

Advancing White Shark Conservation through eDNA-based Population Monitoring and Community Education

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Stanford DOERR SCHOOL OF SUSTAINABILITY
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HART LEADERSHIP PROGRAM

Introduction

Background

White sharks (*Carcharodon carcharias*) are important to the ecological stability of the northeastern Pacific, but they are **difficult to detect/quantify** because of their low density, large ecological niche, and high mobility (Merson et al.).

Environmental DNA (eDNA) is derived from cells organisms shed into their surroundings. It has the potential to:

- Supplement current surveying methods
- Provide more robust information on where white sharks tend to occur and aggregate.



Current surveying methods (acoustic tagging and visual surveys). Image credit: Block Lab, 2024

Though the current literature has identified eDNA as a non-invasive means of detecting the presence of white sharks, its use in quantifying the number of white sharks in an area remains largely unexplored (Merson et al.).

Objectives

Experimental Objectives:

- **Target** regions of the genome (200-400 bps) containing identifying information for individuals.
- **Synthesize** white shark-specific DNA primers that can code and amplify these regions during PCR.

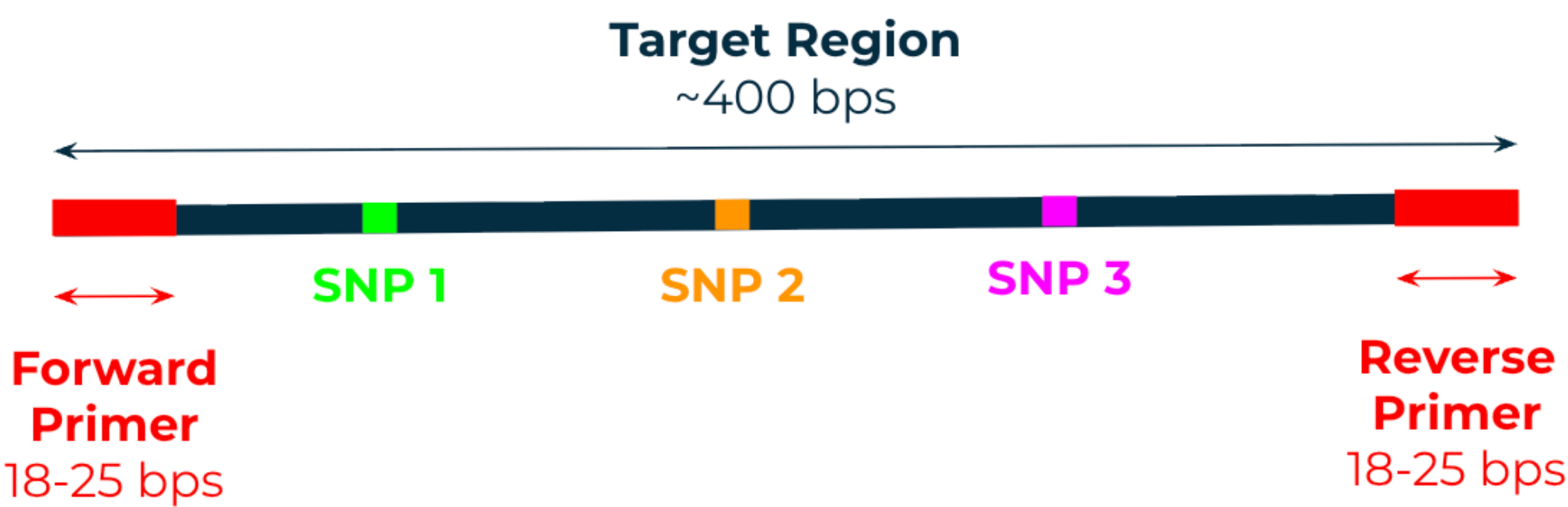
Project Objectives:

- **Support** the development of eDNA as a non-invasive means of quantifying white shark populations.
- **Engage** communities in white shark conservation via the Monterey Bay White Sharks project.

