

Genetic population structure and misidentification reveal the need for regionally informed management of manta and devil rays

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IATTC EBWG 2026

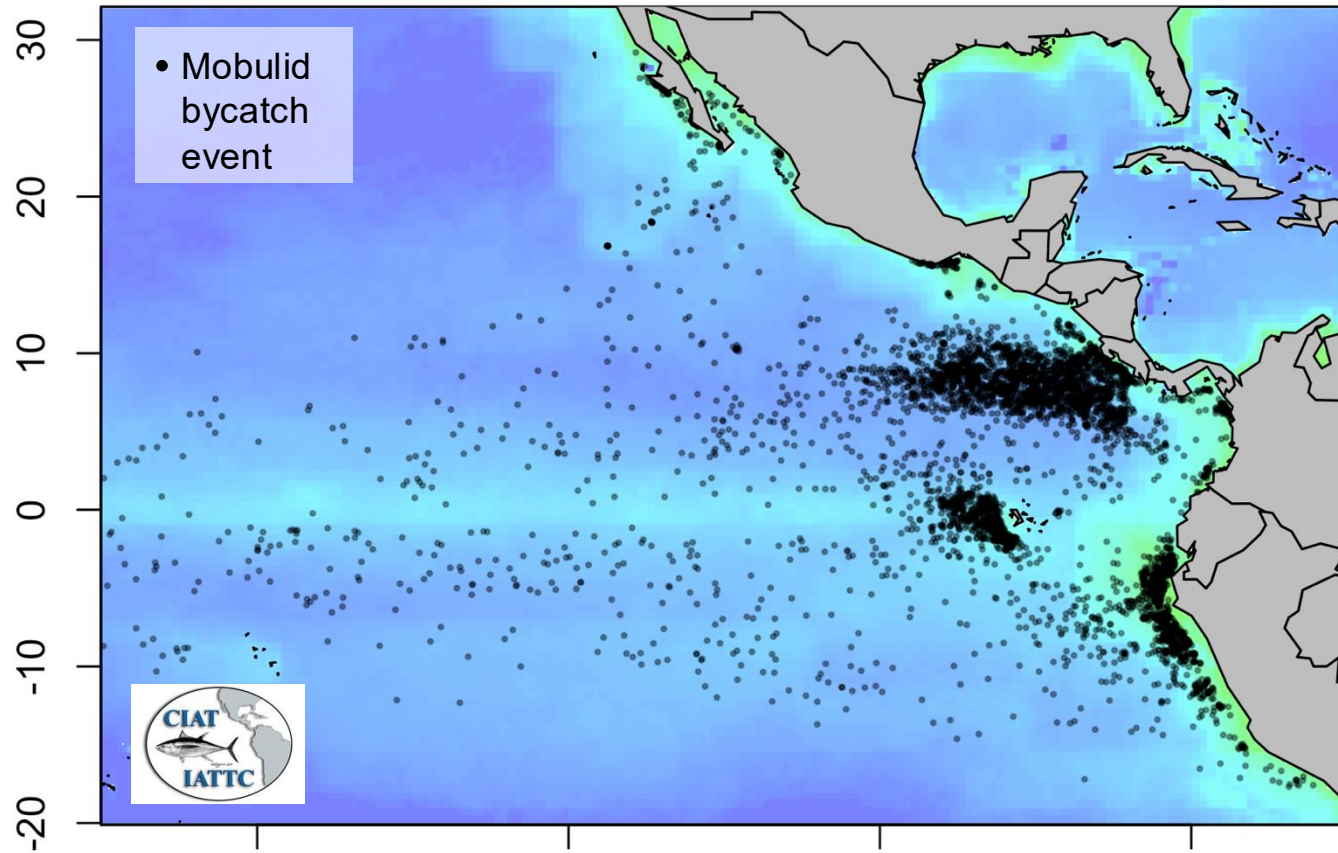


Mobulid (manta and devil ray) life history characteristics

- Late maturation
- Low fecundity
 - 1 pup every 1-2 years
- Very low intrinsic growth rate



