

Development of Genomic Resources for Increased Folate Content in Peanut (*Arachis hypogaea*)

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Tetrahydrofolates are essential in gene expression, the synthesis of lipids and proteins along with the formation of other plastids and cellular macromolecules important in plant development and structure. Biofortification of folate in peanut can be achieved through plant breeding efforts, providing an efficient, economical and sustainable method for fighting nutritional deficiencies in humans. Clinical studies have shown that folate deficiencies in humans can lead to an increased risk of cardiovascular disease (CVD), dementia, certain cancers and pregnancy complications due to the occurrence of neural tube defects caused by folate deficiency-anemia. Knowing that peanut can be a rich source of folate, the objective of this research is to identify molecular markers in order to increase the nutritional content in cultivated peanut (*Arachis hypogaea*) through marker-assisted selection; more specifically, focusing on molecular breeding strategies to facilitate an increase in total folate content found in peanut seed. Using information from a previous study evaluating total folate content of the peanut mini-core germplasm collection, we plan to map quantitative trait loci (QTL) important in the folate biosynthetic pathway. Three plant introductions (PI) selected for high levels of folate were used in the development of a nested recombinant-inbred line (RIL) population with a recurrent cultivar parent, Georgia Green. The three populations, representing ~175 RIL lines in each, were genotyped using a filtered set of polymorphic markers between each PI and the recurrent parent in anticipation for mapping total folate. Large effect QTL identified through this analysis will be used to develop single nucleotide polymorphic (SNP) marker assays for marker-assisted selection. These assays will be used more directly for screening existing peanut breeding populations and selecting advanced breeding lines for increased folate content.