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Population genetic assessments and species abundance with environmental DNA

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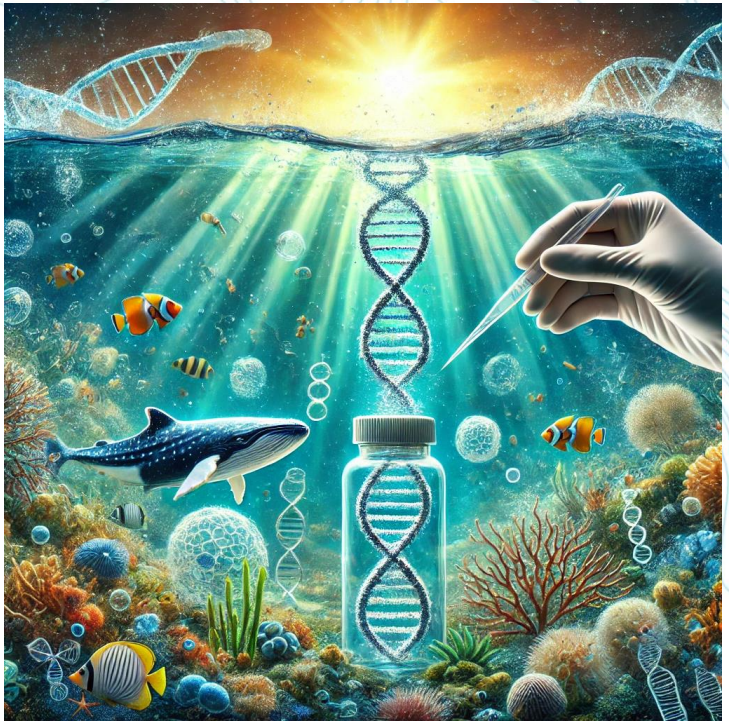
The University of Western Australia

Minderoo Foundation

Population genetics and contributor estimation from eDNA

- Population genetic studies on wildlife species can help inform appropriate conservation measures
- Environmental DNA (eDNA) has the potential to provide non-invasive, affordable and scalable toolkits to study population genetics
- Highly-polymorphic nuclear DNA markers offer higher resolution and range of insights



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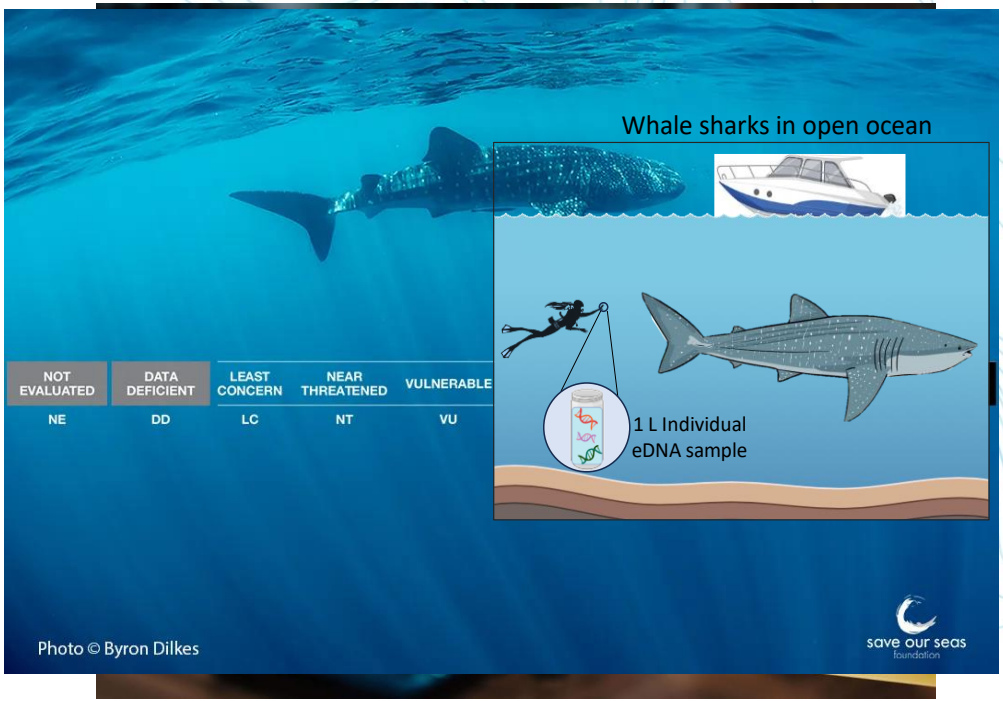
Microhaplotype Markers

