Application of eDNA and Metabarcoding to Routine Stream and Wetland Biomonitoring Programs in California

Eric D. Stein, Raphael Mazor, Bryan White

Southern California Coastal Water Research Project Authority, Costa Mesa, CA, USA

Abstract
Biological monitoring and assessment is routinely used to help answer questions about stream and wetland health or presence of species of interest, such as invasive or sensitive species. Molecular methods, such as traditional DNA barcoding, have been explored as tools to improve resolution and efficiency of biomonitoring programs.   Despite the advantages of these tools, they require intensive sample processing (e.g., sorting individual organisms) and can only detect targeted species. Extracting DNA from environmental samples (eDNA), combined with next generation sequencing offers promise by allowing for relatively rapid detection of species presence without the need to sort individual specimens. However, interpretation of eDNA data depends on understanding issues such spatial fidelity, temporal persistence, and bias among species (i.e. relative probably of detecting one species vs. another).   We have begun to evaluate some of these factors by testing applications of eDNA to biomonitoring programs in California wadeable streams. Here, we present preliminary results testing the use of eDNA to 1) detect the presence of an invasive mussel, the New Zealand Mud Snail, 2) determine how far downstream a eDNA signal may travel, 3) compare assemblage structure based on eDNA to traditional morphology-based analysis of benthic macroinvertebrate samples, and 4) evaluate the ability of eDNA to detect species typically excluded from stream bioassessments.   Our results suggest that eDNA and metabarcoding hold promise for application to routine biomonitoring, but several interpretation and methodological issues remain to be resolved.