



Manifestation of position-specifically ^{13}C -labelled amino acid assimilation and transformation by volatile and lipid fatty acid signatures in marine sediments

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Polar lipid-derived fatty acids (PLFAs) and compound-specific stable carbon isotope analysis are often combined to characterize microbial populations involved in the degradation of organic matter, offering a link to biogeochemical processes and carbon sources used. However, single PLFAs may derive from multiple species and PLFA community patterns are influenced by substrate types. Here we investigated such dependencies by monitoring the bacterial transformation of position-specifically ^{13}C -labelled amino acids of the pyruvate family in coastal marine sediments. Alanine assimilation yielded a PLFA pattern highlighted by uptake into straight-chain FAs, while the incorporation of valine and leucine led to the specific production of even- and odd-numbered iso-series FAs. This suggests that identical microbial communities have adjusted their metabolic pathways according to substrate availability. Transformation into precursor molecules for FA biosynthesis was manifested in increased ^{13}C recoveries of the corresponding segregated volatiles acetate, isobutyrate and isovalerate of up to 39.1%, much higher than for PLFAs (<0.9%). A significant fraction of ^{13}C was found in dissolved inorganic carbon (up to 37.9%), while less was recovered in total organic carbon (up to 17.3%). A clear assimilation discrimination against the carboxyl C was revealed, whereby C2 and C3 positions were preferentially incorporated into PLFAs. Therefore, position-specific labelling is an appropriate approach for reconstructing the metabolic fate of protein-derived amino acids in marine environments.