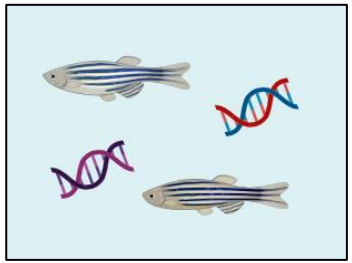
- 100 - 300 bp sequences with > 2 SNPs
- Individual detection, ancestry and lineage from mixed forensic DNA
- Ideal candidate for eDNA studies

Phase 1: Development & optimization of methodology using zebrafish in controlled aquaria

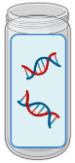
Phase 2: Field-based application towards monitoring of Endangered whale sharks at Ningaloo Reef



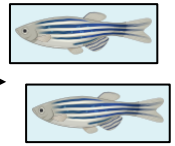
Phase 1: Developing methodology in experimental aquaria using Zebrafish



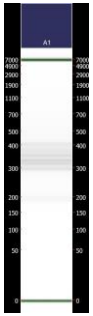
1 L water with eDNA

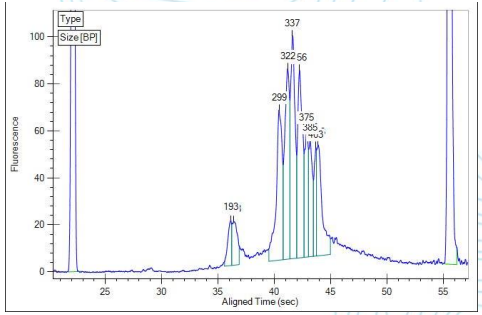


Tissue samples



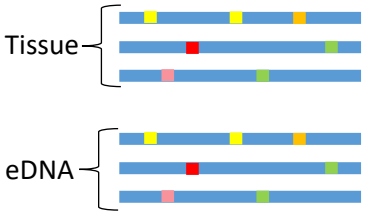
17 Microhaplotypes with 69 SNPs amplified by multiplex PCR & sequenced





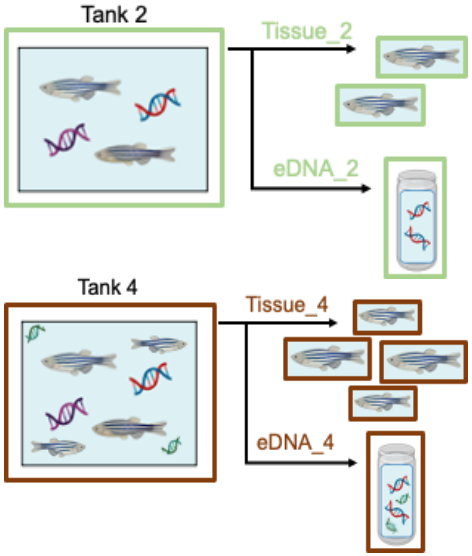
No. of individuals: 2, 4, 10, 20, 25, 50, 100, 200, 300, 411

