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GENETIC DIVERSITY WITHIN THE GOMPHONEMA PARVULUM COMPLEX

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In order to use diatoms as indicators of the ecological quality of running waters, a better knowledge of the taxonomy of species inhabiting rivers is necessary. Many species belonging to the genus *Gomphonema* are often represented in freshwater benthic samples. However, several taxa groups are difficult to identify under light microscopy, and some clarifications and taxonomical reassessments are called for. This is the case of the genus *Gomphonema* and specially the species complex *G. parvulum*, which is widely represented in freshwaters. *G. parvulum* is known to be a species with a great morphological variability and taxonomists often have problems in distinguishing morphologically among taxa belonging to this species complex. Distinction of these varieties and forms is important because they often have different ecological values in the diatom indices.
Molecular biology techniques are powerful alternatives to microscopic observations for studying diatoms. Several examples illustrate how DNA sequences (barcodes) can be used to stabilize taxonomy (Jahn et al. 2008, Evans and Mann 2009). Sequences of 18S rDNA, ITS, *rbc*L and *cox*1 of several strains of *Gomphonema parvulum* and other *G.* species from rivers in French tropical islands (Mayotte, La Réunion), Mainland France, Italy, Luxembourg, Portugal and Spain have been determined and compared together with sequences available in GenBank. Two main group of *G. parvulum* can be distinguished. Geographical distribution does not explain the separation in two clades. The results indicate that the species complex of *G. parvulum* would divide into two segregate species.

References

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