

The Construction of a Chromosome Segment Substitution Line Population for the Systematic Introduction of Wild Alleles from *Arachis batizocoi* and *Arachis stenosperma* into Cultivated Peanut

E.C. BARNES*, Institute of Plant Breeding, Genetics & Genomics, University of Georgia, Athens, GA 30602; S.L.M. LEAL-BERTIOLI, Institute of Plant Breeding, Genetics & Genomics and Department of Plant Pathology, The University of Georgia, Athens, GA 30602; and D.J. BERTIOLI, Institute of Plant Breeding, Genetics & Genomics and Department of Crop & Soil Sciences, The University of Georgia, Athens, GA 30602.

Chromosome segment substitution line (CSSL) populations are a genomic tool first developed in tomato and since constructed in a diverse group of commodity and specialty crops. CSSL populations are formed through the development of an advanced backcross population with introgressions of minimal size from one genome in the background of another genotype, usually a common cultivar. Ideally, each line contains only one introgression with the entire donor genome represented across the population. As a tool, CSSL populations have a wide range of applications, including QTL discovery and gene mapping. They are also commonly employed by plant breeders for the introduction of novel alleles from crop wild relatives. In peanut, one CSSL population has previously been generated through the formation of an *Arachis duranensis* × *Arachis ipaensis* tetraploid hybrid and recurrent backcrossing to cultivated peanut. The aim of this project is to form another CSSL population featuring introgressions of *Arachis batizocoi* and *Arachis stenosperma* in an elite cultivar background. The lines used are previously generated and derive from an *Arachis batizocoi* × *Arachis stenosperma* induced allotetraploid that has been recurrently backcrossed to cultivated genotypes. Currently, a population of 81 lines covering 64.9% of the A subgenome and 45.7% of the B subgenome (based on ThermoFisher Axiom Arachis 48 K SNP array genotyping) are being maintained for this purpose. The introgressions in these lines vary in size from several megabases to nearly entire chromosomes; lines with very large introgressions will be further backcrossed to break down genome coverage into smaller introgressions. The portions of the genome not currently covered by the 81 lines will be recovered through the selection and backcrossing of previous backcross generations with introgressions in these regions. Upon completion, these CSS lines will encapsulate the genetic diversity of two wild species that can be systematically phenotyped and, owing to their tetraploid form and largely cultivated genome, are suitable for the immediate introduction to peanut breeding programs aimed at a multitude of genetic improvement goals.