



Conference Abstract

DNA metabarcoding and morphological methods show complementary patterns in the metacommunity organization of lentic epiphytic diatoms

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Abstract

Diatoms are important organisms in freshwater ecosystems due to their position as primary producers and therefore, analyzing their communities provides relevant information on ecosystem functioning. Diatoms have historically been identified based on morphological traits, which is time-consuming and requires well-trained specialists. Nevertheless, DNA barcoding offers an alternative approach to overcome some limitations of the morphological method. Here, we assess if both approaches are comparable methods to study patterns and mechanisms (including environmental filtering and dispersal limitation) of epiphytic diatom metacommunities using a comprehensive dataset from 22 Mediterranean ponds at different taxonomic resolutions. We used a fragment of *rbcl* barcode gene combined with High-Throughput Sequencing to infer diatom community composition. The overall degree of correspondence between both approaches was assessed by Procrustean rotation analysis and Procrustean randomization tests, whereas the role of local environmental variables and geographical distances was studied using a comprehensive combination of BIOENV, Mantel tests and distance-based redundancy analysis. Our results showed a relatively poor correspondence in the compositional

variation of diatom metacommunity between both approaches. We speculate that the incompleteness of the reference database and the bioinformatics processing are the biases most likely affecting the molecular approach, whereas the limited counting effort and the presence of cryptic species are presumably the major biases related with the morphological method. On the other hand, variation in diatom community composition detected with both approaches was strongly related to the environmental template, which may be related with the narrow ecological niche and the strong preferences for particular substrata of some diatom species. Nevertheless, we found no significant relationship between compositional variation and geographical distances at regional extent.

Overall, our work highlights the importance of DNA metabarcoding to address empirical research questions of community ecology in freshwaters, especially once the reference databases include most genotypes of occurring taxa and bioinformatics biases are overcome.

Keywords

Diatoms, DNA barcoding, *rbcl*, High-Throughput Sequencing, Metacommunity

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