ABSTRACT

Salinity is one of the major abiotic stresses that adversely affects productivity and quality in several crops including soybean (Glycine max (L.) Merr.). Conventional genetic studies have commonly utilized bi-parental mapping populations to identify and characterize genomic regions associated with tolerance to salinity. Even though this strategy has successfully mapped major loci on different chromosomes (Chr.), it has limitations to capture allelic diversity and genomic resolution in parental lines. In this study, a genome-wide association study (GWAS) was performed to detect and map genomic regions for salt tolerance in a diverse panel of 400 exotic soybean plant introductions (Pis), consisting of both cultivated (Glycine max) and wild soybean (Glycine soja). Over 37,000 single nucleotide polymorphism (SNP) markers with minor allele frequency (MAF) ≤ 0.5, generated by the SoySNP50K iSelect BeadChip, were utilized for analysis. The GWAS identified a major locus on Chr. 3 (p-value = 8.08E-34), which was consistently mapped at the same genomic position as the known locus of previous studies. A second minor locus was identified and mapped on Chr. 5 (p-value = 5.93E-06). It was speculated that it could be a novel locus for salinity tolerance in this panel of exotic germplasm. Several candidate genes along with significantly associated SNPs will be helpful to reveal the molecular mechanism involved in salt tolerance and also useful for marker-assisted selection in soybean molecular breeding programs.

RESULTS AND DISCUSSION

Frequency distribution of leaf scorching score (LSS) in soybean germplasm accessions

The distribution of LSS of soybean germplasm accessions (G. max and G. soja) showed that most soybean accessions evaluated were sensitive to salt (Fig. 3).

Phylogeny of soybean accessions

A neighbor-joining (NJ) tree for a diverse set of over 400 soybean accessions was constructed based on Nei’s genetic distance with 35,270 SNPs and a graphical visualization of phylogenetic tree was made (Fig. 4). The resulting NJ tree showed G. max accessions and G. soja accessions were clustered into different groups and diversity of subgroups.

CONCLUSIONS

- Among soybean accessions evaluated in this study, five G. max accessions and four G. soja accessions were identified to be new salt tolerant sources, which can be valuable for salt tolerance improvement in soybean.
- The GWAS identified a major locus significantly associated with salt tolerance located on Chr. 3 (p-value = 8.08E-34). The finding in our study was in agreement with many previous studies.
- A second minor locus was identified and mapped on Chr. 5 (p-value = 5.93E-06); however, additional investigation needs to be conducted to confirm this locus.

FUTURE WORK

- The most significant SNP for salt tolerance was mapped on chromosome 3 but relatively distant from the gene identified in previous studies. Thus, these new sources may have different alleles for tolerance which needs to be confirmed.
- A second locus on Chr. 5 showed a significant but low R-squared value for salt tolerance and the effects of this allele for tolerance needs further study.
- Thus, additional phenotyping of this diverse set of soybean accessions and association analysis conducted with sequence data from the USB whole genome sequencing project is necessary.

ACKNOWLEDGMENTS

This research was supported in part by the United Soybean Board, the Missouri Soybean Merchandising Council, and the National Center for Soybean Biotechnology, University of Missouri. The authors would like to thank Drs. Perry B. Cregan and Quinn Song, Soybean Genetics and Improvement Lab, USDA-ARS, Beltsville, MD 20705, for the development of SoySNP50K iSelect BeadChip used in this study.