

Development of an Early Generation Marker-Assisted Selection Strategy for Virginia-type Peanuts

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Previously, an association mapping study utilizing the Axiom Arachis2 48k SNP array identified 21 marker-trait associations for five traits of interest in Virginia-type peanuts. After observing complete linkage between markers associated with the same trait, but placed on different chromosomes, all 5,346 polymorphic markers were re-mapped to the *A. hypogaea* genome. This refined the 21 associations to ten genomic regions: three each for pod yield and leaf spot, two for *Cylindrocladium* black rot, and one each for *Sclerotinia* blight and tomato spotted wilt virus. PCR Allelic Competitive Extension (PACE) assays were designed for all associated SNPs, plus causal polymorphisms of the high oleic genes *FAD2A* and *FAD2B*. Assays were used to genotype all 46 lines used as parents in the North Carolina State University breeding program the last four years, plus the exotic germplasm line N96076L. Polymorphic SNPs will be run on bulked samples from F_{2:4} lines in an attempt to improve early generation selection efficiency via marker-assisted selection.