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Microbial origin of fluorescent dissolved organic matter: bacterial species fluorescence signatures

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Dissolved organic matter (DOM) is ubiquitous in aquatic systems, undertaking an essential role in global biogeochemical cycling (Hudson et al. 2007). Recent research has seen the increasing use of fluorescence spectroscopy for monitoring naturally occurring fluorescent DOM (FDOM), with advances in the technology and in the analysis of data leading to an improved understanding of the interactions between the ecosystem and FDOM (Hudson et al. 2008, Carstea 2010). This work has defined the origins of FDOM as autochthonous, produced *in situ*, often termed 'microbially derived', and allochthonous, transported into the system from external source, often termed 'terrestrially sourced' (Coble et al. 2014).

Previously at EGU we have presented research that has explored microbial processing and production of Peak T, an autochthonous FDOM peak. Within this work we have identified the autochthonous production of a range of FDOM peaks, including Peak T as well as larger molecular weight compounds solely associated with allochthonous derivation. From this we have begun to understand more about the important role that the underpinning microbial community plays in the transformation, utilisation and production of FDOM.

To further this research and enhance the knowledge surrounding microbially derived FDOM our recent research has focussed on the analysis of the FDOM signature of different bacterial species; *Escherichia coli*, *Bacillus subtilis* and *Pseudomonas aeruginosa*. To do this, we have developed a non-fluorescent media to culture individual bacteria species. By undertaking bacterial growth curves, alongside fluorescence spectroscopy, we have been able to determine FDOM development with population growth, highlighting which FDOM peaks are associated with cell multiplication and which as a metabolic by-product from other processes. We have also analysed the intracellular and extracellular fluorescence signature of each species to understand how the microbial community structure may impact the FDOM signal in aquatic systems. We have also explored the notion that cell lysis is responsible for the presence of microbial larger FDOM compounds (Elliot et al. 2006).

From this work we have been able to identify the different fluorescence signatures of the species analysed, as well as highlight the range of FDOM that can be of microbial origin. This has further informed our understanding of microbial FDOM and the wider impact this can have on aquatic DOM, ecosystem sustainability and biogeochemical cycling.