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NirS-containing denitrifier communities in the water column and sediment of the Baltic Sea

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Abstract:

The aim of this study was to compare structural differences in the denitrifying microbial communities along the environmental gradients observed in the water column and coastal sediments of the Baltic Sea. To link community structure and environmental gradients, denitrifier communities were analyzed by terminal restriction fragment length polymorphism (T-RFLP) based on nirS as a functional marker gene for denitrification. NirS-type denitrifier community composition was further evaluated by phylogenetic analysis of nirS sequences from clone libraries. T-RFLP analysis indicated some overlap but also major differences of communities from the water column and the sediment. Shifts in community composition along the biogeochemical gradients were observed only in the water column while denitrifier communities were rather uniform within the upper 30 mm of the sediment. Specific terminal restriction fragments (T-RFs) indicative for the sulfidic zone suggest the presence of nitrate-reducing and sulfide-oxidizing microorganisms that were previously shown to be important at the suboxic-sulfidic interface in the water column of the Baltic Sea. Phylogenetic analysis of nirS genes from the Baltic Sea and of sequences from marine habitats all over the world indicated distinct denitrifier communities that grouped mostly according to their habitat. We suggest that these subgroups of denitrifiers had developed after selection through several factors, i.e. their habitats (water column or sediment), impact by prevalent environmental conditions and isolation by large geographic distances between habitats.