Conference Abstract

Developing DNA-Based Ecological Classifications for Shallow Streams in Northeastern United States

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Abstract

Several regions in the Unites States have developed algal bioassessment methods for wadeable streams (e.g. Maine, Connecticut). Algal communities and indicator species are correlated with land use, water chemistry, and other watershed metrics to identify ecosystem indicators relevant to local conditions. Taxonomic analysis has historically been performed by microscopic examination and identification of species within a sample. A pilot survey was conducted to assess the use of DNA-based taxonomic methods in algal bioassesments of stream condition in New Hampshire and Maine in the northeastern United States. Algae samples were collected at 60 wadeable streams throughout the region in the summer of 2019. Samples were collected at sites included in long term water quality monitoring networks, to allow comparison with longer term water quality and bioassesment data. Samples were extracted and sequenced with primers targeting 18S for eukaryote species, rbcl for diatoms, and 12S for fish. Algal features were correlated with stream parameters including nutrient concentration, historic Benthic IBI indices, and other water quality metrics. Our results support previous studies indicating that molecular-based methods are a viable approach to water quality assessment. We found that:

- DNA-derived algal communities can be correlated to nutrient categories, and indices developed from multiyear data are reflected in the community.
- DNA-derived algal communities can be correlated to Benthic IBI ratios, and to traditional algal bioassesment categories.

- 18S and rbcl primers were both effective at amplifying target species to identify distinguishable community assemblages.
- Fish were detected in water samples at all sites, and the species identified represent those that are likely to be present based on previous electro-fishing surveys.

Keywords

Streams, assessment, indicators, metabacoding

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