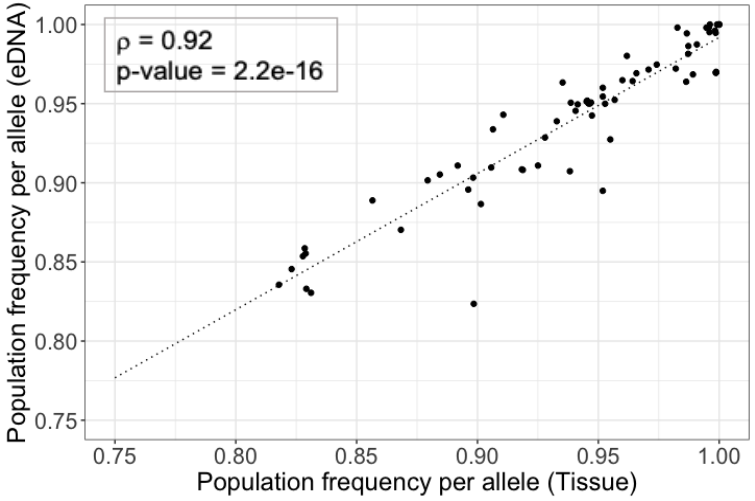
Comparing tissue Vs eDNA genotypes

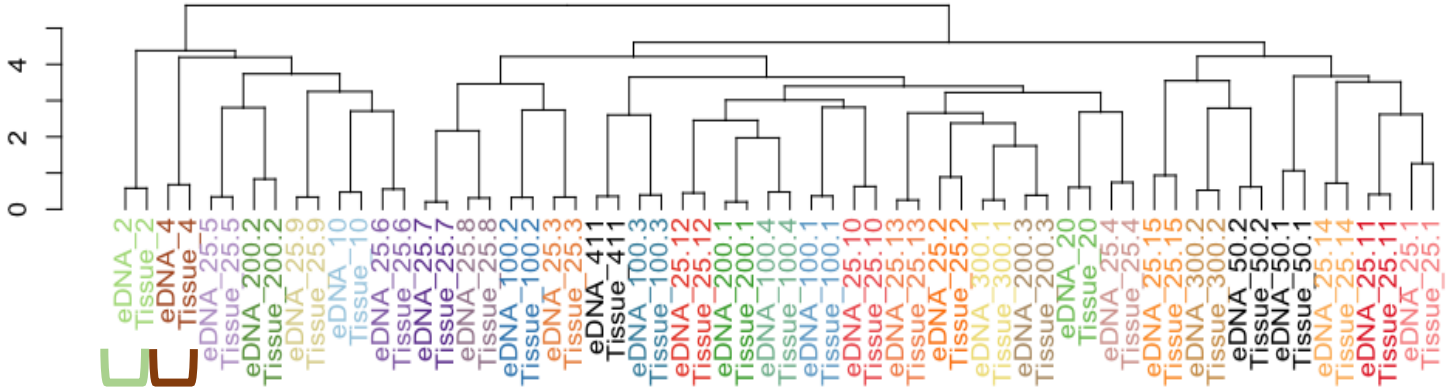


