

Field Evaluation of Peanut Lines with Introgressions Conferring Resistance to Late Leaf Spot

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Late Leaf Spot (LLS) disease caused by *Cercosporidium personatum* (Berk. & M.A. Curtis) Deighton is one of the most costly diseases of U.S. grown peanut (*Arachis hypogaea* L.). IAC 322 is a breeding line that contains three introgressed chromosome segments from a wild species that provides a very high level of resistance to LLS. Although this line has excellent resistance to leaf spot, it does not have acceptable agronomic performance in Georgia. Genetic markers are available for these genomic regions, so marker assisted selection (MAS) to combine resistance with acceptable agronomic performance is feasible. The goal of this research was to identify the genomic regions or combinations of genomic regions that provide the highest level of resistance. 'TifNV-High O/L' was crossed with IAC 322, and 400 resulting F₂ progeny were genotyped. Individuals with single introgressed regions, individuals with all pairwise combinations, and individual with all three introgressions were identified. This material was then advanced to the F₅ generation. We previously reported results on LLS severity on this material from a detached leaf study. In 2018 we planted this material in replicated field studies at two locations. No fungicide sprays were used for leaf spot control. Results indicated that major genes for resistance are contained on the introgressions from the bottom of chromosome A03 and the top of chromosome A02. The third introgressed region was from the bottom of chromosome A02 and did not add significantly to the levels of resistance to LLS. These results can be used to improve the efficiency and effectiveness of MAS to develop leaf spot resistant cultivars.

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