

Pyramiding Alleles from the Wild Crop Relative *Arachis cardenasii* Increases Resistance to Early and Late Leaf Spot in Peanut

M. GONZALES* Department of Plant Pathology, University of Georgia, Athens, GA 30602; R. KEMERAIT JR. and A. CULBREATH Department of Plant Pathology, University of Georgia, Tifton, GA 31793; R. ANDRES and J. DUNNE, Department of Crop and Soil Sciences, North Carolina State University, Raleigh, NC 27695; B. ABERNATHY and D.J. BERTIOLI, Department of Crop and Soil Sciences, University of Georgia, Athens, GA 30602; S.C.M. LEAL-BERTIOLI, Department of Plant Pathology, University of Georgia, Athens, GA 30602.

Early (ELS) and late (LLS) leaf spots caused by *Passalora arachidicola* and *Nothopassalora personata* respectively, are two of the most devastating diseases in peanut that are effectively managed with a multiple fungicide program. Chlorothalonil a commonly used fungicide in disease management programs and one of the most effective for leaf spot control was banned by the European Union (EU) due to its potential risk to wildlife and human health. This new regulation could negatively impact US peanut growers as some countries in the EU are major importers of peanut. Resistant cultivars are needed to reduce the use of fungicides to sustainably mitigate leaf spot diseases. However, cultivated peanut (*Arachis hypogaea* L.) only has low to moderate level of resistance to both ELS and LLS in the US. This study aims to obtain lines with multiple resistances that introgress genomic segments from the wild species *Arachis cardenasii* that confer long-term, high level of resistance to foliar diseases into lines with resistance to root-knot nematode and the high oleic property. BC₁F₂ lines were generated from a cross between cultivar 'Bailey' and an advanced line IAC 321 and crossed with cultivar 'TifNV H/O', all with different *A. cardenasii* segments. To evaluate resistance to foliar diseases in a controlled environment, 100 BC₁F₂ lines were tested using detached leaf bioassays. Six different components of resistance were measured: incubation period (IP), lesion number per leaf area (LN/LA), number of sporulating lesions per leaf area (SL/LA), percent diseased leaf area (DLA), Area under the disease progress curve of the lesions per leaf area (AUDPC_{LN}) and AUDPC of the sporulating lesions per leaf area (AUDPC_{SL}). Lines with wild-derived segments exhibited higher level of resistance to both ELS and LLS with lower values of LN/LA, SL/LA, DLA, AUDPC_{LN} and AUDPC_{SL} than the parents. Resistance to leaf spots was also confirmed under field conditions using 395 BC₁F₂ lines. Same results were obtained in the field wherein lines with segments from both parents have lower disease scores and AUPDC values. Overall results infer that combined wild-type alleles gives strong resistance to both ELS and LLS. Advanced lines with multiple resistances from different wild-derived segment combinations will provide high level of resistance to these fungal diseases that would require minimal spray reducing cost of production and lessening the environmental effects of fungicides.

Breeding, Biotechnology, and Genetics