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Conference Abstract

New trends in bioassessment of aquatic ecosystems: from organisms to DNA-based metrics

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Abstract

Traditionally, the biological quality of aquatic ecosystems is assessed using selected groups of organisms that can be identified morphologically. Recent advances in high-throughput genomic approaches offered new opportunities to monitor biodiversity and assess ecological status using DNA barcoding and metabarcoding. The DNA-based tools have been used in three different ways: (1) to replace morphological identification of biological quality elements in existing biotic indices, (2) to develop new molecular indices based on morphologically inconspicuous groups of potential environmental indicators, and (3) to predict biotic indices from environmental DNA datasets using machine learning methods (Pawlowski et al. 2018). The next steps need to take advantages and challenges of these different approaches into account in view of their future application in routine bioassessment.The Working Group 2 of DNAqua-Net, Biotic Indices & Metrics, has worked with several task forces tackling different organism groups (fish, macroinvertebrates, diatoms, bacteria, protists, meiofauna), because challenges have been shown to be quite different dependent on the target organisms Kahlert et al. 2019. For the fish the eDNA-metabarcoding methods are well developed and give very good results in terms of species detection. The important question is to see if the semi-quantitative data retrieved from the metabarcoding (proportion in eDNA sequences) could be translated to proportions in biomass/numbers that are now used in many indices. The fish researchers are trying to fit these data in, but some correction factors might be needed to correct for differences between molecular and conventional methodsRegarding the macroinvertebrates, much

discussion regarding index development was focusing on the importance of abundance measurements, and it was tested how existing indices would perform if barcoding data would be used instead of morphological data. Still discussion is ongoing on several technical issues, including the use of preservative for DNA extraction from bulk samples, the choice of primers for PCR amplification and the incompleteness of reference databases which impedes the correct assignment of eDNA sequences. Also minimum standards for routine operation are still missing.The diatom group has worked much on practical issues, starting a large initiative to compare diatom metabarcoding protocols used in routine freshwater biomonitoring for standardization (Bailet et al. 2019, Keck et al. 2018, Vasselon et al. 2017). With diatoms, all three approaches to develop molecular indices have been tested and seem promising, i.e. using existing indices with taxa names derived by matching sequences with reference databases, developing new indices based on molecular data only with traditional fixed scores, and using machine-learning techniques (Bailet et al. 2020, Vasselon et al. 2018, Tapolczai et al. 2019, Keck et al. 2018) The micro- and meiobiota group has worked towards an inclusion of microorganisms into aquatic assessment, because the microbial community dynamics are a missing link important for our understanding of rapid changes in the structure and function of aquatic ecosystems, and should be addressed in the future environmental monitoring of freshwater ecosystems (Sagova-Mareckova et al. 2021). Another focus was on how sediment DNA analysis can be integrated into stated goals of routine monitoring applications. It has been an interesting journey, and we WG2 coordinators would like to thank all the people for their engagement! Keep up the good work!

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Presented at

1st DNAQUA International Conference (March 9-11, 2021)

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