

## Indirect selection of macadamia yield through a genome wide association study of component traits

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Current macadamia breeding programs involve a lengthy and laborious two stage selection process: evaluation of a large number of unreplicated seedling progeny, followed by replicated trials of clonally propagated elite seedlings. Yield is an important selection trait, however it is difficult to select due to its polygenic nature and low heritability. Component traits such as kernel recovery and nut weight are more easily measured and have a higher heritability, and as such may be used to indirectly select for yield. A genome-wide association study (GWAS) combined with marker-assisted selection offers an opportunity to reduce the time of candidate evaluation. In this study, a total of 295 progeny from 32 families, and their parents, have been genotyped for 2322 SNP markers. A GWAS will be performed to determine if there are any significant associations between genetic markers and kernel recovery and nut weight. Significant markers and their genome scaffold position will be identified, and this will also determine if the markers are proximally located. Future macadamia breeding could involve pre-screening of individuals for desired traits using these markers, with only predicted elite individuals continuing to the second stage of selection, thus potentially reducing the selection process by 8 years.