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Diatom tolerance metrics to identify total phosphorus as candidate cause of aquatic life impairment in Connecticut, USA freshwater streams



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ABSTRACT

Anthropogenic phosphorus is a major driver of cultural eutrophication in rivers and streams, leading to numerous water quality impairments, including detrimental shifts in biological communities. Phosphorus has not been identified as a cause of aquatic life impairment in the State of Connecticut (CT), USA, rivers and streams. That is because phosphorus effects on aquatic life are complex, varying spatially and temporally, and often have indirect effects on biological communities typically used for water quality assessment, such as macroinvertebrates and fish. Biological tolerance metrics can be useful in identifying biological impairments due to pollutants that do not lend themselves to conventional toxicity testing, like phosphorus, by providing a measure of the sensitivity of aquatic organisms to anthropogenic disturbance over time. Diatom species tolerances to phosphorus have been derived at national and regional scales in the USA, but not specifically for CT. National scale studies often have the advantage of utilizing larger datasets to derive tolerances over a wide range of environmental conditions, however, developing tolerances specific to a region or for CT may better capture localized conditions. Our study aims to identify diatom species tolerance value metrics suited to aiding aquatic life assessments in CT. We developed diatom tolerance metrics using two different methods that combined responses of individual diatom species along the observed phosphorus gradient using data collected in CT. We then compared the existing national and regional diatom tolerance metrics to the CT tolerance metrics. Our results found the best performing metrics for use in CT aquatic life assessments were CT tolerance values derived using a generalized additive modeling approach. These metrics were CT specific, discriminated well between high and low levels of phosphorus concentrations, and had a greater response to phosphorus than alternative ecological gradients (chloride, pH, and water temperature) that also affect diatom species composition. These results show that diatom tolerance metrics for phosphorus can be effectively used in a weight of evidence approach to identify phosphorus as a cause of aquatic life impairment in CT. All source code and data for this project is freely available and open source at: https://github.com/marybecker/DiatomTPMetrics.

1. Introduction

Cultural eutrophication is a serious threat to water quality in the State of Connecticut, USA (CT) (Becker, 2014; CASE, 2014) and is one of the most pressing water quality issues facing the nation (U.S. EPA, 2017). The United States Environmental Protection Agency (U.S. EPA) has identified cultural eutrophication as one of the primary factors resulting in impairment of United States surface waters and encourages all states and tribes to develop strategies to reduce nutrient (nitrogen and phosphorus) pollution that address impairments caused by cultural eutrophication (Grumbles, 2007; Stoner, 2011; U.S. EPA, 2017, 2000). The State of Connecticut Department of Energy and Environmental Protection (CT DEEP) has not identified nutrients as a cause of aquatic

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life impairment in any freshwater stream to date because nutrient effects are complex. They vary across spatial and temporal scales and indirectly affect higher trophic levels, like macroinvertebrates and fish, typically used for water quality assessments.

Biological inference metrics may be particularly useful for identifying biological impairments due to pollutants that do not lend themselves to conventional toxicity testing, like nutrients, that vary dynamically across space and time (CASE, 2014; Karr and Chu, 2000). Biological inference models look at the responses of individual taxa across a stressor gradient and identify where taxa achieve their highest abundance or optima. Biota integrate past disturbances occurring over their lifespan and can therefore provide a more informative measure of environmental conditions over this time period (Karr et al., 1986).





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Inferring environmental conditions from biological observations provides a biologically relevant measure of environmental conditions at a site (Karr, 2006). Thus, these inferences provide a complementary line of evidence that can strengthen a case made with other measurements (Yuan, 2006).

CT DEEP has developed and utilized macroinvertebrate tolerance metrics derived from CT data to infer overall stream health for over 20 years. In aquatic biological assessments, the term tolerance is used to describe how aquatic taxa respond to a gradient of anthropogenic stress. The metrics assist in determining attainment of aquatic life goals in streams. Although these tolerance metrics help to identify whether or not a stream has an aquatic life impairment, they do not help to illuminate the cause of the aquatic life impairment. Tolerance metrics developed to diagnose nutrients as a candidate cause of aquatic use impairments would help to direct effective management action for nutrients in rivers and streams.

Algae are an aquatic life community that are ubiquitous in streams and are primary energy source for many stream food webs (Stevenson, 1996). CT DEEP has more recently begun collecting diatoms, a type of alga that are well-studied indicator of nutrient degradation in aquatic systems (Danielson et al., 2011; Potapova and Charles, 2007; Van Dam et al., 1994). Diatom communities are sensitive to small increases in nutrient levels in streams, making them particularly useful as indicators of nutrient pollution and cultural eutrophication (Black et al., 2011; Pan et al., 2000; Smucker et al., 2013a).

There are a variety of pre-existing diatom metrics to assess water quality and methods to derive metrics (Paul et al., 2017). Because of their wide geographic distribution, diatom indicators and metrics have been successfully applied in regions outside of the area where they were developed (Pignata et al., 2012; Srivastava et al., 2017; Tan et al., 2013). Deriving inferences at a national or continental scale typically have the advantage of utilizing larger datasets and covering a wide range of environmental conditions. However, inference values could be very different for a given taxa depending on the range of data that are collected (Yuan, 2006) and evidence suggests that inferences created specifically for regional areas of similar ecological condition may perform better than those developed at a larger geographic scale (Potapova and Charles, 2007).

