Exploring the Effects of River Sediment Chemical Composition on Microbial Community Diversity Across British Columbia's River Networks

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Introduction

- Microorganisms are essential components of ecosystems, playing a crucial role in processes like nutrient cycling, water purification, and the overall health of the ecosystem.
- The structure and function of microbial communities are influenced by a variety of factors, including the chemical composition of their surroundings.
- In river ecosystems, which are abundant in Canada and vital for human activities like drinking water provision and agriculture, understanding how these factors affect microbial communities is especially important.
- The chemical composition of river sediment often serves as an indicator of pollution. Elevated concentrations of certain elements can reflect the intensity and proximity of pollution, illustrating the potential impact of anthropogenic activities on local environmental conditions.
- This study examines the relationship between the chemical composition of sediments and waters on microbial community structure in rivers across British Columbia.

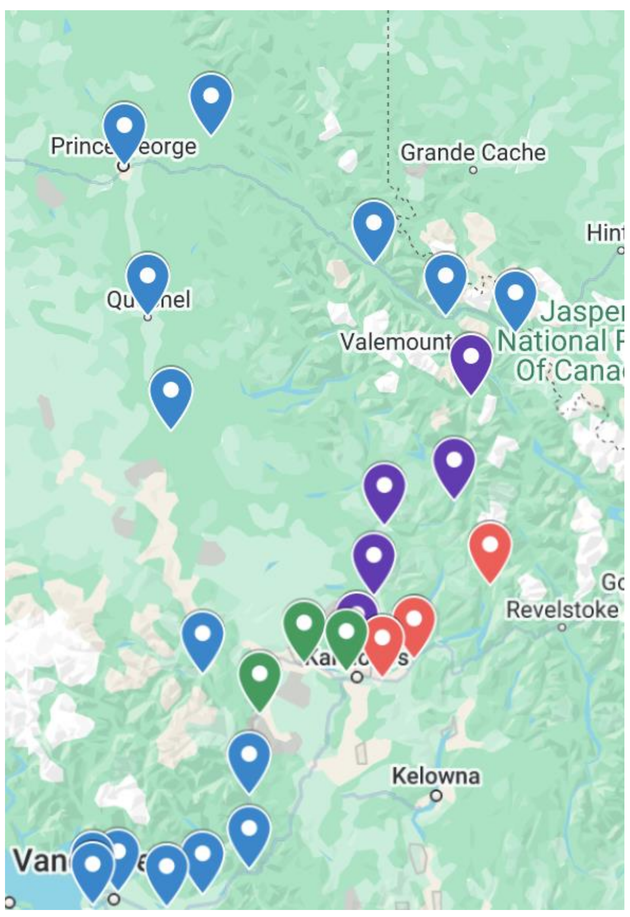

Figure 1. Map of sample sites in British Columbia with blue points representing sites on the Fraser River, purple representing the North Thompson River, red representing the South Thompson River, and green representing the Thompson River.

Hypotheses

- Microbial community composition in sediment samples will be more variable than water samples, due to more variable environmental conditions and reduced mixing.
- The chemical composition of river sediments will be a strong predictor of microbial community structure.

Methods

Sample Collection

- Water and sediment samples were collected from 26 sites along several rivers in British Columbia, spanning from near the river source to just before they flow into the Pacific Ocean.
- Both filtered and unfiltered water samples were collected at each site.
- Sediment samples were taken at triplicate points about 10 meters apart at each site

Microbial Community Structure

- To assess microbial community diversity, DNA was extracted from the sediment samples and water filters, and the 16S rRNA gene was amplified using polymerase chain reaction (PCR).
- Sequencing was performed to identify the microbial species present and determine their relative abundance in each sample.

Chemical Composition

- The chemical composition of the water and sediment was analyzed using Inductively Coupled Plasma Mass Spectrometry (ICP-MS) to determine the concentration of various elements present in each sample.
- Sediment samples (approximately 0.2 g) were digested in 4.5 mL of nitric acid and 0.5 mL of hydrochloric acid, then diluted with 2% nitric acid to a final volume of 50 mL.
- Filtered water samples (approximately 15 mL) were diluted in 2% nitric acid to a final volume of 50 mL.

Data Analysis

Microbial Community Structure

- Beta diversity was assessed to explore variation in microbial community composition across sites using the Bray-Curtis dissimilarity index and visualized using a multidimensional scaling plot.

Chemical Composition

- Principal Component Analysis (PCA) was used to reduce the dimensionality of the chemical data set, allowing us to visualize the most important patterns and correlations of the chemical composition of the sediment and water samples.

Statistical Analysis

- Variance partitioning based on redundancy analysis was used to determine how much variation in the microbial community composition could be explained by spatial variables (PCNM scores derived from site locations) and chemical variables (PCA scores derived from element concentrations).
- About 28% of the variation in the community data could be explained by spatial and chemical variables: 10% explained by spatial data alone, 14% explained by chemical data alone, and 4% explained by both datasets simultaneously.

