



Global Population Genetic Structure and Parentage Analysis of the Bull Shark (*Carcharhinus leucas*)



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Project Synopsis: The bull shark (*Carcharhinus leucas*) is a globally distributed, large coastal shark that occurs in marine, estuarine and freshwater habitats. It has been assessed as near threatened by the IUCN, is caught in recreational and commercial fisheries throughout its range, and shows evidence of recent declines in the Gulf of Mexico. Regional population studies have reported mitochondrial but not nuclear differentiation between the western North and South Atlantic (Karl *et al.*, 2011) and among juvenile *C. leucas* sampled in river systems across northern Australia (Tillett *et al.*, 2012). We expanded on these studies by evaluating the global population genetic structure of *C. leucas* using 12, bi-parentally inherited, nuclear microsatellite loci and a globally distributed set of 470 samples. Our microsatellite data revealed strong genetic differentiation between samples from the western North Atlantic (WNA) and Indo-Pacific (I-P). No population structuring was detected within WNA and Indian Ocean sampling sites. Notably, however, samples from Fiji demonstrated statistically significant genetic structuring from the remaining locations sampled. Assignment testing (GeneClass2) showed evidence of a low-level of first generation migrants from the WNA and western Pacific among the southwest Indian Ocean samples, a surprising finding considering the strongly coastal nature of *C. leucas*. Finally, parentage analysis of 2 litters suggests that the species may be genetically polyandrous, although this hypothesis will need further testing with more litters.

Research Objectives:

- Delineate the global genetic population structure of *Carcharhinus leucas*
- Assess contemporary levels of migration
- Investigate bull shark mating systems

Methods:

- 12 Nuclear Microsatellite Loci
- Statistical Tools: Geneclass 2.0, Genemapper, Genepop 4.0, Gerud2, STRUCTURE 2.3.3

Carcharhinus leucas Distribution and Sample Sizes (total $n = 470$)

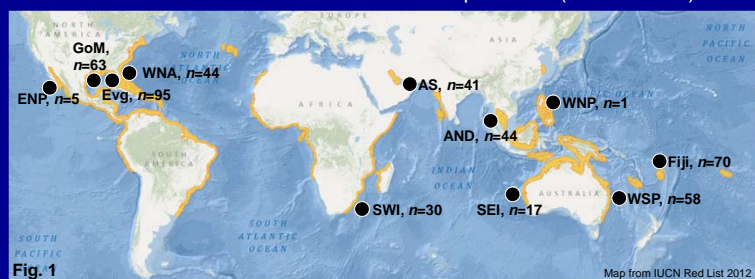


Fig. 1. Species global distribution indicated in gold shading. Sampling locations with fewer than 10 samples were not included in the population-based differentiation statistical analyses (Fig. 2) but were included in the individual-based analyses (Figs. 3 & 4).

Results: Individual-Based Population Subdivision

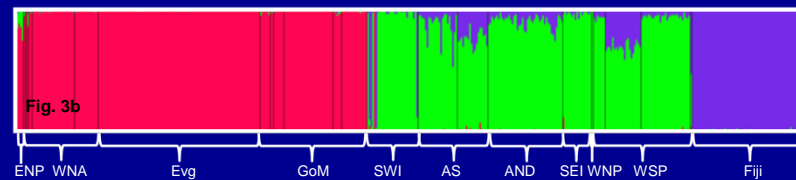
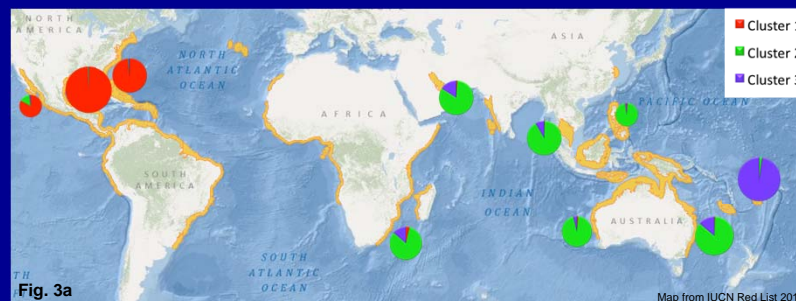


Fig. 3. In Fig. 3a, pie charts indicate the average proportional membership coefficient of individuals in the 3 distinct lineages inferred from nuclear microsatellite genotypes by the program STRUCTURE. Pie chart sizes are roughly proportional to sample sizes. Fig. 3b depicts assignment of individual sharks to each lineage in a conventional bar plot.

Results: Parentage Analysis

	# pups	Minimum fathers
Litter 1 (GoM)	12	3
Litter 2 (WNA)	12	3

Conclusions:

- Individual and population level analyses are concordant in showing at least 3 genetically distinct populations:
 - Western North Atlantic
 - Indo-Australia
 - Fiji
- Three 1st generation migrants were identified, indicating contemporary movement from both the Atlantic and Pacific oceans into the Indian Ocean.
- Complex patterns of migration and population structure require coordinated regional management efforts.
- Parentage analyses of 2 litters revealed multiple paternity in both litters.

Results: Population-Level Genetic Differentiation (F_{ST})

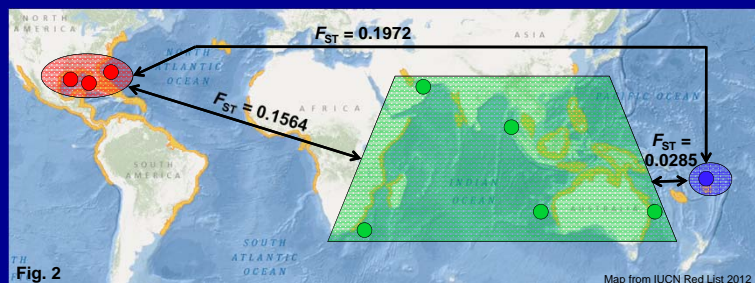


Fig. 2. *Carcharhinus leucas* genetic differentiation based on population-level statistical analyses. Colored shapes (ovals and square) represent genetically distinct populations. F_{ST} values ($p < 0.0000$) between each population pair are indicated by arrows. Sampling locations (indicated by circles) within each population are not genetically differentiated ($p > 0.05$).

Results: First Generation Migrants

Fig. 4. GeneClass2 identified 3 first generation migrants in the Southwest Indian Ocean, all sampled as adults ($p < 0.01$ and $L_h > 3.0$).



Samples kindly provided by:

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