



Title: Understanding freshwater ecosystem health from a microbial perspective

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Freshwater environments are exposed to a variety of stressors that contribute to the decline of freshwater species, ecosystems, and the services they provide. Understanding the causes of these declines is complex, as there are typically multiple, interacting pressures. Additionally, these pressures may be sporadic, for example in the form of pulses of chemical pollution or extreme weather events, which makes directly measuring stressor events a challenge. An established approach to understand both the condition of ecosystems and identify the causes of declines, is the use of bioindicators. These are typically based on the composition of fish, macroinvertebrate, diatom or macrophyte communities. However, bacterial, fungal, and eukaryotic microbial communities dominate freshwater biodiversity, both numerically and in terms of species and genetic diversity. These communities play fundamental roles in the functioning and maintenance of freshwater ecosystem health. They are primarily responsible for the decomposition of organic matter, are key drivers of biogeochemical cycles, photosynthetically fix carbon, and form the base of aquatic food webs. However, we lack an understanding of how microbial communities are structured within freshwaters and, critically, how they respond to ecosystem stressors such as nutrient and organic pollutants, and climatic and hydrological change. Due to the functional importance of these communities, it is a priority to understand more about their composition and distributions across freshwater catchments, as well as explore their ability reveal ecosystem condition.

Advances in High Throughput Sequencing (HTS) of DNA mean that we now can characterise whole microbial ecosystems in unprecedented detail, at low cost and in high throughput. This project will apply HTS of freshwater biofilms collected by the Environment Agency's structured freshwater monitoring programme (the River Surveillance Network). You will utilise both existing data from the RSN and perform field sampling and molecular analysis to develop and refine approaches to enable the utilisation of molecular tools for routine regulatory biomonitoring.

This project will explore novel DNA-based approaches to characterise freshwater microbes, including long-read DNA sequencing (PacBio or Nanopore) to characterise whole communities. These data will be benchmarked against short-read DNA sequencing approaches (Illumina), both generated by you and from the Environment Agency's ongoing work into developing novel approaches for assessing freshwater ecosystem health. There will be opportunities to feed directly into regulatory policy.

The project will address the following key research questions:

1. How are freshwater microbial communities (bacterial, fungal, and eukaryotic) structured across river catchments in England?
2. How do different components of the freshwater microbial community respond to physicochemical and spatial drivers at a national scale?
3. How can novel statistical and machine learning approaches be used to identify bioindicator taxa that can be used determine freshwater ecosystem status and identify stressors?

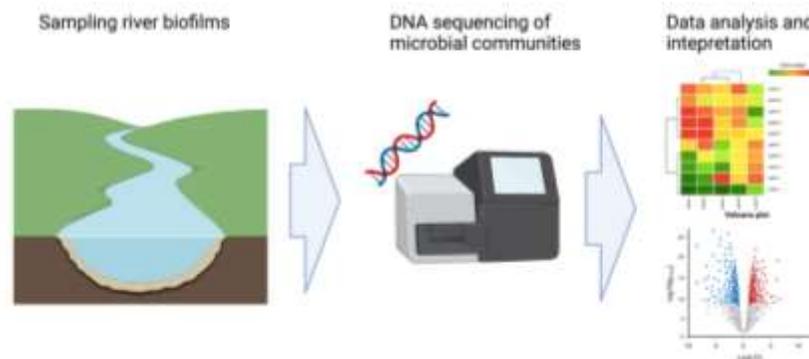


Figure 1 Simplified workflow showing the sampling environment (rivers), DNA sequencing and ecological data analysis.

Training opportunities:

You will receive training in wet-lab skills (DNA extraction, PCR, sequencing on the Illumina MiSeq and Oxford Nanopore platforms) at UKCEH Wallingford and the University of Reading. Training in data analysis and bioinformatics will be supported by Dr. Gweon at the University of Reading, as well as the ability to work with statisticians at UKCEH.

You will spend a three-month placement working within the Climate Change & Resource Efficiency Team within the Environment Agency's Chief Scientist's Group, where you will support the Agency's ongoing efforts to integrate DNA-based tools into regulatory assessments.

As well as training in technical skills, you will have access to UKCEH's training and support via the Researcher Development Programme (RDP). This provides development opportunities via an annual student conference, training in statistical programming, presentation skills, and other personal development opportunities.

Student profile:

You will have a 2:1 or 1st class degree in a relevant subject, such as biology, ecology, microbiology, or environmental science. Further qualifications such as an MSc or MRes in a relevant subject, or equivalent work experience in microbiology, molecular biology, or the analysis of ecological data would be advantageous.

Funding particulars:

This project benefits from CASE funding from the Environment Agency (£1,000 per annum).

References: (optional)

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Tiegs, S. D. *et al.* Global patterns and drivers of ecosystem functioning in rivers and riparian zones. *Sci Adv* 5, eaav0486 (2019).

<https://research.reading.ac.uk/scenario/>