Results

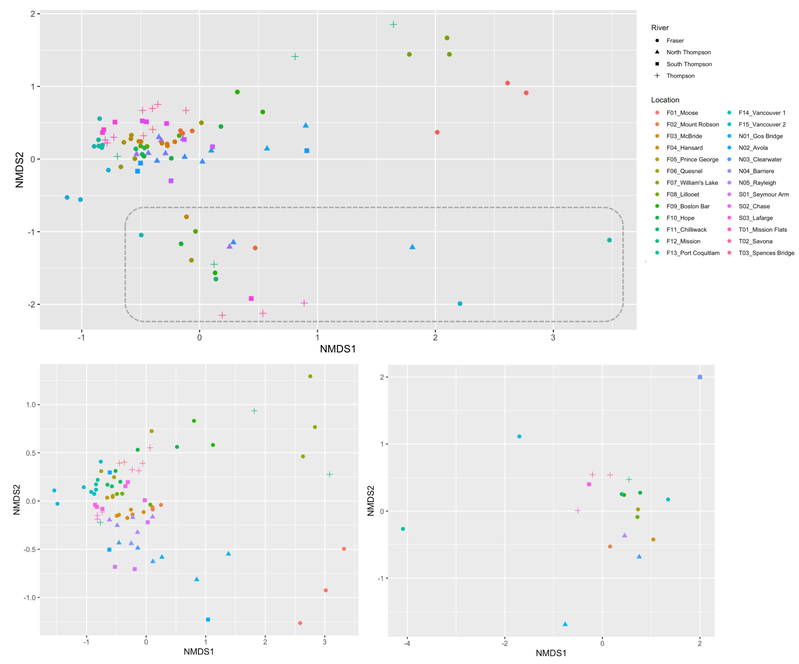

Figure 2. Multidimensional scaling plot illustrating the Bray Curtis dissimilarity in the microbial community composition of all samples with water samples outlined in grey (top), sediment samples (bottom left), and water samples (bottom right).

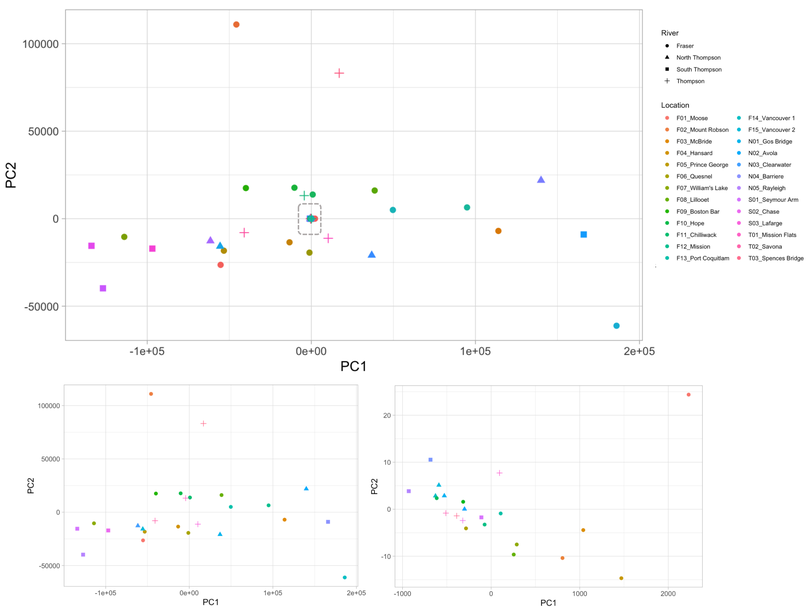

Figure 3. PCA analysis of sample chemical composition of all samples with water samples outlined in grey (top), sediment samples (bottom left), and water samples (bottom right).

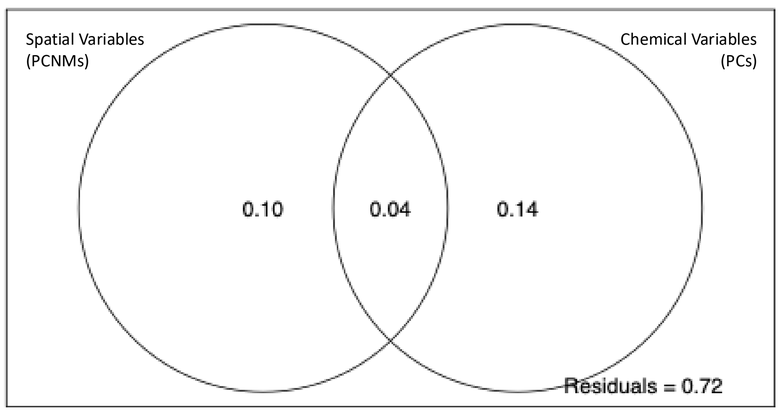

Figure 4. Variance partitioning based on redundancy analysis to determine how much variation in the microbial community composition could be explained by spatial and chemical variables.

Future Work

- Several key elements like nitrogen and sulfur were not measured. These elements are essential nutrients for many microorganisms and their relative abundance will likely contribute to patterns of microbial community structure.
- Locational analyses did not account for the possibility that two sites may be geographically close but located on separate rivers. By considering the differences in river type and spatial distribution, future analyses could more effectively compare the datasets to identify potential regional or river-specific patterns.

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