New Sources of Multiple Disease Resistances from *Arachis diogoi* Introgression Lines

H. T. STALKER*, W. G. HANCOCK, T. G. ISLEIB, and J. E. HOLLOWELL, Department of Crop and Soil Sciences, N.C. State Univ., Raleigh, NC 27695-7629; Y. CHU and P. OZIAS-AKINS, Department of Horticulture, The University of Georgia, Tifton, GA 31793-0748; and A. N. MASSA, R. B. SORRENSEN and M. C. LAMB, USDA-ARS National Peanut Research Laboratory, Dawson, GA 39842.

Introgression lines (2*n* = 40) derived from 'Gregory' x *Arachis diogoi* (GKP 10602) that are fully compatible in crosses with *A. hypogaea* were studied. Five diseases were evaluated in the greenhouse [Sclerotinia blight (SB) and Cylindrocladium black rot (CBR)], field [early leaf spot (ELS) and late leaf spot (LLS)] or both the field and greenhouse [Tomato Spotted Wilt Virus (TSWV)]. Moderately high levels of resistance were identified for both SB and CBR. Many Single Nucleotide Polymorphism (SNP) marker associations were identified with both diseases, with the greatest effects for SB resistance on chromosome A5 and for CBR resistance on A6 and B1. Early leaf spot was most prevalent in North Carolina (75%) and LLS predominated in Georgia (90%). Defoliation was recorded multiple times using a scale of 1 = no disease to 9 = dead, and lesion number was recorded once each in North Carolina and in Georgia. Ten lines expressed high levels of resistance to ELS (in mid-October, ratings = 4 - 4.5, resistant checks = 6, cultivars = 8 - 9). SNP markers were associated with ELS defoliation on chromosomes A2, A3, A5, A6, B1, B4, B5, B8 and B9. One line had a rating of 3.3 for LLS in Georgia (checks = 6 - 9). SNP marker associations with LLS defoliation were found on chromosomes A2, A3, A4, A6, B1, B2, and B9 and for the number of lesions on B10. Up to 63% of field plots had TSWV in North Carolina. Four lines did not express symptoms in North Carolina, three lines in Georgia, and one line (IL 51) was disease free at both locations. SNP associations with TSWV were observed on nine chromosomes, with the strongest associations on A9 and B9. Additional studies are in progress to better associate SNPs with all five diseases.