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ABSTRACT BOOK



AAGB/FT-17: Revealing Peanut Blanchability: Genomic Insights for Identifying Markers and Candidate Genes to Improve Quality and Boost Industry Impact

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Blanching is the process of removing the seed coat (testa) from peanuts (*Arachis hypogaea*), and a genotype's ability to shed the testa is known as blanchability. This trait is of significant economic value in peanut-based food production, yet limited research has focused on it within breeding programs. Blanchability is highly heritable and genetically regulated, suggesting that breeding and selection for this trait should be effective. The aim of this study was to identify high-blanchability genotypes from the ICRISAT minicore collection (184 genotypes) and identify the genomic regions responsible for the trait. Over two seasons, phenotypic data from these genotypes were combined with high-quality SNP data to perform Genome-Wide Association Studies (GWAS). Using the 58K 'Axiom_*Arachis*' array and whole-genome resequencing (WGRS), 58 and 26 marker-trait associations (MTAs) were identified, respectively. These 9 MTAs (from 58K Axiom_*Arachis*) and 6 MTAs (WGRS) were distributed, across 6 chromosomes, with four Chromosomes (Ah01, Ah05, Ah06, Ah17) being common. The MTAs identified on chromosome B07 (from 58K Axiom_*Arachis*) and Ah17 (from WGRS) had highest phenotypic variation of 35.28% and 54.03%; respectively. Of the several candidate genes linked to blanchability were identified in the study, three genes in particular-*xyloglucan endotransglucosylase*, *glucan endo-1,3-beta-glucosidase 8*, and *galactoside 2-alpha-L-fucosyltransferase-like protein*-seem to play key role in controlling blanchability. These genes play a role in the dynamic processes of cell wall construction, modification, and maintenance and have a direct impact on the development of seed coats, the integrity of cell walls, and plant adhesion. We have validated 6 markers which can be used for selecting progenies and genotypes with high blanchability.

Keywords: *Arachis hypogaea*, Peanut, Genotype, Blanchability, GWAS, Candidate genes