Microbial degradation of organics and nitrate leaching from bituminised radioactive waste

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Deep geological barrial is in many countries considered as a potential safe long-term solution for the disposal of radioactive waste. In Belgium, Boom Clay has suitable physico-chemical characteristics to serve as natural barrier for the disposal of low- and intermediate long-lived radioactive waste. Most of this low- and intermediate long-lived radioactive waste is immobilized in a bituminous matrix, and typically contains also a large amount of soluble salts with sodium nitrate as most dominant. Over time, water will infiltrate into the waste monoliths in the repository resulting in the leaching of large amounts of sodium nitrate together with radionuclides and other soluble compounds, mainly originating from chemical and radiolytical degradation of the bitumen itself. These leachates might influence the geochemistry of the Boom Clay in the near field and might influence the migration of radionuclides. In addition, the microbial population present in the repository can have an influence on these leachates as sodium nitrate is a known electron acceptor and most of the other leachates are degradable by microorganisms as well, if proper growth conditions are attained. Borehole water samples from different layers within the Boom Clay have been shown to comprise a highly diverse bacterial community of which a large fraction is active.Batch experiments were performed to investigate more in detail the metabolic potential of the microbial community present in the Boom Clay borehole water. Sodium acetate and sodium formate – known leaching products of bituminized waste – degradation was shown in the presence of regular and aged bitumen, while no degradation was observed without the addition of bitumen. This demonstrates that microorganisms present in Boom Clay borehole water can use acetate and formate as electron donor in the presence of sodium nitrate leaching from the bitumen as electron acceptor. 16S DNA metagenomics was performed in order to investigate putative shifts in the microbial community in the different conditions.

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