

Linking Microbial and Macrofaunal diversity with Benthic Ecosystem Functioning of the Belgium Parts of the North Sea

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Aim of this study: By investigating the link between ecosystem functioning, macrofauna and the microbial communities, we are going to 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.

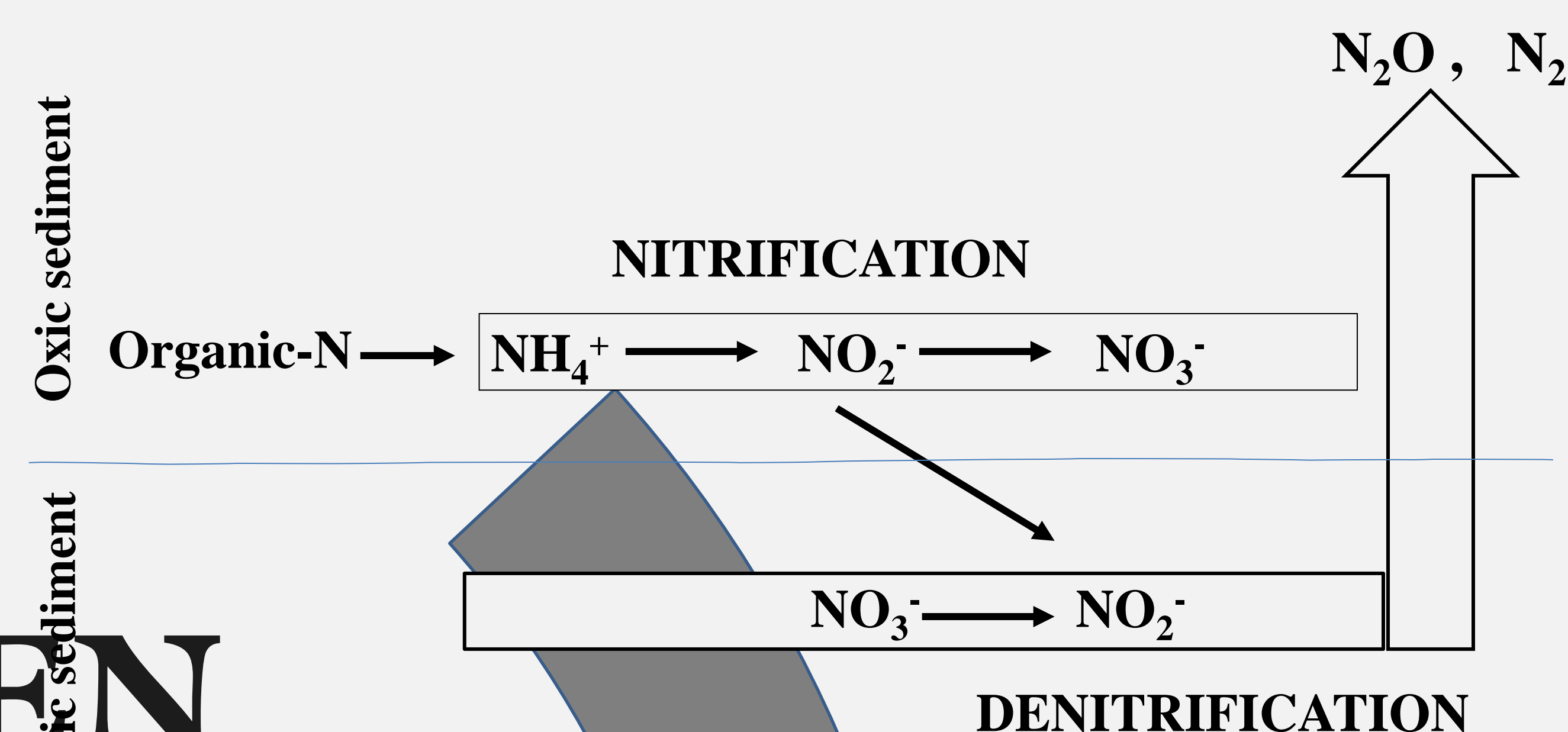
Objectives:

- assessing spatial and temporal distribution of total microbial communities (Bacteria and Archaea), based on the 16S rDNA gene
- assessing metabolically active ammonium-oxidizing archaea (AOA) and ammonium-oxidizing beta and gamma proteobacteria (AOB), based on RNA extraction and amoA gene
- determining the effect of different environmental factors (sediment grain size, sediment O₂, CN, porosity, sediment and water pigment concentrations and nutrient concentrations in the water column) on microbial communities focusing on AOA and AOB
- estimating nitrification and denitrification by measuring fluxes of nutrients (NO₃⁻, NO₂⁻, PO₄⁻³, NH₄⁺) and O₂ across the sediment–water interface during a series of lab incubations

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 oxidisers 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.

