

Quantifying Genetic Diversity of Peanut Cultivars Released by the University of Georgia Using Genotyping by Sequencing.

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Over the course of the University of Georgia's peanut breeding effort, which spans over 80 years, 33 peanut (*Arachis hypogaea* L.) cultivars have been developed and released to the public. Thirty-two of these cultivars were recently genotyped using the targeted genotyping by sequencing (tGBS) method to quantify genetic diversity within and among cultivars. Two spanish, 2 valencia, 7 virginia, and 21 runner types were evaluated. From each cultivar, a total of 12 plants were individually sampled and genotyped to measure variability within inbred lines. The tGBS method used restriction enzyme *Bsp 1286 I* and sequencing was conducted on an Illumina HiSeq X. A total of 37,036 polymorphic SNPs were used to characterize the genetic diversity of these cultivars. Limited variation within inbred lines existed, thus genotype data was combined across individual samples within cultivars to create a composite, and more complete genotype for each of the cultivars. Average genetic similarity of Spanish botanical types to the panel ranged 62.6-63.1%; valencia types 71.0-73.1%; and 82.4-99.2% for Virginia and runner market types. Comparing coefficient of parentage calculations based on pedigree data, revealed a statistically significant, but weak correlation with tGBS-based measurement of genetic similarity ($r_2=0.223$, $p<0.0001$). This tGBS-based genetic diversity study provides an improved understanding of genetic relationships among these peanut cultivars which have had a significant impact on the peanut industry and could be of value to breeding programs for improved crossing decisions.