

Marker assisted selection in legumes

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Marker assisted selection (MAS) has begun to be implemented in some self-pollinating crops such as wheat. The promise of MAS has been on the breeding horizon for over two decades now. With the advent of the *Medicago truncatula* and *Lotus japonicus* genome sequences; numerous SSR-mapped markers in *M. truncatula*, *Medicago sativa*, *Trifolium pratense*, and *Trifolium repense*; and various EST projects in forage legume species, a good genomic infrastructure has been developed. In this context, an exploratory integrated QTL discovery and selection scheme has been implemented in *T. pratense*. *T. pratense* (red clover) is a diploid outbreed species with limited breeding resources due to smaller seed market share, with biomass yield and plant persistence being the overwhelming traits of breeding interest. This makes red clover an ideal test case for determining MAS feasibility, both scientifically and economically. An analysis of a recurrent halfsib selection scheme overlaid with a simultaneous recurrent linkage disequilibrium (LD) QTL discovery and MAS scheme shows substantial increased genetic gain per cycle could be achieved for traits, such as persistence, that are difficult to phenotype and highly quantitative. However, consideration of molecular technology costs, along with correspondingly reduced field evaluation expenditures, makes the genetic gains in MAS selection schemes much more marginal. One of the most powerful uses of molecular markers in a halfsib recurrent selection scheme would be to increase parental control by identifying paternity for truncation selection within field selected halfsib lines. LD QTL discovery methods fit very nicely into recurrent halfsib selection schemes, since almost any marker associations with the trait (real or population structure induced) can be used for either increased parental control or QTL enrichment. Reducing genotyping costs to \$0.03 USD or less per marker per genotype would make MAS very competitive in red clover persistence selection. Even at current cost estimates of over \$0.30 USD per marker per genotype, MAS could play a profitable role in paternity identification and selection schemes.