

ABSTRACT

Genetics of Soybean Resistance to *Coniothyrium glycines*, the Causal Agent of Red Leaf Blotch Disease

Soybean is a high oil and protein-rich legume with several production constraints. Several fungi, viruses, nematodes, and bacteria cause major yield losses in soybean production across the world. *Coniothyrium glycines*, the fungus that cause red leaf blotch disease (RLB) is not extensively studied but causes significant yield loss to soybean. To increase soybean productivity, efforts in understanding genetic diversity in the soybean genetic resources in Uganda is critical. The identification of soybean genotypes and markers associated with resistance to *C. glycines* is needed for sustainable management of RLB in soybean production. The main aim of this study was to generate knowledge and contribute to the development of soybean varieties with resistance to RLB. Specifically, this study sought to (i) determine the genetic diversity and population structure of soybean genotypes maintained by the Uganda Soybean Breeding Program, (ii) identify soybean genotypes with resistance to RLB. (iii) identify genomic regions and candidate alleles associated with resistance to RLB. A total of 282 soybean genotypes were assembled and genotyped using the medium density markers using the DarTSeq with a high throughput of Single-nucleotide polymorphisms (SNPs). After the filtering and the imputation, a total of 6,935 high-quality SNPs were identified across the whole soybean genome. The mean value of genes diversity, major alleles frequency, minor alleles frequency, expected heterozygosity, and the polymorphism information content were estimated at 0.35, 0.77, 0.22, 0.33, and 0.29, respectively suggesting genetic diversity in Ugandan soybean germplasm remains low. Soybean genotypes responded differently to *C. glycines* disease with thirty genotypes showing resistance response. Additionally, resistance to RLB was found to be correlated with some agro-morphological traits, including plant height, number of days to flower and number of days to maturity. These traits can be used for selecting soybean genotypes with resistance to RLB and favorable agronomic traits. GWAS analysis performed on a panel of 279 soybean genotypes identified nineteen significant markers associated with resistance to *C. glycines* on twelve chromosomes. Among these SNPs markers; five SNPs Gm19_44916522 (44.9Mb), Gm16_3302971 (3.3Mb), Gm16_34649045 (34.6Mb), Gm06_20112134 (20.1Mb), and Gm01_17813710 (17.8Mb) were identified at more than one soybean stage of growth and could be useful for MAS for resistance to RLB. Gene annotation for the significant SNP loci identified important genes associated with defences responses against plant diseases. The results of this study provide valuable insights for further dissection of the genetic architecture of resistance to *C. glycines* in soybean and the identified SNP can be used for making genomics-informed selection decisions in the breeding process for improving resistance traits. The SNP markers associated with resistance to RLB can now be used by soybean breeders to track RLB in the breeding pipeline.