High Abundance of Bacterial Families Associated with Pollutant Degradation Identified in Tijuana River Estuary Sediment

Taylor, M.[1] , Belt, M.[1] , Gaudet, J.[1], Villarreal, A.[2] , Jedlicki, J.[3,4]

[1]Cuyamaca Community College, [2]Sweetwater High School, [3]Boz Life Science Research and Teaching Institute, [4]University of California San Diego, Division of Extended Studies

Summary

- DNA was isolated from sediment samples
- 16S rRNA sequencing was performed to identify bacteria.
- The most abundant bacterial families can degrade pollutants
- Wet and dry periods have slightly different relative abundance and diversity of sediment bacteria

Abstract

The Tijuana River Estuary, a critical ecological zone straddling the U.S.-Mexico border, has been increasingly impacted by pollution, including wastewater discharge and urban runoff. This ecological survey characterizes the bacterial composition in the sediment during wet and dry periods using 16S rRNA sequencing. The diversity and composition of sediment microbiome are slightly different between the two sampling periods. We detected abundant bacteria families which are known to metabolize pollutants commonly found in agricultural runoff and sewage. These findings lay the groundwork for future studies on microbial bioindicators and conservation strategies in the Tijuana River Estuary.

Introduction

Hypothesis:

The bacterial taxa composition of the Tijuana River Estuary differs between wet and dry periods.

Background:

- The Tijuana River Estuary is located on the westernmost side of the Tijuana River Valley and is a transitional point where the Tijuana River reaches the Pacific Ocean.
- The estuary is a key location for over 300 species of birds and fish as an important site for feeding, nesting, and breeding.
- Extensive sewage, industrial waste, and urban runoff pollution has led to the San Diego Water Board designating parts of the Tijuana River Watershed as impaired water body segments. (California Regional Water Quality Control Board, 2024)

(A)

(B)

Figure 1. Tijuana River Estuary landscape alterations due to high tide (A) and low tide (B). Water constantly enters and exits the estuary due to tidal events.

Figure 2. Trash in the Tijuana River Estuary. While visiting the estuary, plastic waste was frequently seen.

Materials & Methods

Sample Collection

- Sediment was collected from the estuary at coordinates (32.547251, -117.064224)
- Collection occurred during a dry period on 12/12/2020 and following a wet period on 02/04/2021
  - *Dry period:* At least 14 consecutive days with no precipitation
  - *Wet period:* Precipitation event with over 1.27 cm rainfall within 24 hours

DNA Extraction

- DNA was extracted from sediment using MOBio PowerSoil DNA Isolation Kit
- Quality and quantity checked using Nanodrop spectrophotometer

Library Preparation for 16S Sequencing

- The NEXTFLEX 16S V4 Amplicon-Seq Kit 2.0 for Illumina Platforms was used to target bacterial DNA

Quality Check and Sequencing

- Quality check and sequencing of prepared libraries were performed at Scripps Research Genomics Core
- Samples were sequenced using Illumina NextSeq2000

Data Analysis

- After passing quality check, sequences were aligned to bacterial genome database using DADA2 pipeline v.1.16
- Data were visualized using ggplot2 (v 3.5.1)

Results

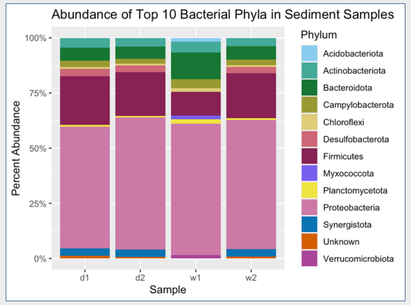

Figure 3. Relative abundance of ten most abundant bacterial phyla in sediment samples collected during dry and wet periods. d1 and d2 indicate the two dry period sediment samples, and w1 and w2 indicate wet period samples. Proteobacteria is the most abundant phylum across all samples.

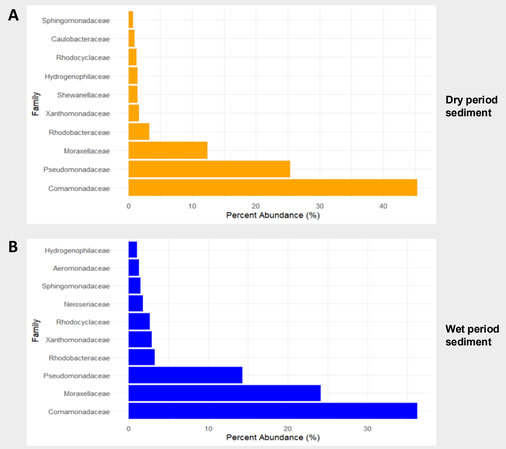

Figure 4. Top ten abundant bacterial families in sediment collected during the (A) dry period and (B) wet period within the Proteobacteria phylum.

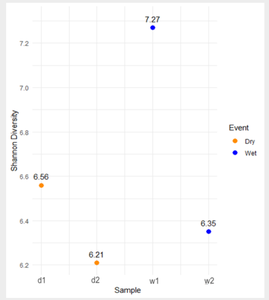

Figure 5. Shannon Diversity Index (SDI) of bacteria in the estuarine sediment during dry and wet periods. d1 and d2 indicate the two dry period sediment samples, and w1 and w2 indicate wet period samples.

Discussion & Conclusion

- Proteobacteria is the most abundant phylum in sediment from both dry and wet sampling periods. They are associated with biodegradation of pollutants and play a critical role in nutrient cycling (Aislabie & Deslippe, 2013).
- Within Proteobacteria, Comamonadaceae is the most abundant bacterial family in both types of sediment samples (Figure 4). They are known to degrade petroleum hydrocarbons (Bacosa et al., 2020).
- Pseudomonadaceae and Moraxellaceae are the 2nd and 3rd abundant families in the dry period sediment (Figure 4A), respectively, but switched places in the wet period sediment (Figure 4B).
- Pseudomonadaceae can degrade pesticides and petroleum products (Mishra et al, 2020). Moraxellaceae are known to degrade pollutants such as fecal matter and agricultural runoff (Rosenberg et al., 2014).
- Episodic pollution events, such as stormwater runoff, likely contributed to the observed variation. Nevertheless, the microbial composition and overall diversity remained unexpectedly similar between the two sampling events (Figure 3-5).
- The high abundance of bacteria that can metabolize pollutants could be a result of long-term contamination of the estuarine environment. These bacteria can also be potentially used for bioremediation.

Limitations & Future Directions

Limitations

- Identifying bacteria present by 16S rRNA sequencing does not determine a cause and effect relationship between the bacteria and pollution (María Bailén et al., 2019).
- Related bacterial species are indistinguishable due to homology between sequences, and bacteria were only identified at the family level (María Bailén et al., 2019).

Future Directions

- Conduct metagenomic analysis to link bacteria taxa with pollutant metabolic pathways.
- Use long-term monitoring to determine sources of pollution.

References

Scan me!