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Ecosystem Indicators for Freshwater Streams

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Ecosystem Indicators for Freshwater Streams

Basic Information

Title:	Ecosystem Indicators for Freshwater Streams
Project Number:	2016NH202B
Start Date:	3/1/2016
End Date:	2/1/2017
Funding Source:	104B
Congressional District:	NH-1
Research Category:	Water Quality
Focus Categories:	Water Quality, Management and Planning, Non Point Pollution
Descriptors:	None
Principal Investigators:	Alison Watts

Publications

There are no publications.

Improved Ecosystem Indicator Tools for Water Quality Management - NH WRRC Annual Report – Alison Watts, University of New Hampshire

Problem

Water resource managers, such as state and federal agencies, municipalities, and watershed groups, must identify and manage multiple interconnected stressors within an individual watershed. Primary stressors include nutrient inputs, invasive species, water clarity, low dissolved oxygen, contaminants in water and sediment, increased impervious cover, and loss of aquatic buffers and wetlands. Many of these are interrelated, and may be temporally and spatially variable. Ideally, assessment of biotic condition will provide information that allows managers to identify loss of ecosystem function, indicate the relative importance of primary stressors, identify measures or methods to reduce the stress and repair the system, and ultimately track progress towards management goals. Misidentification of stressors may lead to expenditure of management resources without benefit, and contribute to further degradation of the system. Current approaches to assessing the biological integrity of surface waters rely on manual identification of individual species of fish, invertebrates or other organisms. While effective, this approach is labor-intensive and expensive. Furthermore, it assumes *a priori* knowledge of which groups of aquatic biota are most likely to be impacted by water quality; these are the target groups for which identification of individual specimens are obtained. Advances in DNA methods and rapid reductions in analytical costs present an opportunity to harness this new technology and fundamentally improve our capacity to monitor biological communities and individual species (Bista et al., 2017; Thomsen and Willerslev, 2015). Environmental DNA (eDNA), or DNA present in an environmental sample, includes whole microorganisms (microalgae, bacteria etc.) and fragments of tissue, reproductive and waste products, and other cellular material.

Objectives

This study has two major objectives: (1) Pilot a sampling program to develop statistical correlations between causal parameters (including nutrients, land use and chloride) and microbiotic species attributes for wadeable streams in New Hampshire; (2) to assess the value of genomic analyses of eDNA as an additional tool to evaluate the ecological health of streams.

Methods

The study is being conducted at wadeable streams across New Hampshire, representing a range of land use and stream characteristics. Samples are collected at existing NH Department of Environmental Services (NHDES) Volunteer River Assessment Program (VRAP) and Long Term Monitoring sites, in coordination with NHDES staff and volunteers. The NHDES VRAP program engages over 150 volunteers to sample 30 sites, and provides data that contributes to stream assessment associated with more than 2,900 miles of rivers and streams in New Hampshire. Volunteers have been trained to collect samples for genomic analysis, and the methods, results, and implications will be shared with volunteers and watershed groups. Water samples collected from these sites 10 times (monthly) in 2016 are being analyzed by amplicon sequencing to provide data on stress response, seasonality, replicability, and trends.

Sampling was conducted from June –October 2016, and over 340 samples were collected. Samples were conveyed to UNH and frozen pending extraction and sequencing of DNA. Most of these samples have been sequenced to identify bacteria, while a smaller subset have been sequenced for animal species. Initial analysis and taxonomic identification was performed via QIIME2 (Quantitative Insights Into Microbial Ecology; Caporaso et al, 2010) with the Genbank database.

Initial findings and significance

We identified approximately 40,000 named bacterial species, and 300 animal species (primarily representing fragments, not whole organisms) in the sample set. Initial analysis of microbial populations indicates strong correlation with water quality parameters (Figure 1).

