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AMINO ACID BIOGEOCHEMISTRY IN VENT SYSTEMS

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For two contrasting vent systems the information contained in amino acids have been used to get insights into the carbon sources and cycling as well as the structure of the respective food chains. The concentration of the individual amino acids, their racemization and their compound-specific isotopic composition have been analysed by HPLC-FD, chiral GC-FID and GC-irmMS for a variety of sample materials.

One type of vent systems investigated were high- and low-temperature hydrothermal vent systems along the Mid-Atlantic Ridge system, where vent fluid and plume water samples as well as selected organisms have been analysed. For most of the fluid and water samples the concentration of the total dissolved amino acids were only slightly higher than adjacent deep and intermediate water masses. But especially at the diffuse venting sites with abundant organisms thriving nearby, the concentrations were elevated. The pattern of abundance of the individual amino acids within the organisms and within the water samples showed marked differences with a strong depletion of the acidic amino acids in the liquid samples.

The racemization of individual amino acids shed insights on the contribution of certain bacterial (endo)symbionts of e.g. *Bathymodiolus thermophilus* (*B. th.*) in distinct tissues or organs. The high abundance of symbiotic methane- and sulphide-oxidizing bacteria in the gills resulted in significantly elevated percentages of e.g. D-alanine in comparison to the foot (or the bulk remainig tissue, see fig. 1). And the differences between organisms, e.g. the mussel *B. th.* and the shrimp *Rimicaris*, underlines the findings of Zbinden & Cambon-Bonavita (03), that the very high numbers of ectosymbionts as well as symbionts within the gut of *Rimicaris sp.* are important for its nutrition – in contrast to findings of van Dover et al. (88).

The compound-specific carbon isotopic composition of individual amino acids depicts the importance of different food sources for the above-mentioned organisms (see fig. 1). Overall the amino acids of *B. th.* are depleted by up to 15 permil compared to *Rimicaris sp.* – which is due to the contributions of methane-oxidising symbiontic bacteria in the mussel. But the similar isotopic composition of most amino acids in the different mussel tissues points to the efficient shuffling of fixed carbon from the symbionts to the host. The compound-specific carbon isotopic composition of the essential amino acids clearly traces the ultimate C sources

for *Rimicaris sp.* – in contrast to difficulties with bulk carbon isotope studies still showing an influence of the juvenile planktonic food sources (Van Dover al., 88).

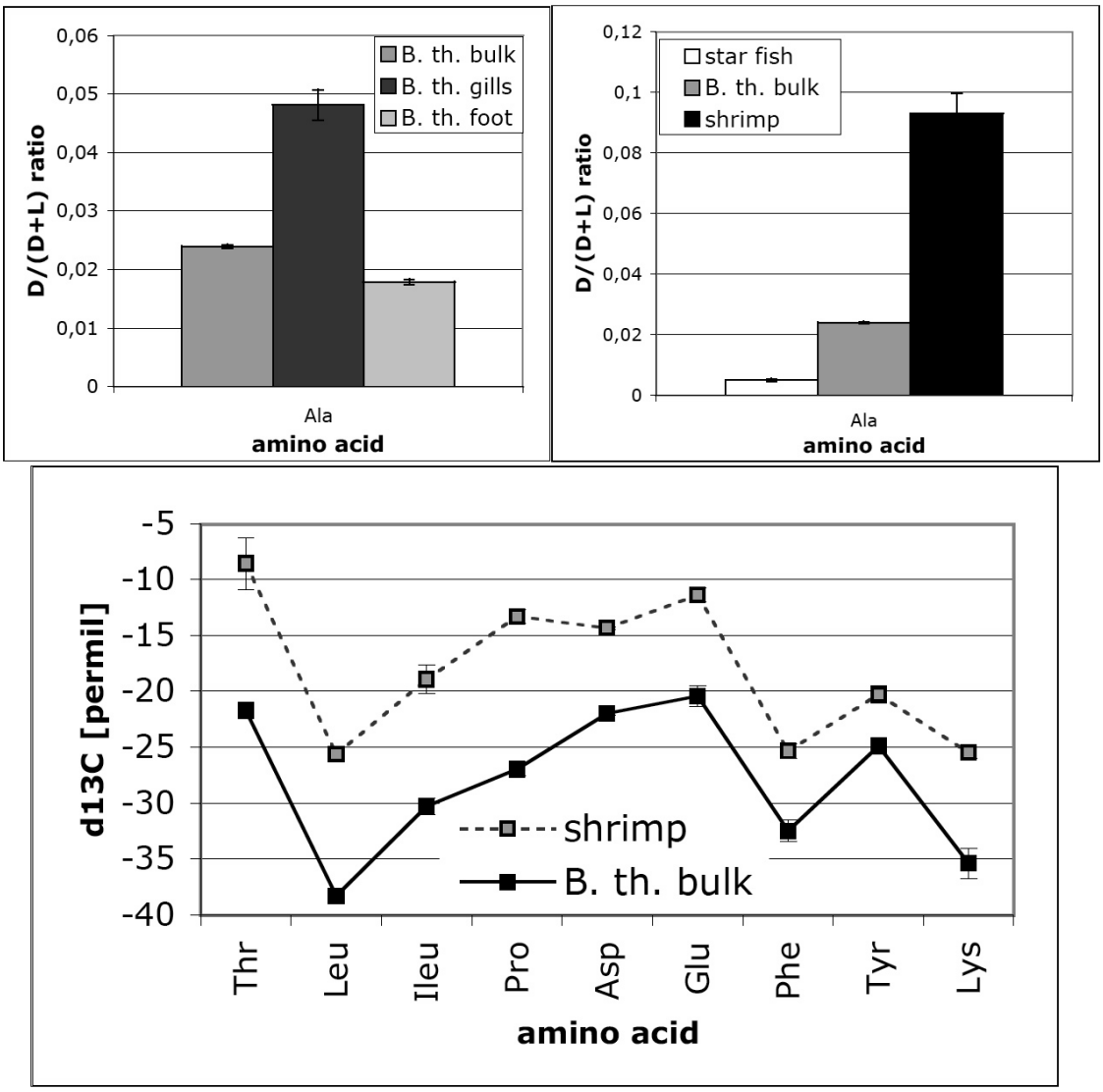

Figure 1. Racemization and compound-specific carbon isotopic composition of amino acids in different organisms at a Mid-Atlantic hydrothermal vent site.

REFERENCES

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