

Developing molecular marker for Verticillium wilt resistance in autotetraploid alfalfa (*Medicago sativa* L.)

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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 disease and abiotic stress resistance loci in alfalfa. This framework provides a statistical basis for analyzing marker-trait association using linkage disequilibrium. We have identified a group of markers and putative candidate functional genes associated with Verticillium wilt resistance. One of these genes encodes an ABC transporter (Figure 1). Validation of the marker linked to this gene has shown high co-segregation with the VW resistance allele in the S&W populations (Figures 2 and 3). Validations of other markers associated with resistance are in progress. After validation, these markers can be used for marker-assisted selection for breeding alfalfa cultivars with improved resistance to the disease.

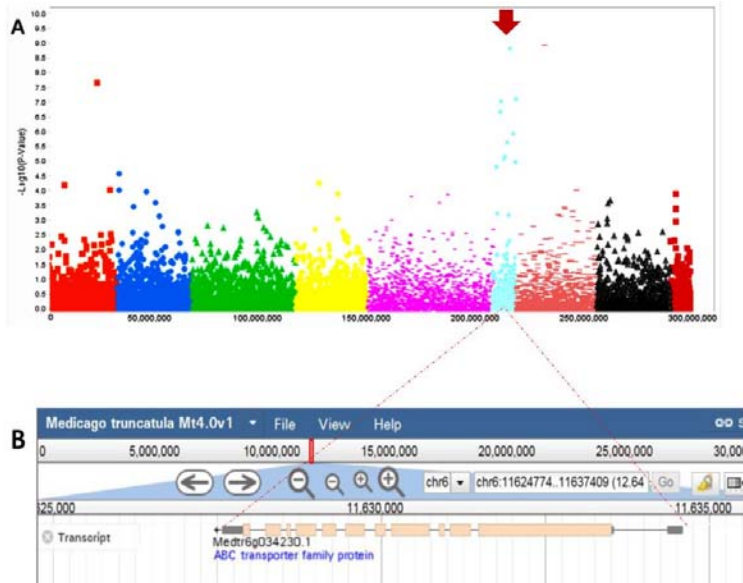


Figure 1. Marker-trait association identified significant loci for VW resistance on Chromosome 5 (A). One of the significant marker hits ABC transporter at the same locus (B).

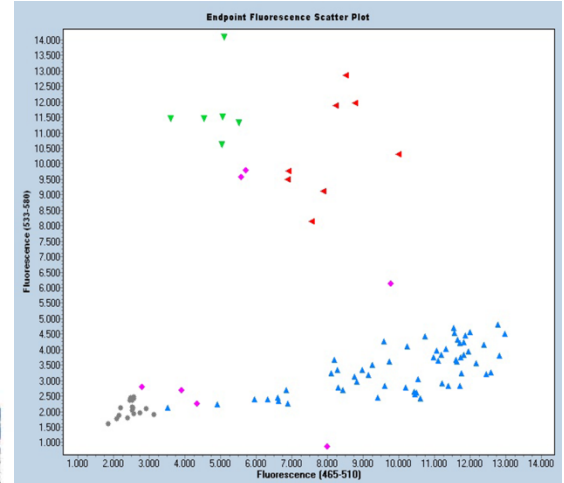


Figure 2. Validation of marker for VW resistance in the S&W alfalfa population using KASP assay

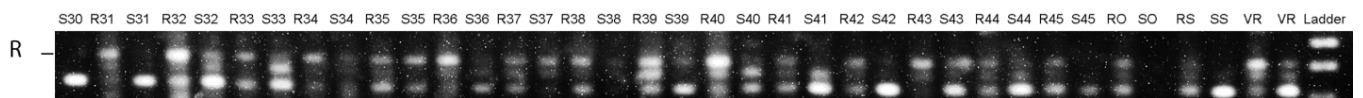


Figure 3. Validation of marker linked to ABC transporter identified from the S&W alfalfa population. The marker showed high co-segregation with VW resistance at the “R” allele.