Prospects for Improving Alfalfa Yield Using Genomic- & Phenomic-Based Breeding

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Alfalfa (*Medicago sativa* L.) is a perennial outcrossing legume that is cultivated as an important forage crop in many parts of the world. Yield is the most important trait for profitable alfalfa production, yet over the last 30 years yield improvement in alfalfa has stagnated. Current breeding methods focus on recurrent phenotypic selection; however, alternatives incorporating genomic- and phenomic-based information may enhance genetic gain and help to address the lack of yield improvement. Here we attempt to increase the yield potential of alfalfa using genomic selection (GS) in combination with high throughput phenotyping (HTP). A total of 193 families from two closely related elite populations were sown in the greenhouse and transplanted into mini sward plots in two locations near Davis, CA in May 2020. The trial was managed as a high-input system under full irrigation. Plants were genotyped by GBS and phenotyped for biomass yield by mechanical harvest and a combination of drone and tower-based remote sensors across 13 harvests, 3 in the establishment year (2020), 7 in the first full year of production (2021) and 3 to date in 2022. Genotyping resulted in a dataset with 90,000 SNPs distributed across the genome. Alfalfa yields ranged from 13-27 tonnes DM/hectare/year. We will discuss these results further in the paper along with the development of our GS model which could significantly reduce the average length of a selection cycle compared to a traditional alfalfa breeding program and provide breeders with the potential to increase the rate of genetic gain for a range of complex quantitative traits including yield.