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Amino acid biogeochemistry in the Laurentian Trough: vertical fluxes and individual reactivity during early diagenesis

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The detailed composition of total hydrolysable (THAA), dissolved free (DFAA) and combined (DCAA) amino acids was studied in settling particles and the solid phase and porewaters of underlying sediments in the Laurentian Trough to evaluate their sources and individual reactivities during early diagenesis. Vertical fluxes of THAA measured at 150 m depth (234-980 [mu]mol/m2/day) represented 3.8% of the average daily primary production and 8-16% of total organic carbon (TOC) and 24-42% of total nitrogen (TN) fluxes. THAA concentrations decreased from 89±39 to 39±4.4 [mu]mol/g from settling particles to the top 3 cm sediments, with no significant change of the %THAA-C and %THAA-N. However, these parameters decreased with depth in the sediments (10-13 to 7-8% and 30-45 to 22-28%, respectively) indicating a selective THAA removal. THAA composition of settling particles and sediments was relatively uniform and showed a marked enrichment in serine, threonine and glycine relative to fresh plankton which is ascribed to the selective preservation of diatom cell-walls. Serine was the more specific diatom tracer; it covaried with diatom lipid biomarkers, was relatively more abundant at a seaward site and increased downcore reflecting the selective preservation of diatom cell-walls. An increasing trend with sediment depth was also observed for aspartic acid whereas glutamic acid and histidine decreased. Porewater DFAA and DCAA accounted for 3-25% of total DOC and showed low levels in the surface zone of most intense solid phase THAA decay. Both fractions showed clear compositional differences related to the prevailing source material: DCAA, as solid phase THAA, were dominated by serine and threonine+glycine, whereas DFAA were enriched in glutamic (Glu) and [beta]-aminoglutaric acids ([beta]Glu), probably originating from bacteria. These patterns changed with depth in the sediments: the proportion of serine and [beta]Glu increased in DCAA and DFAA, respectively, whereas that of glutamine, alanine and Glu decreased in the DFAA pool. The preferential downcore decay and conversion of Glu into [beta]Glu was reflected by a consistent increase of [beta]Glu/Glu ratios, particularly at a landward station where the higher rates of sedimentation and OM burial favor the continued metabolism of bacteria in deeper sediment layers.

Palabras clave: Amino acids, Vertical fluxes, Solid phase, Porewater, Early diagenesis, Reactivity