

Ecological Drivers of Microbial Community Composition Along River Networks of Western Canada



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Introduction

- By understanding how microbial community structure and function differ in environments that vary in both geographical location and chemical composition, we can understand which factors have the greatest impact on these communities.
- Understanding these relationships is crucial due to the abundance of rivers in Canada and our heavy reliance on them for clean drinking water and agricultural practices.
- This study follows several rivers in British Columbia from near their origin, as they pass through various topographies and anthropogenic influences, to just before they flow into the Pacific Ocean.

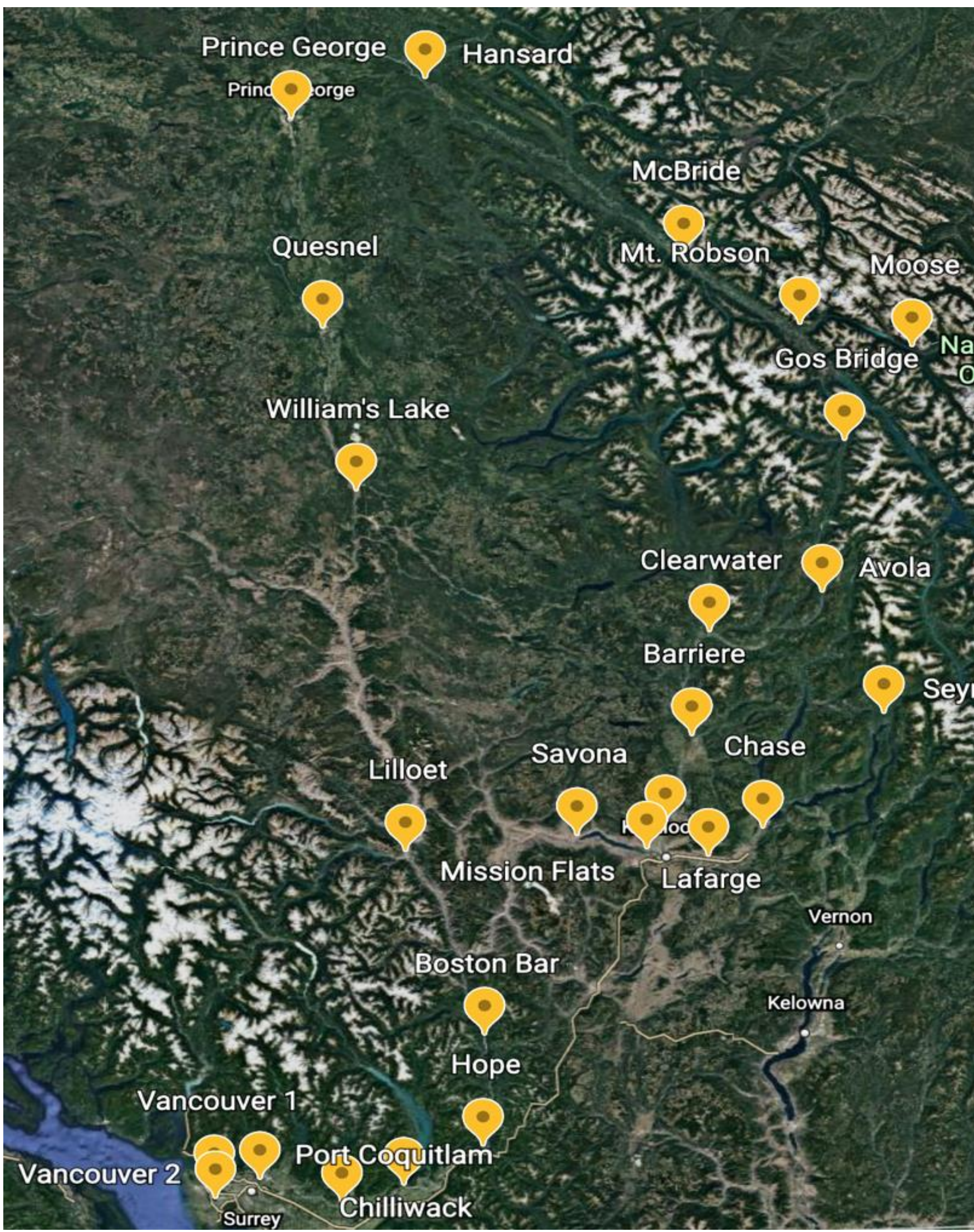


Figure 1. Map of sample sites in British Columbia

Hypotheses

- Sites closer together on a river will have greater similarity in their microbial community composition than those further apart.
- Diversity will increase as microbial communities move away from pollutant sources, and the array of functional genes will be less skewed toward those related to tolerating and breaking down pollutants.
- Sites near anthropogenic pollutant sources will show higher levels of elements such as sulphur, nitrogen, and heavy metals, and this will correlate to an increased abundance of microorganisms that use these elements as nutrient or energy sources.

Methods

Sample Collection

- Sediment and water samples were collected from twenty-six sites along four different rivers in British Columbia.
- Three sediment samples were taken at each location about 10 meters apart.
- One water sample was taken at each location and filtered on site using a Sterivex filter.
- The sampling sites were photographed, and various environmental conditions were recorded.

