

Genome-Wide Association Study of Pod and Seed Quality Traits in Peanut

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Traits like seed size, seed weight, small shelled kernels, kernel weight, hull weight determines quality of peanut seed. Numerous genomic region and gene network are regulating such trait. Identifying such genomic regions will help breeders to develop molecular marker for MAS (Marker Assisted Selection) breeding. A total of 120 accessions from U.S. peanut mini core collection were evaluated for seed quality traits. These accessions were also genotyped using 58K SNP array and we were able to identify 17K high quality SNP for this association panel. Base on results, we observed significant variation for seed quality traits in different accessions and different botanical varieties. Through Genome Wide Association Study (GWAS), we were able to identify multiple regions associated to small shelled kernels, seed weight, kernel weight, hull weight. For instance, marker AX-176823847 (Chr 15), AX-176794068 (Chr 12), AX-177638040 (Chr 10), AX-176794068 (Chr 11) and AX-147216060 (Chr 03) were strongly associated with seed size, small shelled kernel, seed weight, kernel weight and hull weight. Areas surrounding these markers were scrutinized for candidate genes associated with these traits. Multiple genes were identified in the regions that might have important role during seed development. In summary, our work will provide markers that could be incorporated in breeding program to accelerate selection process for seed quality and explore the possibility of function of candidate gene to understand the complex genetic network that governs seed quality.