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Nature or nurture? Testing the correlation between stress tolerance and genotype in *Acropora millepora* on the Great Barrier Reef

Young grew up in Kyoto, Japan. He completed his BSc (hons) in Marine Biology and Ecology at the University of Queensland under the supervision of Sandie Degnan. His Honours research investigated transcriptional responses of heat shock family genes to heat stress in the intertidal abalone, *Haliotis asinina* in an ecological context. Following this, he returned to Japan to pursue a career in molecular genetics at Kyoto University working at the Drosophila Genetic Resource Center, The Center for Ecological Research and the Laboratory of Marine and Biological Function. Here, his passion for evolutionary patterns at the genetic level grew and Young developed an interest in ecological genetics.

A number of studies have shown that corals have both phenotypic plasticity and the capacity for acclimatisation, including studies showing physiological, biochemical and behavioural responses to environmental stochasticity, and the contributions of zooxanthellae clades to the thermal tolerance of the coral holobiont. However, no study has reported functional genotype x environment associations to suggest that corals are locally adapted. Identification of genetic loci for stress tolerance will allow spatial vulnerability mapping and will assist in implementing a range of conservation strategies, including better informed preservation and restoration efforts.

Young's PhD project aims to find multiple genetic markers that correlate with environmental gradients in coral populations and validate the association between the markers and phenotypic response in the reef building coral, *Acropora millepora*.

He found that allele frequency patterns of some genetic loci were significantly correlated with spatial patterns of temperature and nutrient-related variables. He used a Bayesian Belief Network model which suggested multiple causes for the allele frequency patterns, leading him to speculate that the allele frequency of the genes of interest might have been shaped by multiple environmental factors, acting in both interactive and combined manners.