Maximum likelihood of contributor numbers

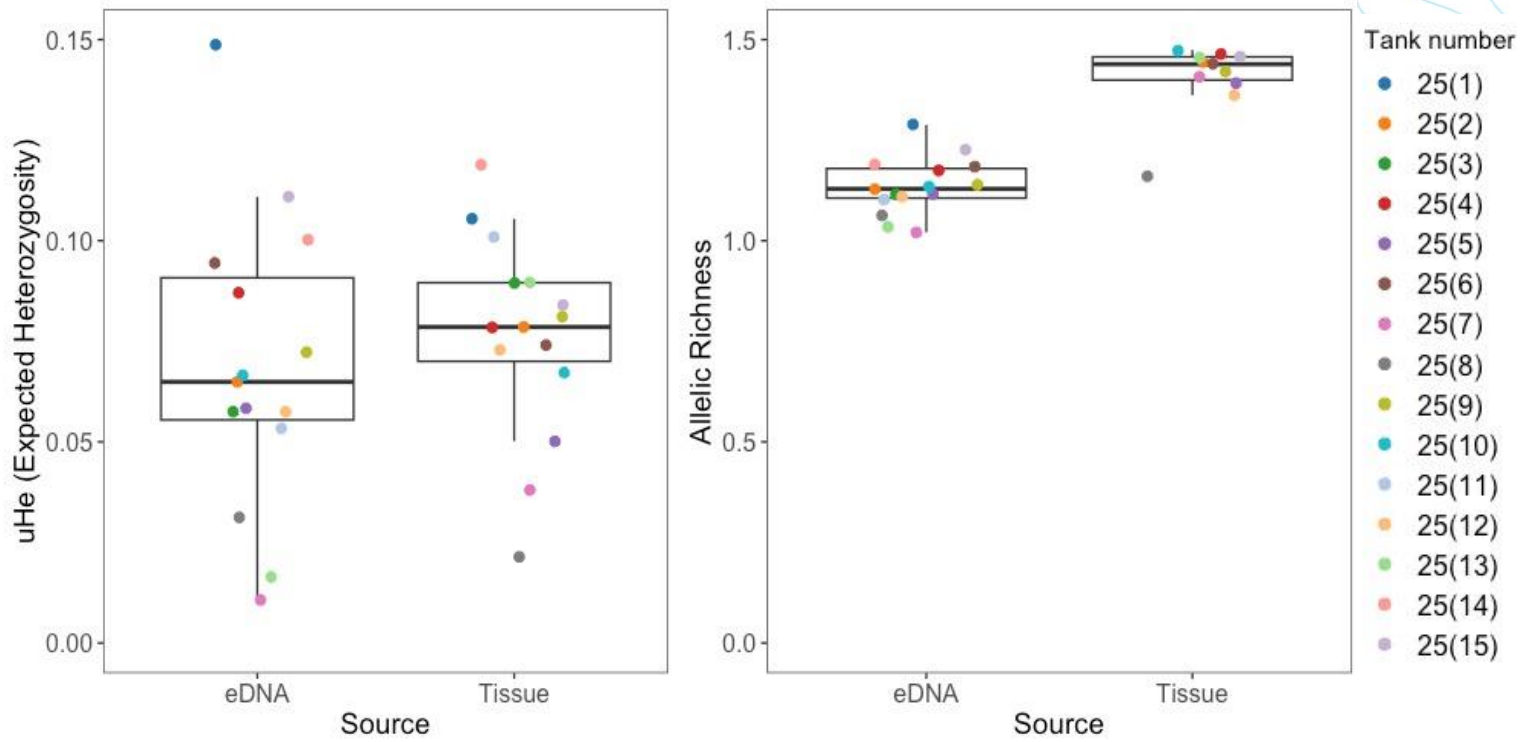
Strongly correlated allele frequencies (69 SNPs)