Species-specific bycatch rates of mobulids unclear



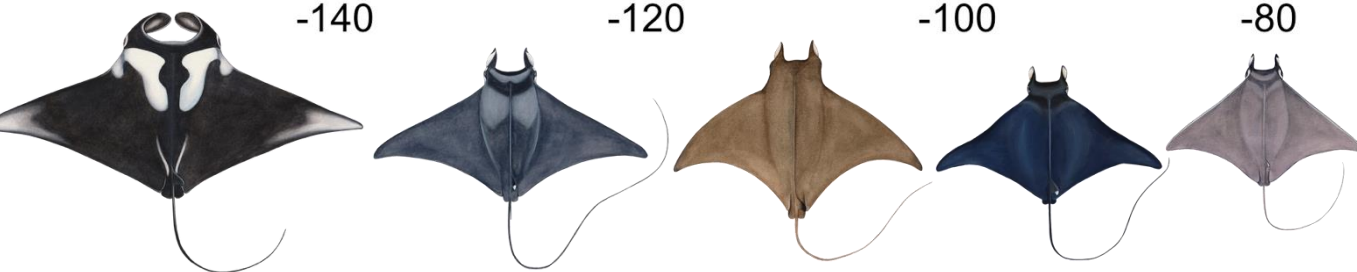
- Different species appear morphologically similar
- **Mortality strongly varies between species** (Stewart et al. 2024)
 - 20-74% post-release survival depending on species

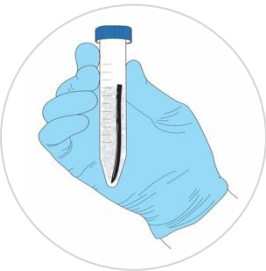
Questions:

1) Which species are caught, and how accurate is species identification?

2) What is genetic population structure?

- Identify correct scale of management





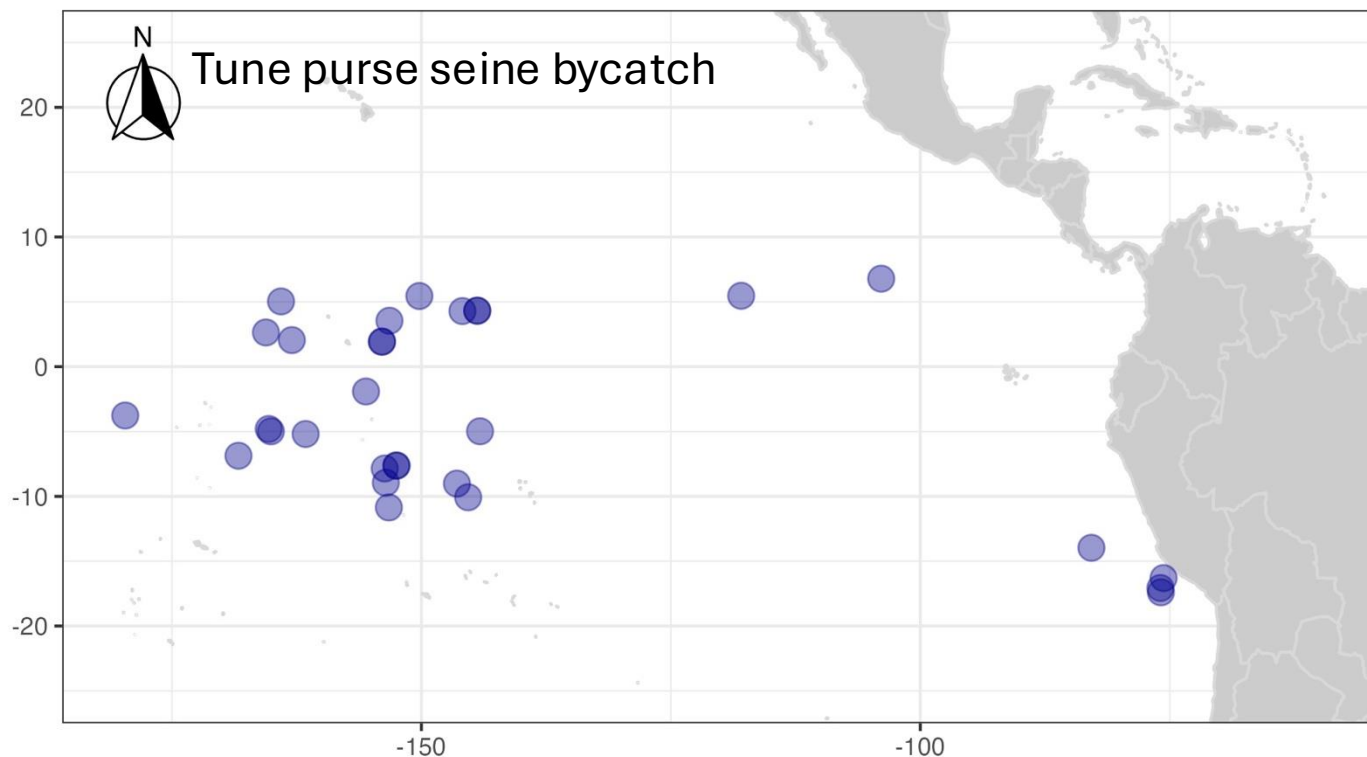
Methods: Genetic tissue sample collection

