

Effect of natural populations of the ecosystem engineering polychaete, *Lanice conchilega*, on abundance and diversity of nitrifying and denitrifying organisms

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Densities and functional diversity of macrofaunal organisms affect the environment on a local scale by introducing fresh oxygenated water into deeper sediment layers thereby altering the physico-chemical properties of the sediment. The tube-building polychaete *Lanice conchilega* can form dense populations, often called biogenic reefs, affecting nitrogen cycling processes due to its irrigation activity. We aimed to investigate how bio-irrigation by *L. conchilega* in different natural densities affects abundance and community composition of metabolically active nitrifying (ammonia-oxidizing bacteria and archaea) and denitrifying organisms.

Sediment was collected by core (78.5 cm² surface area) in October 2014 from the intertidal zone of the seashore of Boulogne-sur-mer, France (50° 44.10' N, 01° 35.25' E) from the reef zones located higher on the beach and exposed at every low water. Three replicate cores were taken from three different areas of the reefs: (i) an area with an average density of *Lanice* individuals of about 25 tubes per core surface (3185 individuals/m²), (ii) an area with lower *Lanice* densities (5 tubes per core surface; 637 individuals/m²) located on the edge of the patches, (iii) and sediments without *Lanice* between the patches.

Cores were transferred to the lab and submerged in tanks containing continuously aerated seawater at *in situ* temperature-controlled room.

Vertical profiles of sediment oxygen concentration were measured (three replicate per core) using Unisense oxygen micro sensors (type ox100) in vertical increments of 250µm. Bio-irrigation activities of *Lanice* individuals was assessed as well, by logging changes in sediment O₂ concentrations at 1.5 and 6mm sediment depths.

At the end of the experiment, the sediment cores were sliced in 0.5cm intervals (0–0.5, 0.5–1, 1–1.5 and 2.5–3cm) and homogenized before collecting subsamples for further microbial analyses. To analyse active microbial communities, RNA was extracted from 4g sediment (wet weight). Functional genes of nitrifying (*amoA*) and denitrifying (*nosZ*) organisms were amplified and sequenced using next-generation sequencing technology (Miseq, Illumina).

Our ongoing results will show the effect of bio-irrigation activity of *L. conchilega* as differences in controls and high density treatments.