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Ecosystem Indicators for Freshwater Streams

Alison Watts
University of New Hampshire, alison.watts@unh.edu

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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:	2/28/2018
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

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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 inter-related, 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 was conducted at wadeable streams across New Hampshire and Maine, representing a range of land use and stream characteristics. Samples were 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 in 2016 and 2017 were analyzed by amplicon sequencing to provide data on stress response, seasonality,

replicability, and trends. Additional samples collected from Maine included attached algae (periphyton) samples collected by the Maine Department of Environmental Services (MEDEP).

Sampling was conducted from June – October 2016,at approximately 30 sites, and 10 sites were re-sampled monthly in 2017. 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 eukaryote animal and plant species. Initial analysis and taxonomic identification was performed via QIIME2 (Quantitative Insights Into Microbial Ecology; Caporaso et al, 2010) with the Genbank database.

Principal 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. Analysis of microbial diversity indicates strong correlation with water quality parameters (Figure 1). Specifically, alpha microbial phylogenetic diversity decreases as certain stressors dominate; decreasing diversity was measured in response to increasing temperature, decreasing dissolved oxygen (which are correlated), and increasing nutrients (nitrogen and phosphorus).

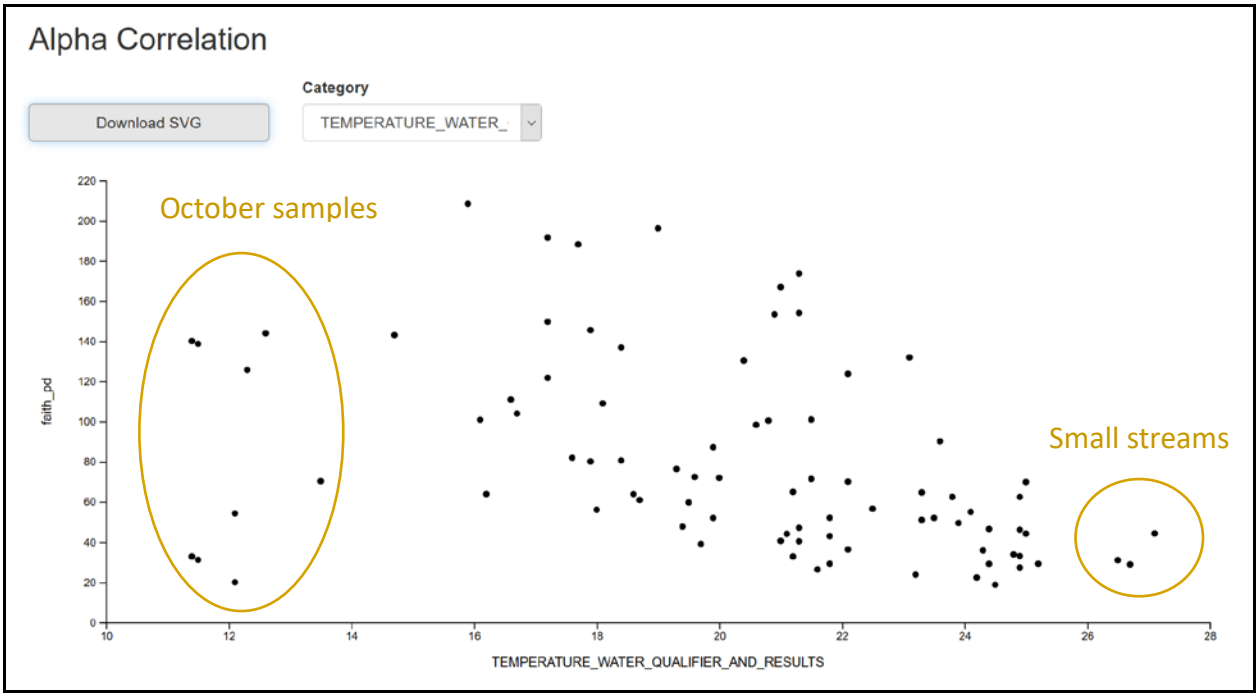

Figure 1. Microbial phylogenic diversity (pd) declines in response to increasing water temperature in NH streams. Samples collected in October show generally higher diversity, indicating that microbial community recovers fairly quickly in the fall when temperatures decrease. A similar trend of decreasing diversity with stressors is seen for nutrients (phosphorus and nitrogen) and dissolved oxygen.

Samples were also collected from stream periphyton (algae) in 2017. Periphyton is used to support stream classification in several states including Maine. Samples were collected from streams in Maine by scraping algae directly from rocks, and in New Hampshire using glass slides as a substrate. Samples were extracted and amplified with an 18S primer to identify eukaryote species. The data set is limited to 20 samples, but shows a potential correlation between stream classification and periphyton species (Figure 2). Samples collected in New Hampshire are distinctly different from samples collected in Maine, which we attribute to the difference in collection methods. The DNA method provides detailed information on number of species, and community composition, but no information on species counts.

