Algal-bacterial interactions:

a study of *Gymnodinium catenatum* and its associated bacteria

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By

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Declarations

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Abstract

Over the last decades, harmful algal blooms (HABs) have increased globally in both frequency and extent, leading to intensified efforts to determine the primary factors that are controlling the population and toxin dynamics of bloom-forming algal species. One poorly understood factor in HAB ecology, yet shown to be of great importance, is that of algal-bacterial interactions.

Efforts to investigate the relationships and mechanisms of interaction are often hindered by the complex composition of the algal-associated bacterial communities, wherefore this present study used simplified algal-bacterial experimental model systems. The model systems are based on the toxin producing dinoflagellate *Gymnodinium catenatum* and two of its associated bacteria, *Marinobacter* sp. DG879 and *Alcanivorax* sp. DG881, both known to support growth and survival of *G. catenatum* in culture. Using the experimental model systems, the work presented in this thesis examined the growth dynamics of *G. catenatum* and its associated bacteria, and studied the effect of bacteria on the toxicity of *G. catenatum.* The abundance of *Alcanivorax* and *Marinobacter* genotypes associated with natural populations of *G. catenatum* in the Derwent Estuary and D'Entrecasteaux Channel, south-east Tasmania was also investigated.

This thesis demonstrates that the bacterial community is important for growth of *G. catenatum* and showed that different bacteria, in particular *Marinobacter* sp. DG879, have a significant effect on the growth dynamics and toxicity of *G. catenatum* laboratory cultures. When grown with *Marinobacter* sp. DG879, *G. catenatum* was found to remain viable in culture for a period longer than ever recorded, suggesting that *Marinobacter* sp. DG879 produce a compound inducing a positive growth response in *G. catenatum,* or that it plays a role in carbon recycling or nitrogen fixation. Toxin analysis of the *G. catenatum* / *Marinobacter* sp. DG879 cultures revealed a toxin profile significantly different to other analysed treatments containing different bacteria. As the experimental design of the study sought to minimise genetic variation among treatments, and with biotransformation generally operating on extracellular toxins (this study focussed on intracellular toxins), the differing toxin profile seen in

the *G. catenatum* with *Marinobacter* sp. DG879 is most likely a response to *Marinobacter* sp. DG879 influencing toxin synthesis indirectly through its effect on dinoflagellate physiology. The field studies also suggest that *Marinobacter* sp. may have an important role in natural populations of *G. catenatum*, preceding *G. catenatum* blooms.

With the use of molecular detection methods becoming more widespread, and with more research on naturally occurring blooms, there is potential that specific elements of the bacterial population, such as *Marinobacter* sp. DG879 could be employed as indicator species of *G. catenatum* and other algal blooms, ultimately allowing for early detection and management of potentially harmful blooms.

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