An integrated genetic linkage map of alfalfa (*M. sativa* L.)

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A high-density genetic linkage map could provide the basis for fine mapping, comparative mapping, and linkage disequilibrium (LD) estimation, and also facilitate marker-assisted selection (MAS) and genomic selection (GS). A number of genetic maps have been constructed for alfalfa. However, most previous maps were poorly saturated or lacked resolution due to the limited number of individuals, recombination events, and polymorphic markers within each mapping population. In this study, we constructed a framework consensus map by integrating five individual maps derived from one tetraploid and three diploid mapping populations. The resulting consensus map spans 767 cM across eight linkage groups and is composed of 316 markers (45 RFLP, 217 SSR, and 54 SNP) with an average density of one marker per 2.4 cM. Quantitative trait loci (QTL) identified from three mapping populations were projected into the consensus reference map to enable QTL meta-analysis. A high level of synteny was observed between the alfalfa consensus map and *M. truncatula* physical map. These results enable alfalfa scientists to make use of well-documented genes in the model species for alfalfa research and breeding.