

2017 USAFRI Research Project Objectives

Maximizing Alfalfa's Yield Potential University of California - Brummer

Project Award: \$49,988

Justification:

- High yield of highly nutritious forage is critical for profitable alfalfa production. Yield advances are being made in other crops, in particular, corn silage, so the need to boost alfalfa's yield potential just to remain competitive with other crops is substantial. Unfortunately, most evidence shows that alfalfa yield potential has not improved over the past several decades, with stagnation in most areas of the country (Brummer & Casler, 2014). Improvements in alfalfa have occurred; undoubtedly, resistant cultivars will have higher yield, particularly later in stand life, under disease or insect pressure.

However, these yield gains are effectively defensive – while they protect yield, they are not advancing yield potential. University variety trials in California show clear indications that even across years, yields have not increased since the 1970s (Figure 1).

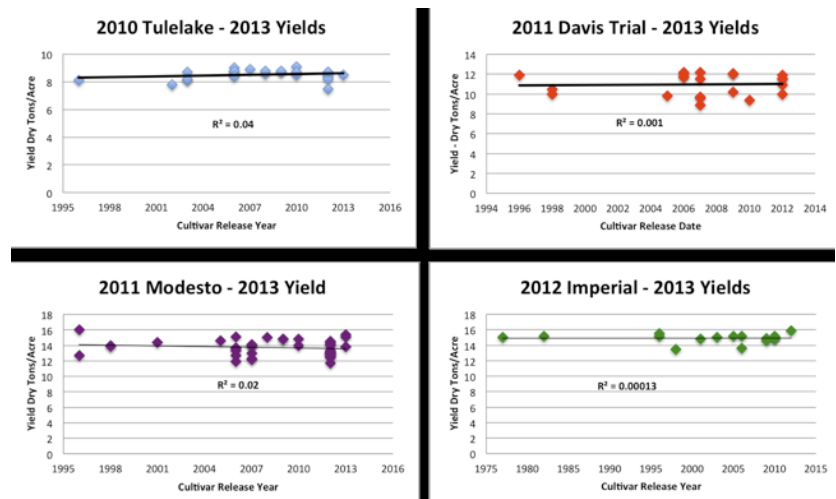


Figure 1. Relationship between year of cultivar release (xaxis) and biomass yield at four CA environments (y-axis). Yield is total annual yield for 2013; the dates trials were planted precede the location name. Locations include Tulelake (north); Davis and Modesto (central), and Imperial (south). Yield data are at <http://alfalfa.ucdavis.edu/>.

My research group is investigating three interlinked objectives related to alfalfa yield – heterosis, yield selection, and dormancy. Heterosis can be defined as the superiority of a hybrid (formed from crossing inbreds or populations) compared to the midparent or the high parent value, with the latter being the more interesting from a commercialization standpoint. Although alfalfa cultivars are typically marketed as synthetic varieties, semi-hybrid cultivars theoretically could be produced and they could express heterosis for yield (Brummer, 1999). We have evaluated the potential for yield heterosis among alfalfa germplasm, exploring both yellow-flowered falcata (Riday and Brummer, 2002; 2005) and non-dormant germplasm (Sakiroglu and Brummer, 2007), complementing conceptually similar work done by Ian Ray's group in the early 2000s (e.g., Segovia-Lerma et al., 2004). The substantial amount of underused germplasm from the USDA-National Plant Germplasm System and other genebanks worldwide could be used to create genetically distinct populations useful to form heterotic groups de novo based on breeding methods such as reciprocal recurrent selection.

We have applied genetic markers to assess yield and yield-related traits (e.g., Robins et al., 2007; Li, Alarcon-Zuniga, et al., 2016). Recently, we have used high-throughput array-based SNP markers (Li et al., 2014a) and genotyping-by-sequencing (GBS) (Li et al., 2014b) to quickly and cost-effectively cover the entire genome. We used GBS markers and yield data from a clonal phenotypic selection program (Li et al., 2015) and also from two Italian half-sib family selection programs (Annicchiarico et al., 2015) to create genetic prediction models. These models suggest that we can accelerate yield improvement using GBS marker-only genomic selection (GS). These markers can also be used for genome-wide association studies (GWAS) (Sakiroglu and Brummer, 2016).

More recently, we have been using GBS markers to assess population distinctiveness. We evaluated populations of CUF101 that had been divergently selected for autumn dormancy – taller or shorter plants in autumn – using GBS markers. Marker loci whose allele frequencies shifted as a result of selection may be associated with dormancy. We genotyped four independent 24 plant bulks of each population. The results show that the four replicate bulks tightly cluster but the three populations are clearly differentiated (Figure 2). The O and H populations are not different phenotypically for plant height in autumn (the selection criterion), yet they can be clearly separated by markers nonetheless. The importance of this experiment is that we can easily separate populations based on the marker allele frequencies in bulked samples. Thus, this opens the door to applying markers more widely in alfalfa breeding where all germplasm pools are populations, not individual genotypes as in inbred crops.

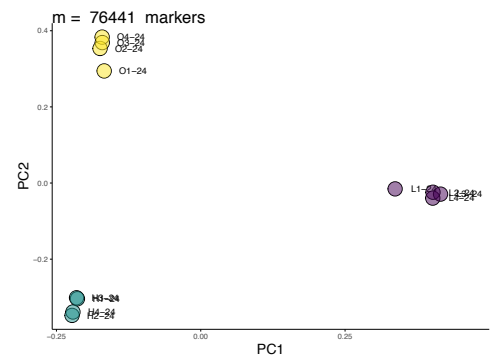


Figure 2. The first two principal components from an analysis of >76,000 GBS-based SNP markers assayed on four replicate 24-plant bulk samples of three populations: CUF101 (O=original) and pops selected for three cycles for short (L) or tall (H) fall growth (Munjaj & Brummer, unpub).

Both conventional and marker-assisted selection depends on accurate phenotypes of the traits under selection. For traits like yield and even plant height, repeatedly measuring large nurseries throughout the year is both arduous and expensive. Automated phenotyping for plant size, growth and development stage, and plant health and stress level has been demonstrated in a number of field crops (e.g., white clover [Inostroza et al., 2016]; cotton [Andrade-Sanchez et al., 2014]; and wheat and soybean [Bai et al., 2016]). Importantly, sensor-based phenotyping has been used to accurately measure alfalfa height (Pittman et al., 2015). Applying these technologies to alfalfa breeding, especially when combined with high-throughput genotyping, could further improve yield gains.

Objectives:

- Our long term objectives are to develop selection methodologies that can help breeders address the yield potential of alfalfa, leading to the release of higher yielding cultivars. In the near term, we will address three objectives related to the overarching research themes described in the introduction: 1) Evaluate the yield gain possible from genomic selection; 2) Classify germplasm by genotyping populations and forming heterotic pools, and 3) Characterize alfalfa growth using proximal and/or remote sensing. All three of these projects build on existing experiments in my program supported by various sources. Thus, these projects leverage current funding and provide opportunities to acquire additional funding in the future.