Influence of different microbial communities on black shale degradation

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Weathering of ancient organic matter contributes significantly to biogeochemical carbon cycles over geological times. The role of microorganisms in this process is not completely understood. Especially the contribution of different microbial groups in degradation of ancient organic matter is unknown. Therefore, we investigated the effect of fungi, Gram positive and Gram negative microbes in the degradation process in a column experiment. Columns contained freshly crushed, not autoclaved black shale material. Two columns were inoculated with either the fungi Schizophyllum commune, the Gram-positive bacterium Pseudomonas putida or the Gram-negative bacteria Streptomyces griseus and Streptomyces chartreusis. The effects were compared to control columns. To one set the same nutrient solution was added as to the inoculated columns and to the other set only sterile deionised water was supplied. To calculate the mass balance CO2 flux and DOC loss were determined. Phospholipid fatty acids (PLFA) were extracted to investigate microbial communities. We used both the compound specific 13C and 14C signal of the PLFA to quantify carbon uptake from black shales. The microbial biomass and the total carbon loss were higher in medium fed columns compared to control columns. The carbon loss in these columns exceeded the amount of added glucose, the major carbon source in the nutrient broth, by approximately 20%. Gram-positive bacteria dominated in the columns. The highest uptake of black shale material was also found using Gram-positive bacteria (18.3%). Our results suggest that especially native, Gram-positive bacteria are able to live on and degrade black shale material. Thus, microorganisms may actively drive weathering of ancient organic matter with implications for the global carbon cycle.