

Marker-aided breeding using QTL-linked SSRs for stolon traits in white clover.

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Characteristics such as superior feeding value, high acceptability by stock, and symbiotic fixation of atmospheric nitrogen make white clover (*Trifolium repens* L.) a valuable forage legume in temperate regions of the world. As unreliable vegetative persistence is a major constraint to white clover performance, significant effort has been directed towards the genetic improvement of persistence of the stolon system - the vegetative unit of white clover.

Phenotypic measurements of component traits of the white clover stolon such as node number, internode length, branching and stolon density, are commonly assessed by breeders. These traits are difficult to measure under sward conditions and are often confounded by genotype-by-environment interaction effects. It is expected that the application of new genomic assisted breeding techniques, such as marker-aided breeding (MAB), will improve efficiency of identification of superior plants.

The QTL discovery and development program within the Pastoral Genomics (an Industry:Government-funded research consortium) program at AgResearch has successfully identified QTL for a range of above and below ground morphological traits in white clover. We have utilised these resources to assess MAB focussing on two stolon traits (Node Number (NN); Internode Length (IL)) of moderate heritability, as a proof of concept in an outbreeding forage legume. Microsatellite markers associated with QTL discovered and verified in replicated mixed sward trials across years and sites were used to screen a multi-parent complex population sampled from an early generation base population of cultivar 'Kopu II'. Significant ($p < 0.0001$) marker:trait associations were identified, with plants carrying beneficial marker alleles exhibiting a 21% and 19% increase in trait mean for IL and NN, respectively. Contrasting polycrosses were made on the basis of phenotypic and marker-based selection indices to generate half-sib families. Assessment of these families in grazed mini-swards indicates the effects are significant ($p < 0.05$) and heritable. These results demonstrate the viability of QTL-targeted MAB in complex white clover breeding populations providing a proof of concept for MAB in forages.