# Bacterial influence on amino acid enantiomerization in a coastal marine sediment

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ABSTRACT: The contribution of D-isomers of aspartate (Asp), glutamate (Glu), alanine (Ala), and serine (Ser) to the total concentrations of dissolved free amino acids (DFAA), dissolved combined amino acids (DCAA), and total hydrolyzable amino acids (THAA) was studied in a <2,300-yr-old coastal sediment. Concentrations of the different amino acid pools were typically 5 (DFAA), 100 (DCAA), and 20,000 nmol cm$^{-3}$ (THAA), but variable amounts occurred, especially in the surface layer. D-amino acids were identified in all three amino acid fractions. The highest concentration of D-isomers occurred in the THAA fraction at a depth of 10 cm, where the maximum bacterial density has been observed (Jørgensen et al. 1990; Mar. Ecol. Prog. Ser. **59**: 39-54). This coincidence suggests that the D-amino acids originated in peptidoglycan of bacterial cell walls. The proportion of D-Asp, D-Glu, D-Ala, and D-Ser increased through the pools of DFAA and DCAA to THAA, suggesting a selective removal of L-amino acids to D-amino acids. The percentage of the four D-amino acids in the THAA pool increased with sediment depth to at least 4.3 m (~2,150 yr). This most likely indicated that peptidoglycan THAA were retained for a longer period of time in a particulate form compared to other proteinaceous material. The contribution of THAA from peptidoglycan to the THAA pool was estimated to range from >9% at the surface to at least 18% at 4.3 m deep, depending on the assumptions used in the calculation. The distribution of amino acid isomers in Aarhus Bay sediment demonstrated that bacterial peptidoglycan contributed to the pool of organic nitrogen (the four analyzed D-amino acids made up about 3% of particulate organic nitrogen [PON]). Although the peptidoglycan concentration increased with sediment depth, our observations do not indicate a long-term accumulation of peptidoglycan-derived amino acids.

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