BARCODING BROOKLYN COLLEGE AQUACULTURE WATER SYSTEMS

Authors

Mary Ogunwale[1], Kako Uemura[2], Theodore Muth[3], Tony Wilson[4]

Affiliations

[1]UBRP, Midwood HS. [2]Science Research, Midwood HS.
[3]Muth Lab, Brooklyn College. [4]Wilson Lab, Brooklyn College.

Abstract

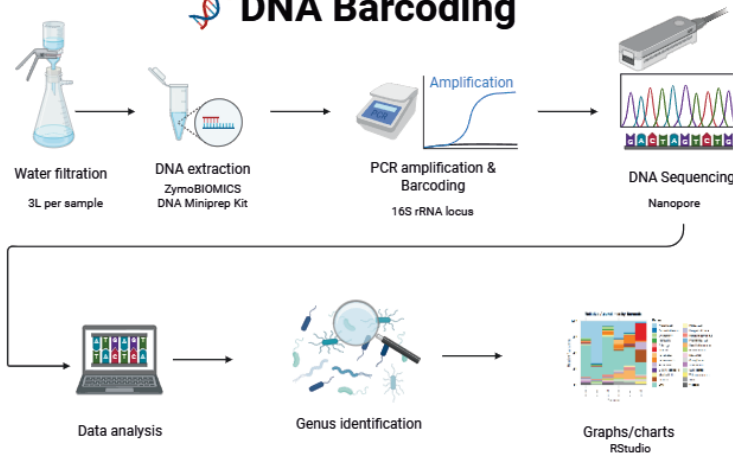
Shifts in environmental microbiota can directly affect health, disease susceptibility, and fecundity, which are all key factors to species conservation. Brooklyn College is home to seahorses and pipefish collected from Australia and New York. The animals are housed in two water systems using artificial salt water prepared from NYC tap water. We characterized the microbial differences between the two water systems with the aim of reflecting the microbial communities impacting the experimental animals. This was achieved by sampling water coming from the tanks from each system back into the filtration system. The study was conducted over multiple days to identify any differences in the microbial communities across different days and times. Our high throughput molecular data and insight into the microbiome of the two systems. Further refinement of the methods will help to reduce sample-level variation. The data revealed >500 microbial OTUs, with clear differences between systems.

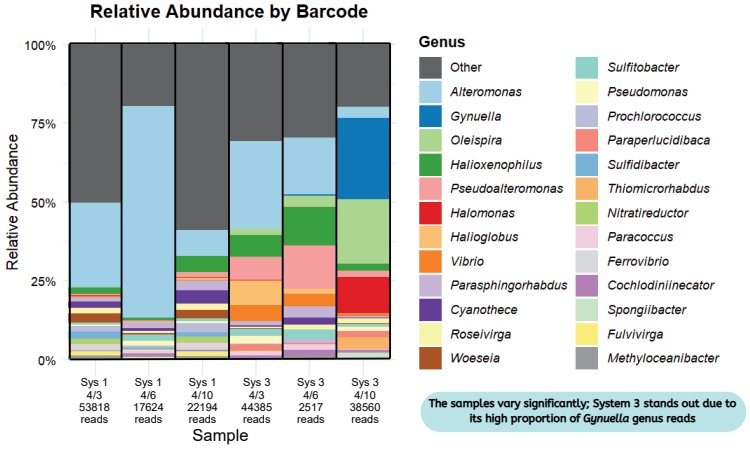
Introduction

The microbial community associated with an organism can reveal extensive information about the environmental conditions it has been exposed to (Govender & Ghai, 2025). Exposure to an unfamiliar microbial population can induce shifts in an organism's microbial community. This study aims to characterize the differences between microbial communities in two aquarium water systems housing Tasmanian *Hippocampus abdominalis* (**system 1**) and New York populations of Hippocampus erectus and *Syngnathus fuscus* (**system 3**). Understanding and analyzing the differences in microbial communities in aquarium systems is crucial because shifts in environmental microbiota can directly affect health, disease susceptibility, and breeding success (Suzuki et al., 2020).

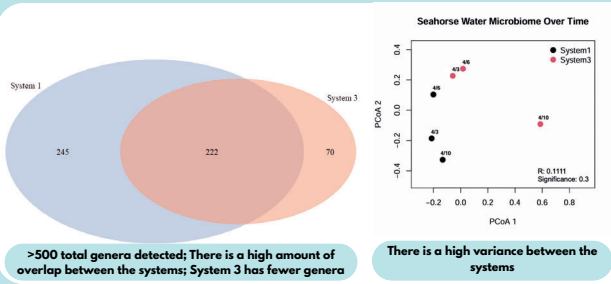
Methodology

DNA Barcoding





The samples vary significantly; System 3 stands out due to its high proportion of *Gynuella* genus reads



>500 total genera detected; There is a high amount of overlap between the systems; System 3 has fewer genera

There is a high variance between the systems

Discussion

The Nanopore sequencing method was straightforward and high throughput. The filtering apparatus was very efficient and reduced the chance of human error when filtering. It also allowed for the filtering of more water in less time compared to manually pushing water through a syringe. This contributed to a high number of reads (3K-54K). The results revealed a total of 537 different genera present. The relative abundance barplot, venn diagram, and PcoA reveal great variance within and between the 2 systems, especially within system 3. Possible causes are sampling errors that may have occurred during water contamination and filtering. Additionally, contamination may have been present during sampling, extraction, and library preparation stages. Rerunning the DNA samples will provide additional sequence data and help to pinpoint whether the observed within-system variation is biologically relevant or due to experimental artifacts.

Acknowledgements

We are grateful to Dr. Wilson for guiding us throughout this significant research project and Dr. Muth for support, especially with the Nanopore sequencing. We would also like to express my gratitude to the Urban Barcode Research Program and the Pinkerton Foundation for making this possible, as well as Brooklyn College for providing the resources and equipment.

References

Álvarez-Mercado, A. I., Navarro-Oliveros, M., Robles-Sánchez, C., Plaza-Díaz, J., Sáez-Lara, M. J., Muñoz-Quezada, S., Fontana, L., & Abadía-Molina, F. (2019). Microbial population changes and their relationship with human health and disease. Microorganisms, 7(3), 68. https://doi.org/10.3390/microorganisms7030068

Ashe, J. L. (2021). Microbial-Host Dynamics and the Evolution of Nearshore Diversity in Hippocampus abdominalis (Doctoral dissertation, City University of New York).

Govender, P., & Ghai, M. (2025). Population-specific differences in the human microbiome: Factors defining the diversity. Gene, 933, 148923. https://doi.org/10.1016/j.gene.2024.148923

Suzuki, A., Akuzawa, K., Kogi, K., Ueda, K., & Suzuki, M. (2020). Captive environment influences the composition and diversity of fecal microbiota in Indo-Pacific bottlenose dolphins, Tursiops aduncus. Marine Mammal Science, 37(1), 207–219. https://doi.org/10.1111/mms.12736