

**MICROBIAL COMMUNITY DYNAMICS WITHIN
IMPACTED COASTAL ECOSYSTEMS**

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CERTIFICATE OF ORIGINAL AUTHORSHIP

I, Richard Linley Carney declare that this thesis, is submitted in fulfilment of the requirements for the award of Doctor of Philosophy, in the School of Life Sciences at the University of Technology Sydney.

This thesis is wholly my own work unless otherwise reference or acknowledged. In addition, I certify that all information sources and literature used are indicated in the thesis.

This document has not been submitted for qualifications at any other academic institution.

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Thesis by compilation

This thesis is formatted in accordance with the requirements of a thesis by compilation.

A thesis by compilation is structured as a single manuscript that comprises a combination of chapters and published/publishable works.

It should be noted that data chapters two through to five, within this thesis, are structured according to the requirements of each respective journal where the manuscripts has, or will be submitted, however formatting has been kept consistent throughout as much as possible.

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Abstract

The microbes that inhabit coastal environments are responsible for high rates of primary productivity and nutrient cycling, and are amongst the first organisms to respond to changes in their habitat. This means that microbes are often the key biological initiators of positive (eg. bioremediation) or negative (eg. algal blooms) outcomes in response to environmental perturbations associated with natural or anthropogenic disturbances. Until now, most investigations of coastal microbiology have only focused on a narrow set of organisms that indicate faecal pollution, and consequently, have overlooked the 99% of environmental microbes that are yet to be cultured. Given this shortfall in our understanding of coastal microbiology, this project aimed to identify the key environmental and biological processes that influence the microbial ecology of coastal ecosystems, including potentially harmful species. To achieve this, a 24 month, high temporal resolution sampling regime was conducted at two urban beaches that experience contrasting hydrology and exposure to anthropogenic influences. Water samples were analysed in several ways using a suite of molecular, computational and statistical approaches, to elicit patterns and interactions between climate, water chemistry and microbial community assemblages. Each of my thesis chapters focus on a particular ecological aspect of the microbial communities extracted from water collected at two beach sample locations. In Chapter 1, I provide a background and overview of microbial ecology in coastal ecosystems. In Chapter 2, the first of my data chapters, 16S rRNA sequencing was combined with threshold indicator taxa analysis and network analysis to capture the dynamics of bacteria at the community-scale, which

revealed contrasting temporal patterns in whole bacterial communities, and seasonal switching between closely related taxa. Broad screening of bacterial communities also detected an interesting pattern in a population of emerging pathogens within the genus *Arcobacter*. This became the focus of Chapter 3, where large peaks were detected in *Arcobacter* abundance during inputs of stormwater and WWSO at the impacted beach, which persisted in high abundance for a further week following rainfall. In Chapter 4, the focus shifted from enteric microbes, to genes that confer resistance to antibiotics, which found 100-fold increases in several antibiotic resistance genes that were strongly correlated with potentially pathogenic enteric bacteria. In Chapter 5, this project closely tracked populations of pathogenic species within the genus *Vibrio*, providing new evidence that directly links blooms in pathogenic *Vibrio* in coastal surface waters with marine heatwave events. Overall, the findings of this project provide new and transformative insight into the microbial ecology of coastal systems, which has highlighted several potential implications for ecological and public health. Specifically, the detection of genes associated with antibiotic resistance and potential pathogens, that persist in beach water even when standard fecal indicators have diminished, has highlighted a need for broader screening tools in the monitoring and management of water quality in swimming beaches.