



Evaluation of phylogenetic markers suitable for *Planktothrix* spp. discrimination

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In Portugal, potentially toxic cyanobacteria from *Planktothrix* genus have become frequently observed in freshwater reservoirs. Identification of *Planktothrix* species through optical microscopy is complicated due to limited morphological differences among them.

The aim of this work was to determine the most suitable phylogenetic markers that could be used for the molecular identification of *Planktothrix* species. In order to do so, several genes of interest were selected: *rpoB*, *rpoC1*, *cpcA*, *cpcB*, *rbcX*, 16S rRNA genes and 16S rRNA-tRNA^{Ile}-tRNA^{Ala}-23S rRNA internal transcribed spacer (ITS), and their sequences retrieved from public databases.

Phylogenetic analysis showed that 16S rRNA, *cpcA*, *rbcX* genes and ITS region trees do not allow a clear discrimination of *Planktothrix* species, however *cpcB* and *rpoB* seemed putative suitable phylogenetic markers for *Planktothrix* species identification. The applicability of these markers was then evaluated in 20 *Planktothrix* isolates, isolated over the years from several Portuguese freshwater reservoirs and maintained in the Estela Sousa e Silva Algae Culture Collection (ESSACC). The selected genes, *cpcB* and *rpoB*, were amplified by PCR and sequenced and the resulting trees compared with the phylogenetic clustering obtained with our previously characterized *rpoC1* phylogenies. The phylogenetic analyses, based on the three gene regions, revealed that *Planktothrix* isolates analyzed in this study could be phylogenetically resolved into their corresponding species.

This work contributes for the discussion of the appropriate genes that can be used in phylogenetic identification of *Planktothrix* species.