TOWARDS UNDERSTANDING THE GENETIC BASIS OF YIELD BY CHARACTERIZING SEGREGATION DISTORTION IN DIVERSE DIPLOID ALFALFA POPULATIONS

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Abstract

Alfalfa (*Medicago sativa L.*) is a widely cultivated forage crop that, due to its outcrossing nature, carries a high genetic load. The effect of this load is often reflected in the form of segregation distortion, which occurs when inheritance patterns deviate from expected Mendelian ratios, often towards one parental genotype. Oddly, in the case of alfalfa, we observe a high extent of distortion significantly skewed towards heterozygosity present throughout the genome. We are interested in deciphering the underlying cause of this phenomenon, particularly considering the stagnation of biomass yield increases in alfalfa despite continued breeding efforts over the past 30 years. This project is a novel approach to better understand the genetics of alfalfa and the genetic factors that might be influencing yield.

To determine the genetic mechanisms responsible for this unexpected pattern, we created a diverse panel of F_2 alfalfa populations including both intra- and inter-subspecies hybrids of *M. sativa* subsp. *caerulea* and subsp. *falcata.* Using these populations, we aim to identify genomic regions consistently exhibiting distortion skewed towards excess heterozygosity, and to create genetic maps of these regions. We have also generated high-quality phased reference genomes for these subspecies and their hybrids to investigate structural variation. Ultimately, we want to identify consensus regions of distortion in whole genome sequences and genetic maps and/or individual loci, and to compare these locations to structural variants.

Key words: Segregation distortion, yield, heterozygosity, reference genome, diploid alfalfa

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