

Genomic Analysis of Verticillium Wilt Resistance and Drought Tolerance in Alfalfa

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Abstract

Alfalfa (*Medicago sativa* L.) is the fourth largest crop in the United States. Changing trends to multipurpose uses increases demand for alfalfa. However, the production of alfalfa is challenged by endemic and emerging diseases and adverse environmental factors. Identification of genes/loci controlling biotic and abiotic stress resistance will facilitate breeding for improving alfalfa production. In the present investigation, we applied an integrated framework of genome-wide association with high-throughput genotyping by sequencing for identifying genes/loci associated with Verticillium wilt (VW) and drought tolerance in alfalfa populations. An integrated pipeline for genotyping by sequencing was used for analyzing allelic variation in autotetraploid alfalfa. Marker-trait association by linkage disequilibrium identified a group of SNP markers significantly associated with VW resistance and drought tolerance, respectively. Alignment of their sequence tags to the reference genome revealed multiple chromosomal locations. Markers associated with VW resistance were located on chromosomes 1, 5, 6, 7 and 8 (Fig.1). BLAST search using the flanking sequences of the resistance loci against *M. truncatula* genome identified candidate genes with disease resistance such as TIR-NBS-LRR protein and MDR-ABC transporter. Markers associated with drought tolerance were located in different chromosomal regions. Major loci identified in this work overlap with the reported QTLs in alfalfa. Our results have been published in peer-reviewed journals. Validation of resistance loci in a broad range of alfalfa populations has been conducting using high throughput strategies. Functional markers closely linked to the resistance loci or derived from functional genes will be developed and used for genomics-assisted breeding for alfalfa with improved resistance to the disease and abiotic stress.