

GENOTYPIC DIVERSITY AND DIFFERENTIATION AMONG BENTHIC FRESHWATER DIATOM POPULATIONS AS REVEALED BY MICROSATELLITE ANALYSIS

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Microsatellite-based studies of natural populations provide insight into the genetic and genotypic diversity within populations and patterns of gene flow between them at different spatial scales. In diatoms and other microalgae, such studies are almost exclusively confined to the marine phytoplankton. Patterns for freshwater microalgae can be expected to be different due to the typically highly fragmented and more short-lived nature of their habitat. We developed 6 microsatellite loci for the epiphytic freshwater diatom *Eunotia bilunaris* “robust” and used these to investigate genotypic diversity and differentiation between *E. bilunaris* “robust” populations at different spatial scales, from ponds within the same pond system, over the same region, to between regions on a Western European scale. For this, 340 isolates from 9 populations were obtained, their species identity confirmed using valve morphology combined with *rbcL* sequences, and their microsatellite allelic composition determined. Analyses show that while in some populations there was a very high genotypic diversity with every strain belonging to a different genotype, in others one or a few genotype(s) made up half of the population. Population differentiation was low between ponds from the same pond system or for a single population sampled twice ($F_{st} < 0.1$) but could already be very high ($F_{st} > 0.2$) for populations from the same region, located some tens of kilometers from each other. These results will be compared with a similar dataset for the benthic freshwater diatom *Sellaphora capitata* (356 isolates from 8 Scottish populations and one Belgian) using 7 microsatellite loci, allowing to test the generality of findings in *Eunotia*. Finally, possible causes for the observed large population differentiation will be discussed.