

NEW BIOMONITORING APPROACHES BASED ON NEXT GENERATION SEQUENCING: A TEST FOR FRESHWATER DIATOM COMMUNITIES

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The EU member states are required to assess rivers quality with diatoms. Species composition and abundance must be defined. As microscopic identification requires time and expertise, the development of a new tool for fast and accurate identification is a major challenge for routine biomonitoring of aquatic ecosystems.

We evaluated the capacity of Next Generation Sequencing to assess the composition of environmental diatom samples. We pyrosequenced 3 mock environmental communities made of known diatom strains (30) with 3 markers (18S, rbcL, cox1) in order to establish their species inventories. Read libraries obtained from pyrosequencing were compared to reference databases (laboratory and GenBank diatom sequences) using metaMatch software to establish the inventories. Their accuracy was tested by comparison to real compositions.

18S sequences have a low resolution. Cox1 seems to have the largest resolving power, but insufficient reference database. Inventories obtained from rbcL are closely related to real inventories. RbcL combines a high resolving power with large reference databases, and coupled to pyrosequencing, could serve as a molecular tool for quick and easy identification of diatom species in environmental samples.