The Fascinating Genomes & Phenomes of Diploid Alfalfa

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Cultivated alfalfa, *Medicago sativa* L., is autotetraploid but wild diploid relatives exist, though they are largely understudied. Tetrasomic inheritance complicates genetic analyses and the resolution of haplotypes from genome sequencing, and although diploid inheritance lacks certain elements seen in tetrapoids – for example, two instead of four possible alleles per locus and three vs. five genotypic classes for a biallelic locus – the possibility of using diploids to dissect quantitative traits, to evaluate the effects of selection, or to identify effects of transgenes suggests that more use should be made of diploid genetic resources.

Over that past several years, we have developed numerous diploid alfalfa populations and identified specific genotypes to use for various genomic, genetic, and breeding projects. Using long-read sequencing, we have assembled multiple haplotypes of both subspecies of diploid alfalfa, purple flowered *M. sativa* subsp. *caerulea* and yellow flowered *M. sativa* subsp. *falcata*. These haplotypes show significant numbers of rearrangements both within and between subspecies. In addition, we have developed genetic maps of over a dozen populations and identified QTL in for yield and yield components in several of them. We have also identified loci involved in extreme segregation distortion toward excess heterozygosity, a pervasive feature of all linkage maps. Finally, we have selected diverse parents to create new germplasms that could be useful for breeding experiments and genetic studies. In this presentation, I will highlight some of the results of our diploid alfalfa experiments and will discuss the value of this research for breeding alfalfa and improving complex traits.