Determining Genetic Factors That Influence Protein Quality & Yield in Alfalfa

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Alfalfa is the most widely grown legume forage crop worldwide due to its adoption in various environments and high quality as livestock feed. However, alfalfa presents challenges for genetic improvement like highly heterozygous genomes and outcrossing biology. Therefore, the genetic basis that influences complex traits like yield or protein degradability is still poorly understood. The objective of this research was to identify molecular markers associated with protein degradability, fall dormancy (FD), and yield in a diverse panel of 200 alfalfa accessions planted in field trials in 3 locations for 3 years. Phenotypic traits were adjusted by single-trial and stagewise analysis in a multi-environmental trial. Multiple significative markers were identified in the present study: seven SNPs were associated with protein degradability, seven SNPs were associated with yield, and 13 SNPs were associated with fall dormancy. Some markers were consistently identified across multiple datasets. E.g., markers associated with FD and located in a locus annotated as protein NUCLEAR FUSION DEFECTIVE 4-like. Markers and associated genes identified in this study will be useful for the genetic improvement of forage quality, yield, and fall dormancy selection in alfalfa.