

LIPID BIOMARKERS AND CARBON FLOW IN HIGH-SALINITY MICROBIAL MATS

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Microbial mats are vertically laminated organosedimentary structures. These small-scaled ecosystems, which are often not more than 5 to 10 mm thick, typically consist of a few functional groups of microbes which interact through their metabolic processes.

In the last few decades increasing interest developed in understanding the nutrient metabolism within microbial mats. The driving force in most of these mats is photosynthesis by cyanobacteria and algae. Sulphate-reducing bacteria, using excretion, lysis, and decomposition products of cyanobacteria, produce sulphide by the dissimilatory reduction of sulphate. The sulphide can be reoxidized to sulphate by colourless and purple sulphur bacteria. These close interactions between autotrophic and heterotrophic microorganisms in the uppermost mat layers lead to almost closed nutrient loops.

In the present study we investigated microbial mats from the sabkha region of Abu Dhabi, United Arab Emirates. Sabkhas are salt flats and are commonly found in the vicinity of sand dunes. These relatively flat and very saline areas of sand or silt form just above the sealevel where the sand is cemented by evaporitic salts from seasonal ponds. The sabkha region of Abu Dhabi in the intertidal area of the Arabian Gulf provides locally different growth conditions. In the most extreme case the water salinity is around 100 to 150 with high evaporation rates of the tidal waters caused by shadowless sunshine exposure for nearly 12 hours a day.

The analysed mat is finely layered and has a rubbery texture (Figure 1). In the uppermost 5 mm differently coloured layers of 1 mm thickness can be distinguished. Assuming that the colours represent differences in the community structure we sliced the mat and compared the results of single-layer analyses with the data for the whole mat.

Phospholipids are main constituents of cell membranes and are easy to extract and identify. Differences in concentrations and distributions therefore will reflect changes in microbial populations. We analysed the polar lipid fatty acids to look for variations between the layers and microbial communities, and selected results are shown in Figure 1.

Because of the extreme environmental condition we were also interested in the carbon metabolism within the mats. For this purpose we applied ^{13}C -labelled substrates to obtain an

insight into the nutrient processing in this unusual natural environment. We arranged our incubation experiment as a time series to follow the metabolic exchange between phototrophic cyanobacteria and the heterotrophic microorganisms. The most interesting point of view was to see where the $\delta^{13}\text{C}$ values change first and how fast the labelled biosynthates are transported into greater depth and were they accumulate. Small mat cores with a diameter of 5 cm and 3 cm height were incubated in artificial seawater, spiked with bicarbonate, which was labelled with ^{13}C to various extents. We took several samples over a complete day-night-day cycle. The cores were sliced into sections according to the visible layers and samples were analysed for their polar lipid fatty acids.

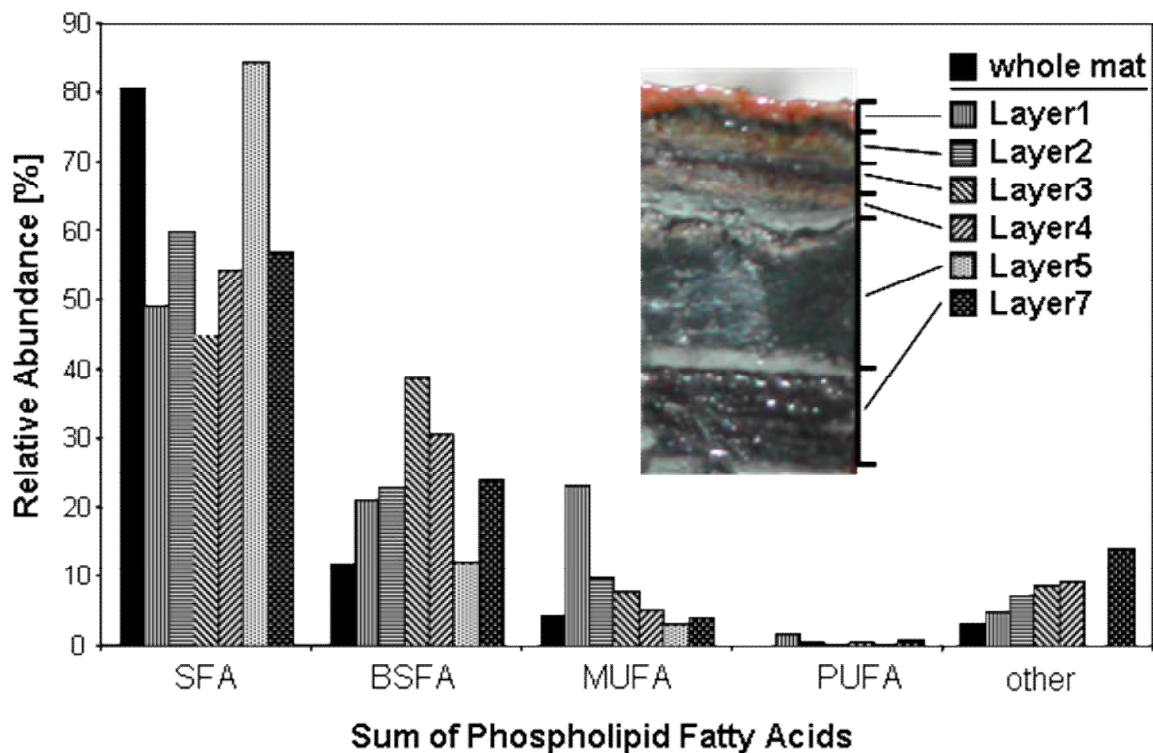


Figure 1. Relative abundances of summed fatty acid groups. The abundances in the whole mat are compared with those in the single layers (whole mat: thickness 12 mm, Layers 1 to 5: each about 1 mm, but separated according to visible layering; Layer 7: starts at 8 mm depth, is 5 to 10 mm thick and consists of several sublayers) (SFA: saturated fatty acids, BSFA: branched saturated fatty acids, MUFA: monounsaturated fatty acids, PUFA: polyunsaturated fatty acids)

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