

Identifying the origins of microbially derived aquatic DOM using fluorescence spectroscopy.

Bethany Fox (1), Robin Thorn (1), Alexandre Anesio (2), and Darren Reynolds (1)

(1) University of the West of England, Bristol, United Kingdom (bethany.fox@uwe.ac.uk), (2) University of Bristol, Bristol, United Kingdom

Dissolved organic matter (DOM) in aquatic systems is an essential support of the microbial population and, therefore, of the entire aquatic ecosystem. Aquatic DOM is also key for global biogeochemical cycling of nutrients and connects land processes to the marine environment via hydrological transportation.

There have been multiple advances in technological assessments of the characteristics of aquatic DOM, with spectroscopy becoming widely used. The extensive use of benchtop spectroscopic instruments has led to the development of in situ sensors, improving the spatiotemporal scale of data acquisition. Whilst this has greatly improved understanding of DOM characteristics and patterns, there are still unknown variables, parameters and interactions of DOM within the aquatic environment. In particular, the interactions of aquatic DOM with the microbial population is still mostly unidentified. It is generally accepted that certain DOM fluorescence regions are autochthonous and microbially derived, such as "peak T" fluorescence. However, the origins and metabolic pathways involved in the production and release of these fluorescent molecules is, as yet, not definitively known.

Our work focuses on the identification of these metabolic pathways from whence this microbially derived DOM originates. The most recent stage of the research has utilised traditional microbiological techniques, such as growth curves and chemostat experiments, alongside DOM fluorescence spectroscopic analysis and flow cytometry. The information gained regarding the microbial production and processing of DOM is central for the development of novel in situ fluorescence technology, the ultimate aim of this project.