

## Conference Abstract

# Let me see your iD: Impacts of Environmental Stressors on Aquatic Ecosystems Assessed by (e)DNA Metabarcoding

Romana K Salis<sup>‡</sup>, Arne Beermann<sup>‡</sup>, Jan N. Macher<sup>‡</sup>, Christoph D Matthaei<sup>§</sup>, Jeremy Jay Piggott<sup>|</sup>, Alexander M Weigand<sup>‡,¶</sup>, Vera Zizka<sup>‡</sup>, Florian Leese<sup>‡</sup>

<sup>‡</sup> University Duisburg-Essen, Essen, Germany

<sup>§</sup> University of Otago, Dunedin, New Zealand

<sup>|</sup> Trinity College Dublin, Dublin, Ireland

<sup>¶</sup> Musée National d'Histoire Naturelle, Luxembourg, Luxembourg

Corresponding author: Romana K Salis ([romana.salis@uni-due.de](mailto:romana.salis@uni-due.de))

Received: 19 Apr 2018 | Published: 18 May 2018

Citation: Salis R, Beermann A, Macher J, Matthaei C, Piggott J, Weigand A, Zizka V, Leese F (2018) Let me see your iD: Impacts of Environmental Stressors on Aquatic Ecosystems Assessed by (e)DNA Metabarcoding.

Biodiversity Information Science and Standards 2: e25983. <https://doi.org/10.3897/biss.2.25983>

## Abstract

Traditionally, taxonomic characterisation of organisms has relied on their morphology; however, molecular methods are increasingly used to monitor and assess biodiversity and ecosystem health. Approaches such as DNA amplicon diversity assessments are a particularly useful tool when morphology-based taxonomy is difficult or taxa are morphologically ambiguous, for example for freshwater bacteria and fungi as well as many freshwater invertebrate species. DNA metabarcoding provides the ability to distinguish cryptic taxa (which can differ markedly in their ecological requirements and tolerances) and in addition it can provide valuable insights into the genetic and ecological diversity of taxa and ecosystems. While DNA metabarcoding has been used mostly on tissue of sampled specimens, recent years have seen an increased use of metabarcoding on environmental DNA samples: DNA extracted not from sampled specimens, but from the surrounding soil or water. However, the ability of metabarcoding of specimens and metabarcoding of environmental DNA (eDNA) to assess biodiversity and the impact of anthropogenic stressors on freshwater ecosystems is largely understudied. In this talk, several studies

that document the advantages and still open challenges of (e)DNA metabarcoding for assessing impacts of environmental stressors on aquatic ecosystems will be presented. These studies, performed in Europe and New Zealand, integrate impacts across different biotic groups, i.e. look at stressor effects on bacterial, protist, fungal and macroinvertebrate communities. Specifically, we use various case studies from freshwater ecosystems to address the following questions:

1. whether eDNA samples, which can be relatively quickly obtained from the water, can act as reliable proxies for catchment-level stressor impacts by comparing these to DNA obtained from local bulk samples, and
2. whether DNA metabarcoding data can also provide quantitative information rather than only presence-absence data.

In view of the case studies presented, a perspective on the urgent next steps that need to be taken in order to include genetic tools in routine biomonitoring will be derived and linked to the vision of the international network *DNAqua-Net*.

## Keywords

DNA metabarcoding, environmental DNA, stressors, bacteria, protists, fungi, macroinvertebrates

## Presenting author

Romana K Salis