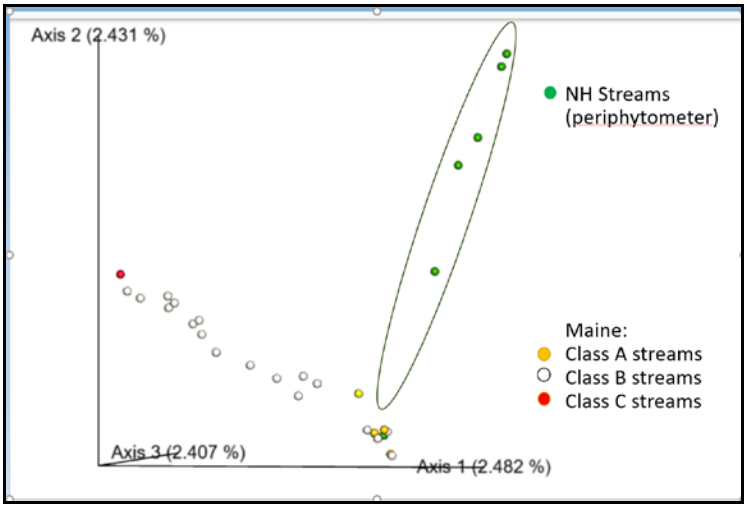

Figure 2. Principal components analysis of algae communities in small streams. Samples which are grouped together have similar algae communities. This preliminary data suggests that amplicon DNA analysis can support stream classification.

These results indicate that DNA-derived periphyton community analysis may be useful for developing or monitoring stream clarification and condition indicators.

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. Society of Toxicology and Chemistry, Minneapolis, MN. Nov 2017.

New technology and New Issues in Watershed Management – eDNA Methods for NH Streams. A. Watts. Lamprey River Symposium. Durham, NH, Jan 2018

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 3).

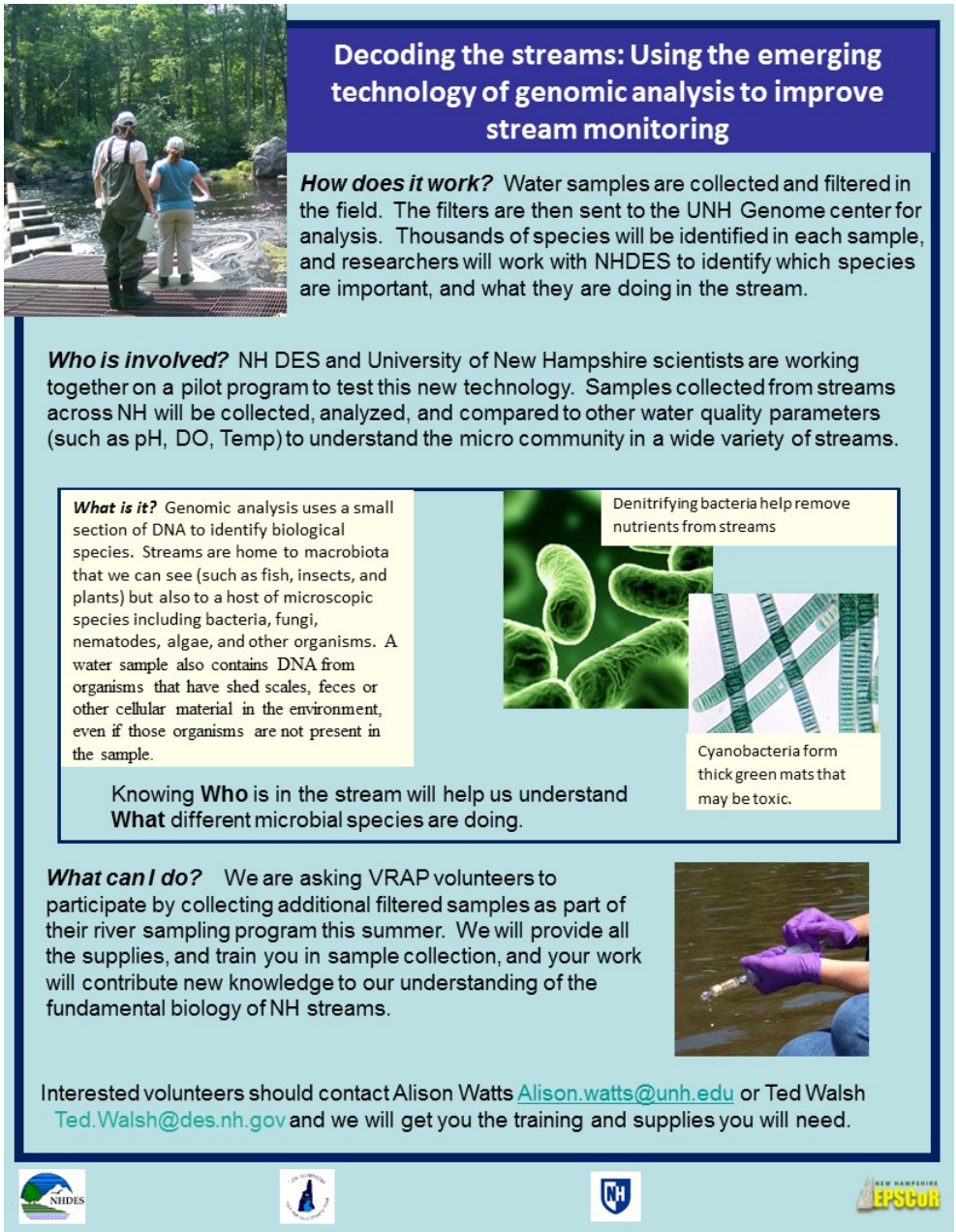

Figure 3. Fact sheet distributed to VRAP volunteers.

Number of students supported
This project has provided partial support for three undergraduate students (Kendra Dow, Tim Sommers, and Cassidy Wallich, all seniors in Environmental and Civil Engineering).

Number and names of faculty and staff supported
Alison Watts, Research assistant Professor