

Development of a White Clover Linkage Map with Cross-Species SSR Markers and Comparative Mapping within the *Trifolieae*

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Allotetraploid white clover (*Trifolium repens*), a cool-season perennial used extensively as forage for livestock, is an important target for marker-assisted breeding. A genetic linkage map of white clover was constructed using simple sequence repeat (SSR) markers based on sequences from several *Trifolieae* species, including white clover, red clover (*Trifolium pratense*), *Medicago truncatula* and soybean (*Glycine max*). An F₁ population consisting of 179 individuals, from a cross between two highly heterozygous genotypes, GA43 and Southern Regional Virus Resistant ('SRVR'), was used for genetic mapping. More than 1,570 SSR primer pairs were screened for amplification and polymorphism. A total of 565 polymorphic primer pairs were selected for genetic mapping. Of these, 479 primer pairs amplified at least one allele. The map consists of 415 loci amplified from 343 SSR primer pairs, including 83 from white clover, 181 from red clover, 77 from *M. truncatula* and two from soybean. Linkage groups for all eight homoeologous chromosome pairs of allotetraploid white clover were detected. Map length was estimated at 1,877 cM with 87% genome coverage. Map density was approximately 5 cM per locus. Segregation distortion was detected in six segments of the genome (A1, A2, B1, B2, C1, and D1). Comparing map location of markers originating from white clover, red clover, and alfalfa (*Medicago sativa*) suggested putative macro-synteny between the three *Trifolieae* species (Fig. 1). This map will link quantitative trait data with the genetic location of SSR markers, and accelerate the improvement of white clover by marker-assisted selection and breeding.

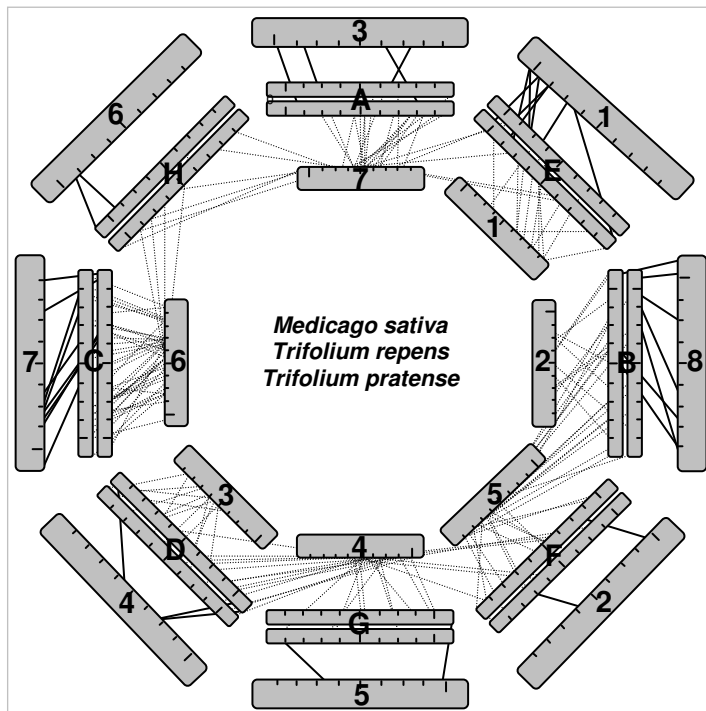


Fig. 1 Consensus comparative map for *M. sativa*, *T. repens*, and *T. pratense*. The three levels of circles represent the genomes of the three species. Outside circle: autotetraploid *M. sativa*; middle circle: allotetraploid *T. repens* with two homoeologous pairs; inside circle: *T. pratense*. Each bar represents one linkage group, and is scaled to the actual map length. Corresponding markers between *T. repens* and *T. pratense* / *T. repens* and *M. sativa* were connected with dashed / solid lines, respectively, based on map distance.