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Short communication

DNA barcoding of chondrichthyans in South African fisheries

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ABSTRACT

South Africa has one of the highest chondrichthyan species diversities in the world, with more than 35% affected by regional fisheries. In order to evaluate the impact of these activities, accurate data on species occurrence is needed. Here, we tested a more robust identification approach of chondrichthyan species in South Africa by sequencing a subsample of specimens (n = 75) collected from different regional fisheries at the mitochondrial cytochrome c oxidase subunit I (COI) gene. Morphological identification of these specimens was evaluated through sequence similarity testing of barcoding sequences available in the Barcode of Life Data (BOLD) database. A total of 23 species from ten families of sharks, skates and rays were identified with an overall agreement of 73% between genetic identification and initial morphological identifications made in the field. Despite some limitations of the COI gene for species identity and the small number of samples analysed in the study, results suggest that a more integrated species identification approach of chondrichthyans can be used to assist conservation of chondrichthyans in South African fisheries.

1. Introduction

The increase in demand for shark meat and other shark-related products coupled with biological and ecological life history traits has placed chondrichthyes (sharks, rays, and chimearas) at high risk for overexploitation (Dulvy et al., 2014). With a 4.5% increase in the global trade of shark meat, South Africa ranked 20th for exporting 942 t of shark meat and 15th for importing 13 t of shark fins valued at USD3 000 000 and USD72 000 respectively each year from 2000 to 2011 (Dent and Clarke, 2015).

South Africa has dedicated and well-established chondrichthyan fisheries including the demersal shark longline fishery and pelagic longline fishery (reviewed in da Silva et al., 2015). Target species include smoothhound *Mustelus mustelus*, whitespotted smoothhound *M. palumbes*, soupfin *Galeorhinus galeus*, bronze whaler *Carcharhinus brachyurus*, dusky sharks *Carcharhinus obscurus*, and broadnose sevengill shark *Notorynchus cepedianus* (da Silva and Bürgener, 2007). In addition, four decommercialised species, the leopard catshark *Poroderma pantherinum*, striped catshark *P. africanum*, spotted gully shark *Triakis megalopterus*, and spotted ragged-tooth shark *Carcharias taurus* are occasionally landed, although the trade in the latter is no longer permitted (da Silva et al., 2015). Limited species-specific management is in place, except for CITES (Convention on International Trade in Endangered Species of Wild Fauna and Flora) Appendix II listed species or look-alikes such as *Sphyrna* spp., *Alopias* spp., *Carcharadon carcharias, Carcharhinus falciformus*, *C. obscurus* and *C. longimanus*. Species-specific fishery dependent and independent data suitable for stock assessments only exists for ten species. As such a limited number of stock assessments have been completed but have been complicated by data inaccuracies. Common data inaccuracies are as a result of grouping of chondrichthyes into “morphogroups” e.g. *Requiem* sharks and mis-identification of similar species, such as triakids, and as a result of changing regional vernacular names with multiple species given the same name in different areas. Additonally, sharks are sometimes only taxonomically identified to genus level such as the smoothhound sharks of the genus *Mustelus.* This issue is compounded when catches are processed at sea and many distinguishing features are removed, resulting in mis-identifications and inaccurate catch composition reports. This could also allow fraudulent activities to go unregulated. Additionally, hybridization and cryptic speciation suspected within a number of genera of South African chondrichthyan biodiversity can complicate the accurate designation of specimen identity (Bester-van

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Table 1
Chondrichthyan species identified through DNA barcoding: (I) indicates a correct identification, (M) indicates a misidentification, and (U) indicates no initial identification. Number of samples barcoded (n) and average total length (s) are denoted below the species name. Specimens in bold are from a demersal hake biomass trawling survey.

