Assessing genomic variation in the hopbush, Dodonaea viscosa, to investigate micro-evolution and adaptation

By Matthew John Christmas

School of Biological Sciences

The University of Adelaide

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“One general law, leading to the advancement of all organic beings, namely, multiply, vary, let the strongest live and the weakest die.”

Darwin, 1859

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Summary

In this thesis I use a range of genomic tools in order to investigate aspects of the evolutionary history of the hopbush, *Dodonaea viscosa* (L.) Jacq. (hopbush). Understanding the past evolutionary processes that have led to the distribution and adaptation of contemporary populations can help to inform on how populations may continue to adapt into the future. A changing climate is altering selection pressures and populations will need to adapt to these if they are to persist. I pay consideration to how plant populations may adapt to a changing climate, as well as what constrains adaptive responses and how an understanding of these constraints can inform conservation management, in a review article (Chapter 2).

Dodonaea viscosa is globally widespread and distributed across the Australian continent where it originated. Within Australia there are seven taxonomically identified subspecies, but subspecies boundaries are not clear. Here, I analysed genome-wide single nucleotide polymorphic (SNP) markers for each of the seven subspecies using genetic structure analysis as well as network-based and Bayesian-based methods to assess phylogenetic relationships and show that defining subspecies for *D. viscosa* based on morphology is not wholly accurate or useful (chapter three). A consideration of a population's geographic location, environment and Pleistocene history appears to better explain the distribution of genetic variation across this species, rather than the presence of distinct gene pools corresponding to morphologically defined subspecies.

The thesis then moves onto an examination of the population history and signatures of selection in the narrow-leaf hopbush, *Dodonaea viscosa* ssp. *angustissima* along an environmental gradient within South Australia. Firstly, I generated a transcriptome reference genome by sequencing RNA from several individuals and used a range of bioinformatic tools to assemble and annotate it (chapter four). This transcriptome was

then used to selectively target a subset of 970 genes via ‘hybrid-capture target enrichment’ in order to develop a set of SNP markers present within putatively functional genes distributed throughout the genome. The SNP markers were used to characterise population genomic metrics of the target populations, such as genetic diversity and structure (chapter five). A range of analytical methods was used, including Principal Component Analysis, Mantel tests, AMOVA, and an F_{ST} outlier analysis algorithm. The data demonstrates there to be three distinct genetic clusters across the study region with low gene flow among them. The potential origins of these clusters are discussed, along with the implications for restoration practice using germplasm derived from these distinct gene pools.

SNP markers within the sequenced target genes were also analysed for signatures of selection, providing evidence for local adaptation driven by climatic factors (chapter six). A combination of F_{ST} outlier analysis and genotype-environment association analyses found 74 SNPs showing strong evidence for selection. Genes containing these SNPs under environmental selection were diverse, including aquaporin and abscisic acid (ABA) genes, as well as genes with ontologies relating to environmental responses, such as ‘response to water deprivation’. Selection acting on these populations has led to clines in allele frequencies in a number of functional genes, including some genes associated with leaf shape and stomatal characteristics, the phenotypes for which have been observed previously to vary along this environmental gradient. The implications for conservation and restoration practice using such data are further discussed.

The thesis concludes with a consideration of the future directions of research that can be informed by and further strengthen the findings of this thesis. Confirmation of adaptive significance of the genomic variation identified here is required. The use of common garden and reciprocal transplant experiments in order to provide evidence for links between genotype and phenotype and to asses the relative roles of genetic adaptation and plasticity in this species are discussed.

Declaration

I certify that this work contains no material which has been accepted for the award of any other degree or diploma in my name, in any university or other tertiary institution and, to the best of my knowledge and belief, contains no material previously published or written by another person, except where due reference has been made in the text. In addition, I certify that no part of this work will, in the future, be used in a submission in my name, for any other degree or diploma in any university or other tertiary institution without the prior approval of the University of Adelaide and where applicable, any partner institution responsible for the joint-award of this degree.

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