Towards a Comparative Map of White Clover (Trifolium Repens) and Barrel Medic (Medicago Truncatula)

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Towards a comparative map of white clover (*Trifolium repens*) and barrel medic (*Medicago truncatula*)

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Introduction Grassland is of pivotal importance to the Irish agricultural industry. This dependence of grass is reflected in the large proportion of land area under grass, approx. 80% of the total land acreage in Ireland. The presence of white clover (*Trifolium repens* L.) in grassland significantly improves the overall nutritional value of the forage by increasing the relative amounts of nitrogen present. Genetic improvement of white clover through breeding of varieties should increase the productivity of grasslands. Advances in plant biotechnology offer the possibility of developing tools that will radically enhance our ability to breed improved plant varieties. The objective of this study is (1) to construct a genetic map of white clover and (2) to assess the level of genome synteny of white clover and *M. truncatula* (the model for legume species) with the use of different molecular markers developed in *M. truncatula*.

Materials and methods Genomic DNA from a F1 hybrid white clover population was extracted using CTAB method. The population consisted of 94 progeny bred in IGER (Wales) from parents, S1S4 and R3R4, and was used as mapping population. In order to provide a basis for the comparison of the genomes of white clover and *M. truncatula*, we are in the process of developing a genetic map of clover, using AFLP markers, microsatellite markers and a set of PCR-based markers derived from genes that have previously been placed on the *M. truncatula* genetic map (Choi *et al*., 2004).

Results To date, the segregation of 170 AFLP markers has been assayed in the mapping population (Figure 1). However, additional AFLP markers will be developed in order to obtain a comprehensive map. This map will then be tagged with a number of molecular markers of known chromosomal location from existing maps of white clover and *M. truncatula*. We have assessed the amplification in clover of 89 (EST and BAC end sequence derived) PCR-based markers mapped in *M. truncatula* by Choi *et al*. (2004). Sixty five (73%) successfully amplified in white clover, of which 22 were single copy amplicons (Table 1). The single copy products are being assessed for polymorphism in our mapping population and, if possible, be placed on the genetic map.

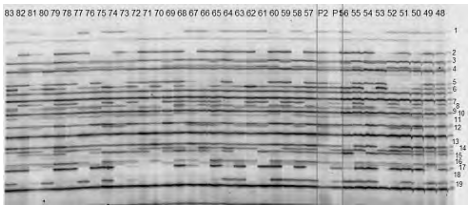

Figure 1 AFLP markers (1-19) representing Pac Maag primer combination on the white clover parents (P1, P2) and some of the progeny (48-83)

Table 1 Successful amplification of *M.truncatula* PCR-based primers applied to white clover

Total no. markers tested to date	95
No. successful in *M. truncatula*	89
No. successful in white clover	65
No. giving single bands in white clover	22
Proportion of amplification in both sp.	73%

Reference

Choi H-K., Kim D., Uhm T., Limpens E., Lim H., Mun J-H., Kalo P., Penmetsa R.V., Seres A., Kulikova O., Roe B.A., Bisseling T., Kiss G.B. and Cook D.R. (2004). A sequence-based map of *Medicago truncatula* and comparison of marker colinearity with *M. sativa*. Genetics, 166: 1463-1502.