Morphotype (Skate/ Ray/Shark)	Taxonomy (Order, Family)	DNA-Based Species ID	IUCN Red List	Morphological ID of Misidentified (M)	Longline (n = 13)	Rod and Handline (n = 26)	Trawl and Commercial (n = 36)
Shark	Carcharhiniformes, Carcharhinidae	*Carcharhinus brachyurus* (n = 5; s = 644 mm)	NT, u	*Galeorhinus galeus*	–	UUUU	M
Shark	Carcharhiniformes, Carcharhinidae	*Carcharhinus brevipinna* (n = 1; s = 798 mm)	NT, u		–	I	–
Shark	Carcharhiniformes, Carcharhinidae	*Carcharhinus galapagensis* (n = 1; s = 830 mm)	NT, u	*Carcharhinus obscurus*	–	M	–
Shark	Carcharhiniformes, Carcharhinidae	*Carcharhinus obscurus* (n = 1; s = 750 mm)	V, d		–	I	–
Shark	Lamniformes, Odontaspididae	*Carcharias taurus* (n = 2; s = 1935 mm)	V, u		–	II	–
Ray	Myliobatiformes, Dasyatidae	*Dasyatis chrysonota* (n = 3; s = 590 mm)	LC, u	*Torpedo marmorata*	–	IIM	–
Shark	Squaliformes, Etmopteridae	*Etmopterus brachyurus* (n = 1)	DD, u		I	–	–
Shark	Carcharhiniformes, Triakidae	*Galeorhinus galeus* (n = 16; s = 1162 mm)	V, d	*Mustelus mustelus*	III	–	IIIIIIIIIIIMM
Shark	Carcharhiniformes, Scyliorhinidae	*Haploblepharus edwardsii* (n = 2; s = 628 mm)	NT, u		–	UU	–
Shark	Carcharhiniformes, Scyliorhinidae	*Holohalaelurus regani* (n = 4; s = 453 mm)	LC, i		–	–	**IIII**
Skate	Rajiformes, Rajidae	*Leucoraja wallacei* (n = 1; s = 734 mm)	LC, u	*Dipturus pullopunctatus*	M	–	–
Shark	Carcharhiniformes, Triakidae	*Mustelus mustelus* (n = 13; s = 1235 mm)	V, d	*Galeorhinus galeus*	IIII	–	IIIIMMMMM
Shark	Carcharhiniformes, Triakidae	*Mustelus palumbes* (n = 5; s = 769 mm)	DD, u	*Mustelus mustelus*	–	UU	MMM
Ray	Myliobatiformes, Dasyatidae	*Myliobatis aquila* (n = 1; s = 627 mm)	DD, u	*Pteromylaeus bovinus*	–	M	–
Shark	Carcharhiniformes, Scyliorhinidae	*Poroderma africanum* (n = 2; s = 832 mm)	NT, u		–	UU	–
Shark	Carcharhiniformes, Scyliorhinidae	*Poroderma pantherinum* (n = 2; s = 660 mm)	DD, u		–	UU	–
Skate	Rajiformes, Rajidae	*Raja straeleni* (n = 1; s = 921 mm)	DD, u		I	–	–
Skate	Rajiformes, Rajidae	*Rostroraja alba* (n = 2; s = 1427 mm)	E,d		II	–	–
Shark	Carcharhiniformes, Scyliorhinidae	*Scyliorhinus capensis* (n = 3; s = 515 mm)	NT, u		–	–	**III**
Shark	Carcharhiniformes, Sphyrnidae	*Sphyrna zygaena* (n = 5; s = 743 mm)	V, d	*Sphyrna lewini*	M	IIUU	–
Shark	Squaliformes, Squalidae	*Squalus blainville* (n = 2; s = 446 mm)	DD, u		–	–	**II**
Shark	Squaliformes, Squalidae	*Squalus megalops* (n = 1; s = 489 mm)	DD, u		–	–	**I**
Shark	Carcharhiniformes, Triakidae	*Triakis megalopterus* (n = 1; s = 860 mm)	NT, u		–	I	–

IUCN Red List listings are given along with population trajectories (IUCN, 2015, version 3). IUCN status: DD, data deficient; E, endangered; LC, least concern; NT, near threatened, and V, vulnerable. Trends: d, decreasing; I, increasing, and u, unknown.

der Merwe and Gledhill, 2015).

Effective surveillance of these chondrichthyan species can be reinforced through the use of complementary identification schemes, such as morphology, species biology and genetics (Ebert and van Hees, 2015). The latter can be accomplished through the use of the cytochrome c oxidase subunit I (COI) partial gene sequence as a standard DNA barcoding marker (Ward et al., 2005). The effectiveness of COI barcoding in species identification of chondrichthyan species has previously been validated (Holmes et al., 2009;Pavan-Kumar et al., 2015; Bineesh et al., 2017; Cariani et al., 2017). There is some evidence showing the limitation of the COI gene in chondrichthyan species identification at the genus level (Wong et al., 2009; Naylor et al., 2012; Marino et al., 2017), possibly due to historic hybridization and/or incomplete lineage sorting (Marino et al., 2017). The utility of this identification tool is reliant on comprehensive sampling and established taxonomic data in order to accurately assign species identity (Meyer and Paulay, 2005). In this study, we evaluated the efficacy of DNA barcoding as an identification tool on a range of chondrichthyan species