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Metagenomic analysis of nitrogen metabolism genes in the surface of marine sediments

Carolina Reyes (1,2), Dominik Schneider (3), Andrea Thürmer (3), Olaf Dellwig (4), Marko Lipka (4), Rolf Daniel (3), Michael E. Böttcher (4), and Michael W. Friedrich (2)

(1) University of Vienna, Vienna, Austria (creyes6@gmail.com), (2) University of Bremen, Bremen, Germany, (3) University of Göttingen, Göttingen, Germany , (4) Leibniz Institute for Baltic Sea Research (IOW), Warnemünde, Germany

In this study, we analysed metagenomes along with biogeochemical profiles from Skagerrak (North Sea) and Bothnian Bay (Baltic Sea) sediments, to trace the prevailing nitrogen pathways. NO_3- was present in the top 5 cm below the sediment-water interface at both sites. NH4+ increased with depth below 5 cm where it overlapped with the NO_3- zone. Steady state modelling of NO_3- and NH4+ porewater profiles indicates zones of net nitrogen species transformations. Protease, peptidase, urease and deaminase ammonification genes were detected in metagenomes. Genes involved in ammonia oxidation (amo, hao), nitrite oxidation (nxr), denitrification (nar, nir, nor) and dissimilatory NO_3- reduction to NH4+ (nap, nfr and otr) were also present. 16S rRNA gene analysis showed that the nitrifying group Nitrosopumilales and other groups involved in nitrification and denitrification (Nitrobacter, Nitrosomonas, Nitrospira, Nitrosococcus, and Nitrosonomas) appeared less abundant in Skagerrak sediments compared to Bothnian Bay sediments. Beggiatoa and Thiothrix 16S rRNA genes were also present suggesting chemolithoautotrophic NO_3- reduction to NO_2- or NH4+ as a possible pathway. Although anammox planctomycetes 16S rRNA genes were present in metagenomes, anammox protein-coding genes were not detected. Our results show the metabolic potential for ammonification, nitrification, NO_3- reduction, and denitrification activities in Skagerrak and Bothnian Bay sediments.