- Collaborative sampling with IATTC, fisheries from:



- target fisheries
- existing collections
- tuna purse seine bycatch (collected by observers)

- Regional intra- and interspecies comparison within EPO and with outgroup in Indian Ocean





Methods: Restriction-site Associated DNA (RAD) Sequencing

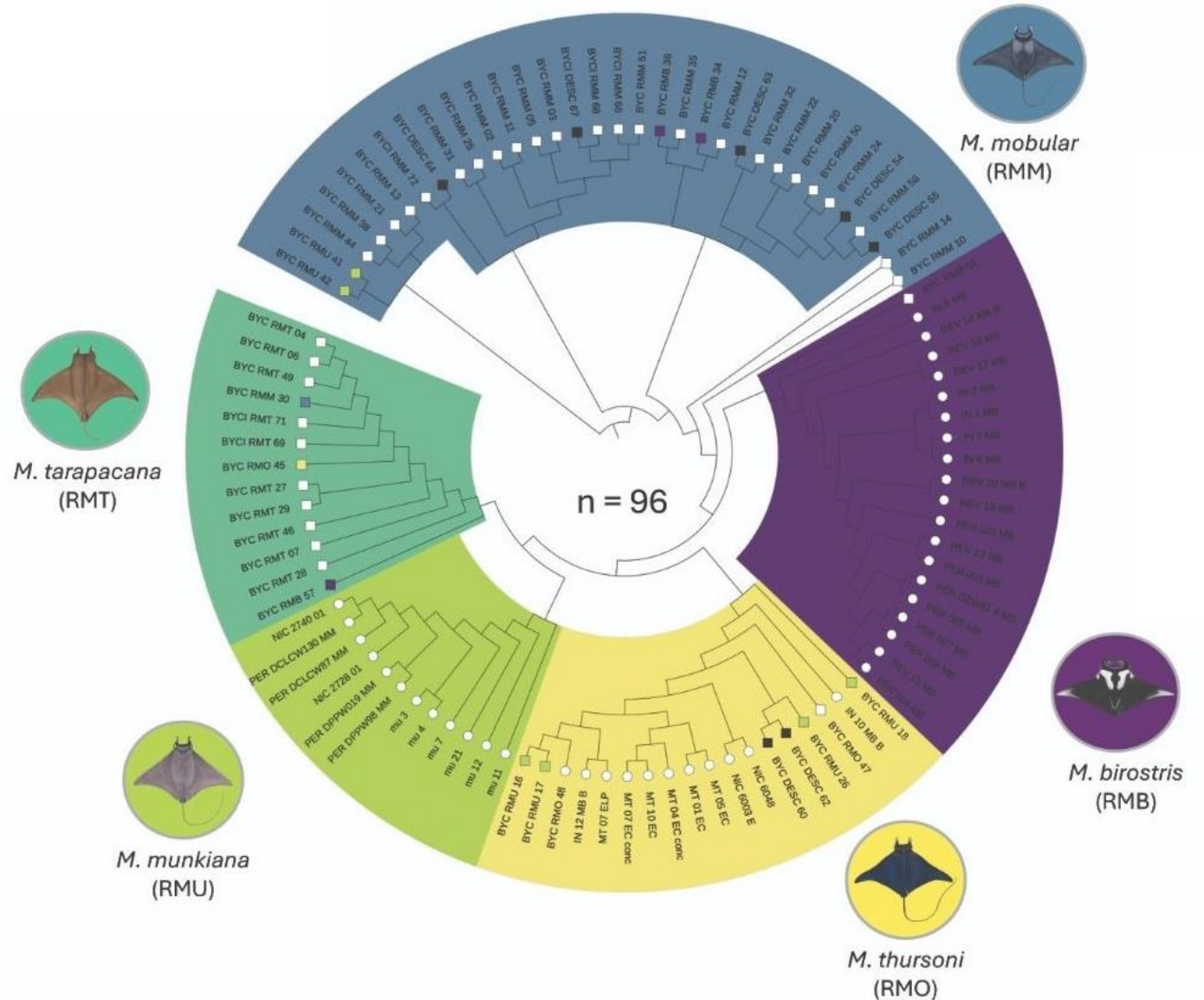
- Sequencing with Illumina HiSeq platform
- Single-nucleotide polymorphism (SNP) discovery and filtering using *STACKS*; *populations* pipeline
- *STRUCTURE* Bayesian clustering analysis
- Identify outlier loci under selection (using *pcadapt*)
- Bioinformatics, genomic statistics using *genodive*





