1999

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Doctor of philosophy (applied microbiology)

University of Dar es salaam, College of Natural and Applied Science, 1999

Sulfate reduction and methanogenesis processes were studied in Tanzanian mangrove sediments. Focus was on the role of methanogenesis and sulfate reduction in the microbial degradation of organic matter and to the importance of dimethylsulfide (DMS) as a catabolic substrate. Sampling and field experiments were done at Mtoni mangrove sediments along Mzinga creek, Dar-es-Salaam. The sediments were characterised by a high organic matter content and total counts of bacteria which decreased with depth. There were remarkable differences between and within sampling sites. In areas with high deposition of leaves and without aerial roots of mangrove (due to mangrove cutting), very high sulfide concentration, high methane emission and low redox potential were encountered. On the contrary, in areas with aerial roots, low sulfide concentration, low methane emission and high redox potentials were found. This indicated that aerial roots are responsible for sediment oxidation and cutting of mangrove trees will endanger this ecosystem.

The rates of sulfate reduction decreased with depth and were 10 to 200 times higher than methane production rates. Acetate, H2/CO2 and formate stimulated sulfate reduction and methanogenesis in the sediment but the major part of these substrates were converted through sulfate reduction. Addition of methylated substrates (methanol, trimethylamine and DMS) to the sediment slurry had a major stimulatory effect on methane production. These findings and the results for most probable number counts clearly indicate that methanogens and SRB co-exists in mangrove sediment.A new methanogenic archaea, strain MD1 , which utilises DMS was isolated from the sediment. The name Methanosarcina semesiae sp. nov. was proposed. Cells are coccoid bodies 1.4 ± 0.2 fun in diameter occurring as individual cells, which lysed in freshwater or sodium dodecyl sulfate and stained Gram positive. DMS, methanethiol (MT), mono-, di-, and trimethylamines (TMA) and methanol were used for growth and methanogenesis. Analysis of the 16S rRNA gene sequence showed that strain $MD1^T$ was phylogenetically closely related to members of the genus Methanosarcina, but clearly differed from all described species of Methanosarcina (94-97% sequence similarity). The Genbank/EMBL accession number for the sequence of the 16S rRNA gene of strain $MD1^T$ is AJO12742.Cell free crude extract of Methanosarcina semesiae grown on

DMS exhibited methanogenic activity exclusively with DMS and MT. When cells were grown on TMA the extract only produced methane from TMA. This shows that methyl transfer reactions involved are specific for each substrate, DMS, TMA and methanol, and have to be induced. It was also shown that DMS conversion proceeds in a manner similar to methyltransferases involved in methanol and TMA conversion, but with a different reduction source. A sulfate reducing bacterium, strain SD1, which utilises DMS as the only catabolic substrate was enriched and isolated from the sediment. The cells of strain SD1 were short rods, motile, 1.1 ± 0.2 pm width and 2.2 ± 0.5 pm long. They occurred as single cells, double or aggregated, and stained Gram positive. The isolate utilises DMS, MT. pyruvate and butyrate. This is the first DMS utilising SRB isolated from a marine environment.