

CONSTRUCTION OF AN IMPROVED LINKAGE MAP OF DIPLOID RELATIVES OF ALFALFA

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An improved genetic map of diploid ($2n=2x=16$) relatives of alfalfa has been constructed by analyzing the inheritance of more than 900 genetic markers on a F₂ population containing 137 plant individuals (1). The F₂ segregating population derived from a self pollinated F₁ hybrid individual of the cross of the yellow flowered *Medicago sativa* ssp. *quasifalcata* and the blue flowered *Medicago sativa* ssp. *coerulea*. This mapping population was the same one that had been used for the construction of the basic genetic map of alfalfa (2). The genetic analyses were performed by using classical (3) and specific (4) maximum-likelihood equations and related computer programs. In this map, the linkage relationships of some markers on linkage groups 6, 7, and 8 are different from the previously published map. The cause of this discrepancy was that the genetic linkage of markers displaying distorted segregation (characterized by an overwhelming number of heterozygous individuals) had artificially linked genetic regions that turned out to be unlinked. To overcome the disadvantageous influence of the excess number of heterozygous genotypes on the recombination fractions, recently described maximum-likelihood formulas (4) and colormapping (5) were used which allowed us to recognize the misleading linkages and to estimate the genetic distances more precisely.

The genetic map is being developed permanently and the improved genetic map of alfalfa in its present form contains more than 1800 markers (8 morphological, 10 allozyme, 26 seed protein and more than 1700 DNA-based markers) of which more than 300 represent loci with known function or sequences in the genome. The markers of the eight linkage groups cover approximately 760 cM genetic distance. The average correlation between the physical and the genetic distance is about 1000 kb/cM taking the DNA content of the haploid genome as about 1000 Mbp (6). This genetic system has been used to map protein markers originating from nodule and seed tissue as well (7).

Other linkage studies (cited in 1) also report segregation distortion, which is a common feature of F₂ families involving diploid relatives of alfalfa. Nonetheless, improved genetic map of alfalfa is suitable for comparative mapping studies. It has already been used successfully to facilitate the fine mapping of a non-nodulation trait in tetraploid alfalfa (8), and can serve as a useful tool in mapping other important tetraploid traits in the future. The determination of the degree of synteny between the genetic maps of *Medicago sativa* s.l., *Medicago truncatula*, *Pisum sativum*, and other legumes is underway.

References

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