Microbial roles in marine carbon export: Insights from compound-specific isotope analysis

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Microbial and metazoan heterotrophy are the major agents acting on marine particles to reduce (via respiration or disaggregation) or enhance (via repackaging) vertical carbon flux in the water column, but the relative importance of each mechanism remains difficult to quantify using current models or data. Compound-specific stable isotope analysis of amino acids (AA-CSIA) has shown promise for distinguishing these mechanisms, both through carbon AA-CSIA “fingerprinting” approaches and nitrogen AA-CSIA trophic indicators. Here we apply both techniques to size-fractionated particles from the oligotrophic North Pacific to determine how microbial biomass and degradative processes are partitioned across particle size classes and evolve as particles sink from the surface to bathypelagic depths. Our dataset encompasses the largest CSIA assessment of size-fractionated marine particles to date and explains the large differences between the $\delta^{15}N$ values of large and small particles in the deep ocean. Combined with concurrent zooplankton CSIA data, the results allow us to distinguish new signatures of microbial vs. zooplankton heterotrophy and to identify specific depth zones of microbial biomass accumulation, microbial enzymatic degradation, and zooplankton influence on particles in the water column. Based on these results, we introduce a multivariate AA-CSIA framework to classify the origins and trophic history of detritus of unknown provenance. Finally, we suggest that carbon isotope fingerprinting of amino acids may not accurately quantify bacterial biomass: the technique assumes de novo synthesis, but in bacteria this appears to vary with organic nitrogen availability.