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Identification and comparison of QTL for resistance to *Pythium ultimum* var. *ultimum* in two soybean RIL populations

*Kelsey Scott**, Department of Plant Pathology, The Ohio State University, Ohio, USA

Jonell Winger, Department of Plant Pathology, The Ohio State University, Ohio, USA

Anne Dorrance, Center for Soybean Research, The Ohio State University, Ohio, USA

Leah McHale, Department of Horticulture and Crop Science, The Ohio State University, Ohio, USA

Pythium seed and root rot of soybean can cause severe stand losses, particularly in cool and damp growing conditions. The soilborne oomycete *Pythium ultimum* var. *ultimum* is one of the most prevalent and pathogenic *Pythium* species that contributes to disease development in Ohio. This seedling disease can be managed with the use of cultivars with quantitative resistance to *Pythium*. To identify sources of resistance, the parents used to develop the soybean Nested Association Mapping (NAM) population were first evaluated for resistance to isolates of *Pythium ultimum* var. *ultimum* collected from fields in Ohio using a greenhouse cup assay. NAM parents HS6-3976 and 4J105-3-4 were found to be as resistant as the moderately resistant check according to root rot scores and mean root weight data. Thus, our objective was to identify the quantitative trait loci (QTL) that confer resistance to *P. ultimum* var. *ultimum* in two RIL populations derived from crosses HS6-3976 x IA3023 and IA3023 x 4J105-3-4, which are part of the larger NAM population. Composite interval mapping was performed separately on both populations using genome-wide logarithm of odds thresholds of 3.0 and 3.3 (type I error rate of $\alpha = 0.5$) for the HS6-3976 and 4J105-3-4 populations, respectively. Two QTL were detected in the HS6-3976 population on chromosomes 2 and 18. One QTL was detected in the 4J105-3-4 population on chromosome 3. These three QTL are potentially useful sources of quantitative resistance to *P. ultimum* var. *ultimum*.