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Short communication

Differential gene flow patterns for two commercially exploited shark species, tope (*Galeorhinus galeus*) and common smoothhound (*Mustelus mustelus*) along the south–west coast of South Africa

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ABSTRACT

South Africa's demersal sharks are threatened by over-exploitation, lack of species-specific catch data and non-cohesive fishing regulations. Two of the species most affected by fisheries are the common smoothhound (*Mustelus mustelus*) and the tope shark (*Galeorhinus galeus*) for which regional population structure is largely unknown. In this study, the population genetic structure of *M. mustelus* ($n = 105$) and *G. galeus* ($n = 124$) landed off the south–west coast of South Africa was investigated. Genetic diversity and gene flow patterns were compared based on genotype data generated from 12 microsatellite markers previously developed in closely related Triakidae species. Summary statistics and Bayesian analysis indicated significant population differentiation for *M. mustelus* and moderate to high gene flow between sampling sites for *G. galeus*. The different patterns of gene flow detected for these two species might be attributed to species-specific habitat preference and movement patterns and could have potential implications for fisheries management pertaining to these sharks.

1. Introduction

The demersal shark trade in South Africa has been gradually increasing for over two decades with shark fins and fillets increasingly being exported to support a demand in the international market (da Silva and Bürgener, 2007). In 2012, the landed dressed weight of five commercially important shark species was 316, 330, 145, 147 and 67 tonnes (t) for shortfin mako (*Isurus oxyrinchus*), blue shark (*Prionace gluaca*), tope shark (*Galeorhinus galeus*), common smoothhound (*Mustelus mustelus*) and copper shark (*Carcharhinus brachyurus*) according to South Africa's National plan on action, NPOA-sharks (DAFF, 2012), respectively. Total landed dressed weight of chondrichthyans for 2012 was 2527 t (DAFF, 2012). *M. mustelus* and *G. galeus* are the two shark species within the hound shark family, Triakidae that are considered to be most affected by the increased exploitation of demersal sharks in South Africa. Both these species are highly vulnerable to overfishing due to *K*-selected traits such as long generation time, late sexual maturity and low fecundity. Despite the paucity of data that limit the use of stock assessment models, there are observable trends for these species. McCord (2005) and da Silva (2007) showed respectively that *G. galeus* is fully exploited and *M. mustelus* is marginally overexploited. *M. mustelus* is a relatively small coastal-benthic species found in shallow waters. Reproduction is viviparous and sexual maturity is reached at a total length (TL) of 70–112 cm for males and 107.5–124 cm for females (Smale and Compagno, 1997; Saïdi et al., 2008). *G. galeus* on the other hand is a comparatively larger species (TL 148–200 cm) distributed in anti-tropical waters. Reproduction is viviparous with sexual maturity attained at TL 107–135 cm for males and 118–150 cm for females depending on the ocean basin (Ebert, 2003; Lucifora et al., 2004; McCord, 2005).

G. galeus is a principal target of directed shark fisheries in South Africa, targeted when high value teleost catches are low. Both *M. mustelus* and *G. galeus* are caught as targets or bycatch in the hake long-line, demersal longline, commercial linefishery, seine and gill-net, and trawling fisheries along the South eastern and South western Cape coast of South Africa (DAFF, 2012). *G. galeus*, locally known as soupfin, was one of the original targeted chondrichthyan species in Western Cape fishing villages when commercial exploitation of chondrichthyans began in the 1930s (von Bonde, 1934). Targeting of sharks increased after the Second World War with

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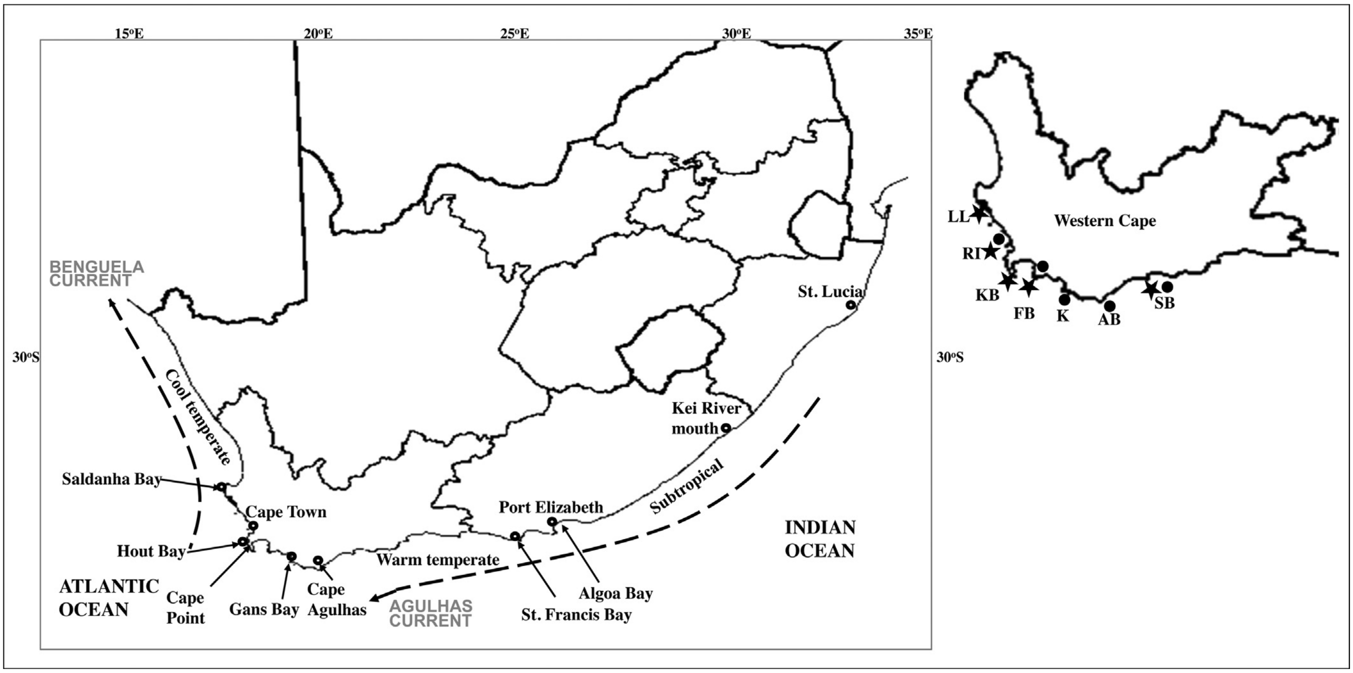

