

De novo assembly and characterisation of transcriptomes from *Amphidinium* species

Gurjeet S. Kohli^{a, b}, Juan Jose Dorantes-Aranda^c, Tsvetan R. Bachvaroff^d, Allen R. Place^d, Arjun Verma^a, Shauna A. Murray^a

^a Climate Change Cluster, University of Technology Sydney, Ultimo, NSW 2007, Australia

^b Alfred-Wegener-Institute Helmholtz Center for Polar and Marine Research, Bremerhaven, 27515, Germany

^c Institute for Marine and Antarctic Studies, University of Tasmania, Hobart, Tasmania 7001, Australia

^d Institute of Marine and Environmental Technology, University of Maryland Center for Environmental Sciences, 701 East Pratt Street, Baltimore, MD 21202, USA

Amphidinium Claparede et Lachmann is one of the most abundant and diverse dinoflagellate genera found in marine benthic, sand dwelling and pelagic habitats. Species of *Amphidinium* have been widely studied for their potential to produce natural products, in particular, long chain and linear polyketide and macrolide compounds. More than 40 compounds produced by different species of *Amphidinium* have been isolated. These compounds with varying bioactivities are being investigated for their efficacy as antimicrobial and/or therapeutic agents. Some compounds produced by *Amphidinium* species have bioactivities against fish gill cells, and may lead to fish kills. Structural elucidation of many toxic compounds produced by dinoflagellates suggest that they may be based on a polyether ladder backbone, and that polyketide synthase (PKS) enzymes may have a role in their biosynthesis. The aim of our study was to screen *Amphidinium* species for the production of polyketide compounds and test their toxicity. We conducted a transcriptomic sequencing study to determine the presence of PKS genes (both mono-functionally expressed catalytic domains and genes encoding multimodular PKS enzyme complexes) in *Amphidinium*. The ketosynthase domain encoding transcripts were found to form distinct clades in the phylogenetic analysis, in comparison to similar genes from other organisms. We also show the presence of genes encoding six key enzymes essential for fatty acid production in *Amphidinium*. The results presented here are a step forward towards recognising the genes encoding critical steps in toxin biosynthesis and designing tools to monitor for and mitigate human illnesses due to harmful algal blooms.