A Tree of Relationships of Section Arachis of Unprecedented Scope and Detail

C. CHAVARRO*, Institute of Plant Breeding, Genetics & Genomics, University of Georgia, Athens, GA; D.J. BERTIOLI, Institute of Plant Breeding, Genetics & Genomics, University of Georgia, Athens, GA and Department of Crop & Soil Sciences, The University of Georgia, Athens GA, USA; G. SEIJO, Institute of Botanics of Northeast -IBONE, Corrientes, Argentina; C. SIMPSON, Texas A&M University, Texas AgriLife Research, TX 76401, Stephenville, Texas, USA; J.F.M. VALLS, M.C. MORETZSOHN, Embrapa Genetic Resources and Biotechnology, CEP 70.770-917, Brasília, DF, Brazil; S. TALLURY, USDA- Agricultural Research Service, Plant Genetic Resources Conservation Unit, 30223, Griffin, GA, USA; H.T. STALKER, Department of Crop Sciences North Carolina State University, Raleigh, North Carolina 27695, USA; S.C.M. LEAL-BERTIOLI, Institute of Plant Breeding, Genetics & Genomics, University of Georgia, Athens, GA and Department of Plant Pathology, The University of Georgia, Athens, GA.

The 33 described species within the botanical section Arachis, the wild species most closely related to cultivated peanut (*Arachis hypogaea*), are of particular interest because they can be used as sources of diverse alleles in breeding. They have been the subject of intense collection and characterization. Here we studied 659 germplasm samples representing deposits in national collections in EMBRAPA (Brazil), IBONE (Argentina), USDA (USA) and seeds from active research programs in Texas A & M, North Carolina State and the University of Georgia. These 659 samples represent 296 accessions, virtually all collections of wild peanuts within the Arachis section ever made. The DNA of these germplasm samples was characterized with 14K informative SNPs after the genotyping using the Axiom Arachis Array with 48K SNPs. This matrix of data was used to generate a phylogenetic tree of relationships of the 588 diploid germplasm samples after curation and a tree with 287 germplasm accessions with a unique sample per accession. These trees broadly supported the division of the section into the six genome types with almost all accessions assigned to A genome species forming a well-defined clade. The non-A species form another clade with clear separation of genome types; the most derived B genome clade being associated with the F, D, K and 2n=18 clades in increasing genetic distance respectively. *A. hoehnei*, a species of as yet undefined genome type, is positioned at the periphery of this non-A group. Some species classifications were well-supported: for instance, *A. duranensis* and *A. stenosperma* accessions cluster in well-defined monophyletic clades. The genetic structure of the 35 accessions of *A. stenosperma* strongly supporting the theory of its use and transport by Amerindians prior to the European discovery of South America. Other species showed clear polyphyletic groupings, for instance *A. kuhlmanni* clustering in at least four distinct groups. Still others, such as *A. correntina* form paraphyletic groups. A group of miscellaneous and new collections positioned between the A and non-A clades may represent undescribed species. In summary, this analysis of unprecedented scope and resolution gives a powerful tool to confirm accession identities, and explore and revise the species structure of the section Arachis.