Phylogenetic tree of samples included in this study

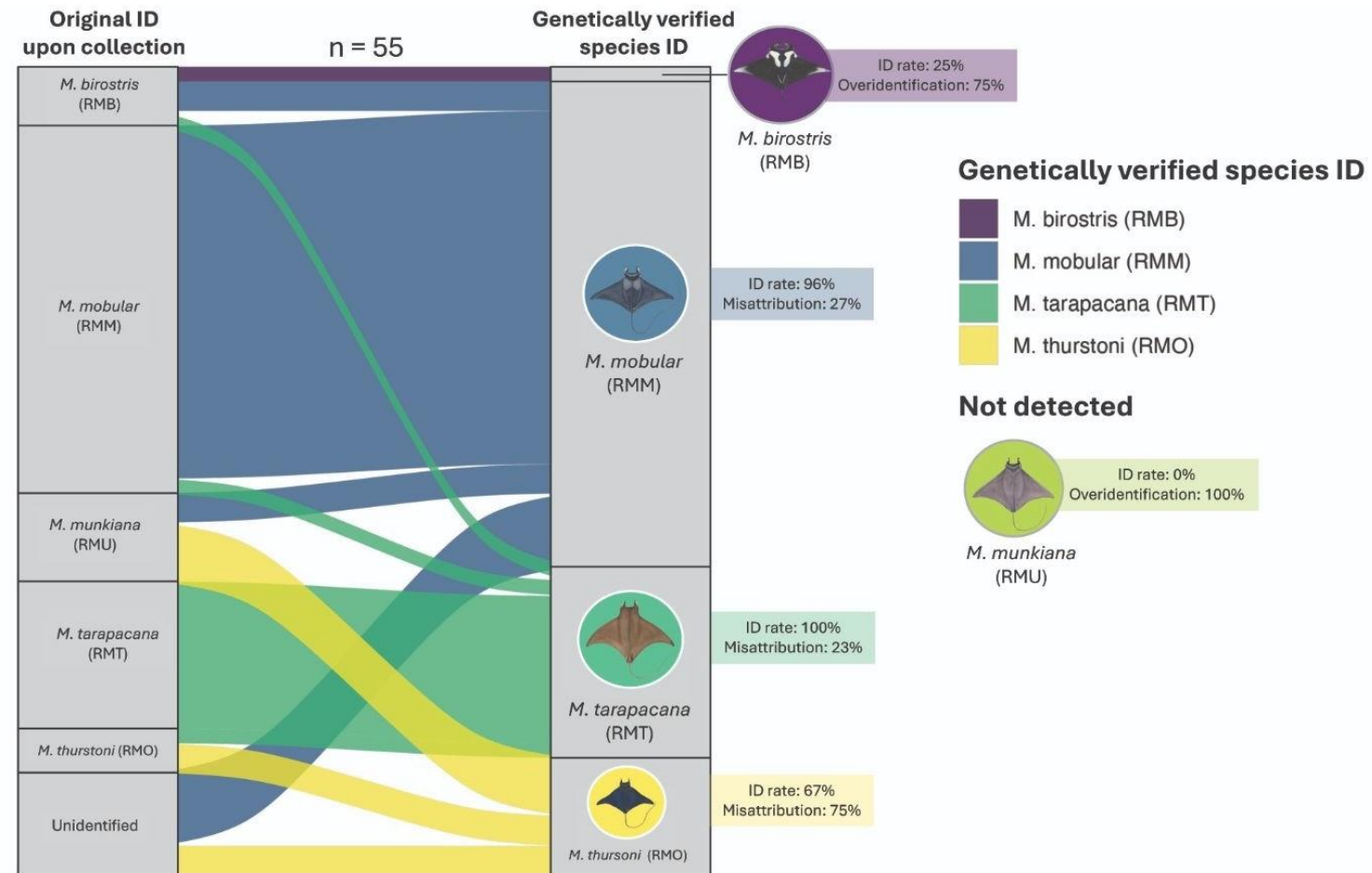
- 96 samples from 5 species usable after filtering for degraded DNA and low coverage samples
- 55 of these samples were from EPO tuna purse seine bycatch





