Bacterial Community Homogeneity Across Dolphin Enclosures in the San Diego Bay

Grace Ye[1], Sarah Pan[2], Katelyn Zhang[1], Jackson Gage[3], Feng, Z.[4], Deviney, B.[4,5], Jedlicki, J.[4,5], Lu, J.[4,5], McClain, A.[4,6], Bozinovic, G.[4]

[1]Del Norte High School, [2]Brooks School, [3]Canyon Crest Academy, [4]Boz Life Science Research and Teaching Institute, [5]UC San Diego Division of Extended Studies, [6]U.S. Navy Marine Mammal Program

Summary

- Bacterial DNA were isolated from mussels and sequenced to study the microbial community in dolphin enclosures
- No statistically significant variation in bacterial composition was detected

Abstract

San Diego Bay is home to many marine animals, and should be protected to preserve its ecosystem from pollution. To survey the bacterial composition of the waters in the U.S. Navy Marine Mammal Program Facility, mussels were collected from five sites. Bacterial DNA was isolated and sequenced, revealing diverse and similar microbiomes across the sites.

Introduction

Hypothesis:

- Dolphin enclosures close in proximity at the marine mammal facility in the San Diego Bay should have similar bacterial composition.

Mussels found along the California coast. Photo by California State Parks.

Background:

- Bacteria can enter San Diego Bay through urban runoff and sewage (Pendergraft, 2023)
- Effective monitoring methods should be developed to detect harmful bacteria
- The similarity between bacterial communities is negatively correlated with distance (Bell, 2010).

The polluted Tijuana River flowing into coastal waters near San Diego Bay. Photo by NBC News.

Methodology

1. Sample Collection
- Mussels were collected from five sites around the Marine Mammal Program's dolphin enclosures in the San Diego Bay

Figure 1. Sampling locations (red pins) in the dolphin enclosure area.

2. Mussel Dissection
- Collected mussels' digestive organs

3. Bacterial DNA Extraction
- Used Powerfood™ Microbial DNA Isolation Kit

4. Library Preparation
- Used Nanopore 16S Barcoding Kit 24 V14

5. Nanopore 16S Gene Sequencing
- Prepared library was sequenced with MinION sequencer

6. Data Analysis
- Sequencing reads were aligned to 16S sequences with EPI2ME
- Bacterial read counts were analyzed in RStudio

Results

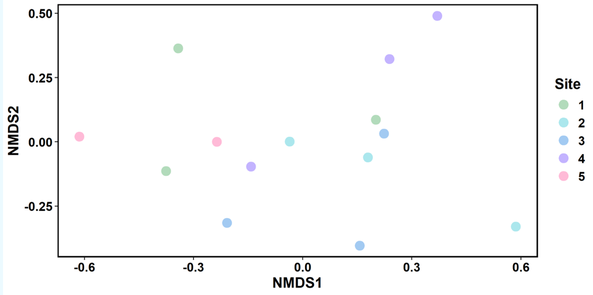

Figure 2. Samples did not cluster by study site on NMDS plot. NMDS analysis of relative abundance levels per bacterial species did not result in apparent grouping patterns. Stress = 0.1416.

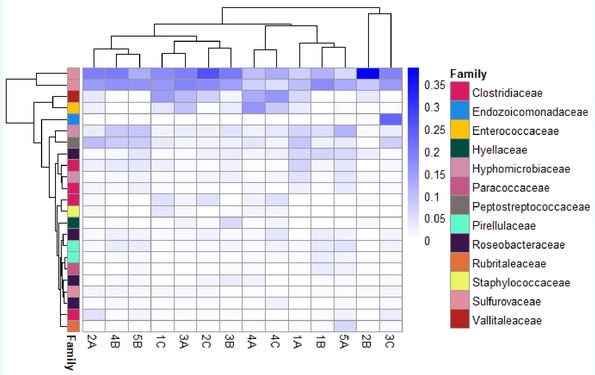

Figure 3. *Sulfurovaceae* species are highly abundant across study sites. Each row represents a bacterial species, and each column represents a mussel sample. Darker colored cells indicate higher abundance. Variations in bacterial composition across sites are not significantly higher than within-site variations (PERMANOVA, $p > 0.1$), as illustrated by the hierarchical clustering.

Bibliography

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Discussion & Conclusion

Our hypothesis was supported by our data, which showed similar bacterial composition across study sites (Figure 2-3)

- Mussels were collected at sites within 30-70m of each other (Figure 1)
- This is likely because the environmental conditions and ecological processes were similar across the sites
- Potentially harmful bacteria in the *Staphylococcaceae* and *Enterobacteriaceae* families were detected
- Our results confirm the consistency of this bacteria sampling and identification method
- Sampling a wider geographical range will allow for the identification of location-specific bacterial composition variations, which could be useful for monitoring water quality for dolphin populations

Study Limitations

- Samples were only collected during one season, and fluctuations in seasonal temperature were not accounted for
- There were only two samples for Site 5, as the library preparation step failed for the third one

Future Directions

- Sampling can be conducted over a larger timescale and range
- Bacteria can be isolated from other marine animals in the San Diego Bay
- Functional analysis of bacteria can be conducted to explore their interactions with their hosts