AN INTRODUCTION TO ADaPtE: A EUROPEAN UNION - FUNDED PROJECT COMPARING THE STRUCTURE AND DYNAMICS OF NEUTRAL AND ADAPTIVE GENES IN QUEENSLAND'S SPOTTED GUMS.

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In plants, the dynamic interactions of migration and selection act to establish genetic structure within and between populations of a species. It is this variation and its distribution within and amongst population that ultimately defines the ability of a species to respond to a changing environment and shifting selection pressures. Traditionally genetic diversity on forest tree species is measured at molecular markers which are neutral. There is however concern among forest scientists that the extent of genetic variation at such markers does not reflect that of adaptive traits and therefore may be of little value for genetic resource improvement and forest management.

Indeed, the description of genetic variation encoding adaptive traits within natural populations has been problematic. In the past, some well-characterised morphological and phenotypic traits known to confer fitness advantages and to be under single -locus control following Mendelian segregation analysis (e.g. flower colour) have been available. However, such systems tended to be the exception not the rule and, since only a few such characters were available, they defined the extent of the ecological questions that could be posed. The recent scientific revolution in the fields of genomics and transcriptomics has allowed a paradigm shift for the field of ecological genetics, and now these new techniques offer the potential of studying the distribution of genetic variation encoding for ecologically important and relevant traits (Schenk et al. 2000), i.e. those that have evolved in response and are maintained by environmental extremes and selection pressures.

ADaPtE (Adaptive Diversity and Population Structure in Eucalypts) is a recently started EUfunded project which therefore aims at producing a fine scale map of the distribution of neutral and adaptive gene variation in spotted gum populations distributed across a steep cline of water availability in central Queensland by 1) Quantifying neutral genetic structure and dispersal parameters using available microsatellite markers and well characterised population genetics analytical methods. 2) Identifying gene markers for drought tolerance using state-ofthe-art functional genomics tools and mapping their distribution across the region. The empirical work will be complemented with simulation modelling to improve our understanding of the role of selection in shaping the distribution of genetic and phenotypic variation across environmental gradients (Bacles et al. 2004).

REFERENCES

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