

Quantitative Trait Loci Mapping of Seed Dormancy in a Recombinant Inbred Line Population of Peanut (*Arachis Hypogaea* L.)

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Peanut sprouting/germination prior to harvest/digging results in significant loss of pod yield and possible preharvest aflatoxin contamination. We developed a recombinant inbred line (RIL) mapping population from Tifrunner (dormancy) and GT-C20 (no dormancy) for quantitative trait loci (QTLs) mapping for fresh seed dormancy and identification of markers and candidate genes. Fresh seed dormancy was carried out immediately after dug for two years, and the RIL population was genotyped using the peanut 58K SNP Array. A genetic map was constructed with 1147 SNP markers and used for QTL analysis. Total 47 QTLs were identified with phenotypic variance explained (PVE) from 10.77% to 51.60%. One QTL with 51.60% PVE was in linkage group A05, and another QTL with 43.15% PVE was in linkage group A04. The flanking sequence of the major QTLs were used for blasting to the reference genome, and a 98kb physical interval on Chr.15 was identified. According to the searches of the peanut genome database, a total of 11 genes were revealed in this genome region and one candidate gene was under-investigation for possibly response to the fresh seed dormancy. The identified QTLs associated markers and the potential candidate genes will be studied further for possible application in breeding for fresh seed dormancy in peanut.