

Framework Genetic Linkage Map for Alfalfa

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A classic genetic linkage map is the foundation for genetic studies and breeding applications. Alfalfa includes two main subspecies, *M. sativa* subsp. *sativa* and *M. sativa* subsp. *falcata*, and two ploidy levels, diploid and tetraploid. We developed genetic maps for diploid alfalfa using populations derived from intra- and inter-subspecies crosses and compared those maps with a *M. truncatula* physical map. We found that the genetic maps and the *M. truncatula* physical map showed overall synteny. A few minor differences in marker orders were also found, which was likely due to the low confidence deriving from limited population sample size and/or rare informative recombinants among tightly linked markers. We also observed high levels of segregation distortion in both intra- and inter-subspecies crosses. As more and more molecular markers are available and the cost of genotyping decreases, we suggest that a random mating advanced diploid population (RMAD) be used to construct a classic reference map for alfalfa. The advantages of RMAD populations are (1) relatively simple genetic inheritance compared to tetraploid populations; (2) providing full segregation information of markers compared to tetraploid populations; (3) increased number of recombinants improving resolution power compared to F₁, F₂, and backcross populations; (4) lower segregation distortion level by breaking the linkage between segregation distortion loci and surrounding markers compared to F₂ and backcross populations.