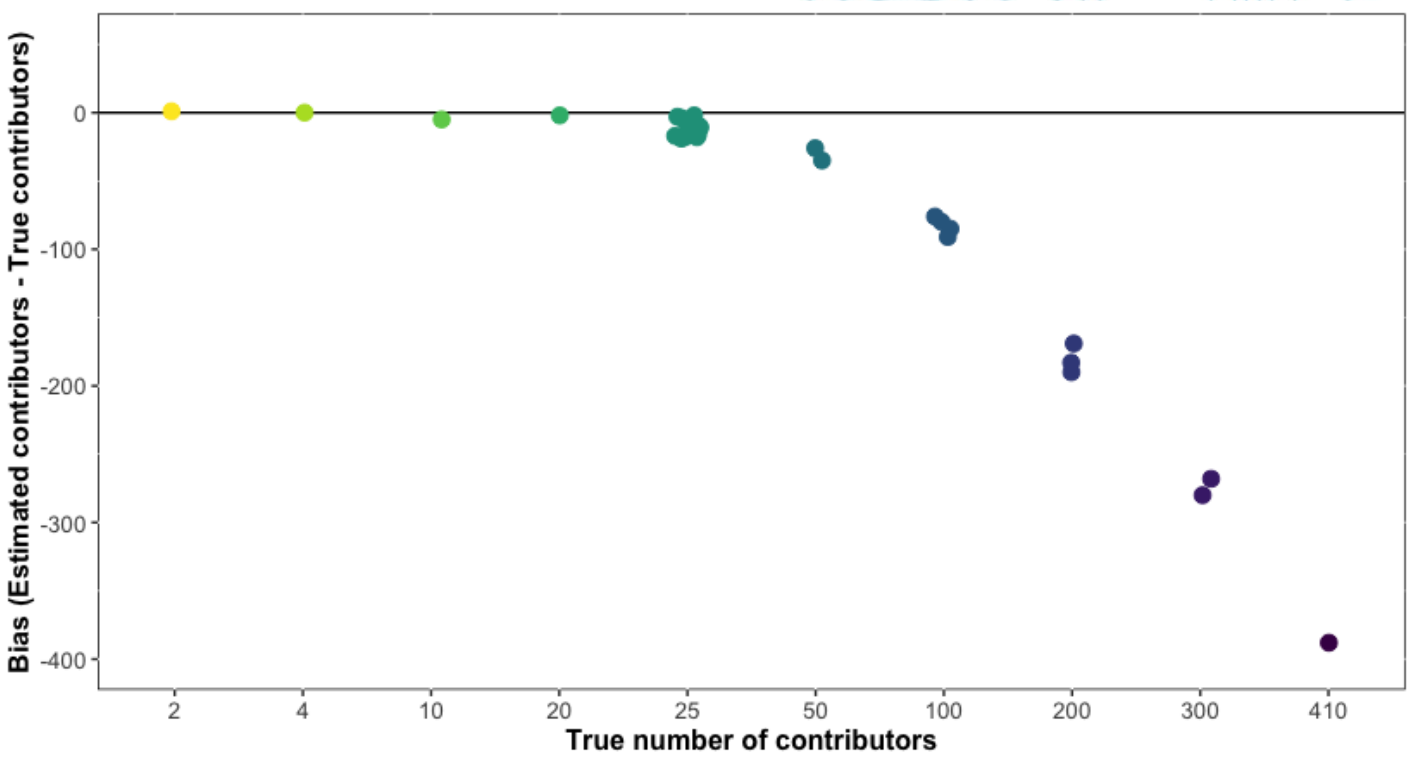




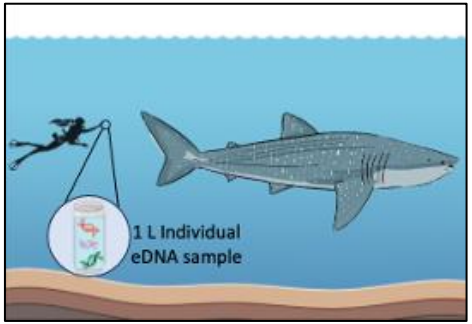
Genetic diversity estimates from tanks with 25 zebrafish



Contributor estimation from eDNA



Phase 2: Application towards monitoring whale sharks at Ningaloo Coast World Heritage Area

