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Mapping host resistance genes to soybean sudden death syndrome

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Soybean Sudden Death Syndrome (SDS) is a disease caused by a soil-borne fungus, *Fusarium virguliforme*. In addition to seed treatments, disease resistant varieties are the cornerstone of SDS management. Many genetic studies have attempted to identify genes responsible for the quantitative host resistance to SDS. Three recombinant inbred line (RIL) populations were evaluated for foliar SDS resistance at a naturally infested field site in Decatur, Michigan during the 2014 and 2015 growing seasons. Lines were evaluated for disease severity (DS) on a 1-9 scale, disease incidence (DI) as an estimate of the percentage of plants with symptoms per plot, and disease index (DX) as a metric which integrates DS and DI. A subset of RILs from each population were genotyped with the SoySNP6K Illumina Infinium BeadChip. Linkage maps unique to each population were constructed using Joinmap. Composite interval mapping was done using WinQTLCartographer. Two quantitative trait loci (QTL) were identified across multiple years and/or populations. One QTL was on Chromosome 10, and appears to be in close proximity to the *E2*maturity locus. Further mapping will be collected to determine if this QTL is truly responsible for SDS resistance, or if maturity conflated SDS phenotyping. The other QTL identified was on Chromosome 18, in a region which has been demonstrated to provide SCN and SDS resistance in many studies (*Rhg1/Rfs2*). RILs from the three populations were selected with residual heterozygosity in the QTL regions. Kompetitive Allele Specific Primers (KASP from LGC Genomics) were developed to identify recombination events within the residual heterozygous lines (RHL) which were selfed in the greenhouse. RHL with recombination events were evaluated in the field site in Decatur, MI during the 2016 and 2017 growing season to fine map the genes responsible for SDS resistance.