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## Sources and sinks of dissolved free amino acids and protein in a large and deep mesotrophic lake

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ABSTRACT: We studied the microbial cycling of dissolved free amino acids (DFAAs) and protein in mesotrophic Lake Constance, Germany, by examining their release by phytoplankton and various heterotrophic organisms and incorporation by heterotrophic bacterioplankton. Release processes of both substrate classes, measured by an isotope dilution approach, comprised, as an annual mean, 15% of primary production and as much as 64% during the clear-water phase. DFAAs accounted for ~70% of total release during the spring bloom, in the early phase predominantly as photosynthetic extracellular products of rapidly growing algae and toward the end as a result of copepod grazing. Thereafter, during the clear-water phase, when daphnids were most abundant, release was dominated by protein. At this time, and again in late summer, lysis of grazing-damaged and senescent algae, including as well the hydrolytic activity of attached bacteria was one of the most important sources of protein. Rotifers, protozoans, and release processes in the fraction <1 μm were minor sources of DFAA 1 protein. Concentrations of dissolved combined amino acids (DCAAs) and protein ranged between 750-1,900 and 1-280 nM, respectively, and peaked duringphytoplankton blooms in spring and summer. As an annual mean, concentrations of labile protein constituted 8% of DCAAs, and the ratio of DFAAs to DCAAs was 0.16. About 50% of the DCAAs occurred in the molecular weight fraction between DFAA and 3 kDa and 30% in that >30 kDa. Concentrations of DCAAs >3 kDa were closely correlated to chlorophyll a, suggesting their phytoplankton origin and thus a ready availability. Protein was the preferred bacterial substrate. As an annual mean, its incorporation supported 45% of bacterial biomass produc-tion, compared with 13% by DFAAs. During winter and spring, when DFAA concentrations were highest, DFAA incorporation constituted up to 40% of bacterial production. Annually, the sum of DFAA 1 protein supported 58% and 80% of the bacterial C and N demand, respectively, indicating that they were the most important bacterial C and N sources.

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