16S rRNA Gene Sequencing

- DNA was extracted from both the sediment and water samples using DNeasy PowerSoil and PowerWater kits.
- PCR was completed using 16S rRNA primers to amplify bacterial and archaeal DNA.
- The 16S rRNA amplicons were sequenced to determine which organisms were present, and in what abundance, in each sample.



Figure 2. Species richness of sediment samples from sites moving down each river.

Results

Microbial Community Composition

- Diversity tests on the 16S rRNA sequencing results showed the triplicates from each site had very similar microbial community compositions.
- Sites closer together on the same river showed a greater similarity than sites further apart or from different rivers.

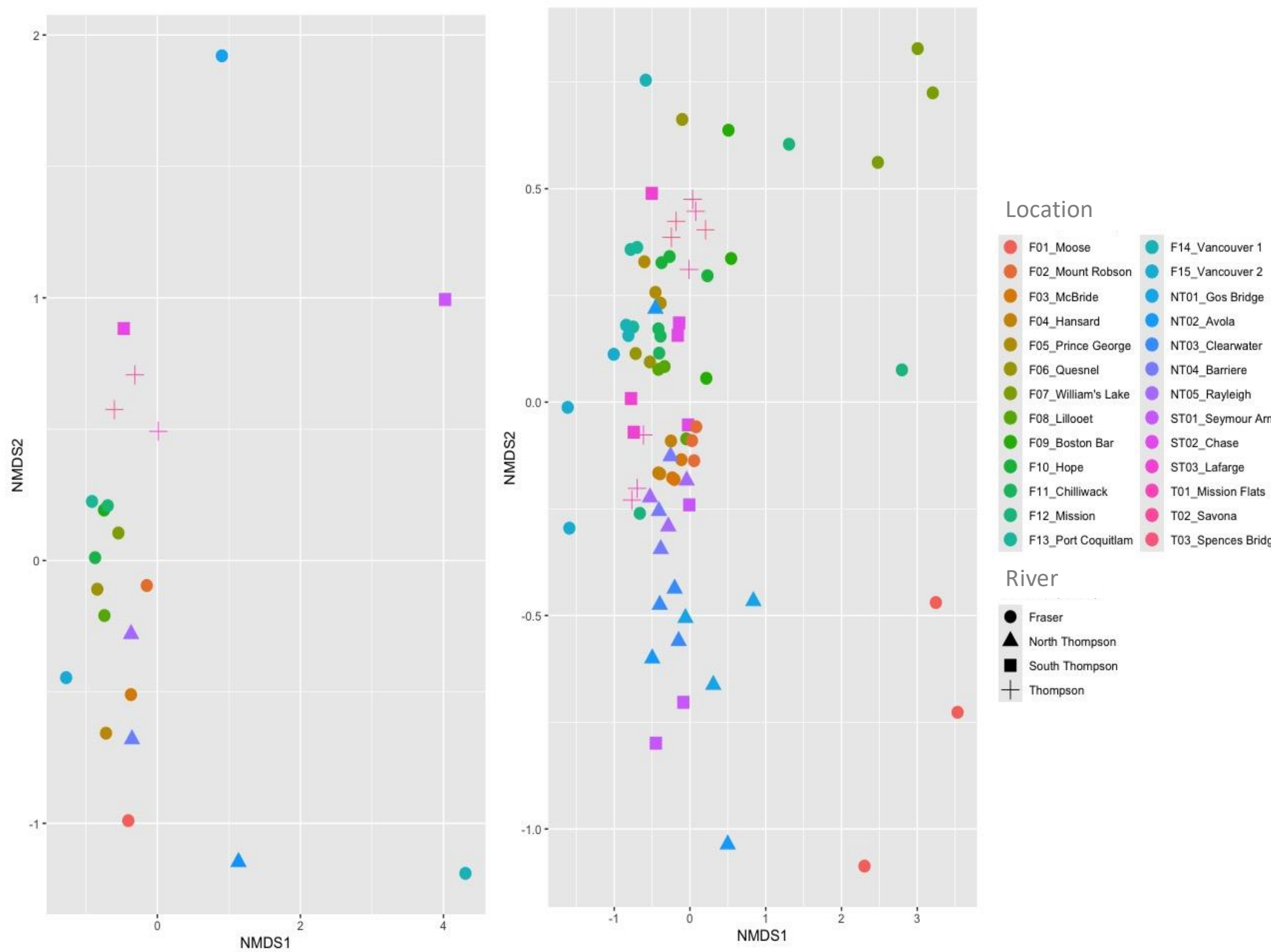


Figure 3. Multidimensional scaling plot illustrating the Bray Curtis dissimilarity in the microbial community composition of water samples (left) and sediment samples (right).

Conclusion

Microbial communities from sites close together within the same river showed greater similarity compared to sites further apart. Communities located in different rivers, but in areas with similar anthropogenic influence also showed greater similarity than those found in areas with drastically different levels of anthropogenic influence. There is no support for the hypothesis that alpha diversity increases with distance from river origin, as the species richness from each site did not increase linearly moving down each river.

Future Work

- Elemental compositions of water and sediment samples are being determined by inductively coupled plasma mass spectrometry (ICP-MS).
- Analysis of ICP-MS data along with the analyses of the 16S rRNA results will determine which factor, whether it is geographical space or the chemical composition of a community's habitat, is the greatest contributor to the variance in the structure and function of microbial communities in river sediment and water.