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Genome wide dissection of resistance to *Pythium sylvaticum* in soybean

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Pythium root rot (PRR) is an increasing threat for soybean growers in the United States. The disease is caused by several oomycete pathogens classified to the genus *Pythium*, such as *P. sylvaticum*, *P. oopapillum*, and *P. irregulare*. Previous studies have identified several putative quantitative trait loci (QTL) that confer resistance to *P. irregulare*, however, little study has been done for resistance to *P. sylvaticum*, which is the most prevalent *Pythium* species hosting soybean in Michigan. In our study, a genome wide association panel consisting of 99 accessions of MSU developed elite lines and 125 accessions from Plant Introductions (PI) were genotyped by BARCSoySNP50K BeadChips and used for genome wide association study (GWAS). Further analysis suggested general linear model (GLM) to be more suitable for association analysis. Using a cut-off of $q < 0.05$, 11 significant markers were identified, each explaining 9.8% - 10.7% of phenotypic variation. 10 markers were located on chromosome 10, and distributed within a 50kb region between markers Gm10-42963703 and Gm10-43014268, with the most significant three markers Gm10-42965189, Gm10-42975806, and Gm10-43004105 ($p = 2.36 \times 10^{-6}$). The other marker was located on chromosome 20 (Gm20-2245263), with p value of 6.05×10^{-6}. Moreover, a RIL population of 113 F4:7 lines derived from E09014 x E05226-T was used for genome wide QTL mapping. 87 RILs were genotyped with BARCSoySNP6K BeadChips at F4:5, and a high density linkage map with 1390 single nucleotide polymorphism (SNP) markers were constructed into 28 linkage groups. The rest of the RILs were genotyped at F4:7 using the same method. QTL analysis using 87 lines identified four QTLs on chromosomes 9, 10, 19 and 20. Of them, q10 (LOD = 3.36, $R^2 = 10.5\%$) was flanked by Gm10-44137020 and Gm10-44274964, and q20 (LOD = 3.52, $R^2 = 11.3\%$) was mapped between Gm20-1348454 and Gm20-3078662. Q10 was located about 1.4 Mb close to the significant region identified by GWAS, while q20 was co-localized with the GWAS marker Gm20-2245263. Further, we combined genotypes of all 113 RILs for QTL mapping, which confirmed q10 with higher significance (LOD = 4.94, $R^2 = 13.8\%$), while a new QTL was identified on chr. 18 (LOD = 2.87, $R^2 = 7.4\%$). Our results suggested that q10, q20 and the significant markers on chromosome 10 could be used for marker assisted breeding for resistance to *P. sylvaticum*.