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Current progress in assessing pathotype variability in North Central United States
Phytophthora sojae populations

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Phytophthora root and stem rot of soybean, caused by the oomycete *Phytophthora sojae*, is a devastating soybean disease that accounted for the loss of 32,864,000 bushels of soybean across the North Central region of the United States in 2014. This pathogen is most effectively managed by R-gene mediated resistance, and consequently, assessment of current *P. sojae* populations is of great importance to soybean disease research groups. The aim of this study is to characterize the pathotype diversity of *P. sojae* populations across the states of Ohio, Indiana, Kentucky, Michigan, Illinois, Iowa, Minnesota, Nebraska, and South Dakota. This characterization will allow for the assessment of the effectiveness of *Rps* genes in conferring resistance against populations of *P. sojae* across this region. Each state has collected soil samples from multiple locations with a known history of Phytophthora root and stem rot. Soil samples are baited with the susceptible cultivar Sloan for the recovery of *P. sojae*. These isolates are then pathotyped using 14 soybean differentials to assess their virulence against commonly deployed *Rps* genes, including *rps*, *Rps1a*, *Rps1c*, *Rps1d*, *Rps1k*, *Rps2*, *Rps3a*, *Rps3b*, *Rps3c*, *Rps4*, *Rps5*, *Rps6*, *Rps7* and *Rps8*. Currently, over 900 soil samples have been collected across 92 fields in 7 states, and isolate collection efforts have led to the recovery of over 200 *P. sojae* isolates from Ohio soil samples alone. From this survey, we expect to see a greater level of pathotype diversity compared to earlier surveys, which will provide greater awareness of the virulence that exists towards *Rps* genes and which ones should be deployed across the North Central soybean producing region of the U.S.