

## Identification and Genetic Mapping of Novel Sources of Resistance to Groundnut Rosette and Late Leaf Spot Diseases in a Collection of *Arachis* Wild Derivatives

D. A. ESSANDOH\*, T. L. ODONG, Department of Agricultural Production, Makerere University, Kampala, P.O. Box 7062; D. KALULE OKELLO, National Semi-Arid Resources Research Institute (NaSARRI), Serere, Uganda, P.O. Box 56; D. FONCEKA, Centre d'Etudes Régional pour l'Amélioration de l'Adaptacion a la Secheresse (CERAAS), Thies, Senegal, P.O. Box BP 3320; A.C. BALLEEN-TABORDA, M.C. CHAVARRO, D.J. BERTIOLI and S-L BERTIOLI, Department of Plant Pathology, The University of Georgia, Tifton, GA 31793-0748.

Late leaf spot (LLS) and Groundnut rosette disease (GRD) are the most destructive diseases of groundnut in sub-Saharan Africa. Limited resistance is available therefore, novel sources of resistance are required in cultivated groundnut varieties. Three hundred and sixty-six (366) interspecific lines that bring wild alleles-genetic variation from four different wild species (*A. batizocoi*, *A. valida*, *A. duranensis* and *A. ipaensis*) were evaluated in two agro-ecological zones in Uganda at Nakabango and Serere. Phenotyping of the three populations identified several interspecific lines with good agronomic, and disease resistance traits. One genotype, from the population (Fleur11 x (*A. valida* x *A. duranensis*)<sup>4x</sup>), B7-25-22-8 was particularly useful in combining high yields and disease resistance and could be used as a parent in the groundnut breeding program.

Individuals from population (Fleur11 x (*A. batizocoi* x *A. duranensis*)<sup>4x</sup>) consisting of 133 lines were genotyped with Axiom\_Arachis1 SNP array to generate a genetic map consisting of 1440 markers in four (4) linkage groups (LG). QTL analysis identified four QTLs for GRD on linkage groups B01, B04, B05 and A08 with phenotypic variance explained (PVE) of 11.04, 12.56, 11.51 and 7.90 % respectively. Two QTLs were identified for LLS on linkage group B04 with PVE of 9.43 and 9.60%. QTL analysis allowed us to verify the effect of wild alleles on disease resistance. The QTLs identified for LLS and GRD were contributed by wild parent (*A. batizocoi* x *A. duranensis*) with the exception of GRD severity whose lower values were contributed by the recurrent parent, Fleur 11. The QTLs identified for LLS and GRD resistance provides additional tools for marker-assisted breeding to advance groundnut improvement and for molecular characterization of disease resistance.