

Tracking of Wild Allele Introgressions in a Peanut Chromosome Segment Substitution Line Population

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Cultivated peanut arose from the hybridization of the diploids *Arachis duranensis* (A genome progenitor) and *Arachis ipaensis* (B genome progenitor), followed by spontaneous chromosome doubling to yield the current allotetraploid state (AABB; $2n=4x=40$). This genetic heritage, short period since polyploidization, self-pollinating breeding system, and domestication bottleneck have resulted in a crop with reduced diversity. In order to harness polymorphism from its wild relatives, a chromosome segment substitution line (CSSL) population was created via the tetraploid route to interspecific hybridization. The CSSL population was derived by crossing the A and B genome progenitors, *doubling the chromosomes of the cross, and introgressing chromosome segments from the resultant synthetic allotetraploid into the background of a cultivated variety (Fleur 11)*. Through SNP genotyping, we have developed high-resolution sets of markers that have enabled us to precisely delineate the regions of wild genetic introgression. In addition, we have observed evidence of tetrasomic recombination events in the population. By comprehensively phenotyping the population, we have uncovered significant variation in canopy, below ground, as well as seed composition traits. Analysis of the genotype and phenotype data has enabled us to deduce how chromosome segments from the wild alter the expression of traits in the cultivated genetic background. This study improves our understanding of how the wild relatives of peanut can be used to confer beneficial traits to cultivated peanut varieties.