



Conference Abstract

Novel DNA-based test for the identification of benthic diatoms of European freshwater waterbodies (WAT-DIMON)

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Abstract

Diatoms are unicellular eukaryotic organisms, which have been exploited over the years for effective freshwater bioassessment. Therefore, they are excellent bioindicators, routinely used in national environmental monitoring programs all over Europe within the Water Framework Directive (WFD) 2000/60 /EC (Foster et al., 2000) and CEN standards (CEN, 2018).

Over the years, new technologies have been introduced to this field to maximise and improve the time and cost required for freshwater bioassessment. The application of DNA metabarcoding for the characterisation of benthic diatom communities for WFD was recently introduced (Vasselon et al. 2017, Kelly et al. 2018). Through this technique, the identification of the species present in one environmental sample, is established using

genetic variability and is characterised by a short DNA fragment called a barcode (Vasselon et al., 2019).

The Wat-Dimon Eurostars project aim at creating a novel genomic test for the identification of European benthic diatoms. This new DNA-based test could be routinely implemented in national environmental monitoring programs all over Europe within the Water Framework Directive (WFD) 2000/60 /EC and CEN standards. In the near future, metabarcoding can complement and/or replace the traditional ecological assessments based on the morpho-taxonomy methodology approach needing taxonomic expertise and been subjected to scientific bias. Additionally, the project aims at developing a complementary bioinformatics tool for the biotechnological interpretation of the results. Such product will allow the prompt response to the environmental needs, the early assessment of environmental quality and early treatment response. The study will be developed and validated along a longitudinal gradient in the south part of Europe (Portugal, Spain, Cyprus), including four different biogeographical regions (Macaronesia, Atlantic, Alpine and Mediterranean). The method will cover all steps, from sampling and DNA extraction of diatom assemblages and amplification of DNA barcodes using universal primers for diatoms. The amplified products will be sequenced using Illumina MiSeq. Then, existing bioinformatic pipelines will be adjusted to quality-filter the high number of sequences from the samples and identify them by comparison with reference databases (Diat.Barcode, BOLD, GenBank). Enhancing these databases with diatom species prevalent in the different biogeographical regions assayed will be essential as existing databases are biased to more northerly regions and do not take into consideration harsh, extreme climatic conditions which are prominent in the Mediterranean and Macaronesia regions (Fig. 1). The project focuses on the *rbcl* gene and will used 18S gene only as an alternative or complementary tool if any problematic taxa appear.

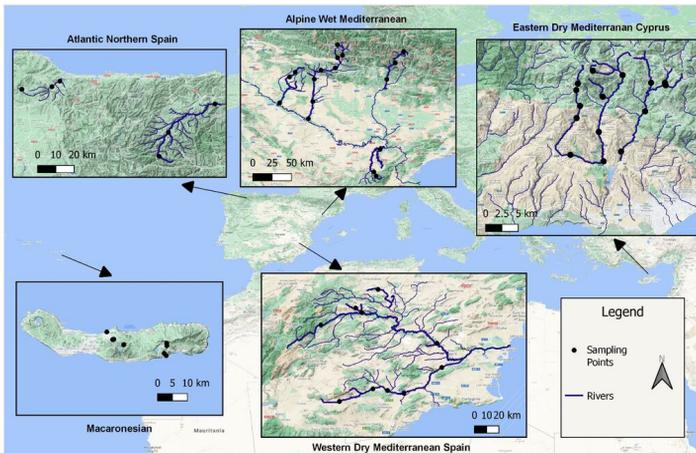


Figure 1. [doi](#)

Compiled map for the representation of European specific monitoring network for the Wat-Dimon project

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