

Investigating the role of benthic-pelagic coupling of microbial communities in carbon cycling within the Western Channel Observatory

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Project description

Continental sea shelves occupy 7-10% of the global ocean area but are responsible for the majority of benthic biogeochemical cycling of organic matter [1]. However, the microbial processes and taxa involved are currently understudied. The Western Channel Observatory (WCO) offers an excellent opportunity to study benthic biogeochemical cycling as it is affected by anthropogenic and riverine input from hydrolytic events (e.g. rainfall) of increasing severity. It also contains one of the most sampled microbial communities in the world, with rich legacy metadata spanning 10+ years. The WCO benthic time-series has highlighted shifts in the microbial community following a plankton bloom with concomitant decreasing oxygen levels 2-3m above the sediment (the maximal depth of current pelagic sampling). This depletion may represent the edge of a hypoxic gradient that extends to the sediment surface and would provide a strong selection pressure for shaping microbial communities and their biogeochemistry. Current data indicates that the benthic microbial community plays an important, but understudied role in the degradation of carbon.

By using the latest sequencing technologies coupled to novel bioinformatic techniques, we will identify the key taxa and metabolic processes involved in the degradation of marine carbon within the benthic community. Crucially, these pathways will then be validated using laboratory methods. A working hypothesis is that predicted regions of hypoxia are shaping microbial communities. The existence of such a layer would fundamentally alter the biochemistry of DOC remineralisation; sediment/water metal exchange; and would offer an opportunity to investigate a novel but potentially important microbial component of the WCO.

The aims of the project will be 1) to assess the formation of hypoxic bottom water following a plankton bloom in the WCO; 2) to use sequence-based bioinformatic network analyses of time-series community profiles to formulate hypotheses of taxonomic interactions in the degradation of DOC by benthic communities and their pelagic counterparts; 3) to validate hypotheses from (2) using protein stable isotope probing (pSIP) [2] to follow the carbon from a planktonic bloom through a microcosm community under hypoxic and oxic conditions; 4) to investigate the novel microbiology of any identified regions of hypoxia within the WCO.

Students will be offered training in the latest bioinformatic techniques for microbial community taxonomic and

functional analysis. Students will learn the laboratory techniques to validate the hypotheses generated from bioinformatics and will emerge as experienced in both wet lab environmental microbiology and bioinformatics, providing a strong foundation for a career in science in the age of 'big data'.

[1] Bauer, J. E. et al. *Nature* 504, 61-70 (2013); [2] Jehmlich, et al. *ISME J*, 2.11, 1122-1133 (2008).