

MICROBIAL DYNAMICS IN SYDNEY HARBOUR: A HIGHLY URBANIZED ESTUARY

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Resumo:

The abundant and diverse microorganisms that inhabit aquatic systems are both determinants and indicators of aquatic health, providing essential ecosystem services such as nutrient cycling but also causing harmful blooms and disease in impacted habitats. Estuaries are among the most urbanized coastal ecosystems and as a consequence experience substantial environmental pressures, providing ideal systems to study the influence of anthropogenic inputs on microbial ecology. Here we use the highly urbanized Sydney Harbour, Australia, as a model system to investigate shifts in microbial community composition and function along natural and anthropogenic physicochemical gradients, driven by stormwater inflows, tidal flushing and the input of contaminants and both naturally and anthropogenically derived nutrients. Using a combination of amplicon sequencing of the 16S rRNA gene and shotgun metagenomics, we observed strong patterns in microbial biogeography across the estuary during two periods: one of high and another of low rainfall. These patterns were driven by shifts in nutrient concentration and dissolved oxygen leading to a partitioning of microbial community composition in different areas of the harbour with different nutrient regimes. Patterns in bacterial composition were related to shifts in the abundance of *Rhodobacteriaceae*, *Flavobacteriaceae*, *Microbacteriaceae*, *Halomonadaceae*, *Acidomicrobiales* and *Synechococcus*, coupled to an enrichment of total microbial metabolic pathways including phosphorus and nitrogen metabolism, sulphate reduction, virulence and the degradation of hydrocarbons. Additionally, community beta-diversity was partitioned between the two sampling periods. This potentially reflected the influence of shifting allochthonous nutrient inputs on microbial communities and highlighted the temporally dynamic nature of the system. Combined, our results provide insights into the simultaneous influence of natural and anthropogenic drivers on the structure and function of microbial communities within a highly urbanized aquatic ecosystem.

Palavras-chave: bacterioplankton, metagenomics, estuary, 16S rRNA

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