Weighted averaging models are the most common approaches to developing diatom indicators (Danielson et al., 2011; Kireta et al., 2012; Potapova et al., 2004; Potapova and Charles, 2007). Weighted average models often identify an optima, which can then be used to infer tolerance to nutrients (Yuan, 2006). Other methods exist and have been used to infer macroinvertebrate tolerance to nutrient stressors (Yuan, 2004).

The aim of our study was to identify tolerance value metrics suited to aiding bio-assessments in CT. Previous research has identified ecologically relevant total phosphorus (TP) concentration thresholds in CT streams (Smucker et al., 2013a). This study builds on that research to provide an additional line of evidence towards diagnosing TP as a cause of aquatic life impairment in CT. Our goal was to identify biological tolerance metrics that best discriminate between low and high TP concentrations at sites to use in bio-assessments as a line of evidence to diagnose TP as a candidate cause of aquatic use impairments freshwater streams in CT. To achieve that goal, we developed metrics using CT specific data and compared those metrics to nationally and regionally derived metrics to see which performed best in discriminating between sites with high and low TP concentrations. We replicated methods in a national study (Potapova and Charles, 2007) using data collected and derived in CT. We also used an alternative statistical method for deriving species-specific tolerance values (Yuan, 2004) using CT data. We then tested the specificity of response for the TP species tolerance metrics by examining their relationship to alternate ecological gradients (pH, temperature and chloride) previously identified as affecting variation in diatom species composition (Porter-Goff et al., 2013; Potapova and Charles, 2002).

2. Materials and methods

2.1. Study site characteristics and sampling

CT has a total land area of approximately 13,000 km² and encompasses approximately 9383 km of rivers and streams at the 1:100,000 map scale (CT DEEP, 2017). CT is in northeastern United States and is located in the Northeastern Coastal Zone and Northeastern Highlands level III ecoregions (U.S. EPA, 2013). The Coastal Zone was glaciated, but is not as hilly and mountainous as the Highlands in the northwest corner of the State. Both ecoregions have rocky, nutrient poor soils. Mature natural vegetation is dominated by hardwood and mixed hardwood and coniferous forest. Annual average rainfall varies from approximately 1000 mm to 1500 mm (Auch, 2016; Kambly, 2016). Large areas of developed land are found east along Long Island Sound Estuary and northward along the Connecticut River in the center of the State while the remaining land is typically residential and forested (Fry et al., 2011).

Two sets of CT data were used in this study. One was used to develop CT specific tolerance values for diatom species and tolerance metrics (calibration dataset) and the other was an independent dataset used to test the metrics and compare the performance of the CT metrics to the nationally derived metrics (test dataset). The calibration dataset included 155 samples from 114 sites. Locations were selected using an integrated approach that combined probabilistic and targeted monitoring designs (Becker, 2012). Composited periphyton samples were identified at the Patrick Center for Environmental Research of The Academy of Natural Sciences of Drexel University in Philadelphia (ANSP). The test dataset included 55 samples from 50 sites. Locations were selected using a targeted approach designed to capture the TP gradient in CT (Becker, 2011, 2010). Composited periphyton samples were identified by EcoAnalysts. For both datasets, diatom samples were processed using nitric acid to remove organic material before mounting on slides using NAPHRAX[™]. Diatoms were identified to the lowest practical taxonomic level, typically species, and approximately 600 valves were enumerated per sample.

Drainage basins for sample sites were estimated by accumulating the area of National Hydrography Dataset (USGS, 2011) catchments at a 1:24:000 scale using code developed in R (R Development Core Team, 2016). The drainage area upstream of the sites ranged from 1.3 to 1844.5 and 3.4 to 1463.1 square kilometers in the calibration and test datasets, respectively. TP yields were estimated for each site in the calibration and test datasets using the USGS SPAtially Referenced Regressions On Watershed attributes (SPARROW) TP model for the Northeastern and Mid-Atlantic U.S. (Moore et al., 2011) and compared to statewide TP yields in all streams to ensure that sampling sites were representative of the TP gradient in Connecticut streams (Fig. 1). We divided SPARROW model TP yields for all streams in the state into 4 categories by percentiles: 0–25th (low), > 25th–50th (mediumlow), > 50th–75th (medium high) and > 75th (high). Study sampling sites were representative of the statewide TP gradient with 22.8%, 24.6%, 24.6% and 28% of the sampling sites falling into the low, medium-low, medium-high and high categories, respectively, in the calibration dataset and 16%, 32%, 24% and 28% of the sampling sites falling into the low, medium-low, medium-high and high categories, respectively, in the test dataset.

In both datasets CT DEEP collected epilithic diatom samples in the late spring and summer primarily in June and July under base-flow conditions. Samples were collected by scraping periphyton off of cobble-sized substrate within a 150 m stretch of wadeable riffle or run sections of the stream (Becker, 2012, 2011, 2010). Periphyton is a complex mixture of microscopic algae (including diatoms), bacteria and fungi that grows on the bottom substrate of a river or stream. Periphyton was scraped from the entire top surface of 5 rocks distributed within a 150 m reach and composited into one sample (Becker, 2012, 2011, 2010).

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