

Genome-Wide Association Studies of Verticillium Wilt Resistance in Alfalfa using Genotyping by Sequencing

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Quantitative traits such as biotic and abiotic stress resistance are most likely under the control of multiple genes and interact with environmental factors. Identification of resistance loci that contribute to variation in such complex traits, is a primary challenge in plant breeding and population genetics. In the present study, we used an integrated framework that merges a QTL mapping approach called “genome-wide association (GWA)” with high-throughput genome sequencing methodology called “genotyping by sequencing (GBS)” to map Verticillium wilt resistance loci in alfalfa. This framework provides a statistical basis for analyzing marker-trait association using linkage disequilibrium. We have identified 15 significant GBS markers associated with VW resistance and there are located on different chromosomes. Validation of the markers is in progress. Once validated, these SNP markers can be used for marker-assisted selection.