

Comparative Mapping and Genomics in *Medicago* and *Trifolium* to Identify Candidate Genes for Seed Production QTL.

Brent Barrett¹, Mary Sledge², Derek Woodfield¹, and Ian Ray³

¹ AgResearch, Palmerston North, New Zealand; ² The Noble Foundation, Ardmore, OK, 73401; ³ New Mexico State University, Las Cruces, NM, 88003.

Previous work involving comparative linkage mapping of EST-SSR markers derived from *M. truncatula* demonstrated macrosyntenic relationships between *M. truncatula*/*M. sativa* linkage groups 7, and the homeologous linkage groups C1 and C2 of *T. repens* (white clover). Comparative sequence analysis of 60 EST-SSR markers from *T. repens*, that were previously mapped to homoeologous group C, identified 9 markers with strong alignments to *M. truncatula* BACs that mapped to *Medicago* linkage group 7. These results confirmed previous findings and suggest reasonably high levels of colinearity between *T. repens* homoeologous group C and *Medicago* linkage group 7. One of these nine *T. repens* markers was also associated with a QTL strongly influencing inflorescence density, maturity, and seed yield in white clover. Closer analysis of the *M. truncatula* BAC, to which this *T. repens* marker aligned, indicated that the BAC belonged to a larger *M. truncatula* contig. This contig contained a cluster of 3 sequences with homology to the flowering time (FT)-like gene previously identified in *Arabidopsis* and other model species. A *T. repens* SSR marker at the QTL LOD peak was located 51kb from the FT-like homologous sequences; indicating that they may be candidates for functional marker development targeting seed production/inflorescence density traits in white clovers. A second flanking *T. repens* marker was also identified on this *M. truncatula* contig and was located 53kb from the candidate genes. These results demonstrate the value of *Medicago* genomic sequence data to provide insight into forage legume genetics, and as a candidate gene resource. Phenotyping, mapping and genome sequencing efforts in *Trifolium* and/or *Medicago* are likely to provide useful information for improving important traits in both genera.