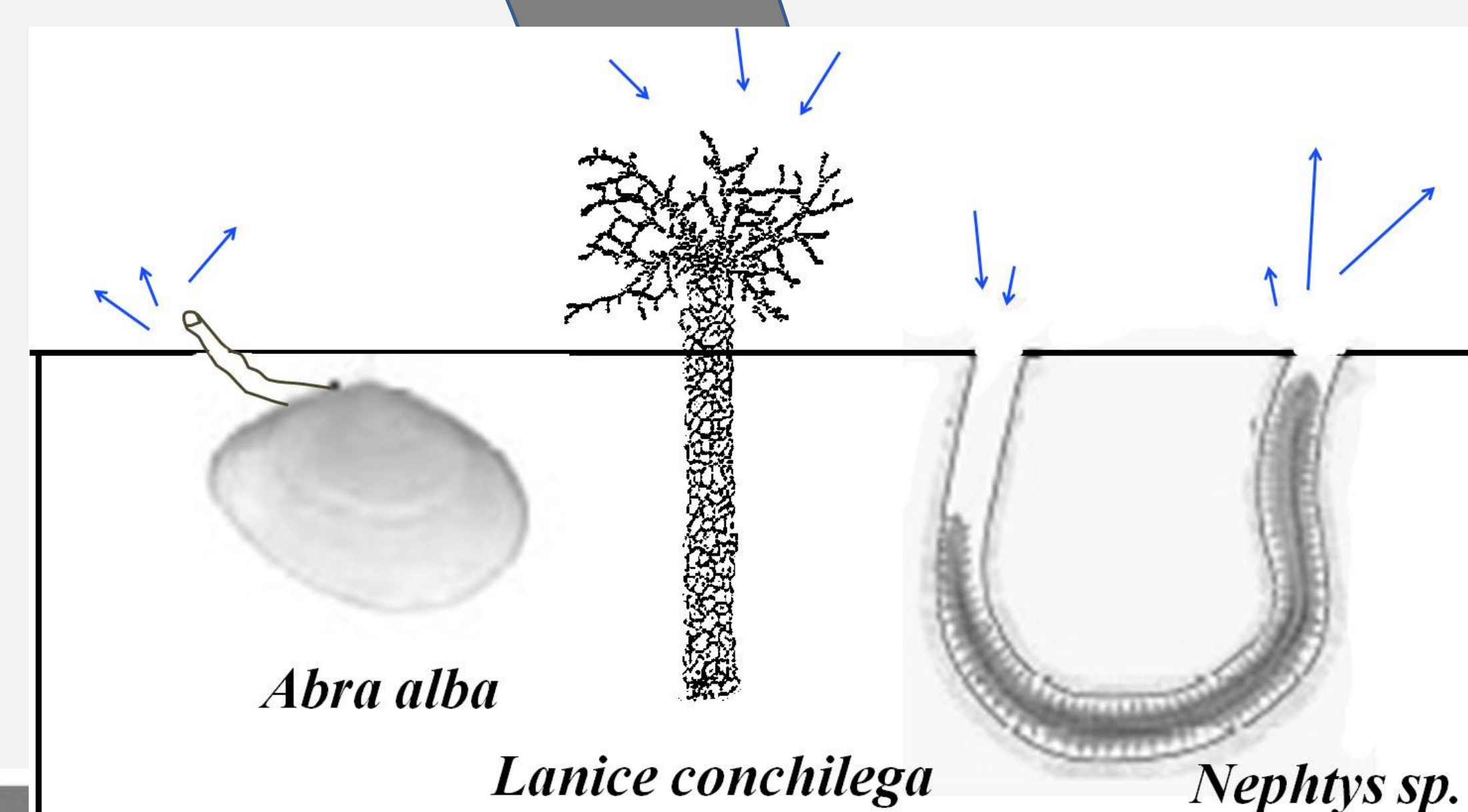
NITROGEN CYCLE



Microbial communities are influenced by

Various environmental variables (e.g. sediment type, nutrients, porosity,.....)

Macrofaunal organisms by their burrowing, feeding, locomotive, respiratory and excretory activities



Sampling: sediment was collected deploying a Reineck box corer monthly from April to September 2010 in 7 sampling stations covering a wide variety of sediment types in Belgium part of the North Sea. Sampling was performed during the peak spring bloom (April), shortly after bloom (June) and during the period of highest mineralisation rates (September).

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.

