EVALUATION OF CANDIDATE BARCODE MARKERS ON THE DIATOM GENUS *FRUSTULIA*

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Traditionally, the identification of diatoms has been based on the size, outline, and ultrastructural features of their silica frustules. However lately, the integrative taxonomical approach showed that molecular techniques are often essential for species level identification and that morphological examination usually enables only the identification to the higher taxonomical levels. Even though this crude classification may be sufficient for biomonitoring and paleoecology, it is absolutely unsatisfying once we aim to study diversity or biogeography of diatoms. Possible solution to this problem seems to be DNA-barcoding; however, despite several attempts to find a suitable barcode marker for diatoms a consensus has not yet been made and thus there is a need to examine other "model systems" and DNA regions.

Our data, which were primarily collected for phylogenetic and biogeographical analysis of the genus *Frustulia*, enabled the evaluation of one new (plastidial psbA) and five candidate barcode markers (partial SSU (V4), partial LSU (D1-D2) and 5.8S+ITS2 nuclear rDNA, plastidial rbcL-3P and mitochondrial coi-5P). In order to assess the power, practicality, and universality of each marker both more distantly related *Frustulia* species and sister species from pseudocryptic complex *F. rhomboides* were included in the analysis. In accordance with previous studies all tested markers were suboptimal in at least one of three decisive criteria.

Although the "perfect" diatom barcode marker has not yet been found, it seems advantageous to adopt a unified barcoding methodology including culturing, vouchering and DNA preservation. Thus, once the suitable marker is found its sequences can be still obtained. All in all, we trust that nomenclaturally effective DNA-barcoding will contribute to more stable diatom taxonomy, which has currently the utmost priority in diatomology.