

D:L-amino acid modeled turnover of microbial biomass

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Decades of ocean drilling have demonstrated wide spread microbial life in deep sub-seafloor sediment, and surprisingly high microbial cell numbers. Despite the ubiquity of life in the deep biosphere, the large community sizes and the low energy fluxes in the vast buried ecosystem are still poorly understood. It is not know whether organisms of the deep biosphere are specifically adapted to extremely low energy fluxes or whether most of the observed cells are in a maintenance state.

Recently, we developed and applied a new culture independent approach – the D:L-amino acid model – to quantify the turnover times of living microbial biomass, microbial necromass and mean metabolic rates. This approach is based on the built-in molecular clock in amino acids that very slowly undergo chemical racemization until they reach an even mixture of L- and D- forms, unless microorganisms spend energy to keep them in the L-form that dominates in living organisms. The approach combines sensitive analyses of amino acids, the unique bacterial endospore marker (dipicolinic acid) with racemization dynamics of stereo-isomeric amino acids.

Data from different sub-seafloor oceanic settings, ages and organic matter quality will be presented together with a thorough discussion of the input parameters to the D:L-amino acid model.