~One third of mobulids caught in PS fisheries were not correctly identified

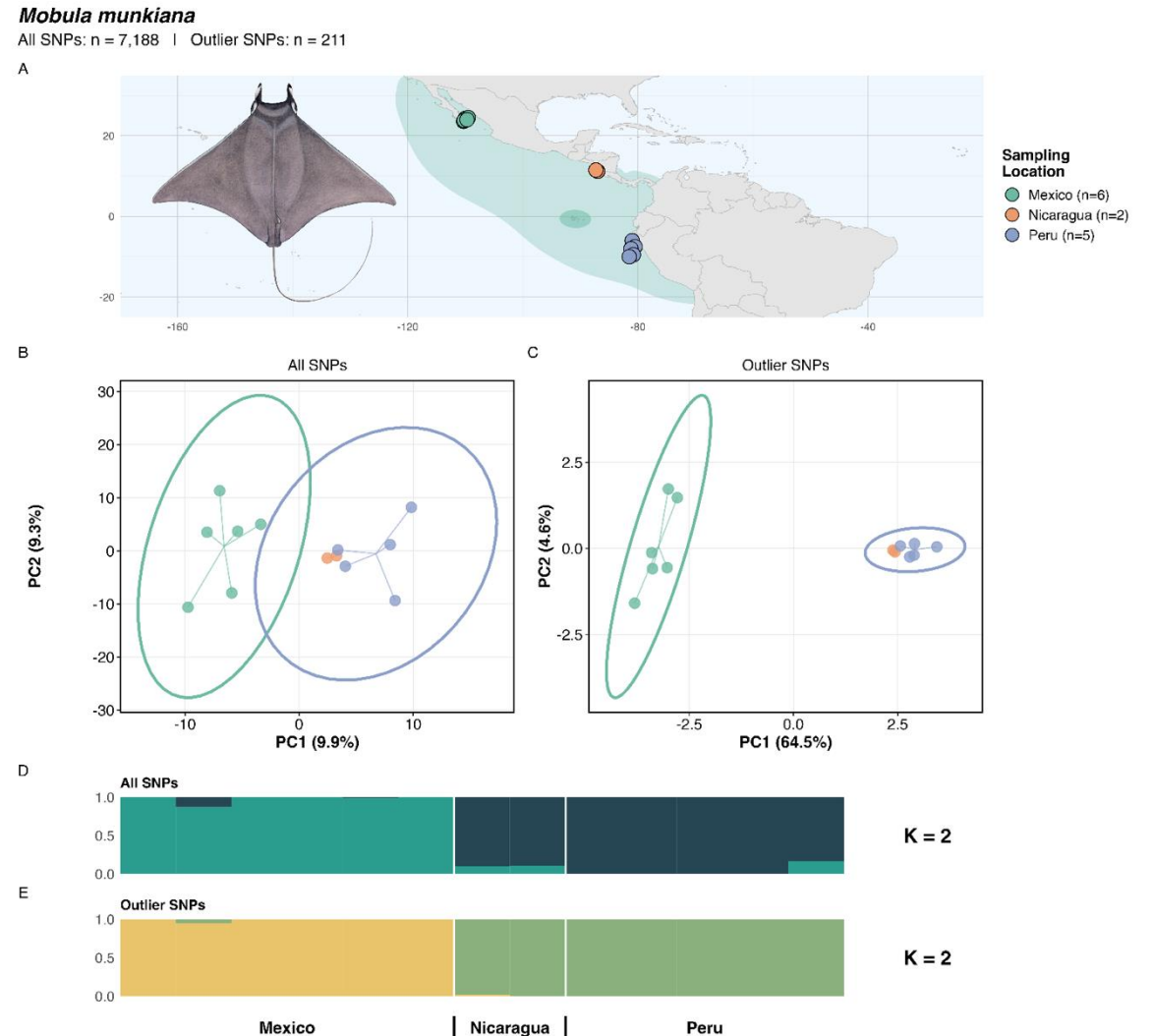
- Giant oceanic manta (*M. birostris*) and Munk's devil ray were over-identified
- Continued observer training is needed to distinguish mobulids species