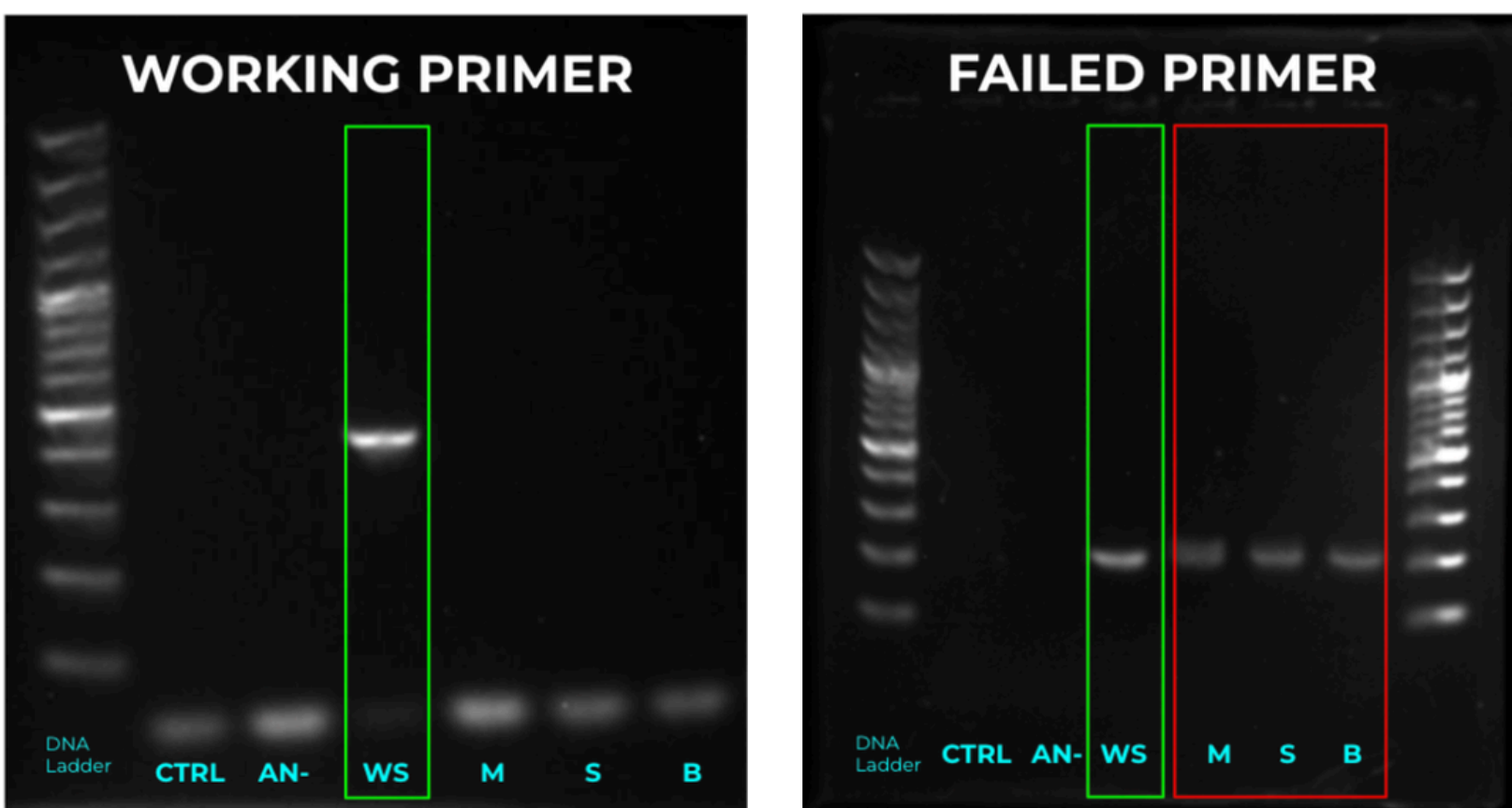
Experimental Design

Methods

Part I: Identify SNP-dense regions and generate primers on Primer-BLAST



