

Biogeochemical dynamics of amino acids in deep-subsurface marine sediments

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Amino acids in sediment pore waters are key compounds in metabolic activities of sedimentary microbes and in remineralization of carbon and nitrogen. However little is known about their biogeochemical dynamics (e.g., sources and transformation processes) in deep-subsurface sediments.

As a new approach to constrain the sources of dissolved amino acids in sediment pore waters, this study reports and compares compound-specific $\delta^{15}\text{N}$ and enantiomer ratio (%D) of total hydrolysable amino acids (THAA) in solid phase and dissolved hydrolysable amino acids (DHAA) in pore waters from the same sediment samples. Samples were collected from deep-subsurface sediments (down to 172.9 m below seafloor) at the Sagami Trough (NW Pacific) during D/V Chikyu cruise CK09-03 (Expedition 905: December 2009).

In the sediments deeper than 9 mbsf, average %D values of DHAA were 25.9% in alanine, 24.8% in aspartic acid, 11.3% in serine, and 16.3% in glutamic acid, and average %D changes from THAA were +15.3% in alanine, -0.4% in aspartic acid, -8.1% in serine, and 4.6% in glutamic acid. Compound-specific $\delta^{15}\text{N}$ analysis showed that $\delta^{15}\text{N}$ values of alanine are higher in the DHAA than the THAA and that $\delta^{15}\text{N}$ values of glycine and glutamic acid are similar between the two fractions ($\delta^{15}\text{N-DHAA} - \delta^{15}\text{N-THAA} = +5.8$ permil, +1.9 permil, -0.3 permil, respectively). These results suggest that the DHAA fractions have different $\delta^{15}\text{N}$ and %D signatures from the THAA fractions, and that hydrolysis of the THAA could not be the sole source of the DHAA. Alternatively, the $\delta^{15}\text{N}$ and %D signatures of DHAA are consistent with the idea that in situ release of proteinaceous materials from sedimentary microbial biomass (such as peptidoglycan of Gram-positive bacteria) is an important source of DHAA. This suggests that recycle of dissolved amino acids by microbes would be an important process during amino-acid degradation and microbial metabolism in the deep-subsurface sediments.

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