

# Linking microbial and macrofaunal diversity with benthic ecosystem functioning of the Belgium parts of the North Sea

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Ecosystem functioning is a broad term that encompasses a variety of phenomena and natural processes like cycling of nutrients which is influenced by fauna through functional and species diversity as well as abiotic factors. Nitrogen (N) is most often implicated as the nutrient limiting primary production in the coastal ocean. Nitrification, the oxidation of ammonia to nitrate via nitrite, is central to the cycling of nitrogen in the environment and, when coupled with denitrification, alleviates the effects of eutrophication through removal of nitrogen to the atmosphere as nitrous oxide or dinitrogen gas. Coupled nitrification/denitrification constitutes an important aspect of marine benthic ecosystem processes. It has been well-known that microbial oxidiser including ammonium-oxidizing archaea (AOA) and ammonium-oxidizing beta and gamma proteobacteria (AOB) play a central role in nitrogen cycling in coastal and estuarine systems. AOA and AOB can be studied in detail by assaying their functional gene *amoA*. Various environmental variables (e.g. sediment type, nutrients, porosity) affect the spatial distribution of the microbial communities. In addition, macrofaunal organisms are important as well as their burrowing, feeding, locomotive, respiratory and excretory activities affect the environment on the local scale. Nevertheless, it is still unclear how ecosystem functioning rates, presence of macrofaunal organisms and diversity and activity of microbial communities are related.

Therefore, spatial and temporal aspects of the community structure of bacteria and archaea in general, and of AOB and AOA in detail, were evaluated in 7 sampling stations covering a wide variety of sediment types. Sampling was performed during the peak spring bloom (April), shortly after bloom (June) and during the period of highest mineralisation rates (September) in the Belgian part of the North Sea in 2011.

In our study we use a molecular method based on Denaturant Gradient Gel Electrophoresis (DGGE), which is a widely used method for mutation analysis and for studies of microbial diversity. Total microbial diversity, based on the 16S rDNA gene will be assessed in order to investigate the relationships between microbial diversity and environmental factors (sediment grain size, sediment O<sub>2</sub>, CN, porosity, sediment and water pigment concentrations and nutrient concentrations in the water column). In addition, the link between the metabolically active AOA and AOB will be investigated as well. During a series of lab incubations, fluxes of nutrients (NO<sub>3</sub><sup>-</sup>, NO<sub>2</sub><sup>-</sup>, PO<sub>4</sub><sup>-3</sup>, NH<sub>4</sub><sup>+</sup>) and O<sub>2</sub> across the sediment-water interface were measured, and will be linked with the community composition and diversity of the AOA and AOB present in these incubations.

By investigating the link between ecosystem functioning, macrofauna and the microbial communities, we close the gap that exists between marine 'macro-ecologists' (focusing on the link macrobenthos-ecosystem functioning) and marine 'micro-ecologists' (focusing on the link microbial communities-ecosystem functioning) and increase the knowledge about the mechanisms underpinning some of the important benthic ecosystem functions.

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