

Genotypic Characterization of the U.S. Peanut Core Collection

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Cultivated peanut (*Arachis hypogaea*) is an important oil, food, and feed crop worldwide. The USDA peanut germplasm collection currently contains 8,982 accessions. In the 1990s, 812 accessions were selected as a core collection based on phenotype and country of origin. The present study reports genotyping results for the entire available core collection. Each accession was genotyped with Arachis_Axiom2 SNP array, yielding 14,430 high-quality, informative SNPs across the collection. Additionally, a subset of the core collection was replicated, using between two and five seeds per accession to assess heterogeneity within these accessions.

The genotypic diversity of the core is mostly captured in five genotypic clusters, which have some correspondence with botanical variety and market type. There is little genetic clustering by country of origin, reflecting peanut's rapid global dispersion in the 18th and 19th centuries. A genetic cluster associated with the *hypogaea/aequatoriana/peruviana* varieties, with accessions coming primarily from Bolivia, Peru, and Ecuador, is consistent with these having been the earliest landraces. The genetics, phenotypic characteristics, and archaeological records are all consistent with previous reports of tetraploid peanut originating in Southeast Bolivia. The present genotype results indicate an early genetic radiation, followed by regional distribution of major genetic classes through South America, and then global dissemination that retains much of the early genetic diversity in peanut. Comparison of the genotype data relative to alleles from the diploid progenitors also indicates that sub-genome exchanges, both large and small, have been major contributors to the genetic diversity in peanut.