

# Distribution of archaeal communities along the coast of the Gulf of Finland and their response to oil contamination

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## Abstract

© 2018 Yan, Yu, Hui, Naanuri, Viggor, Gafarov, Sokolov, Heinaru and Romantschuk. The Baltic Sea is vulnerable to environmental changes. With the increasing shipping activities, the risk of oil spills remains high. Archaea are widely distributed in many environments. However, the distribution and the response of archaeal communities to oil contamination have rarely been investigated in brackish habitats. Hence, we conducted a survey to investigate the distribution, diversity, composition, and species interactions of indigenous archaeal communities at oil-contaminated sites along the coast of the Gulf of Finland (GoF) using high-throughput sequencing. Surface water and littoral sediment samples were collected at presumably oil-contaminated (oil distribution facilities) and clean sites along the coastline of the GoF in the winter 2015 and the summer 2016. Another three samples of open sea surface water were taken as offshore references. Of Archaea, Euryarchaeota dominated in the surface water and the littoral sediment of the coast of the GoF, followed by Crenarchaeota (including Thaumarchaeota, Thermoprotei, and Korarchaeota based on the Greengenes database used). The unclassified sequences accounted for 5.62% of the total archaeal sequences. Our study revealed a strong dependence of the archaeal community composition on environmental variables (e.g., salinity, pH, oil concentration, TOM, electrical conductivity, and total DNA concentration) in both littoral sediment and coastal water in the GoF. The composition of archaeal communities was season and ecosystem dependent. Archaea was highly diverse in the three ecosystems (littoral sediment, coastal water, and open sea water). Littoral sediment harbored the highest diversity of archaea. Oil was often detected in the littoral sediment but rarely detected in water at those presumably contaminated sites. Although the composition of archaeal community in the littoral sediment was sensitive to low-input oil contamination, the unchanged putative functional profiles and increased interconnectivity of the archaeal core species network plausibly revealed resilience and the potential for oil degradation. Halobacteriaceae and putative cytochrome P450 pathways were significantly enriched in the oil-contaminated littoral sediment. The archaeal taxa formed highly interconnected and interactive networks, in which Halobacteriaceae, Thermococcus, and methanogens were the main components, implying a potential relevant trophic connection between hydrocarbon degradation, methanogenesis, sulfate reduction, and/or fermentative growth.

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## Keywords

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