



## Hydrographic controls on marine organic matter fate and microbial diversity in the western Irish Sea

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Cycling of organic matter (OM) is the key biological process in the marine environment<sup>1</sup> and knowledge of the sources and the reactivity of OM, in addition to factors controlling its distribution in estuarine, coastal and shelf sediments are of key importance for understanding global biogeochemical cycles<sup>2</sup>. With recent advances in cultivation-independent molecular approaches to microbial ecology, the key role of prokaryotes in global biogeochemical cycling in marine ecosystems has been emphasised<sup>3,4</sup>. However, spatial studies combining the distribution and fate of OM with microbial community abundance and diversity remain rare. Here, a combined spatial lipid biomarker and 16S rRNA tagged pyrosequencing study was conducted in surface sediments and particulate matter across hydrographically distinct zones associated with the seasonal western Irish Sea gyre. The aim was to assess the spatial variation of, and factors controlling, marine organic cycling and sedimentary microbial communities across these distinct zones. The distribution of phospholipid fatty acids, source-specific sterols, wax esters and C<sub>25</sub> highly branched isoprenoids indicate that diatoms, dinoflagellates and green algae were the major contributors of marine organic matter, while the distribution of cholesterol, wax esters and C<sub>20</sub> and C<sub>22</sub> polyunsaturated fatty acids have highlighted the importance of copepod grazing for mineralizing organic matter in the water column<sup>5</sup>. This marine OM production and mineralisation was greatest in well-mixed waters compared to offshore stratified waters. Lipid analysis and 16S rRNA PCR-DGGE profiling also suggests that sedimentary bacterial abundance increases while community diversity decreases in offshore stratified waters. The major bacterial classes are the Deltaproteobacteria, Clostridia, Flavobacteriia, Gammaproteobacteria and Bacteroidia. At the family/genus level most groups appear to be associated with organoheterotrophic processing of sedimentary OM, ranging from degradation of complex organic matter (e.g. *Tepidibacter* sp.) to sulfur-dependent utilisation of simple organic molecules (e.g. Desulfobulbaceae and Desulfuromonadaceae).

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