

Genomics 2018: Genome-wide evaluation of loci and candidate genes underlying important traits in soybean (*Glycine max* L. Merr.): A Review Article- Wenbin Li, Northeast Agricultural University, China

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Disease resistance and seed quality were important traits for soybean breeding. Better understanding of the genetic architecture and genomic landscape of soybean germplasm with targeted traits is the precondition of molecular design breeding of soybean. Construction of a favorable data platform including phenotyping and genotyping pools and efficient analytical approaches were the fundamental tasks for molecular breeding work. Therefore, more than 500 diverse soybean accessions were sequenced using specific-locus amplified fragment sequencing (SLAF-seq) to establish a genotype database. In total, 64 141 single nucleotide polymorphisms (SNPs) with minor allele frequencies (MAFs) > 0.05 were found among the 512 tested accessions. The genotyped soybean germplasm has been phenotyped for some important soybean quality traits including soybean fatty acid components and seed vitamin E content under multi-environmental conditions. Resistance to many different pathogens including resistance to soybean cyst nematode (SCN), soybean white mold (SWM), soybean root rot (SRR) and soybean mosaic virus (SMV) has been also phenotyped. A set of loci were found to be associated with the above traits by GWAS and some of them were confirmed by biparental mapping which has been used for molecular assisted selection breeding. A set of candidate genes for disease resistance that have been evaluated via sequence polymorphism and differential expression in special donors were cloned and were staged in functional genomics research.

Lately, affiliation examines have been acted in grain soybean for plant engineering and yield-related attributes, and they have made extraordinary progress in distinguishing loci with high planning accuracy. Through genomic results of determination and GWAS, an aggregate of 125 applicant choice locales were recognized of 9 agronomic qualities and 5 potential competitor qualities were anticipated. Zhang et al. (2016) led a genome-wide affiliation concentrate in a populace of 309 soybean germplasm promotions, distinguished 22 loci of minor impact and anticipated 3 applicant qualities on chromosome 19. Tooth et al. (2017) gathered 809 soybean materials worldwide and played out a two-year phenotypic assurance of 84 agronomic

attributes in three areas, and distinguished 245 SNPs, including referred to qualities like Dt1, E2, E1, Ln, Dt2, Fan and Fap, just as 16 unreported loci, which are pleiotropic for various characteristics. Diers et al. (2018) played out an affiliation planning for the NAM populace of 5600 ingrained lines, and SNP information uncovered 23 critical marker-quality relationship for yield, 19 for development, 15 for plant tallness, 17 for plant housing, and 29 for seed mass. Affiliation planning has been utilized to distinguish altogether related locus for blooming stage, grain filling stage, development stage, yield and 100-SW of soybean, and recognized nine, six, four, five and two essentially related SNPs, separately. A sum of 58 SNPs that were essentially connected with internode number (IN), plant stature (PH), seed weight (SW), and seed yield per plant (SYP) were recognized by GWAS, and 28 related competitor qualities were anticipated. By utilizing GWAS, 14 quantitative attribute nucleotides (QTNs) were distinguished to be related with seed length, 13 with seed width and 21 with seed thickness in four tried conditions. Utilizing the multilocus GWAS techniques, an aggregate of 118 QTNs of 100-seed weight were recognized, and three potential competitor qualities were distinguished in soybean. Albeit a ton of investigates for plant design and yield-related characteristics have been completed in soybean, the sub-atomic instrument hidden these qualities in soybean stays indistinct because of their intricacy hereditary system. Plant design related attributes and 100-SW of soybean are unpredictable quantitative characteristics impacted by numerous QTLs and are helpless to ecological elements. Past investigations were led to take apart the hereditary premise of plant engineering related qualities and 100-SW in biparental populaces. Many QTLs were distinguished across the entire genome of soybean, with many being at the same time identified in various populaces. These investigations exhibited that the hereditary planning of quantitative qualities utilizing hereditary linkage maps is a proficient methodology for distinguishing QTLs. As of now, various specialists utilize atomic markers to recognize QTLs controlling these significant agronomic characteristics.