

QTL Mapping of Plant Architectural Traits in Diploid Alfalfa

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Alfalfa (*Medicago sativa* L.) is a perennial legume grown widely as a forage crop for highly nutritious hay, silage, and grazing. Breeding for yield improvement in alfalfa is mostly based on recurrent phenotypic selection; however, yield improvement has plateaued in the last three decades. Alternative modern breeding strategies such as molecular marker assisted breeding are being adopted to accelerate breeding, but genomic tools connecting phenotype to genotype are still needed. Thus, alfalfa plant architectural traits potentially affecting yield need to be studied. To explore architectural traits in diploid alfalfa, this study uses multiple segregating F2 mapping populations derived from phenotypically divergent parents in traits such as presence of pubescence; stem erectness, length and thickness; leaf size and number; internode length; and maturity. Parents were selected from existing diploid alfalfa research germplasm at UC Davis and F1 plants were self-pollinated to create F2 populations of 100-300 individuals. Currently, the F2 mapping populations growing in greenhouse environment are premature for phenotyping but have been sampled (F1 and parents too) for genotyping. DArTseq technology will be used to obtain genotype data and traits will be measured to obtain phenotype data. Single nucleotide polymorphism (SNP) molecular markers will be used to develop a genetic linkage map for associating regions of DNA with phenotypic variation. The objective of this study is to identify major QTLs for plant architectural traits which can provide novel target regions of study and be directly used in marker assisted selection to accelerate alfalfa breeding programs. We will discuss initial results of genetic mapping in these populations.

References

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