THE *ZOSTERA MUELLERI* SEAGRASS MICROBIOME

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CERTIFICATE OF ORIGINAL AUTHORSHIP

I, Valentina Hurtado McCormick, declare that this thesis, is submitted in fulfilment of the requirements for the award of Doctor of Philosophy, in the Faculty of Science - School of Life Sciences at the University of Technology Sydney.

This thesis is wholly my own work unless otherwise referenced 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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'Absence of evidence is not evidence of absence' - Carl Sagan (Martin Rees)

THESIS FORMAT STATEMENT - 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 experimental chapters (Chapters 2 - 4) within this thesis are structured according to the requirements of each respective journal where the manuscripts have been published or submitted. However, formatting has been kept consistent throughout as much as possible.

LIST OF PUBLICATIONS

Hurtado-McCormick, V., Kahlke, T., Petrou, K., Jeffries, T., Ralph, P.J., & Seymour, J.R. (2019). Regional and Microenvironmental Scale Characterization of the *Zostera muelleri* Seagrass Microbiome. *Frontiers in Microbiology*, 10 (1011). doi:10.3389/fmicb.2019.01011

Hurtado-McCormick, V., Tschitschko, B., Ralph, P.J., Seymour, J.R. (n.d.). Shifts in the seagrass leaf microbiome associated with seagrass wasting disease in *Zostera muelleri*. *Marine and Freshwater Research* (under review).

Hurtado-McCormick, V., Kahlke, T., Krix, D., Larkum, T., Ralph, P., Seymour, J.R. (in press). Seagrass leaf reddening alters the microbiome of *Zostera muelleri*. *Marine Ecology Progress Series*. doi: 10.3354/meps13409.

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THESIS ABSTRACT

As many other terrestrial macroorganisms, marine benthic animals and plants establish tight relationships with a collection of microbes widely known as the microbiome. These interactions are maintained in a delicate ecological equilibrium that affects hosts' metabolism and health, and ultimately the biogeochemical processes and ecosystems that rely on them. Seagrasses are aquatic angiosperms that play critical ecological roles and provide very valuable ecosystem services. These plants are now considered holobiont models in the ocean, given the increasing evidence of the relevance of their associations with a wide range of microorganisms. However, seagrass microbiome research is still on its infancy, and our understanding of their dynamics at different spatial scales and the influence of the external environment is still very limited, particularly for the seagrass species *Zostera muelleri*. Despite the undeniable importance of microscale heterogeneity for marine microbial ecology, most investigations on the seagrass microbiome have identified microbial associates within the phyllosphere and rhizosphere, rather than at smaller microenvironmental scales that are likely most relevant to the organisms of interest.

The aims of this thesis were to identify the microbial communities that live in association with *Z. muelleri* and to investigate how changes in the environment or the host influence the seagrass microbiome. Microbial community structure, diversity and levels of conservation, and co-occurrence patterns of bacterial, microalgal and fungal members were explored at the regional and plant scales in a variety of marine locations characterised by different environmental conditions. The dynamics of the *Z. muelleri* microbiome were also investigated within the contexts of disease and environmentally-driven physiological changes of the host, to assess how and to what extent intrinsic features of the plant influence its associated microbiota.

Throughout the thesis, it was consistently demonstrated that the seagrass microbiome is highly dynamic and influenced by environmental and host-associated factors, and as a consequence significantly different microbial communities associate with disparate microenvironments or tissue types within a single plant. I also showed that certain core members within these communities are conserved at larger spatial scales, although this biogeographical signal can be lost in a diseased holobiont. Moreover, I demonstrated that substantial microbial changes in the phyllosphere, with potential detrimental effects, are concomitant with physiological responses of the host against climate stressors.