



Long-term fate of microbial nitrogen, carbon, hydrolysable amino acids, fatty acids, and carbohydrates in sediment

Bart Veugel (1), Dick van Oevelen (1), Jack J. Middelburg (1,2)

(1) NIOO-KNAW, CEME, Yerseke, Netherlands, (2) Faculty of Geosciences, Utrecht University, Utrecht, The Netherlands

We experimentally investigated the long-term fate of microbial carbon, nitrogen, hydrolysable amino acids (HAAs), carbohydrates, and fatty acids in sediment. The microbial community of a tidal flat sediment was labeled with stable isotope tracers ^{13}C and ^{15}N , sediment was incubated *in vitro* in permanent darkness for up to 1 year, and ^{13}C and ^{15}N were traced into bulk sediment, hydrolysable amino acids (by GC-c-IRMS), fatty acids (by GC-c-IRMS) and monosaccharides (by LC-IRMS). This unique suite of compound-specific stable isotope analyses allowed us to investigate the long-term fate of total benthic microbial biomass and –detritus and its major biomass components (proteins, lipids, and carbohydrates). Results showed slow loss of ^{13}C and ^{15}N from the various compounds reflecting slow turnover of microbial detritus combined with recycling of degradation products by the active microbial community. Losses of ^{13}C and ^{15}N were closely coupled despite partly being present in different compounds and partly being derived from different microbial sources. This indicates very similar recycling efficiencies for microbial C and N and no selective preservation of either C or N during early diagenesis. Differences in loss rates between compound groups were small with highest loss rates for fatty acids and lowest rates for monosaccharides. Changes in molecular composition of the different compound groups were small. For the hydrolysable amino acids, changes included increased relative abundances of glycine, proline and lysine. Analysis of ^{13}C and ^{15}N in D-alanine revealed no selective preservation of peptidoglycan or peptidoglycan remnants. Compositional changes in fatty acid pools primarily reflected an increased contribution by heterotrophic bacteria involved in reworking of labeled organic matter.