

Genomic basis of adaptation to climate change (Climate Change)

The overarching goals of this project are to elucidate the genetic potential of species with different ecologies to adapt to climate change, to build that knowledge into predictive models of species distributions under climate change, and to transfer those models to end-users. We are well advanced towards achieving these broad goals, although progress on some Milestones concerned with the genomics is a few months behind schedule.

Elucidating Genetic Potentials

In respect of elucidating genetic potentials to adapt, we have obtained the foundational genomic data for our project, being high quality genome assemblies for 24 Australian drosophilid species variously distributed along a north/south climatic gradient. Furthermore we have been improved the assemblies of genome data produced by other groups for 20 other *Drosophila* species and are now adding those assemblies into our downstream annotation pipelines. In the process we have had to develop improved methods for assembly, annotation and analysis in order to reliably identify key gene gain and loss events associated with differences in climate adaptation among our species. These methods will themselves be publishable. We are also well advanced in the development of a transcriptome-based phylogeny for over 250 drosophilids, which will be a key resource for understanding the evolutionary processes underlying the genetic differences emerging from our genomic data.

Heritability estimates and heat tolerance

The other foundational genetic resource we needed to develop for our project was a database of heritability estimates for the key climate variables for the core Australian *Drosophila* species above. To this end we have obtained estimates for desiccation, cold and heat tolerance for 19 of the species. The results for the first two parameters have generally been consistent with our earlier evidence from just a few species, namely that the climate specialists have lower heritabilities than the generalists. Interestingly however we found no such relationship for the key heat tolerance parameter.

We are still considering the implications of this latter finding in light of evidence for a more adaptive transcriptomic response to heat stress in a heat specialist than a generalist that is emerging in our comparative transcriptomic work. Also notable in our comparative transcriptomic work is a finding that even relatively rainforest specialists with little heritability for desiccation stress can apparently mount a significant transcriptomic response to it. Notably our work on desiccation stress in *Erebia* butterflies is also bearing out the findings from the drosophilids above that rainforest specialists have less heritable variation for desiccation stress than generalist congeners.

Only one of three major *Drosophila* population genomics experiments planned has been completed so far. This study, an association study in *D. melanogaster*, found complex genetic associations with desiccation stress involving several hundred single nucleotide polymorphisms (SNPs). A study of two repleta species differing in heat tolerance along a climate gradient is at the DNA sequencing stage and a study of three montium species differing in desiccation stress is at the DNA preparation stage.

A survey of *Eucalyptus microcarpa* across climatic transects has revealed several climate-associated SNPs. A comparative analysis of several provenances from different climates grown in a 'common garden' is also now being analysed.

A framework for physiological limits and adaptive capacity

The work undertaken on incorporating consideration of adaptive capacity into modelling of biological responses to climate change was broader in scope than what was envisaged in the original project proposal. The most significant addition was the development of a novel conceptual and methodological framework for describing, estimating and predicting key parameters relating to physiological limits and adaptive capacity. This framework opened the way to making more effective use of best-available information from a range of sources in estimating and factoring adaptive capacity into modelling for a very wide variety of non-model organisms.

A new approach was developed for accommodating adaptive capacity in modelling shifts in the distribution of individual species. This approach was operationalised in a new software package *Adaptor*, the value of which was then demonstrated through its application to distributional data, and estimates of adaptive-capacity parameters, for 17 species of *Drosophila*.

New approaches were also developed for accommodating adaptive capacity in community-level modelling. The first of these was an extension of the use of Generalised Dissimilarity Modelling (GDM) to project turnover in community composition under climate change. The value of this extended approach was demonstrated for the Australian continent using distributional data and estimates of physiological limits for 78 reptile species and over 7,500 plant species. The second approach was an extension of the M-SET metacommunity model, which was demonstrated using the subset of plant species occurring in Tasmania.

Workshops and publications

Two workshops focusing on the modelling component of the project were held with state and federal agency and NGO representatives. The first workshop (held in April 2014) introduced participants to the new modelling approaches being developed, and sought input on potential case studies (species, biological groups, regions) for testing these approaches. The second workshop (held in December 2015) presented results from the case-study applications of developed modelling approaches and software. This workshop also provided a forum for comprehensive communication of the findings from all components of the project (not just the modelling component) and to identify and discuss practical implications of these for policy and management.

We also organised two other workshops with a wide range of stakeholders to further the process of technology transfer. Although not sponsored by this project, one of us (Prof Hoffmann) also played a leading role in two other workshops aimed at transferring the implications of our work to stakeholders.

We have published 27 papers from the project in international journals and given 26 invited papers on it at international meetings.