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Genome-wide QTL mapping for *Pythium irregulare* resistance in soybean
*Paul Collins**, Department of Plant, Soil and Microbial Sciences, Michigan State University, Michigan, USA

Feng Lin, Department of Plant, Soil and Microbial Sciences, Michigan State University, Michigan, USA

Zixiang Wen, Department of Plant, Soil and Microbial Sciences, Michigan State University, Michigan, USA

Soybean (*Glycine max* (L.) Merr) is an essential oil and protein crop worldwide, particularly in the United States. *Pythium* root rot is one of the significant diseases of soybean in the United States causing seed and seedling rot. *Pythium* can rot soybean seeds and seedlings both before and after emergence. Many oomycetes pathogens belonging to the genus *Pythium* such as *P. irregulare*, *P. oopapillum*, and *P. sylvaticum*, are responsible for the occurrence of this disease. Till now, scanty reports are available on the identification of putative quantitative trait loci (QTL) responsible for resistance to *P. irregulare* which is one of the aggressive diseases causing root rot under Michigan conditions. The aim of the present study was to identify QTL for resistance to *P. irregulare* using a recombinant inbred line (RIL) population of 124 F3:4 developed from a cross between moderately resistant line E09014 and a moderately susceptible line E05226-T. A subset of 113 lines from the RIL population were genotyped with BARCSoySNP6K BeadChips. The final linkage map contained 1,336 markers grouped into 28 linkage groups, which correspond to the 20 chromosomes of soybean. A major QTL for RRW with LOD score 3.6 was identified on Chromosome 20 (LG I) and was flanked by markers Gm20_3078662 and Gm20_30417244 explaining a phenotypic variation of 11.1%. This QTL passed the 1000 permutation at 0.5 % test of significance with a fare margin. One putative QTL for RRW was also found on chromosome 18 (LG G) having a LOD score 3.2, flanked by markers Gm18_54717680 and Gm18_57346419 and explained 9.42% of the phenotypic variation. Both these QTLs were contributed by the parent E05226-T, a less resistant parent, suggesting transgressive segregation. Further work is in progress to fine map the QTL and develop markers for MAS.