

Breeding alfalfa in the genomics era:
We're moving faster, but where are we going?

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The recent expansion of basic research on the model legume *Medicago truncatula* bodes well for the alfalfa (*M. sativa*) community if the genomics tools developed in the model can be usefully applied to crop improvement. No one will deny that our knowledge of genetic systems has increased dramatically due to application of the various technologies, but the utility of genomics tools to improving breeding methodology needs to be critically examined. Manipulation of single gene traits using biotechnological approaches has been clearly successful, even in alfalfa, but will these tools be as useful for enhancing complex quantitative traits such as yield in heterogeneous populations of heterozygous individuals in outcrossing species at higher ploidy levels?

Improvements in alfalfa breeding should be focused in four main areas: (1) constructing a comprehensive picture of both cultivated and wild genetic resources, (2) streamlining selection procedures to shorten cycle time and increase heritabilities, (3) developing alternative cultivar types that harness the genetic potential within and among germplasm groups, and (4) facilitating the creation and maintenance of genetic variation for major quantitative traits in diverse breeding populations. The major traits of winter survival, multi-year persistence, regrowth, biomass yield, and seed yield cannot be thoroughly assessed in the autogamous, annual, diploid model species. As this list makes clear, the types of problems of interest to alfalfa breeders and to the model legume community differ considerably. Thus, in order for genomics tools to be used to develop better alfalfa cultivars for farmers, breeders will need to apply the technology directly in alfalfa improvement programs.

Overlooking the facts that one of the biggest dilemmas facing alfalfa improvement is a dearth of breeders, and that many improvements in cultivar development could be effected by simply spending more money on traditional selection methods, genomics offers potential means to attack each of the four research areas mentioned above. Genetic markers linked to genes of interest, isolation of chromosomal regions and genes involved with agronomically important traits, and evaluation of gene expression patterns will allow effective manipulation of quantitative traits, at least in certain situations. The promise of genomics may be overstated, however, and unless new methods of using these tools are developed, they may not have a large impact on population improvement programs. In particular, using markers to select desirable individuals during recurrent selection programs is hindered by our limited knowledge of population structure, including linkage disequilibrium and allelic diversity at important loci, in any alfalfa germplasm source, and our inability to identify haplotypes in an easy manner. The use of genomics methods to use exotic germplasm, dissect quantitative traits, and identify candidate loci may help ease some of these problems. In the end, we need to ask whether we are using genomics tools to solve serious breeding problems, or inventing breeding problems that are solvable by genomics methods.