Metabolism of Corrosive Microbial Communities in Oil-containing Environments

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Abstract Petroleum hydrocarbons present in oil-containing environments pose significant threats to the integrity of steel infrastructures by providing essential nutrients for microbial survival, consequently altering the microbial composition and metabolic pathways of microbial communities. To investigate potential keystone taxa that drive the MIC process in these environments, we employed culture-dependent methods, including metagenomic sequencing and quantitative PCR (q-PCR), to characterize the *in situ* corrosive microbial communities in the initial phase of our study. The findings indicated that sulfate-reducing bacteria (SRB), often regarded as the primary contributors, are not always the predominant keystone groups. Instead, archaea including methanogens (*Methanolobus*, *Methanohalophilus* and *Methanocalculus*), fungi including mould (*Aspergillus*, *Fusarium*) and yeast (*Yamadazyma*), and oil-degrading bacteria (*Alcanivorax* and *Marinobacter*), were the abundant corrosion-related members that exhibited higher relative abundances than SRB [1,2]. Furthermore, we futher explored their metabolic features that may attribute to corrosion by using experimental culture-dependent and microcosm tests [1,3]. The results demonstrated that petroleum hydrocarbons enhanced not only microbial oxygen respiration and aerobic hydrocarbon degradation but also nitrate reduction and anaerobic hydrocarbon degradation processes, highlighting the need to consider these microbial groups and their related corrosion-causing mechanisms in oil-containing environments.

Keywords Biocorrosion, petroleum degradation, archaea and fungi, steel corrosion

Reference

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