

Rocking the cradle of life: Delineating key processes in modern microbial mats using innovative analytical and next-generation technologies

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Modern microbial mats can provide key insights into early Earth ecosystems, and Shark Bay, Australia, holds one of the best examples of modern microbial mats. Identifying the spatial distribution of microorganisms with mat depth will facilitate a greater understanding of specific niches and potentially novel microbial interactions, including those that lead to mineral precipitation. High throughput sequencing of small subunit RNA, coupled with elemental analyses and *in situ* microelectrode measurements of two distinct mat types (smooth and pustular) in Shark Bay were undertaken. The bacterial composition along vertical sections at 2 mm intervals was assessed. A total of 8,263,982 sequences were obtained, which were affiliated to 58 bacterial and candidate phyla. We observed that bacterial diversity increased with depth in smooth mats, while remaining relatively constant with depth in pustular mats. The surface of both mats was dominated by Cyanobacteria, accompanied with members of Alphaproteobacteria and Bacteroidetes. The deeper anaerobic layers of smooth mats were dominated by Chloroflexi, whilst Alphaproteobacteria dominated the lower layers of pustular mats. *In situ* microelectrode measurements revealed O₂ concentrations reached a maximum at the surface layer, increasing levels of sulfide were observed at depths under the oxic zone. Specific elements (Mo, Mg, Mn, Fe, V, P) could be correlated with specific mat types and putative phylogenetic groups. Statistical analyses indicated that molybdenum alone accounted for 32 % of the overall variance between the mat community structures. The combination in this study of a high throughput sequencing approach with corresponding elemental profiles has significantly enhanced our understanding of putative microbial niches and functional roles of different bacterial groups in these evolutionally significant ecosystems.