Genomic Diversity Characterization and Genome-Wide Association Mapping of the North Carolina State University Peanut Breeding Lines and Virginia-Type Cultivars.

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Significant phenotypic variation exists among the breeding lines and cultivar releases from the North Carolina State University peanut breeding program for several economically important traits of interest to the Virginia-Carolina region. These extensively tested lines and cultivars coupled with genome-wide single nucleotide polymorphic (SNP) markers allow for the characterization of diversity within the breeding program and the identification of marker-trait associations for use in selection for improved yield, seed and pod characteristics, flavor and quality traits, and biotic and abiotic stress resistances. More than 200 lines, including developed breeding lines and cultivar releases from 1991-2018, were genotyped using a 48K SNP marker array. The post-processed marker set, (~12,000) found to be polymorphic among the submitted lines, were subjected to population structure and diversity analysis. Population sub-structure, estimated using principle component analysis and other molecular marker derived relationship estimates, was detected among these lines, which represent nearly four decades of the breeding program. Diversity estimates increased over this time period most likely resulting from intraspecific hybridization of the *A. hypogea* subspecies and botanical varieties used in the crossing program. In addition to the population structure and diversity estimates, phenotypic data were related to the genotypic information for these lines to establish genome-wide associations for yield, early and late leaf spot defoliation ratings, Cylindorcladium black rot (CBR) incidence, Sclerotinia blight incidence, and tomato spotted wilt (TSW) incidence. A total of 8,064 SNPs were used in identifying a multiple marker associations among each of these traits. These associations, given the extensive phenotypic evaluations on these lines, provide a basis for implementing marker-assisted selection (MAS) for improving the parental population and offer opportunities to impose a genomic selection pipeline for cultivar development and release.

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