**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, Genopop 4.0, Gerud2, STRUCTURE 2.3.3

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

**Results: Individual-Based Population Subdivision**

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

**Results: Parentage Analysis**

**Conclusions:**
- Individual and population level analyses are concordant in showing at least 3 genetically distinct populations:
  - Western North Atlantic (WNA)
  - Indo-Pacific (I-P)
  - 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.

Samples kindly provided by: