Development and Characterization of Two Peanut RIL Mapping Populations.

C.Y. CHEN*, USDA-ARS National Peanut Research Laboratory, Dawson, GA 39842; B. Z. GUO, USDA-ARS Crop Protection and Management Research Unit, Tifton, GA 31793; C.C. HOLBROOK, USDA-ARS Crop Genetics and Breeding Research Unit, Tifton, GA 31793; M.L. WANG, USDA-ARS Plant Genetic Resources Conservation Unit, Griffin, GA 30223; and A.K. CULBRETH, Department of Plant Pathology, The University of Georgia, Tifton, GA 31793.

An appropriate mapping population, suitable marker system, and the software for analyses of data are the critical elements for genetic linkage map construction and quantitative trait loci (QTLs) identification. We have developed two RIL mapping populations that derived from the crosses of ‘Tifrunner’ x ‘GT-C20’ and ‘SunOleic 97R’ x ‘NC94022’. The parents used in the crosses possess very divergent traits either in agronomic phenotypes or disease resistance. The progenies of a total of 248 F2:7 lines for ‘Tifrunner’ x ‘GT-C20’ and 352 F2:7 lines for ‘SunOleic 97R’ x ‘NC94022’ have been assessed under field conditions for descriptive traits on plant, pods, and seeds and TSWV resistance in two growing seasons. Two hundred sixty nine and 173 SSR polymorphic markers also have been used to assess these two populations, respectively. The descriptive statistics for agronomic traits and resistance to diseases were computed considering the maximum, the mean and the minimum values, the standard deviation, the coefficient of variation, and the distribution of frequency. Cluster analysis and estimation of genetic distances among and within populations were conducted with SSR marker data. The repeatability coefficient was calculated to estimate the accuracy of the phenotypic measurements through the methods variance analysis, principal components analysis, and structure analysis. Our results showed that the two progenies segregated for resistance to TSWV and other traits, thus illustrating the usefulness of genetic linkage map construction and QTLs identification.