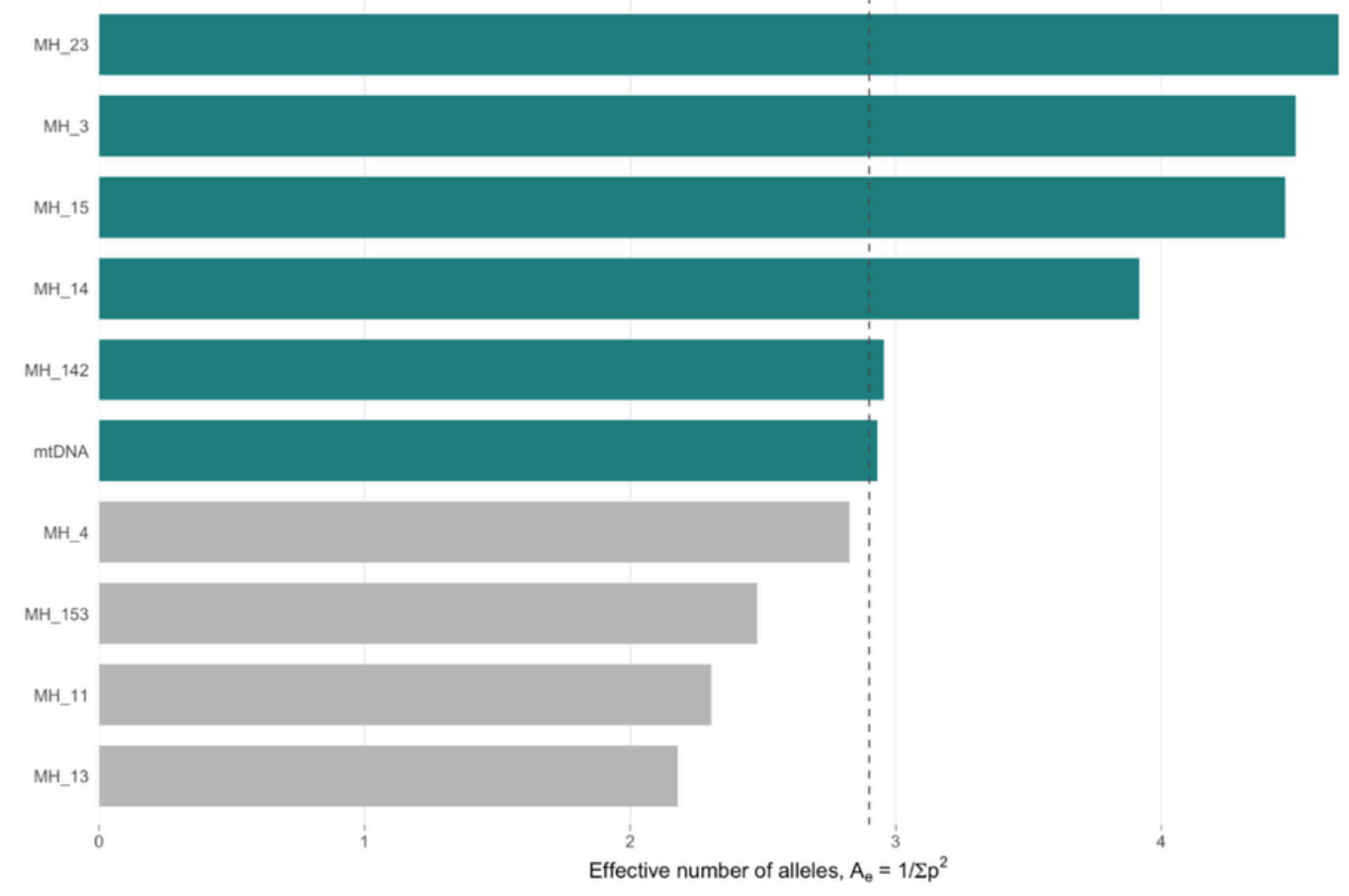
Part II: Test primer specificity to white sharks in-lab via Touchdown PCR



Results

Effective Number of Alleles (Ae)

