



Microbial communities inhabiting hypersaline microbial mats from the Abu Dhabi sabkha

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Microbial mats are organo-sedimentary structures that are typically found in areas with extreme environmental conditions. Since these ecosystems are considered to be representative of the oldest forms of life on Earth, the study of microbial mats can inform our understanding of the development of life early in the history of our planet. In this study, we used hypersaline microbial mats from the Abu Dhabi sabkha (coastal salt flats). Cores of microbial mats (ca. 90 mm depth) were collected within an intertidal region. The cores were sliced into layers 2-3 mm thick and genomic DNA was extracted from each layer. A fragment of the 16S rRNA encoding gene was amplified in all DNA extracts, using barcoded primers, and the amplicons sequenced with the Ion Torrent platform to investigate the composition of the microbial communities down the depth of the cores. Preliminary results revealed a high proportion of Archaea (15.5-40.8% abundance) in all layers, with Halobacteria appearing to be more significant in the first 40 mm (0.4-10.3% of the total microbial community). Members of the Deltaproteobacteria were dominant in almost all layers of the microbial mat ($\leq 48.6\%$ relative abundance); however this dominance was not reflected in the first 8 mm, where the abundance was less than 2%. Chloroflexi and Anaerolinea, representing $\sim 93\%$ of bacterial abundance, dominated the first 8 mm depth and decreased at greater depth ($\leq 3\%$ relative abundance). Cyanobacteria were found only in the top 10 mm, with unexpected low abundance ($\leq 3\%$ of the total number of reads). These results show a vertical zonation of microbial communities and processes in the microbial mats. Further analyses are underway to investigate if these patterns are repeated at other sites along a transect of the sabkha, and to relate the microbial composition to the physical-chemical conditions of the sites.