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Summary

Project ID 281

Project Description: Analysis of Molecular Diversity in Valencia Peanut Core Collection

Valencia peanuts [*Arachis hypogaea* L. subsp. *fastigiata* Waldron var. *fastigiata* (Waldron)

Krapov. & W. C. Greg.] are well known for their in-shell market value. Assessment of genetic diversity is key to the success of developing improved cultivars with desirable agronomic and quality traits. Seventy-eight U.S. Valencia core collection accessions together with 36 Valencia accessions representing the global peanut mini-core collection were used to study population structure and diversity and to identify genetically diverse Valencia germplasm for use in peanut breeding. Fifty-two simple sequence repeats loci amplified 683 alleles, with an average of 13 alleles per locus. The mean polymorphism information content and gene diversity, respectively, were 0.270 and 0.335. The pairwise genetic distance ranged from 0.143 to 0.474, with an average of 0.631. Neighbor-joining clustering, principal coordinate analysis, and STRUCTURE analysis consistently separated the Valencia germplasm into five clusters with two distinct major groups. The first major group consisted of genotypes from South America (64%) with few accessions from Africa, North America, Caribbean, and European regions. The second group consisted of accessions mostly from diverse regions of Africa, North and South America, Asia, and the Caribbean. However, the structuring was not related to the geographic origin and several admixtures were observed. The information generated in this study and phenotyping of this material for biotic and abiotic stress responses and yield-quality traits will facilitate selection of trait-specific, genetically diverse parents for developing Valencia peanut cultivars with a broad genetic base.