

Genetic Dissection of the Crop Maturation Trait in Peanut

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Crop maturation is one of the most recognized characteristics of peanut, and it is crucial for adaptability and yield. However, not much is known regarding its genetic and molecular control. We studied the molecular-genetic components that control the maturity level in three segregating populations derived from the crosses of Virginia X Virginia (HH), Virginia X Runner (RR) and Virginia X Valencia (CC). Crop maturation was studied directly by phenotyping the maturity level and through other “component traits” such as flowering pattern and branching habit. Genotyping was performed using the Axiom_*Arachis2* SNP-array. 13 QTLs were found for maturity level in total, with the phenotypic explanation ranging in 5.3%-9.9%. Common QTL were found between maturity level and harvest index (in RR and CC), branching habit (in HH), flowering pattern (in CC) and pod size (in CC). Further investigations were done to identify genes that control maturity level and the component traits. A map-based cloning approach was performed based on the HH population, identifying a major candidate gene for branching habit, a novel *AhMADS-box* gene (*AhMADS*). Sequence alignment between the parental lines found SNPs in *AhMADS* that cause exon/intron splicing alterations. Another candidate gene was identified for the flowering pattern trait, a *Terminal Flowering 1-like* (*AhTFL1*) gene, located within a small segment in chromosome B02. A 1492 bp deletion was found in *AhTFL1* that completely co-segregated with the flowering pattern phenotype in the CC population and in two independent EMS-mutagenized M₂ families. *AhTFL1* was significantly less expressed in flowering than non-flowering branches. Field trial showed that a Hanoch-based EMS line mutagenized in *AhTFL1* with a sequential flowering pattern had a higher maturity level (~18%) than the parental line Hanoch. The results revealed new insights into the molecular basis for crop maturity in peanut and generated new information that will promote informed targeting of peanut idiotypes by marker-assisted selection.