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Improving Diagnostic Capacity of Bioassessment: New Tools and the Role of Molecular Methods

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Abstract

Traditional measures of water or soil chemistry provide a limited view of environmental health through the presence of pollutants or contaminants of concern at a specific point in time and space. In contrast biological measures provide an integrated view of the condition or health of a specific environment through direct measure of the resident organisms that are exposed to contaminants of concern through multiple pathways (e.g. ambient contact, ingestion). In aquatic environments, such as streams, wetlands, and coastal waterbodies, primary producer communities (e.g. algae) and primary consumer communities (e.g. benthic invertebrates) are often used as bioassessment indicators.

Over the past 20 years, numerous indices have been developed worldwide that provide simple measures of health (or condition) based on algal and benthic invertebrate community composition. Although these tools have been broadly successful, they have some limitations. In particular, as the number and complexity of environmental stressors increases, there is a desire to improve the diagnostic power of bioassessment tools. Such improvements can occur through application of causal assessment frameworks, development of new “predictive” scoring tools, use of multiple indicators, development of targeted metrics that are sensitive to specific stressors, and by measuring functional response of the ecosystem to stress. Molecular tools, such as DNA barcoding and metabarcoding provide opportunities to support many of the “next generation diagnostic assessments” by increasing taxonomic resolution, broadening the suite of taxa that can be evaluated, and providing tools to measure functional aspects of the ecosystem. In this talk, I will explore several diagnostic approaches, the role of molecular methods in supporting these approaches, and the science needed to advance these tools to broadscale application for environmental monitoring and assessment.