

SNP Array Technology in Peanut

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Association of molecular markers with a trait through genotyping of populations and statistical analysis of linkage is a precedent for application of marker assisted selection (MAS) in breeding. MAS reduces the time, effort and cost of incorporating a trait into improved germplasm. While numerous molecular marker types have been developed for peanut, the most abundant molecular marker type in genomes is the single nucleotide polymorphism (SNP), and SNP assays enable cost-effective genome-wide genotyping. The Axiom_Arachis2 SNP array has been the most extensively used genome-wide SNP genotyping platform to date for peanut. The array, designed by Josh Clevenger and Walid Korani and provided through ThermoFisher Scientific, can assay over 48K SNPs for a cost of \$28 per sample. It has been widely used for assaying diversity (mini core, core, African germplasm), mapping populations for disease resistance, seed size, and maturity traits, and quantifying the dynamic interaction of subgenomes in interspecific hybrids. These applications have greatly advanced our knowledge of peanut genetics and accelerated breeding.