

# KATE QUIGLEY

[katemarie.quigley@my.jcu.edu.au](mailto:katemarie.quigley@my.jcu.edu.au)

PhD candidate 2013 to 2016

School of Marine and Tropical Biology

Endeavour IPRS

Supervised by:

Prof. Bette Willis (JCU)

Dr. Line Bay (AIMS)

Dr. Bill Leggat (JCU)

## Molecular and environmental basis for Symbiodinium specificity in the coral-dinoflagellate association

Kate was born and raised in southern Spain, but has lived in a number of countries including Italy, Cuba, the United States, and Peru. With a passion for all things invertebrate, she decided to pursue research aimed at the coral-dinoflagellate symbioses in tropical oceans for both her Masters and PhD.

Numerous field and lab based reports suggest that hermatypic coral tolerances to stressors are in part dependent on the diversity of Symbiodinium that they host. Further hypothesis suggest that corals may shuffle and switch their symbiont complements in order to gain increased potential to acclimate to stressors like increased water temperatures.

However, this potential for flexibility in hosting new and diverse Symbiodinium may be limited by host and environmental factors. These factors and their contribution to symbiont-host specificity must be understood in order to evaluate the potential for acclimation to stressors through changes in the Symbiodinium consortium inside corals.

The relationship between dinoflagellates of the genus Symbiodinium and Cnidarians is extremely complex. Although recognized as functionally important for the coral host and reef ecosystem in general, relatively little is known about the molecular mechanisms that underpin that symbioses and control of Symbiodinium diversity and abundance in-hospite. Kate's PhD will focus on what is driving the specificity of this relationship from a biogeographical and cellular perspective.

The most exciting result so far has been the groundtruthing of 454 Next Generation Sequencing technology for the detection and quantification of Symbiodinium communities and the development of a bioinformatics pipeline to deal with large numbers of sequence reads achieved with this method.