

Short communication

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Change of bacterial community structure in nonylphenols-degrading sediments

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ABSTRACT. The present study investigated the shift in bacterial community structure in response to NP attenuation in the Gulf of Finland bottom sediments. High levels of NP_s (300 mg/kg) in sediments can be biodegraded by the autochthon microorganisms. NP_s addition showed no impact on diversity of microbial community structure. However, NP_s amendment led to significant change in bacterial community structure in NP_s – amended microcosm. Illumina MiSeq sequencing analysis indicated that *Firmicutes*, *Gammaproteobacteria*, *Deltaproteobacteria* were the three most abundant bacterial groups in NP_s-degrading sediment, suggesting that these groups might have a specific role in NP_s degradation. The involvement of a wide range of microorganisms related to NP_s biodegradation enlarges the possible risk of reduction of NP_s in environment.

Keywords: nonylphenols, bottom sediments, biodegradation, bacterial community, Illumina MiSeq sequencing

Nonylphenols (NP_s) – are toxic, xenobiotic substances classified as endocrine disruptors, which have a negative effect on the hormonal system of humans, fish, and other organisms. NPs are ubiquitous in many environmentally relevant matrices (e.g. influent and effluent water from sewage treatment plants, reservoirs, river water, lake water, marine water, groundwater, bottom sediments and others) (Acir and Guenther, 2018). Once released in the aquatic environment, highly hydrophobic (log Ko/w = 4.48) NP_s tend to adsorb to suspended matter and accumulate in bottom sediments. The NP_s content in sediments of marine and freshwater ecosystems are several orders of magnitude higher than that in water and can reach 3500 mg/kg. Highly persistent in the aquatic environment, NP_s are accumulated by aquatic organisms and thus induce direct or indirect toxic effects in them (Staniszewska et al., 2017). Nonylphenols have been found to cause oxidative stress in cells of diatoms, green algae, cyanobacteria (Liu et al., 2010; Gao and Tam, 2011; Zaytseva et al., 2015; Medvedeva et al., 2017). Environmentally relevant concentrations of NP_s cause significant changes in activity of hydrolytic enzymes in the terrestrial fungi involved in organic matter degradation in bottom sediments. It was found that NP_s contributes to the activation of pigments, exopolysaccharides and proteolytic enzymes, considered as potential fungal virulence factors (Kuzikova et al., 2015; 2016; 2017). Biodegradation of

NP_s can reduce the toxicological risk. The knowledge of the NP_s degradation potential in contaminated sediment is very important for the management of sediments for bioremediation.

Sediments (0-10 cm depth) used for microcosm construction was collected from Gulf of Finland in July 2018 (Kopor Bay located at 59.99186° N latitude and 28.96622° E longitude). In this microcosm experiment, initial concentration of NPs (300 mg/kg dw) decreased to 121 mg/kg dw during 240 days, whereas that in control microcosm with autoclaved sediments did not change, indicating that Gulf of Finland sediments contain NPs-degrading activity by microorganisms. The time taken for 50% of initial concentration of NP_s to dissipate (T₅₀) based on a first-order model, was 177 days. Illumina MiSeq sequencing analysis indicated that the structure of the prokaryotic communities in the control sediment has been mainly formed by the phyla of *Proteobacteria*, *Actinobacteria*, *Bacteroidetes*, *Firmicutes*, *Acidobacteria*. *Proteobacteria* have the largest portions in the sediment microbiom. Our study indicated that according to the Shannon and Chao1 indices values, NP_s addition showed no impact on diversity of microbial community structure. However, NP_s amendment led to significant change in bacterial community structure in NP_s – amended microcosm. *Firmicutes* (34.4%), *Gammaproteobacteria* (22.6%), *Deltaproteobacteria* (7.4%) were the largest bacteria groups in NP_s-degrading sediment after 240 days of incubation. The

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relative share of archaea and *Bacteroidetes* decreased and share of *Actinobacteria*, *Firmicutes* and *Chloroflexi* increased in the NP_s – amended microcosm. In this study, 10 bacterial strains capable to degrade the nonylphenols were isolated from NP_s contaminated bottom sediments. By sequencing a fragment of the 16S rRNA gene sequence, the most active strain *Bacterium* sp. 8 was identified as *Raoultella planticola* (Phylum: *Proteobacteria*; Class: *Gammaproteobacteria*).

In conclusion, high levels of NP_s (300 mg/kg) in sediment can be biodegraded by the autochthon microorganisms. NP_s addition showed no impact on diversity of microbial community structure. NP_s amendment and subsequent biodegradation significantly induced the shift in the bacterial community structure in the NP_s-amended microcosm. *Firmicutes*, *Gammaproteobacteria*, *Deltaproteobacteria* were the three most abundant bacterial groups in NP_s-degrading sediment, suggesting that these groups might have a specific role in NP_s degradation. The involvement of a wide range of microorganisms related to NP_s biodegradation enlarges the possible risk reduction of NP_s in environment.

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