Quantitative trait locus analysis of morphogenetic and developmental traits in an ssr- and aflp-based genetic map of white clover (*Trifolium repens* L.)

M.T Abberton[1], N.O.I. Cogan[2], K.F. Smith[3], G. Kearney[3], A.H. Marshall[1], A. Williams[1], T.P.T. Michaelson-Yeates[1], C. Bowen[1], E.S. Jones[4], A.C. Vecchies[2] and J.W. Forster[2]

[1]Legume Breeding and Genetics, Institute of Grassland and Environmental Research, SY 23 3EB, UK, Email: michael.abberton@bbsrc.ac.uk [2]Primary Industries Research Victoria, Plant Biotechnology Centre, La Trobe University, Bundoora, Victoria 3086, and Molecular Plant Breeding Cooperative Research Centre, Australia, [3]Primary Industries Research Victoria, Hamilton Centre, Mount Napier Road, Hamilton, Victoria 3300, and Molecular Plant Breeding Cooperative Research Centre, Australia, [4]Crop Genetics, Pioneer Hi-Bred International, 7300 NW 62nd Avenue, Johnston, Iowa 50131-1004, USA

Overview Molecular marker-assisted plant breeding is a key target for the temperate legume pasture crop white clover (*Trifolium repens* L.). The first genetic linkage map of white clover has been constructed using self-fertile mutants to derive an intercross based fourth and fifth generation inbred parental genotypes (F_2[I.4R x I.5J]). The framework map was constructed using simple sequence repeat (TRSSR) and amplified fragment length polymorphism (AFLP) markers. Eighteen linkage groups (LG) corresponding to the anticipated 16 chromosomes of white clover (2n = 4x = 32), with a total map length of 825 cM were derived from a total of 135 markers (78 TRSSR loci and 57 AFLP loci). The F_2(I.4R x I.5J) family has been subjected to intensive phenotypic analysis for a range of morphogenetic and developmental traits over several years at IGER, Aberystwyth, Wales and East Craigs, near Edinburgh, Scotland. The resulting phenotypic data were analysed independently to identify QTL (quantitative trait loci) for the various traits, using single marker regression (SMR), interval mapping (IM) and composite interval mapping (CIM) techniques. Multiple coincident QTL regions were identified from the different years and different sites for the same or related traits. The data were reanalysed using a meta-analysis across years and sites and Best Linear Unbiased Estimates (BLUEs) were derived for the plant spread, petiole length, leaf width, leaf length, leaf area, internode length, plant height and flowering date traits. A total of 24 QTLs were identified on 10 of the linkage groups. Three regions on LGs 2, 7 and 12 all demonstrated overlapping QTLs for multiple traits (Figure 1). A meta-analysis approach can quickly identify regions of the genome that control the trait in a robust predictable manner across multiple spatial and temporal replication for rapid targeted genetic enhancement via marker-assisted breeding. This first genetic dissection of agronomic traits in white clover provides the basis for comparative trait-mapping studies and the enhanced development and implementation of marker-assisted breeding strategies.

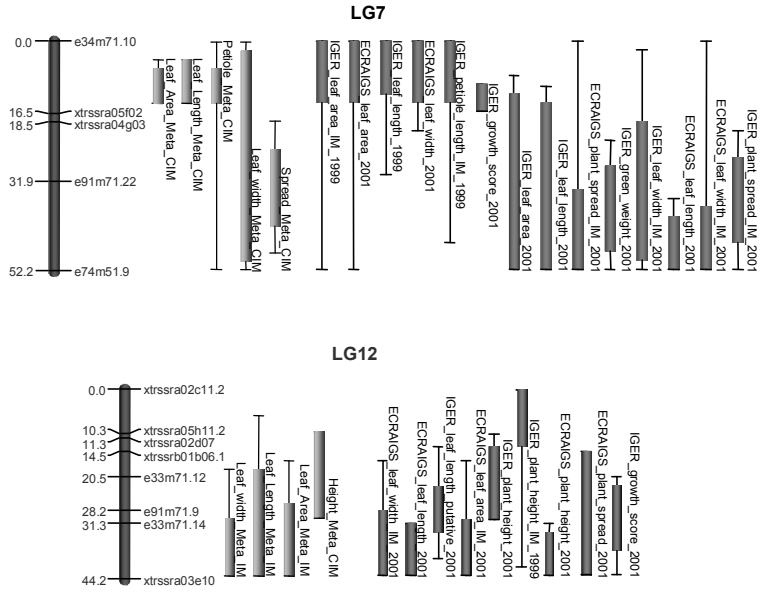

Figure 1 Linkage groups 7 and 12 from genetic map of the F_2(I.4R x I.5J) mapping population, with QTL regions identified. The QTL identified using the meta-analysis are indicated, along with comparison to QTLs from the separate datasets.

Acknowledgements The authors are grateful for financial support from (UK) Defra and BBSRC and (Australia) Victorian DPI, DA, MLA, GGDF and MPB CRC