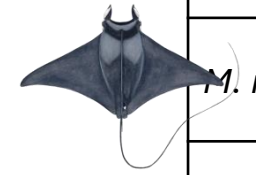
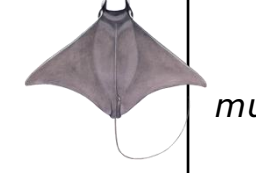
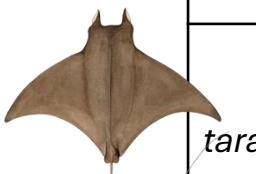
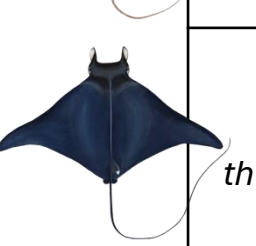
Population structure varies among mobulid species

- All-loci analyses suggest **high connectivity** ($F_{ST} = 0.0010-0.0115$)
- Outlier loci show **geographically mediated population structure**
- **Strongest signal: *M. munkiana***, with Mexico distinct from Nicaragua-Peru
 - Outlier $F_{ST} = 0.3712$
- Weaker outlier structure:
 - *M. birostris* outlier $F_{ST} = 0.1503$;
 - *M. tarapacana* outlier $F_{ST} = 0.1018$
- Very weak outlier structure
 - *M. mobular* outlier $F_{ST} = 0.0497$
 - *M. thurstoni* outlier $F_{ST} = 0.0195$





Selection occurs at some level for all species

| | Species | N | SNPs | Outlier loci | Population structure | Research needs |
|---|----------------------|----|--------|--------------|--|---|
|  | <i>M. birostris</i> | 22 | 12,045 | 165 | Weak structure from all loci ; India distinct from eastern Pacific | Increase sampling to western/central Pacific and Indian Ocean, to test basin-scale structure or sampling gaps. |
|  | <i>M. mobular</i> | 33 | 51,936 | 1,003 | Weak structure | Expand sampling to western and central Pacific |
|  | <i>M. munkiana</i> | 13 | 7,188 | 211 | Clear structure from all loci ; Mexico distinct from Nicaragua-Peru | Add intermediate eastern Pacific sites to clarify the geographic boundary between northern and southern populations |
|  | <i>M. tarapacana</i> | 13 | 43,738 | 1,922 | Weak structure but geographically unresolved | Add more evenly distributed samples across regions |
|  | <i>M. thurstoni</i> | 28 | 1,191 | 41 | Weak structure from outlier loci ; possibly influenced by related individuals | Add more evenly distributed samples, improve SNP coverage and account for related individuals |



Why is population structure weak in mobulids despite selection occurring?

- **Metapopulations:** High mobility and occasional long-distance movement may maintain gene flow from structured populations
- **Slow evolution:** low mutation rate, long generation times, low fecundity, and slow growth
- **Large historical population sizes** can also retain ancestral genetic variation
 - Structure accumulates very slowly
- **Low and uneven sample sizes** may limit our ability to detect subtle structure
 - More sampling is needed to detect signal



Additional findings from genomic analyses

- Genetic diversity varies among species, should be tracked as part of long-term monitoring
- One animal (*M. tarapacana*) was caught as bycatch by a purse seine vessel two days in a row
 - Re-ran all genetic analyses to rule out lab contamination
 - Likely a vessel fishing on the same FAD



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Conservation and management implications

- Ongoing efforts to improve species identification for mobulids will improve data quality
- Mobulid post-release mortality should be considered a minimum estimate given potential for cumulative impacts
- Regional management units could preserve what diversity exists
 - More dedicated sampling is needed to delineate formal management units





Thank you!

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