

Development of Newly Synthesized Amphidiploids and Their Genome Composition

Y. CHU, **C. M. LEVINSON***, and P. OZIAS-AKINS Department of Horticulture, The University of Georgia, Tifton, GA 31793-0748; H. T. STALKER, Department of Crop and Soil Sciences, N.C. State Univ., Raleigh, NC 27695-7629; S. C. M. LEAL-BERTIOLI, Department of Plant Pathology, The University of Georgia, Athens, GA; and D. BERTIOLI Department of Crop and Soil Sciences, The University of Georgia, Athens, GA 30605.

Cultivar improvement for peanut is limited by the narrow genetic base of this species. In order to introduce new genetic resources into peanut breeding programs, crosses were made among A-genome wild peanut diploids species (male) with several B genome species (female). Nine new amphidiploids were established by colchicine treatment producing a total of 115 S_0 seeds. Four out of the nine new amphidiploids were advanced to S_1 generation yielding 824 seeds. The most productive amphidiploid hybrid was [*A. ipaënsis* KG37006 x *A. correntina* 9530]^{4x}. Genotyping of the amphidiploids and their respective parental lines revealed frequent gene conversion between the parental alleles. Evidence suggests that most of the conversion occurred at the diploid stage. However, further gene conversion was observed in both the S_0 and S_1 generations of the new amphidiploids suggesting genome instability of these new materials. Therefore, these new genetic materials should not be treated as a homogenous bulk for breeding programs. However, crossing the new amphidiploids with cultivated peanut yielded viable F_1 hybrid seeds which have the potential for introducing additional genetic variation into breeding populations and lead to improved lines for agronomic traits.