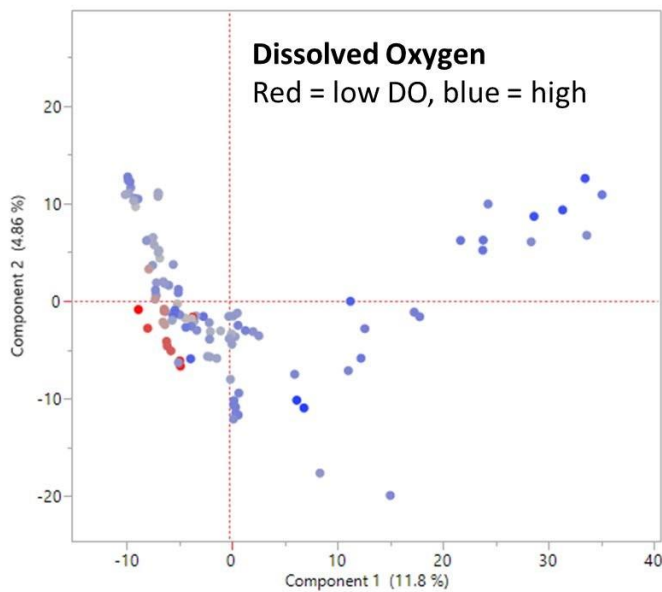


Figure 1. Principal Components analysis of most abundant microbial species show strong correlation between certain assemblages and water quality parameters such as dissolved oxygen.

Additional sampling will be performed at selected sites in 2017 to provide information on the annual variability of microbial populations in streams. 2016 was an unusually dry year, which provides an opportunity to compare results under drought conditions and (potentially) more normal conditions.

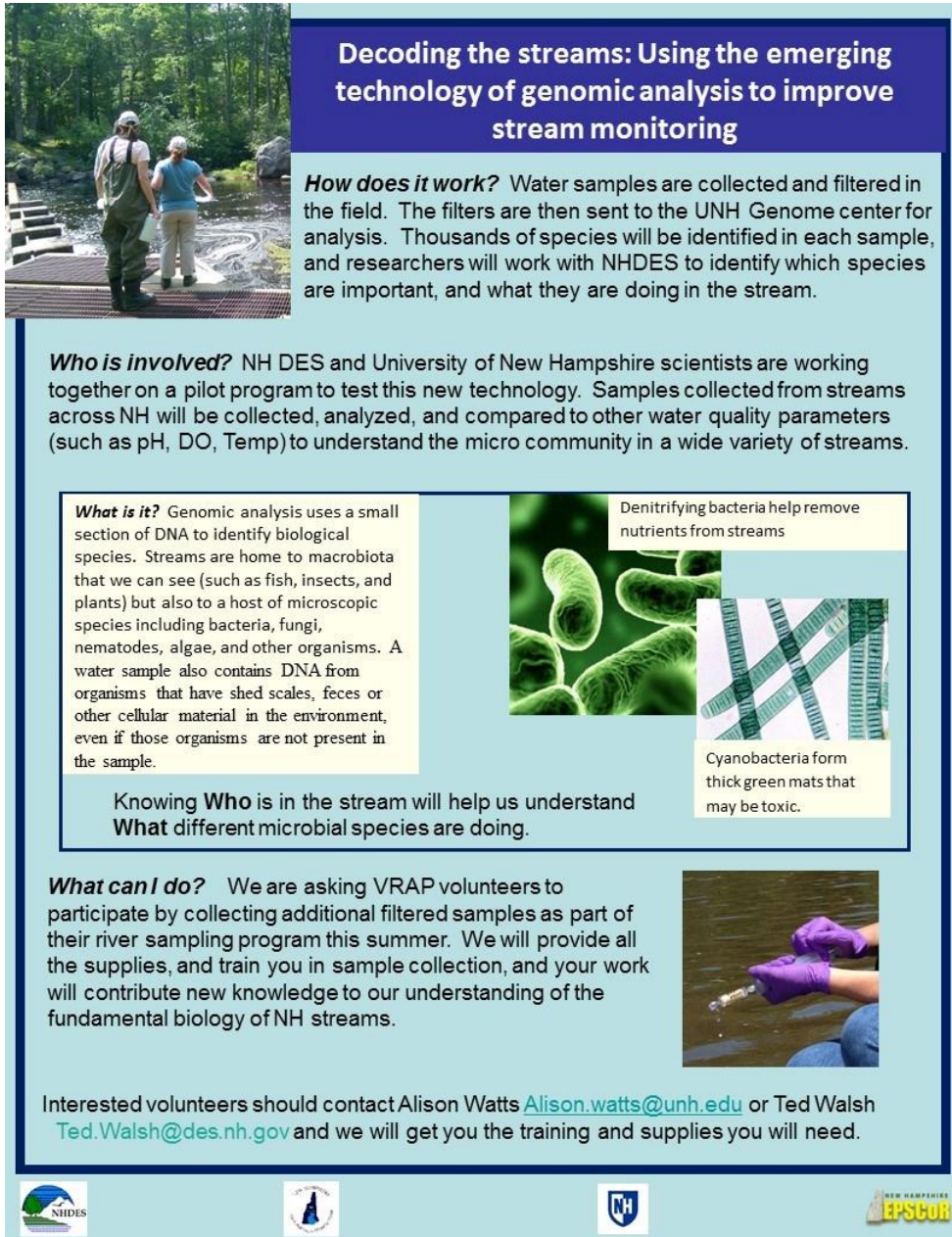
More detailed analysis of the correlation between site characteristics and microbial conditions will be conducted on the full data set in 2017.