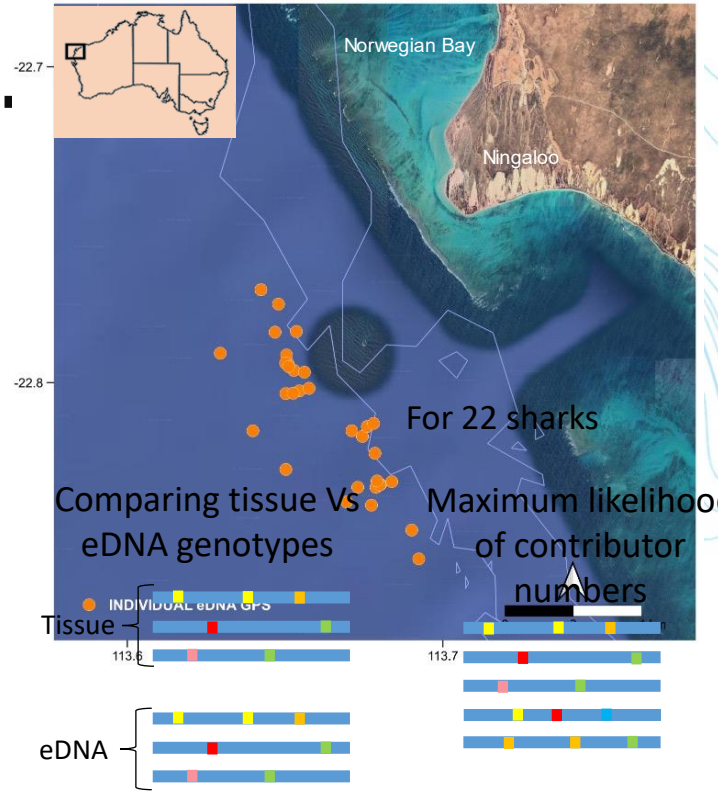


For 33 sharks

Skin biopsy tissue sample

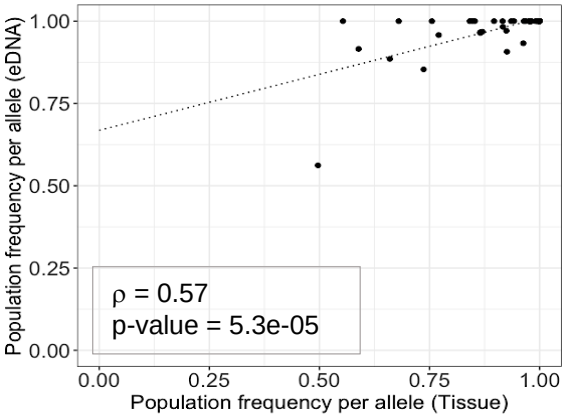
Seawater sample

20 Microhaplotypes with 56 SNPs amplified by multiplex PCR & sequenced

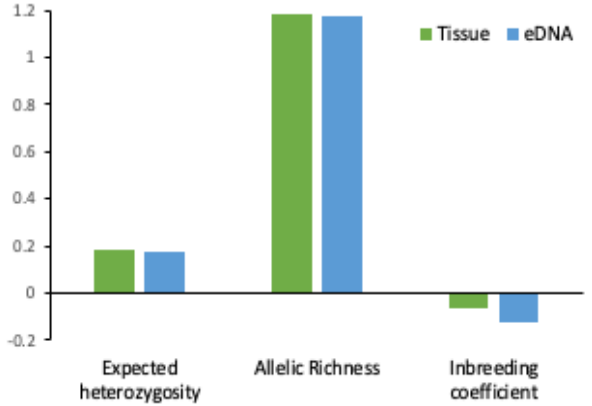


Strongly correlated allele frequencies, genotype profiles & diversity estimates

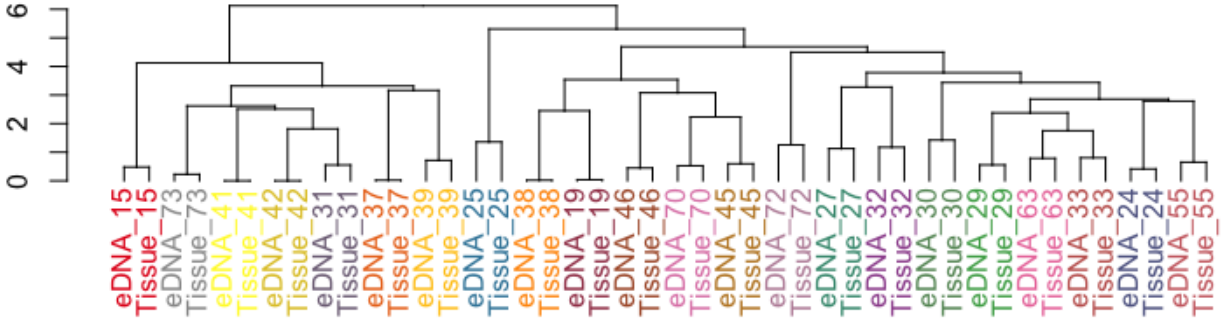
Population allele frequencies



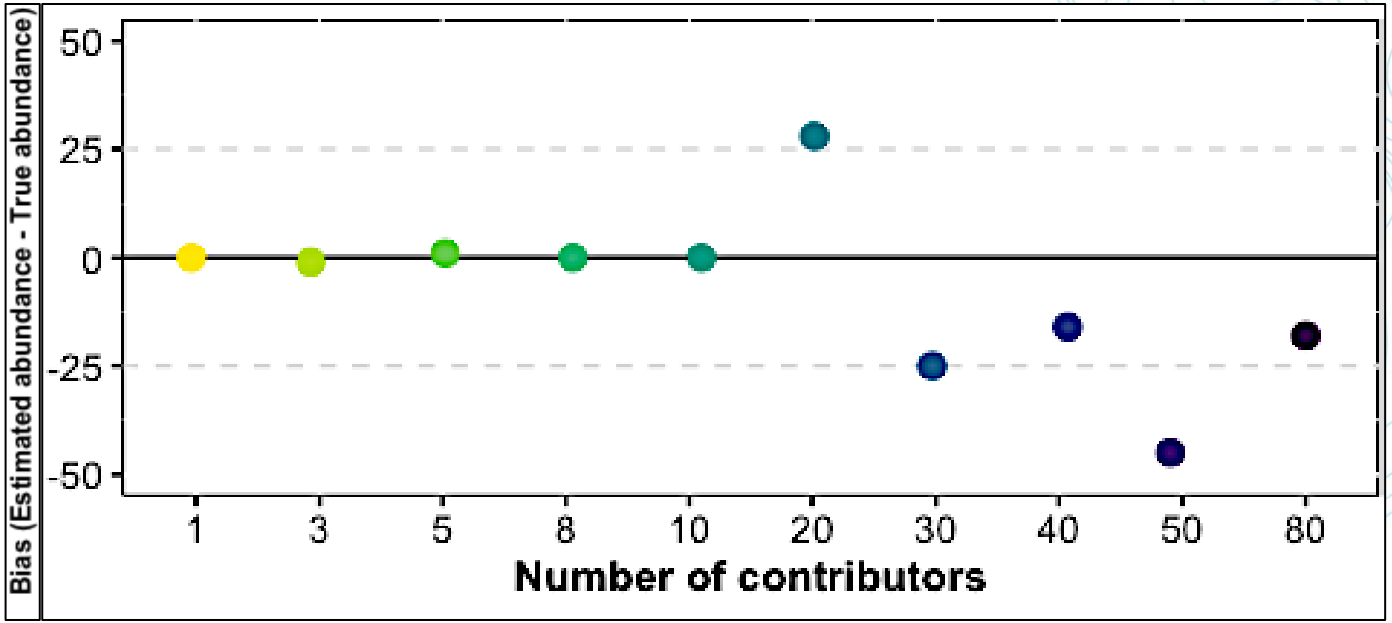
Genetic diversity estimates



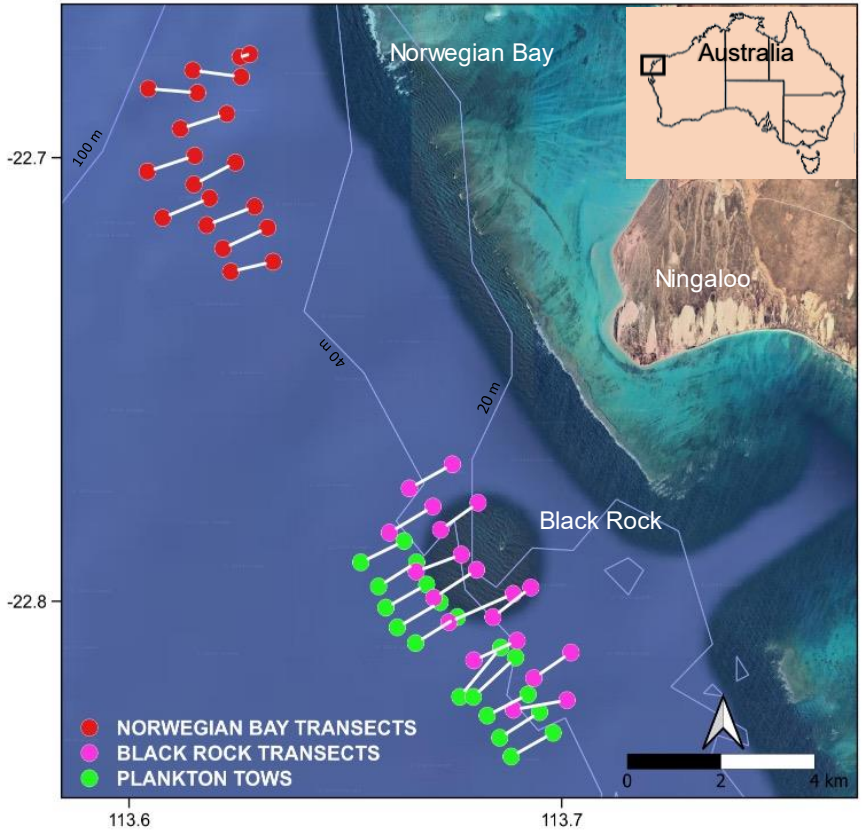
Individual genotype profiles



Contributor estimation from simulated tissue DNA mixtures



