

Reefshark Genomescapes:

Overfishing has severely depleted marine populations worldwide, including within protected areas. Illegal and unreported fishing are major contributors to this decline. Large-bodied apex predators such as sharks are among the most affected, with overfishing driving dramatic species declines and ecosystem destabilization through trophic downgrading. Key barriers to effective marine conservation and management include: data deficiencies that hinder population benchmarks and impact assessments; limited surveillance, which allows illegal fisheries to disproportionately target apex predators; and insufficient capacity in vulnerable nations to monitor and protect species within their waters.

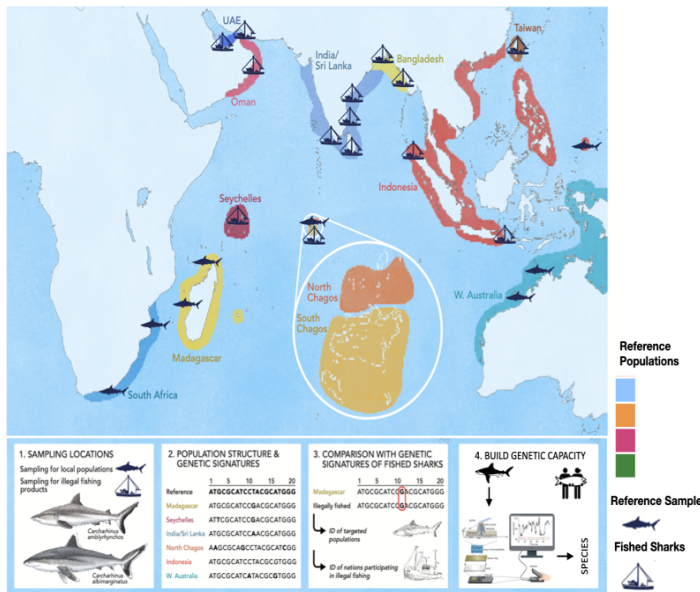
Our study, led by **Shaili Johri** in collaboration with colleagues, communities, and institutions across 12+ countries, addresses these challenges through a novel genomic framework that enables assessment of shark population diversity and health while also improving fisheries traceability by detecting instances of illegal fishing across the Indian and Pacific Oceans. We present the **Reefshark Genomescape**, the first genome-wide reference database for Indo-Pacific reef sharks, which provides an assessment of genetic diversity, structure, and connectivity of two key species across their Indo-Pacific range and allows geographic assignment of fished individuals using population-specific genetic signatures.

We show that **grey reef shark (*Carcharhinus amblyrhynchos*)** populations exhibit high genetic diversity, strong population structure, and elevated F_{st} values, with previously unknown connectivity between the central and western Indian Ocean and clear isolation of populations in the Andaman Sea. In contrast, **silvertip sharks (*Carcharhinus albimarginatus*)** display high connectivity but show genomic signals of declining population health, supporting a reassessment of their IUCN status. Using supervised machine learning with Monte Carlo cross-validation, we assigned geographic origins to fished grey reef sharks with **96% accuracy**.

These findings provide critical insights into the population structure, connectivity, and health of two ecologically important reef shark species, while establishing a robust method for assigning geographic origin. We anticipate this framework will support regional conservation assessments and targeted management. Moreover, by enabling the identification of fishing hotspots and detection of IUU fishing, it lays the groundwork for a broader traceability system in marine ecosystems. Much like the landmark elephant ivory tracing study, this approach has the potential to transform marine conservation globally.

 **Preprint:** <https://doi.org/10.1101/2025.09.22.676358>

Preprint of Manuscript in review: <http://dx.doi.org/10.2139/ssrn.5387526>



Graphical Abstract:

We developed the Reefshark Genomescape, a genomic framework for assessing shark population health and fisheries traceability across the Indo-Pacific. Genome-wide data from grey reef and silvertip sharks revealed contrasting patterns, unexpected connectivity, and genomic signals of decline. Geographic assignment of fished individuals reached 96% accuracy, enabling detection of illegal fishing and identification of hotspots. This framework strengthens regional management, supports IUCN reassessments, and lays the foundation for global marine traceability systems.

