

Abstract

Increasing global urbanization poses significant risks to biodiversity through habitat degradation and overfishing that threaten species like the potbellied seahorse (Hippocampus abdominalis), native to New Zealand and south-eastern Australia. To address these challenges, our study investigates the genetic diversity of a captive-bred pot-bellied seahorse population produced by Seahorse Australia, an aquaculture facility that aims to reduce the harvest of animals from natural populations. Using mitochondrial DNA D-loop sequencing, our research aims to assess the genetic variation of 47 *H. abdominalis* individuals (24 males and 23 females) sourced from this captive population. Our genetic results provide insight into the maternal genetic lineage of this population, guiding future breeding strategies to maintain genetic health and reduce the risk of inbreeding. Our research provides important insights that may help the management of threatened seahorse populations and improve seahorse aquaculture.

Introduction

The global urban population is poised to grow by 2.5 billion over the next 30 years, a development that is expected to lead to habitat and biodiversity loss (Simkin., et al., 2022). Urbanization can contribute to vulnerability and extinction in a variety of species. A species that is vulnerable to this factor is the *Hippocampus abdominalis*, a seahorse species who inhabits New Zealand and south-eastern Australia. According to the International Union of Conservation of Nature's Red List of Threatened Species, the current status of the seahorse species is considered to be data deficient and vulnerable (IUCN, 2024). Habitat degradation and overfishing are the leading factors for the sensitivity. Furthermore, the commercial value seahorses hold for industries such as traditional medicine contribute to their endangerment. Millions of seahorses are collected each year to meet the high demand of the Chinese medicine market where millions of seahorses are harvested annually (Koning and Hoeksema, 2021). The demand for the *Hippocampus abdominalis* is unsustainable, posing a serious threat to the longterm survival of the species.

From Fins To Genes: Exploring the Mitochondrial DNA of Captive Seahorses Lily Huang, Saoirse Healy, Dr. Tony Wilson Midwood High School, Scholar's Academy, Brooklyn College

Materials & Methods

•Fin clips were collected from 47 captive-bred *Hippocampus abdominalis* for genetic analysis

•Genomic DNA extracted using DNeasy 96 Tissue Kit (Qiagen).

DNA purity and concentration assessed with a NanoDrop spectrophotometer.

•Mitochondrial control region was amplified using tRNA ThrF and tRNA PheR primers.

•PCR reactions were performed in 25 µL volumes containing EconoTaq polymerase, reaction buffer, MgCl₂, dNTPs, primer, and DNA.

•Thermal cycling: 94 °C for 3 min; 40 cycles of 94 °C (30 s), 50 °C (30 s), 72 °C (1 min); final extension at 72 °C for 5 mın.

•Agarose gels were prepared with TAE buffer and ethidium bromide.

•Samples were mixed with loading dye and run to visualize PCR products.

•PCR products were sequenced; sequence data were edited and aligned using geneious. Aligned sequences were compared to assess genetic variation and construct a family tree.

Results

Population genetics map: The genetic map shows the pulation structure of seahorses from these regions, providing context for interpreting the genetic diversity observed in the labbased samples.



The phylogenetic tree shows substantial genetic diversity, with several distinct mitochondrial lineages. Some individuals are more distantly related.







Shared by ≥ 3 populations: These alleles are found in three or more populations across the study area (either within AU or NZ regions)

PCR amplification was successful for most seahorse DNA samples, as shown by clear bands on the agarose gel.



Funded by:

The Pinkerton Foundation

Discussion

-We successfully amplified and sequenced DNA from most individuals, and the family tree revealed substantial genetic diversity, with several distinct maternal lineages, suggesting genetic variation is being maintained in the population.

- SH238 appeared closest to the root of the tree and is likely the original maternal lineage.

- PCR amplification was mostly successful, but a few samples failed to show bands. This could be due to errors in PCR setup.

- Include nuclear DNA markers for a more complete genetic picture.

- This study provides valuable insights into genetic variation and emphasizes the importance of maintaining genetic diversity in captive

populations. This is crucial for both conservation and breeding strategies, ensuring the long term survival of the species in both captive and natural environments.

References

Bahr, Angela., Stefan Sommer., Beat Mattle., & Anthony B. Wilson. "Mutual Mate Choice in the Potbellied Seahorse (Hippocampus abdominalis)." Behavioral Ecology, vol. 23, no. 4, 1 July 2012, pp. 869-878, academic.oup.com/beheco/article/23/4/869/222935, https://doi.org/10.1093/beheco/ars045.

Ferreira, Tomas, and Santiago Rodriguez. "Mitochondrial DNA: Inherent Complexities Relevant to Genetic Analyses." Genes, vol. 15, no. 5, 12 May 2024, pp. 617–617, <u>www.mdpi.com/2073-</u> 4425/15/5/617, https://doi.org/10.3390/genes15050617

IUCN. "The IUCN Red List of Threatened Species." IUCN Red List of Threatened Species, 2024, www.iucnredlist.org/en.

Simkin, Rohan D., et al. "Biodiversity Impacts and Conservation Implications of Urban Land Expansion Projected to 2050." Proceedings of the National Academy of Sciences of the United States of America, vol. 119, no. 12, 22 Mar. 2022, pubmed.ncbi.nlm.nih.gov/35286193/,

https://doi.org/10.1073/pnas.2117297119.

Acknowledgements

We would like to thank Dr. Wilson for being our mentor and guiding us throughout this significant research project. We would also like to express our gratitude to the Urban Barcode Research Program for their support, as well as Brooklyn College for providing the essential resources and equipments.