

Despite their size, prokaryote (bacteria and archaea) biomass is estimated to represent between 15 and 30% of total living biomass^{1,2}. Prokaryotes play major roles in marine ecosystems and in global biogeochemical cycling^{3,4}. Molecular phylogenetic approaches have revolutionised microbiology and have revealed that the complexity of microbial life is orders of magnitude greater than previous estimates based on cultivation-based approaches⁵. This highlights how little we currently know about the microbial world and the clear potential of this vast untapped resource for human application. Here we present the first in-depth analysis of microbial community diversity and composition in the Irish Sea. The western Irish Sea is characterised by distinct hydrographic conditions, resulting in summer stratified offshore deeper waters and settling of fine mud, while well-mixed waters and coarser sediment type dominate in the south and coastal regions. We wished to assess whether these factors play ar ole in prokaryote abundance and diversity.



Barcoded pyrosequencing has highlighted a diverse range of sedimentary microbes, of which have diverse metabolic capabilities or have not been cultured. Clustering according to the distinct regional hydrographic zonation.

Discussion & Future Work

To date we have identified a complex range of bacterial groups of known and unknown metabolic capabilities. The most abundant bacterial phyla in the western Irish Sea are the Proteobacteria, Bacteroidetes and Firmicutes. δ-proteobacteria are a major group, and those found here are associated with groups important in sulfur and organic matter cycling under anaerobic conditions. Complex syntrophic relationships between bacteria mediating the degradation of organic matter are evident. We have also shown distinct trends in diversity and abundance associated with known hydrographic conditions in the region. Factors such as particle size, organic matter concentration and type are likely important parameters controlling the distribution of certain bacterial groups. The vast majority of bacteria found have not been cultured and could provide future novel biotechnological and biomedical applications. For example, contamination of the marine environment with persistent organic pollutants is a global concern and has been documented in the Irish Sea⁷. We now wish to explore the potential for pollutant degradation among marine bacteria and hope to identify and isolate groups with high bioremediation potential.

References: 1. Whitman et al., 1998) Proc Natl Acad Sci 95, 5088-5090; 2. Kallmeyer et al., (2012) Proc Natl Acad Sci 109, 16213-16216. 3. Deming and Baross, (1993)Plenum Press, NY. 4. Gooday, (2002) J Oceanogr 58, 305-332. 5. Pace et al., (1997) Science 276, 734-740. 6. O'Reilly et al., 2013. Estuar Coast Shelf Sci, under review. 7. Charlesworth and Gibson, (2002) Mar Pollut Bull 44, 1421-1426