

Genomic Characterization of North Carolina State University's Germplasm and Breeding Lines

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The peanut breeding program at North Carolina State University has historically utilized traditional methods, such as single seed descent, to produce cultivars for release. In the age of high-throughput and cost-effective sequencing, it is essential to integrate genomic tools into the breeding process to enhance the accuracy and productivity of the program.

As the foundation for genomic work in the NCSU program, cultivar 'Bailey II' (*Arachis hypogaea* subsp. *hypogaea* var. *hypogaea*) was assembled as the reference genome for Virginia-type peanut. The assembly quality and utility of the Bailey II reference genome will be discussed. Subsequently, whole genome sequencing (WGS) was conducted for ninety six lines that represent the diversity relevant to the NCSU breeding program. WGS data were used to identify variants throughout the entire length of the Bailey II genome. This data, along with known pedigree information allowed introgression blocks to be identified. The composition of variants in this data along with confirmed introgression blocks will be presented. The findings in this study will inform the future development of markers for use in marker assisted selection and a genotyping strategy suitable for genomic selection.