

## Study of microbial activity in marine sediments of the Iceland basin

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Subseafloor sediment harbors a large proportion of microorganisms- about  $3 \times 10^{29}$  according to the recent census by Parkes et al. 2014. Microbial cells in these very stable and oligotrophic settings catabolize at a much slower rate than model organisms in nutrient rich cultures. Microbial metabolic activity depends upon various factors like pH, temperature, pressure, sedimentation rates and distance from the land. In order to increase our understanding of the life in deep biosphere, we carried out a study on turnover times of bacterial necromass and biomass using newly developed D:L-amino acid racemization model in marine sediments from the Iceland basin. Sediment cores were up to 5 meters long and covered a time scale from present to  $\sim 57,000$  years. Sediment cores were analyzed for total hydrolysable amino acids (THAA), the bacterial endospore marker dipicolinic acid (DPA), and amino acid enantiomers (L- and D-form) of aspartic acid. The amino acid carbon content, and the ratio between the protein amino acids and their respective non-protein degradation products were used for determining the degradation state of the organic matter with the sediment depth and age. Endospores quantified using DPA quantification method were found to be as abundant as vegetative cells. The D:L amino acid modeled microbial necromass was estimated to be recycled over the range of  $0.2-1.1 \times 10^4$  years, while the turnover times for the microbial biomass were in the range of tens of years. Studies with deeper sediment cores will further improve our understanding of the energetic limits of life in the deep biosphere.