Fig. 1. A map of South Africa showing the biogeographic regions, the oceanic currents and the major landing sites of *Mustelus mustelus* and *Galeorhinus galeus* (left). The sampling sites included in this study for *M. mustelus* (stars) and *G. galeus* (black circles) are indicated on a map of Western Cape. Abbreviations of sampling sites are listed in Table 1.

the demand for shark products decreasing with the synthesis of vitamin A. By the late 1940s soupfin shark catches were in decline (Kroese and Sauer, 1998). Catches have not returned to pre-war levels and there are limited relative abundance data to assess their population dynamics. A lack of well-designed catch regulations that hypothetically allow for unlimited fishing of the species (da Silva, 2007) across multiple fisheries and management frameworks complicates this recovery. Major landing sites for both *M. mustelus* and *G. galeus* across South Africa include Saldanha Bay, Cape Town, Hout Bay and Gans Bay on the west and south coast, and occasional landing sites include Mossel Bay, St. Francis Bay and the Kei River on the east coast. Landing sites on the west coast are within the Atlantic Ocean exclusive economic zone (EZZ), while those on the east coast are in the Indian Ocean EZZ of South Africa (McCord, 2005; da Silva, 2007).

There are two oceanic currents at play along the South African coastline; the cold Benguela flowing northwards along the west coast and the warm Agulhas flowing southward along the Indian Ocean on the south–east coast (Hutchings et al., 2009). These currents meet between Cape Point and Cape Agulhas resulting in three major marine biogeographic regions; the cool temperate on the west coast, the warm temperate on the south–east coast, the subtropical region on the east coast. Phylogeographic patterns of various marine species have been associated with these biogeographic zones (reviewed in Teske et al., 2011) and both the Benguela Current and the Agulhas Current have shown to influence migration and gene flow of many coastal species (Teske et al., 2013).

To implement cohesive management and conservation measures for both *M. mustelus* and *G. galeus* in South Africa, the assessment of species-specific gene flow and population structure is necessary. Maintaining the genetic diversity of a species is crucial for its ability to survive (Hoban et al., 2013) and several studies highlight the importance of investigating genetic connectivity of commercially exploited shark species in achieving sustainable resource management (Schrey and Heist, 2003; Veríssimo et al., 2010; Daly-Engel et al., 2012). Microsatellite markers have successfully been used to detect genetic structure of elasmobranchs on regional as well as global scales (Ovenden et al., 2009; Veríssimo et al., 2010). Although species-specific microsatellites are available for a number of species such as scalloped hammerhead (*Sphyrna lewini*) (Nance et al., 2009), dusky smoothhound (*Mustelus canis*) (Giresi et al., 2011), tope (Chabot and Nigenda, 2011) and brown smoothhound (*Mustelus henlei*) (Chabot, 2012), *de novo* development of microsatellites has shown to be arduous and expensive (Guichoux et al., 2011). An alternative approach to *de novo* development is the cross-amplification of microsatellite primer sets amongst closely related species and the downstream application thereof in kinship analysis, genetic diversity assessment and population structure inference (Barbará et al., 2007). In a recent study, 22 microsatellite loci previously developed in three Triakidae species including *G. galeus*, *M. henlei* and *M. canis*, were successfully cross-amplified across 12 endemic and/or commercially important elasmobranch species occurring in South Africa (Maduna et al., 2014). All 12 species, including *M. mustelus* and *G. galeus*, showed polymorphism levels ranging from 31.8% to 95.5% and the polymorphism information content (PIC) was shown to be indirectly proportional to the evolutionary distance from the source species. In this study, 12 of the 22 microsatellite loci optimised in Maduna et al. (2014), was used to assess genetic diversity and population connectivity of *M. mustelus* and *G. galeus.* Since both these species are heavily exploited between the west and south coast of South Africa, a region that features two oceanic currents and the Atlantic/Indian Ocean boundary, it was important to investigate the possible differential effects of this barrier to gene flow. Incorporating this information into fisheries management practices and stock assessments could aid in sustainable fisheries of these and other exploited elasmobranchs in South Africa.

2. Materials and methods

2.1. Sampling and molecular analyses

Fin clip or muscle tissue was sampled from a total of 229 samples of adult *M. mustelus* and *G. galeus* according to protocols and