

Scientific Paper:

J Appl Microbiol (2022) 132, 2795-2811

Structure and functional capacity of benzene-mineralizing nitrate-reducing microbial community

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Abstract:

Aims: How benzene is metabolized by microbes under anoxic conditions is not fully understood. Here, we studied the degradation pathways in a benzene-mineralizing, nitrate-reducing enrichment culture.

Methods and results: Benzene mineralization was dependent on the presence of nitrate and correlated to the enrichment of a *Peptococcaceae* phylotype only distantly related to known anaerobic benzene degraders of this family. Its relative abundance decreased after benzene mineralization had terminated, while other abundant taxa—*Ignavibacteriaceae*, *Rhodanobacteraceae* and *Brocadiaceae*—slightly increased. Generally, the microbial community remained diverse despite the amendment of benzene as single organic carbon source, suggesting complex trophic interactions between different functional groups. A subunit of the putative anaerobic benzene carboxylase previously detected in *Peptococcaceae* was identified by metaproteomic analysis suggesting that benzene was activated by carboxylation. Detection of proteins involved in anaerobic ammonium oxidation (anammox) indicates that benzene mineralization was accompanied by anammox, facilitated by nitrite accumulation and the presence of ammonium in the growth medium.

Conclusions: The results suggest that benzene was activated by carboxylation and further assimilated by a novel *Peptococcaceae* phylotype.

Significance and impact of the study: The results confirm the hypothesis that *Peptococcaceae* are important anaerobic benzene degraders.

Keywords: anaerobic benzene degradation, anammox bacteria, dissimilatory nitrate reduction, *Peptococcaceae*, putative anaerobic benzene carboxylase