Conference Abstract

DNAqua-Net: Advancing Methods, Connecting Communities and Envisaging Standards

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Abstract

Water covers over 70% of our planet's surface and it is a key resource for the survival of all organisms, among them humans. Unfortunately, water resources face increasing pressures due to the exponential expansion of and resource exploitation by human beings. The consequences of this on water ecosystems represent hallmarks of the Anthropocene such as chemical pollution, warming, scarcity of clean drinking water, ocean acidification and a dramatic loss of biodiversity. As a consequence, the direct and indirect benefits humanity obtained from these ecosystems as cheap services, such as clean water, biomass production, climate regulation and matter fluxes, are increasingly at risk. Therefore, it is of utmost importance to assess the ecological state of aquatic ecosystems and to protect and manage them in a sustainable way. In order to assess the ecological status of a given water body, aquatic biodiversity data are collected by morphological identification of bioindicator species and a comparison of site-specific species lists to those of fairly natural reference water bodies. Quantifying the differences between the lists guides subsequent management actions. Examples of European standard bioasseessments (so far morphologically-based) are Marine Strategy Framework Directive (2008/56/EC) and the Water Framework Directive (2000/60/EC). While the implementation of biomonitoring programs is already a great success, there is room for improvement. In the field of

molecular genetics, revolutionary high-throughput DNA-based analyses have been developed. These can be applied to assess taxon lists of hundreds to many thousands at once and greatly improve speed and accuracy of assessments. However, while these novel genetic tools have attracted a lot of interest, they are not implemented in any of the regular legal biomonitoring programs. In order to change this, the European Co-Operation in Science and Technology (COST) program's Action CA15219 'DNAqua-Net' was launched in November 2016 (Leese et al. 2016). The Action aims to gather existing knowledge and complement those standard procedures by developing and implementing these novel genomic DNA-based approaches for biomonitoring and bioassessment. The Action is comprised of five working groups (WGs): WG1: DNA Barcode References; WG2: Biotic Indices & Metrics; WG3: Lab & Field Protocols; WG4: Data Analysis & Storage and WG5: Implementation Strategies & Legal Issues.

However, central to this is the standardisation of the various protocols, methods and biotic indices and integration of DNA-based datasets (e.g. resulting from DNA metabarcoding, mito- and metagenomics) with existing data standards. Here, the TDWG community will be of central importance and its participation in DNAqua-Net is highly desirable. Moreover, the innovative open access journal *Metabarcoding & Metagenomics* (MBMG) has been recently initiated to promote open science and enhance data exchange in this field as well as to connect the diverse actors and communities (Leese et al. 2017).

Keywords

EU COST Action CA15219, biodiversity data standards, DNA-based biomonitoring, metabarcoding, metagenomics

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