidence suggest the unidentified shark carcass is an *O. ferox*. As expected, the second best species match was its only other living congener, *O. noronhai* (KERRI 283-08), with 93.72% of genetic similarity.

DISCUSSION

Based on local fishery dynamics and traditions, it can be deduced that the ragged-tooth shark was captured the day before. The carcass was 144 cm in length with an interdorsal distance (ID) of 41.7 cm. This ID value was back-calculated to an estimated total length (ETL) of 247 cm using proportional morphometric information from a specimen caught off Mexico (Bonfil, 1995). Based on this ETL, the specimen was a sub-adult (Fergusson *et al.*, 2008).

The genetically-matched individual herein represents only the third record of *O. ferox* from the south-western Atlantic and the ninth from the western Atlantic and as proposed by Compagno (2001) this species is spottily distributed and probably circumglobal in warm-temperate and tropical waters.

The monitoring of fisheries associated with rigorous attention to any morphological character available (even on a carcass) and techniques such as DNA bar coding could provide accurate species identification. This is the base of any fishery management and useful as well as for an understanding of distribution and habitat use of this and other poorly known sharks.

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