



The Side-Effects of Fisheries Induced Bottlenecks: Gauging Extinction Risk from the Genome of *Carcharhinus melanopterus*

48 months

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Motivation

This study will serve as a model for the application of genomics in the conservation biology in marine ecosystems. We will provide a profound resource for understanding how wild marine predators respond to the negative anthropogenic effects of overfishing and climate change; a concern facing many fisheries on a circumglobal scale. One highly innovative aspect of this proposal is to design functional markers for inbreeding risk that can be applied by sampling water from the reef, in the form of species-specific eDNA analysis. Such analyses can provide routine, cheap, completely non-invasive assessment of critical population parameters (e.g. local effective population size) and occurrence of deleterious variation for species monitoring.

Aims and Objectives

1. Infer the recent inbreeding history of *C. melanopterus* throughout the Maldivian archipelago
2. Determine the presence of functional detrimental variants and connect them to the phenotypic data obtained from observations in the wild
3. Characterize the functional genomic basis for inbreeding risk, specifically directed towards deleterious alleles that impact the survival of the juvenile individuals
4. To create non-invasive tools to monitor inbreeding risk in wild populations of *C. melanopterus*

Method

Traditionally, species and populations monitoring requires exhaustive sampling and tracking over extended periods of time. These sampling and tracking techniques usually require species and habitat specific approaches that are time consuming and expensive. For marine species in particular, tracking and sampling requires even more specific skills, and many of the monitoring techniques developed for iconic terrestrial species, usually large mammals and birds, can not be easily applied underwater. Conversely, recent advancements in genomics technology has allowed for functional and population genomics insights with a fraction of the individuals required for species and population monitoring. Moreover, the genomics tools can be applied to any species. To further understand the disorder, the disease phenotype will be characterized through photographs and acoustic tracking data during field-based surveys. Acoustic tracks are highly complementary to genomics as it provides key details of fine-scale movements between islands. This will allow for a simpler elucidation of the trends surrounding connectivity between these reef sharks populations like mediation of gene flow and population differentiation. These spatial components can strongly influence the genomic subdivisions between islands. Ultimately, long-term monitoring will be the primary vector for conservation management. We propose for an environmental DNA (eDNA) based field test to be developed to non-invasively track the presence of deleterious alleles.

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