Assessing the **quality** of each microhaplotype

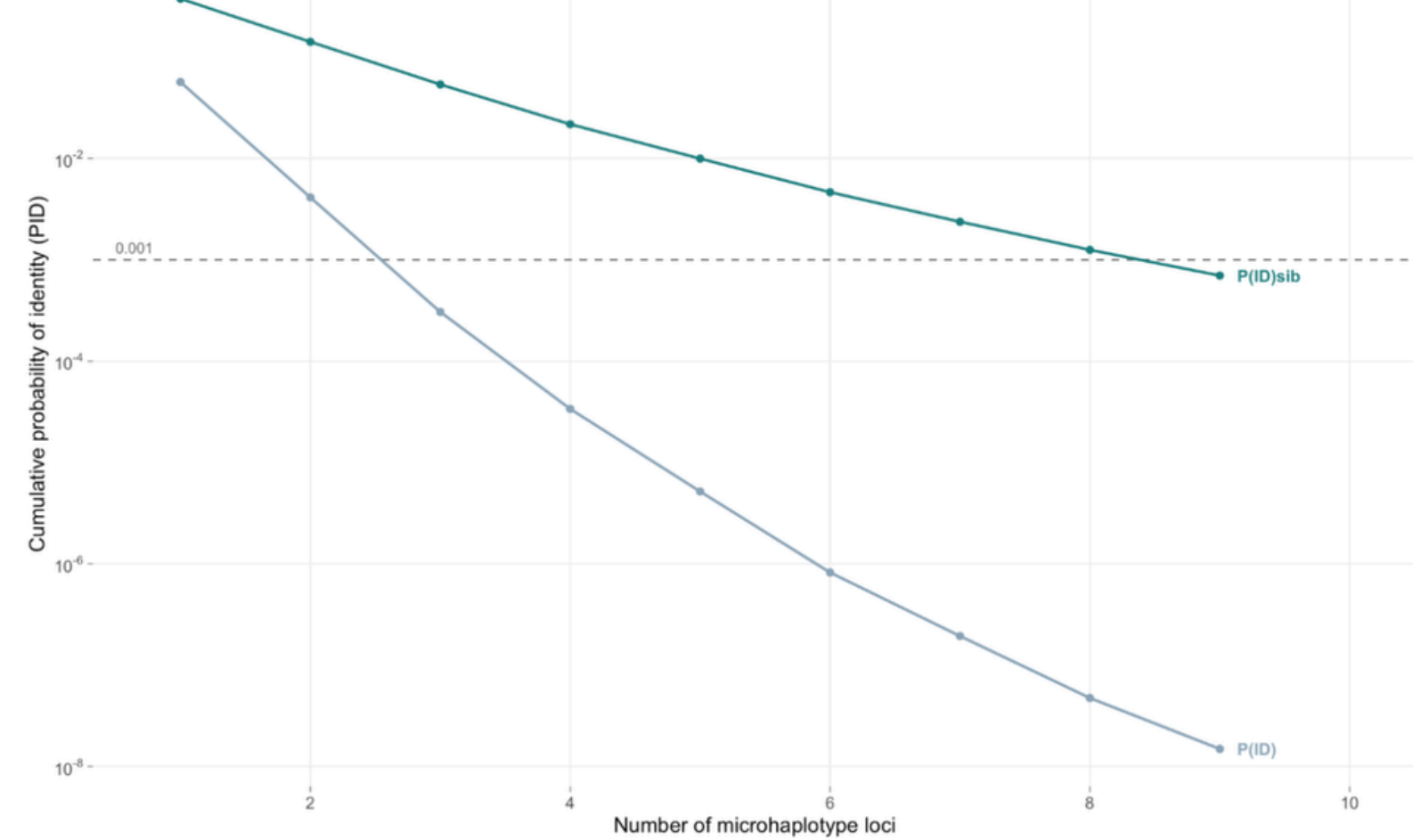


Ideal microhaplotype for mixed sample detection/deconvolution should contain **3+ SNPs** (Kidd et. al.).

6 pass threshold (Ae < 2.9) **4** near threshold (2 < Ae < 2.9)

PID & PID(sib)

Assessing the **efficacy** of the microhaplotype panel



Threshold = 0.001

(WS population in central California = 200-300 individuals) (Kanive et al.)

PID = Probability of Identity for unrelated individuals
Passed at **3rd** microhaplotype

PID(sib) = Probability of Identity for siblings (account for higher genetic % similarity)
Passed at **9th** microhaplotype

Discussion & Conclusions

Discussion

Limitations:

- No publicly available nuclear genomes assembled for salmon sharks (*Lamna ditropis*) and blue sharks (*Prionace glauca*), reducing efficacy of Primer-BLAST.

Next Steps:

- Test the function of primers in a combined multiplex PCR reaction – check if it amplifies all target regions.
- Check the accuracy of the microhaplotype panel in quantifying the number of individuals in a sample.

Community Education: Our goals with MBWS were to:

- Counteract the fear and aversion around white sharks due to popular culture
- Make conservation science (and scientists) more accessible to people of all backgrounds

Conclusion

Key Takeaways:

- Identified **two new DNA primers** that amplify microhaplotypes in the white shark genome.
- Added to microhaplotype panel created by Raksha Doddabele, bringing PID & PID(sib) values below 0.001.
- If successful in a multiplex PCR, this microhaplotype panel could help **quantify white sharks** in the Monterey Bay National Marine Sanctuary through eDNA.
- Complemented eDNA work with **educational content** via the Monterey Bay White Sharks (MBWS) project.

By taking this two-pronged approach to conservation science, the intent is to equip scientists with **tools to effectively monitor populations while making conservation accessible and engaging to the public.**

Kanive, Paul, et al. "Estimates of regional annual abundance and population growth rates of white sharks off central California." ScienceDirect, 21 April 2021, <https://www.sciencedirect.com/science/article/pii/S0006320721001567>. Accessed 31 August 2026.
Merson, Zachariah, et al. "eDNA metabarcoding detection of nearshore juvenile white sharks (*Carcharodon carcharias*) and prey fish communities." ScienceDirect, 31 January 2025, <https://www.sciencedirect.com/science/article/pii/S0022098125000048>. Accessed 31 August 2026.