

Evaluation of Leaf Spot Resistance in Wild *Arachis* Species of Section *Arachis*

A.N. MASSA*, R.S. ARIAS, R.B. SORENSEN, V.S. SOBOLEV, M.C. LAMB, USDA-ARS National Peanut Research Laboratory, Dawson, GA; S.P. TALLURY, USDA-ARS Plant Genetic Resources Conservation Unit, Griffin, GA; H.T. STALKER, Crop and Soil Sciences, North Carolina State University, Raleigh, NC.

Wild diploid *Arachis* species are a valuable source of resistance to early (ELS) and late (LLS) leaf spot diseases caused by *Passalora arachidicola* (syn. *Cercospora arachidicola* Hori), and *Nothopassalora personata* (syn. *Cercosporidium personatum* (Berk. & Curt.) Deighton], respectively. Within section *Arachis*, limited information is available on the extent of genetic variation for resistance to these fungal pathogens. The present study evaluated 148 accessions of 20 diploid species of section *Arachis* from the U.S peanut germplasm collection to identify novel sources of resistance to both ELS and LLS. Screening for resistance was conducted under field conditions at the NPRL in Dawson, Georgia, during 2017-2018. The extent of genetic diversity within and between species was determined by genome-wide single nucleotide polymorphism (SNP) genotyping using a 48K SNP Array. Relatively high levels of resistance were identified for both diseases, with LLS being the predominant pathogen during the two years of observation. On average, 56% of the field plots exhibited symptoms of ELS (13%), LLS (27%), or both (16%). Patterns of genetic variation within and between species were resolved with more than four thousand SNPs distributed across the ten peanut chromosomes. The presence of both ELS and LLS enabled the selection of promising germplasm for further introgression and pre-breeding. Additional studies are in progress to better understand the genetic basis of naturally occurring variation in leaf spot resistance.