

Genesis and Characterization of New Interspecific Hybrids to Increase Genetic Diversity in Cultivated Peanut

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Peanut *A. hypogaea* (L.) underwent a significant bottleneck with regards to genetic diversity in its origin and domestication. Wild relatives harbor significant genetic diversity and useful alleles, but they are sexually incompatible. The development of greenhouse induced wild derived allotetraploid hybrids is a way to harness these alleles. We undertook a process that includes crossing wild species representing both A and B genomes, germinating and growing the hybrids, testing for hybridity, and using colchicine to induce chromosome doubling. The resulting synthetic allotetraploids would then be available to begin a breeding program to introgress valuable traits into cultivated peanut. We were able to produce 26 hybrids utilizing 17 accessions from 11 different wild species. Hybrids were confirmed using six primer sets and performing Kompetitive Allele Specific PCR ensuring the presences of both genomes. These hybrids varied with respect to branching patterns, leaf size, shape, and coloration along with other morphological differences. Viable pollen counts for hybrids ranged between 0 and 42% as compared to parentals which were consistently above 98% viable pollen. There was also variation at the cellular level. Stomata and epidermal cells as well as trichomes were counted. Based on the variation seen in all of these morphological characteristics, it is easy to see how these hybrids can be beneficial to increase the genetic diversity within cultivated peanut, and provide resistance to specific diseases and insects, as well as incorporating other value added traits.