POSTER PRESENTATION

DIATOM QUALITY ASSURANCE PROTOCOLS: METHODS, DIFFICULTIES AND SUGGESTIONS FOR IMPROVEMENT

Diane Winter, Dennis Vander Meer, Wease Bollman

Rhithron Associates, Inc., 29 Fort Missoula Road, Missoula, Montana 59804

Biological monitoring using freshwater diatoms can provide a baseline for a sampling location, allowing comparison with subsequent sampling intervals, or it can determine the current status and 'health' of a location through comparison with data from previous sampling intervals and/or ideal, unimpaired conditions. Current diatom analytical methods of such studies should ideally involve regular quality assurance (QA) checks to ensure consistency and reliability of taxonomic data. The large diversity of diatom species allows detailed representation of assemblages present in differing environments as well as provides the potential for analytical error or inconsistency. This issue is often addressed by two or more analysts counting designated transects and comparing the outcome. Maintaining consistency in identification through comparative counts is hindered by differing species concepts as well as morphologically similar species.

Comparative similarity between analyses is determined through application of the Bray-Curtis similarity index, calculating the inclusive percentage of similar taxa observed in each count, acceptable levels falling between 60-75%, dependant on sample diversity. Our comparisons note a range of 56.5-93.68% similarity for samples analyzed during 2006-2009, with a 79.6% average. Four analysts were employed in this work during this time, one responsible for the original counts and three external QA analysts. Application of a variety versus a nominate form, such as *Achnanthidium minutissimum* and *A. minutissimum* var. *gracillima*, is a common source of irregularity between counts. Other species, such as *Rossithidium pusillum* and *Achnanthidium biasolettianum*, represent morphologically similar species that could be identified interchangeably by different analysts. Commonly interchanged species in our QA data include *Amphora inariensis* vs. *A. pediculus*, *Encyonema minutum* vs. *E. silesiacum*, and *Staurosira construens* var. *venter* vs. *Staurosirella pinnata* vs. *Pseudostaurosira brevistriata*. Incorrect identification of some, such as *Nitzschia palea* vs. *N. paleacea*, can result in ecological misinterpretation (see Lange-Bertalot, 1979).

Using a shared-image database(s) and an accepted list of species has been used successfully in previous projects involving several different labs (e.g. PIRLA, SWAP and NAWQA). Additionally, defining specific publications and illustrations that best show critical characteristics for species presented with a range of morphological variation in the literature would be useful. Definition of criteria used to draw morphological boundaries between different species (and varieties) is an essential step in maintaining consistency. We suggest a further step would be to promote external QA between several labs, seeking to ensure consistency in taxonomy and analytical methods, which would be of benefit to all.