How can genomics be used to demonstrate whether an organism has the capacity to adapt to climate change?

Marine heatwaves have caused biodiversity losses in Australian coastal ecosystems and will become more frequent as climate change progresses. To focus conservation efforts, we need to be able to predict the capacity of organisms to adapt to climate change, including predicting individual variability and phenotypic plasticity in thermal tolerance. We also need to determine whether losses of biodiversity can be attributed to climate pressures. Molecular changes characteristic of either acute stress or adaptation following a thermal challenge have been identified. Linking these signals to (i) the ability of an organism to withstand successive heat shocks; (ii) heritability of the adaptive traits; and (iii) parameters that predict the outcome for populations and communities, not just individuals, remains a science challenge.

Climate Change and Biodiversity

Australian waters are warming due to anthropogenic release of CO_2[1]. The temperature increase is not necessarily gradual and linear, but may instead be increased suddenly in Extreme Climate Events or marine heatwaves[2,3]. These Marine Heatwaves have already altered Australian coastal ecosystems by causing widespread mortality of habitat forming species such as corals, kelp, and sea grass[2]. Tolerance of extreme temperature events is variable, between both species and individuals[4]. Predicting whether individuals and communities can withstand climate related pressures is important for conservation and resource management.
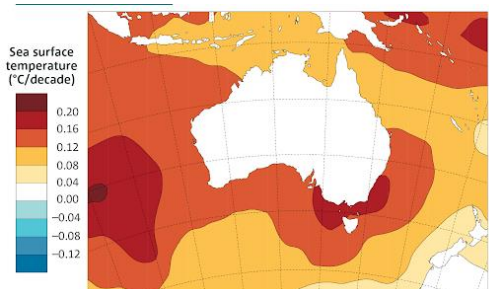

Figure 1 Change in Sea Surface Temperature Around Australia. Image taken from BOM, 2018 State of the Climate Report

Cellular Stress Response

The ability of organisms to withstand these events may be related to their phenotypic plasticity[5], or ability to adjust traits to current environmental conditions. The molecular response of an organism to temperature shocks could be used to determine its phenotypic plasticity and consequently, its susceptibility to future marine heatwaves and climate pressure. Multicellular organisms have a conserved response to cellular stress known as the *Cellular Stress Response.*[6] In response to damaged proteins, increases in the transcription of Heat Shock Proteins (HSPs), proteolysis enzymes, factors involved in cell cycle arrest, and ultimately, induction of apoptosis (or programmed cell death)[6]. These changes happen rapidly after the onset of temperature stress, making them an ideal indicator of susceptibility. Induction of the cellular stress response correlates with decreased overall fitness in heat stressed organisms.[7] Other studies have found additional transcriptional changes related to metabolic function[8], suggesting the possibility of energetic challenges even in species that were able to withstand temperature challenges[9]. Studies in fish have indicated that a lack of molecular changes corresponds to a limited capacity to adjust to climate pressures[7].

Case Study: Can Resilience to Climate Change be used to Predict Fisheries Performance?

Many fisheries have historically been over-exploited, and then recovered when fishing pressure is reduced or removed, such as orange roughy and school shark. However, other southern Australian fish populations have not recovered to harvestable levels, despite reduced fishing pressure. The cause of the failure to recover has not been identified. As southern Australia has some of the fastest warming waters globally, warming waters associated with climate change has been identified as a potential explanation. To date, no mechanism to test this hypothesis exists. The genome, epigenome, and transcriptome may interact to provide phenotypic plasticity in the face of a thermal challenge. We seek to compare one struggling population with one that is thriving to differentiate between adaptive signals and those that indicate comprised fitness to identify if climate can explain lack of recovery. To test the applicability of using omics as an enabling technology to predict climate resilience, we seek to compare the bight redfish (*Centroberyx gerrardi*), which is thriving, to the common redfish (*Centroberyx affinis*), which has not recovered despite apparently reduced fishing pressure for both species. These two fishes are from the same genera and have similar life histories, and overlapping distributions, so presumably, have experienced similar historical pressures.

To test whether climate resilience is affecting the ability of the common redfish to recover from historical fishing pressure, we would first compare the response of the two species to a temperature challenge. Redfish and bight redfish would be collected from areas that have experienced different temperature pressures (e.g. the Bass Straight and coastal NSW). Once organisms are acclimated to laboratory conditions, we would present both fishes with a temperature challenge comparable to a marine heatwave, and compare (inter individual and inter species) variability in:

   a. Thermal tolerance as respiration rate and burst swimming speed

   b. Transcriptomic responses (e.g. At what temperature do we see induction of the cellular stress response? Does it differ between different species?)

Differences in genome content (e.g. differences in the structure of the promoter region; differences in the numbers of orthologues or paralogues of key functional genes); differences in the epigenome, which determines how gene expression is regulated, could also be identified.

Figure 2. *Centroberyx gerrardi¸*the bight redfish (left) and its distribution, compared the common redfish (*Centroberyx affinis*) and its disitribution

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