

Abstract

In past decades, molecular methods helped to discover extensive diversity hidden in morphologically delimited diatom species. Diatom taxonomy awaits revision and molecular methods will play an important role in this pursuit. DNA-barcoding is a relatively cheap and rapid way to incorporate molecular data in the diatomological research. The crucial step, which determines its efficiency, is marker selection. Therefore, we examined the performance of candidate barcode markers in the model genus *Frustulia*. Molecular data from the study helped to support delimitation of two new species, *Frustulia curvata* and *Frustulia paulii*. Similar to previous research, the best-performing markers were part of the large ribosomal subunit and part of the RUBISCO gene. We encountered a case where these two markers disagreed. Similar gene tree discordances might compromise molecular species delimitation, which is based on single molecular loci. The use of both markers in a dual-locus barcode can mitigate the risk and draw attention to problematic cases that merit further study. However, the superior mean of species delimitation, which we used to set species limits in the complex *Eunotia bilunaris-flexuosa*, provides algorithms that use multiple loci and accommodate our understanding of molecular evolution.

Several studies showed that the discovered genetic diversity has a bearing on diatom ecology. Therefore, diatom ecology warrants re-examination in the context of newly discovered diversity. We explored two, approaches that might help us to achieve this goal. The first combines molecular-assisted alpha-taxonomy with computer-based automatic identification of frustules from natural diatom assemblages. We used this approach to examine the diversity of *Frustulia* species in northern Europe; the study revealed a positive correlation between species abundance, realized pH niche breadth, and geographical distribution. To test potential drivers behind this pattern, it is necessary to use the second approach: a controlled laboratory experiment. An example comprises my second study, in which we measured fundamental niches (i.e. pH tolerance) of 15 closely related lineages from the complex *Eunotia bilunaris-flexuosa* and compared them with their respective realized niches (i.e. source locality pH). The experiment showed significant differences in pH-dependent growth of individual species and strains and proved that the physiological response to pH significantly correlates with their distribution in nature. The results of both studies suggest that species hidden by their similar morphologies might be ecologically diverse. This stresses the need to correctly identify diatom species because only then can we understand diatom biology and fully exploit diatom-based applied sciences.