

Mapping & Validation of Resistance to *Aphanomyces euteiches* in Alfalfa

Steve Damon, DLF USA

Steve Wagner, DLF USA

Justin Valletta, DLF USA

Tara Tarnowski, Corteva Agriscience

Lindsey Rushford, University of Wisconsin-Madison - Extension

Aphanomyces euteiches is an economically important soilborne oomycete pathogen of alfalfa (*Medicago sativa*) in North America. The pathogen thrives in saturated soils, resulting in seedling root rot and loss of plants in new alfalfa fields. Due to climate change, extreme weather events can cause soil saturation throughout the dormant alfalfa dairy region of North America. Genetic resistance is available for both race 1 and 2 of *A. euteiches*, however, race 2 (APH2) continues to be an important problem for the industry in the face of climate challenges. Four breeding populations of DLF Seeds alfalfa germplasm were phenotyped for resistance to APH2 and genotyped on a high density SNP microarray platform. A major effect QTL, likely a disease resistance gene (R-gene), was detected on chromosome 4 in each population. Based on linked SNP markers and segregation ratios in each mapping population, the putative R-gene displays complete dominance, with only one allele required to confer resistance. To validate the discovery, 8 plants with two copies of the putative R-gene were intermated to create a new population. This progeny population displayed greater than 80% resistance to several isolates of APH2, much higher than typical varieties developed through phenotypic selection. The conclusion drawn is that marker assisted selection (MAS) may improve resistance levels beyond phenotyping alone by increasing the allele frequency of dominant resistance genes in alfalfa breeding populations and commercial varieties.