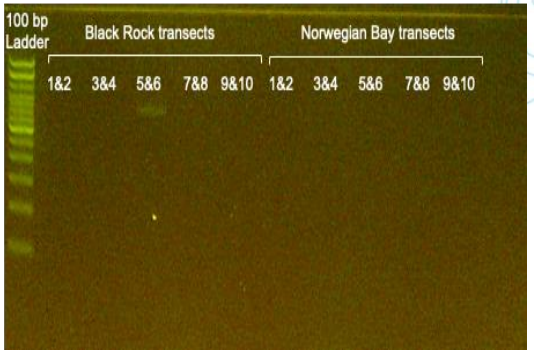
Transect sampling at the Ningaloo whale shark aggregation area



10 L water samples across transects

Plankton tows

WSCR screening on transects (Dugal et al. 2022)



Dugal, L., Thomas, L., Jensen, M. R., Sigsgaard, E. E., Simpson, T., Jarman, S., Thomsen, P. F., & Meekan, M. (2022). Individual haplotyping of whale sharks from seawater environmental DNA. *Molecular Ecology Resources*, *22*(1), 56–65.

Conclusion

- Microhaplotypes from eDNA reliably captures population genetic diversity, individual genotype profiles and abundance estimates.

- Optimizations required for increased read depth, recovery of rare alleles and informative loci in panel.

	Avg. read counts per sample	No. of SNPs recovered
eDNA	260.4 (± 223.2)	6 - 39
Tissue	9370.8 (± 802.5)	56

- This study offers a promising framework for expanding eDNA applications in genetic monitoring and application towards a broader range of aquatic species

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THANK YOU!

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Thanks to PhD supervisors:

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