Reinventing Peanut: Origin, Evolution and Domestication of [*Arachis ipaënsis* x *Arachis duranensis*]^{4x} neopolyploids

S. LAMON*, Institute of Plant Breeding, Genetics and Genomics, The University of Georgia, Athens, GA 30605; S. LEAL-BERTIOLI, Institute of Plant Breeding, Genetics and Genomics and Department of Plant Pathology, The University of Georgia, Athens, GA 30605; and D.J. BERTIOLI, Institute of Plant Breeding, Genetics and Genomics and Department of Crop & Soil Sciences, The University of Georgia, Athens, GA 30605.

Allotetraploid peanut (*Arachis hypogaea* L.; 2n = 4x = 40; AABB), originated less than 10,000 years ago from the spontaneous hybridization of two diploid wild *Arachis* species, *A. duranensis* (2n = 2x = 20, AA) and *A. ipaënsis* (2n = 2x = 20, BB), and a consequent whole genome duplication event. The polyploidization process, given the narrow origin base, generated reduced genetic diversity in peanut, which also found itself isolated from the other diploid *Arachis* species due to ploidy inequalities. On the other hand, the merging of different genomes during peanut origin caused in peanut a genetic shock, which in return produced different types of genetic and epigenetics rearrangements in the peanut genome and gene expression alterations. These genetic instability phenomena increased the overall peanut phenotypic variability and conferred to peanut the phenotypic plasticity and adaptability characteristics typical of polyploid plants. Therefore, regardless of the adverse initial conditions, peanut evolved morphologically diverse, colonized different environments, and become the candidate species for domestication in the *Arachis* genus. In this study, we are recreating the evolution and domestication processes of peanut in controlled greenhouse conditions using colchicine induced [*Arachis ipaënsis* x *Arachis duranensis*]^{4x} (IpaDur) neopolyploids. IpaDur plants have been advanced for about ten generations and showed increased variability for several agronomic traits, such as stem length, flower color, flowering time, seed weight, seed number, growth habit, leaf shape and leaf color. Selection for contrasting phenotypes such as heavy and light seed weight has been carried out for four generations with IpaDur plants and wild diploid ancestors to investigate early peanut genomic plasticity and recreating human domestication process. Increased allelic variability was identified in IpaDur plants and opposite selection was effective.