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ABSTRACT BOOK

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Genetic enhancement of Valencia core collection and molecular characterization of U.S. peanut mini core collection using SSR markers

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A core collection is a gateway for the utilization of diverse accessions with beneficial traits in applied breeding programs. 630 USDA Valencia peanut germplasm and a control cultivar (New Mexico Valencia C) were evaluated for 26 descriptors in augmented design for two seasons. The accessions were stratified by country of origin, and data on morphological and agronomic descriptors were used for clustering following Ward's method. About 10% or a minimum of one accession from each cluster and region was selected to develop core subset of 77 accessions. The similarity in correlation coefficients in entire collection and core subset suggest that this core subset has preserved most of the co-adapted gene complexes controlling these associations. The peanut breeders engaged in improving the genetic potential of Valencia peanuts will find this core subset useful in cultivar development.

Peanut improvement is hampered by limited genetic variability in the germplasm available to breeding programs. This study was conducted to characterize the core of the core collection (COC) of peanut germplasm for the US peanut industry using microsatellites or simple sequence repeat markers (SSR). Seventy two peanut accessions were genotyped using 73 markers (twelve of which are mapped SSR loci) and scored for their haplotype states using high throughput fragment analysis. We found that the four market types represented in the COC can be grouped consistently. Substantial genetic variation was found to exist in the core of the core collection. A group of twelve unlinked markers with known map positions was found sufficient to identify both botanical and market types and gave a clustering pattern similar to the entire marker set. The genetic variation observed indicate that SSR markers are highly suitable for development of a genetic map of cultivated tetraploid peanut.

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