This project also catalyzed several interconnected initiatives:

In collaboration with **Lankika Anjani, Daniel Fernando, and Akshay Tanna at Blue Resources Trust, Johri** extended efforts to **Sri Lanka**, a critical hub for shark fishing and trade, where the demand for shark and ray products such as meat, gill plates, and fins continues to escalate. Many of these species are subject to legal restrictions under IUCN and CITES listings, yet effective regulation is hampered by the difficulty of visually identifying body parts, fins, and gill plates in trade. To address this, we established a **DNA reference library** focusing on species found in Sri Lankan waters. Constructed from 150 samples spanning 50 shark and ray species (with three replicates per species), the library captures the region's unique genetic diversity, with particular emphasis on species commonly caught in Sri Lanka. This resource mitigates the risk of misidentification and now serves as a robust tool for species identification at export points, strengthening CITES trade enforcement and enhancing species-level trade data analysis.

Preprint of Manuscript in review: <https://doi.org/10.1101/2025.06.03.657733>

Similar work in **Bangladesh** has generated key insights into the demographics and species composition of the country's prolific shark and ray fisheries. This work, led by **Fahmida Khalique Nitu** with mentorship from Johri and in collaboration with **Dilshad Farahnaz Tasnim, Sultan Ahmed, and Md Kutub Uddin**, has produced a manuscript now available as a preprint.

Preprint of Manuscript in review: <https://doi.org/10.1101/2025.06.26.660850>

In the Chagos Archipelago, mitochondrial DNA analyses led by Nishad Jayasundara (Duke University) in collaboration with Johri (Stanford) revealed variable mutation rates among grey reef shark populations across the archipelago, whereas silvertip sharks exhibited uniformly low and homogeneous mutation rates.

In collaboration with **Dhir DeRay (Georgia Tech University)**, Shaili co-developed an **Artificial Intelligence tool** capable of identifying 30+ shark and ray species with 93% precision. With further development, this tool has the potential to assess the conservation status of sharks and rays across the Indian Ocean, including critically endangered species, enabling timely and targeted conservation actions.

Finally, working with researchers at the **University of Miami Rosenstiel School of Marine, Atmospheric, and Earth Science**, we pioneered innovative remote biodiversity monitoring methods, including fluid lensing-assisted drones and low-cost underwater cameras, which have expanded survey capacity in developing countries. These advances have uncovered previously unknown biodiversity hotspots, enabling rapid and effective protection measures in regions where conservation action is most urgently needed.

Manuscript in review: *Automated Motile Marine Wildlife Detection in Coral Reefs using Airborne Fluid Lensing.*

Manuscripts currently in review and revision from this work include:

- *Mapping Risk and Resilience Across Indo-Pacific Reefs with Shark Genomes* — bioRxiv (2025.09.22.676358)
- *First Chromosome-Scale Reference Genomes of Carcharhinid Sharks Reveal Low Genetic Diversity and Ancient Bottlenecks* — SSRN (5387526, 2025)
- *Establishing a DNA Reference Library for Elasmobranchs in the Indian Ocean* — bioRxiv (2025.06.03.657733)
- *Unveiling the Diversity and Demography of Sharks and Rays in Bangladesh* — bioRxiv (2025.06.26.660850)
- *Automated Motile Marine Wildlife Detection in Coral Reefs using Airborne Fluid Lensing.*

Broader Impacts:

Together, these efforts establish a scalable, interdisciplinary framework for shark and ray conservation — uniting genomics, AI, and remote monitoring to strengthen fisheries traceability, support international trade enforcement, and expand conservation capacity in vulnerable nations. By bridging fundamental science with applied tools, this work provides a model for protecting apex predators and the ecosystems they sustain across the Indo-Pacific and beyond