

## **Morphological Characterization and Genomic Analysis of *Arachis hypogaea* × *A. diogeni* Introgression Lines**

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Eighty-seven introgression lines developed from a cross between cultivated peanut (*Arachis hypogaea* L) and the diploid wild species *A. diogeni* Hoehne were analyzed for a series of morphological characters and for the introgression of *A. diogeni* chromatin to the cultivated genome. The interspecific hybrid-derived population was developed using the triploid-hexaploid introgression method. Numerous pod, seed, and plant architectural traits were measured. Introgression lines were genotyped using a Single Nucleotide Polymorphism (SNP) marker array. The majority of introgression lines were morphologically intermediate to the two parents with some transgressive segregation for individual traits. Several introgression lines had acceptable seed size for a virginia market-type cultivar, but the majority of lines possessed seed size acceptable for the runner market-type. Of the 7,017 total SNP markers polymorphic between cultivar Gregory and *A. diogeni*, 6,626 markers identified *A. diogeni* chromatin introgression in one or more lines. *Arachis diogeni* introgressions were observed as both large blocks and as single markers. The average amount of *A. diogeni* introgression was 8.12% across the genome of the 87 lines and ranged from 3.00% to 18.14% on individual chromosomes. The average percent *A. diogeni* introgression for single introgression lines was 7.70% and ranged from 0.17% to 51.12%. More introgression was present in the A genome (8.82%) than the B genome (7.42%). No entire *A. diogeni* chromosome or chromosome arm was found in any of the introgression lines suggesting that introgression is due to crossing-over and reciprocal recombination involving both genomes rather than chromosome substitution. Principal component analysis of morphological data and SNP marker data revealed similarities and groupings of introgression lines. A preliminary marker-trait association analysis revealed a large number of significant marker-trait associations for the measured morphological traits. This research demonstrates the potential value of utilizing wild diploid *Arachis* species for peanut improvement.