Characterization of Alfalfa Populations Contrasting for Root System Architecture (RSA)

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ABSTRACT

The root system architecture (RSA) of plants affects the capacity for nutrient and water uptake. Different root structures could impact biomass yield production and may contribute to the persistence of perennial plants. The objectives of this study were to phenotype the roots of three alfalfa populations and identify differences between genotypes. Alfalfa seedlings from a base population and two populations resulting from two cycles of field-based selection for branched vs. tapped roots were grown in controlled greenhouse conditions. The roots from multiple individuals from each population were harvested, washed, imaged and analyzed using WinRhizo software to aid characterization of root traits. Differences in the percent of tertiary roots was a key factor to differentiate between the tapped vs. branched root phenotype. Individuals from each of the populations contrasting for root architecture were identified and are being genotyped using genotyping-by-sequencing to identify genetic differences underlying variation in root traits. Candidate genes and transcription factors associated with root growth and development were mined from the literature and used for primer development. A subset of genotypes contrasting for root traits (strong tap root vs. fibrous network of roots) were genotyped using the developed primers to identify single nucleotide polymorphisms (SNP) that were assayed with a high-resolution melting (HRM) approach. Ongoing efforts include development of mapping populations generated from crosses between individuals with tapped and branched roots. The segregating populations will be evaluated for root growth and genotyped to identify and/or validate QTL associated with root traits. Understanding genetic determinants underlying root system architecture can be utilized to identify the ideal root ideotype in alfalfa that will increase both biomass yields and persistence.