Publications and presentations

Presentation: *Metabarcoding and aquatic bacteria in streams: What can microbiology tell us about the big picture?* A. Watts, T. Walsh, T. Danielson. New England Association of Environmental Biologists, Hartford, CT, March 2017.

Outreach or Information Transferred

We have engaged volunteer organizations in sampling collection in NH streams. Outreach materials and fact sheets have been prepared for volunteers (Figure 2)



Decoding the streams: Using the emerging technology of genomic analysis to improve stream monitoring

How does it work? Water samples are collected and filtered in the field. The filters are then sent to the UNH Genome center for analysis. Thousands of species will be identified in each sample, and researchers will work with NHDES to identify which species are important, and what they are doing in the stream.

Who is involved? NH DES and University of New Hampshire scientists are working together on a pilot program to test this new technology. Samples collected from streams across NH will be collected, analyzed, and compared to other water quality parameters (such as pH, DO, Temp) to understand the micro community in a wide variety of streams.

What is it? Genomic analysis uses a small section of DNA to identify biological species. Streams are home to macrobiota that we can see (such as fish, insects, and plants) but also to a host of microscopic species including bacteria, fungi, nematodes, algae, and other organisms. A water sample also contains DNA from organisms that have shed scales, feces or other cellular material in the environment, even if those organisms are not present in the sample.

Denitrifying bacteria help remove nutrients from streams

Cyanobacteria form thick green mats that may be toxic.

Knowing **Who** is in the stream will help us understand **What** different microbial species are doing.

What can I do? We are asking VRAP volunteers to participate by collecting additional filtered samples as part of their river sampling program this summer. We will provide all the supplies, and train you in sample collection, and your work will contribute new knowledge to our understanding of the fundamental biology of NH streams.

Interested volunteers should contact Alison Watts Alison.watts@unh.edu or Ted Walsh Ted.Walsh@des.nh.gov and we will get you the training and supplies you will need.





   

Figure 2. Fact sheet distributed to VRAP volunteers.

Number of students supported

This project has provided partial support for one undergraduate student (Kendra Dow, senior in Environmental and Civil Engineering), and will support up to two additional students in the summer of 2017.

Number and names of faculty and staff supported

Alison Watts, Research assistant Professor

