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Role of Bacteria, Archaea and fungi involved in methane release

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Abandoned coal mines release substantial amounts of methane which is largely biogenic. The aim of this study was to understand the microbial processes involved in mine-gas formation in two abandoned coal mines in Germany. Therefore, untreated coal- and mine timber samples and anaerobic enrichment cultures derived from them were subjected to DGGE analyses and quantitative PCR. The primers used were specific for Bacteria, Archaea, fungi, and the key functional genes for sulfate reduction (dsrA) and methanogenesis (mcrA). Original samples and enrichment cultures harboured a broad spectrum of facultative aerobes, fermenters, nitrate- and sulfate reducers belonging to all five groups (α - ε) of the Proteobacteria, as well as the Bacteroidetes, Tenericutes, Actinobacteria, Chlorobi and Chloroflexi. Only two groups of Archaea (representing 0.01% of the bacterial abundance) were detected. Based on specific 16 S-rRNA primer sets Methanosarcinales comprised 34% of these, corresponding to 45% detected with primers specific for the mcrA gene. The second group (55%) were uncultivated Crenarchaeota with an unknown metabolism. The detected Fungi (Ascomycetes and Basidiomycetes) were typical wood degraders. To get a perception ofdevelop a metabolic model for the ongoing processes, we linked the detected phylogenetic groups to possible activities promoting methane release.