ABSTRACT

Soybean (*Glycine max* [L] Merrill) is one of the most important legume crops worldwide due to its multiple uses and wide adaptations. Its production is, however, affected by several biotic and abiotic factors such as insect pests, diseases, pod shattering and sensitivity to photoperiod. Diseases are the most important biological constraints, of which soybean rust (SBR) caused by *Phakopsora pachyrhizi* is one of the most serious and widespread foliar diseases of soybean causing high yield losses world-wide. The objectives of this study were to: (i) determine combining ability and mode of inheritance of SBR resistance, (ii) identify and map quantitative trait loci (QTLs) associated with resistance to SBR in UG-5 line, and (iii) determine putative candidate genes associated with resistance to SBR on the detected QTLs of UG-5. Ten parental lines comprising five resistant, two moderately resistant and three susceptible soybean lines were used for the study and crossed using a half diallel mating design (Griffing's method 2, Model 1). F_2 segregating populations derived from all crosses were evaluated for SBR resistance along with their parents. Data on lesion type, rust severity and sporulation level were scored at two reproductive stages (R4 and R6). Ninety-seven F_2 mapping progenies, developed from a cross between Wondersoya (highly susceptible) and UG-5 (highly resistant), were used to identify and map QTLs associated with resistance to SBR. Phenotypic (disease severity) and genotypic (SSR markers) data were collected and analyzed using QTL IciMapping software. Bioinformatics tools from the online available databases were used to identify genes on the vicinity of the putative QTLs associated with SBR resistance in line UG-5. The physical positions for the flanking markers of the putative QTLs were searched on the SoyBase database genome browser based on the Glyma 1.01 assembly. The putative candidate genes and annotated functions of the surrounding genes were discovered in the vicinity using SoyBase and Phytozome databases. The F_2 segregating populations and parents showed significant differences for disease severity and sporulation levels. General and specific combining abilities were highly significant suggesting the importance of both additive and non-additive gene actions in the inheritance of SBR resistance. The high GCA/SCA (1.50 – 2.30) and Baker's (0.75 – 0.82) ratios suggested the predominance of additive gene action in the inheritance of SBR resistance. The narrow-sense (0.73 – 0.82) heritability estimates were high, indicating the possibility of improving resistance to SBR through selection in the early generations. UG-5, Maksoy 3N, Maksoy 4N and Maksoy

5N had negative GCA effects for rust severity and sporulation level, suggesting their positive contributions to resistance. Three putative QTLs associated with resistance to SBR were identified on chromosome 6, 9 and 18 with LOD scores ranging from 3.47 – 8.23 and phenotypic variance explained by the QTLs (PVE) ranging from 18.3 – 25.6%. The putative QTL detected on chromosome 9 was novel and has not been reported elsewhere, and hence could be used as an additional source of resistance to SBR. A total of 18 putative candidate genes were predicted on approximately 482.7 kb region of the QTL detected on chromosome 18, which was mapped to the same region of the previously reported *Rpp1-b* gene. Among these, three putative candidate genes (Glyma18g51930, Glyma18g51950 and Glyma18g51960), Glyma18g51970, Glyma18g52050 and Glyma18g51890 were found to encode leucine-rich repeat (LRR), Ser/Thr protein phosphatase, leucine-rich repeat receptor-like protein kinase (LRR-RLK) and chitinase related proteins, respectively, which are associated with plant defense signaling pathways. Moreover, F-box and leucine-rich repeat, glycosyltransferase and serine/threonine-protein phosphatase 2A catalytic subunit coding genes (Glyma.09G10550, Glyma.09G104700 and Glyma.09G105000) were predicted on the novel putative QTL detected on chromosome 9. It can, therefore, be concluded that the parental genotypes with high negative GCA effects could be used as a source of resistance to SBR and the F_2 progenies with high negative SCA effects could be advanced in future soybean improvement programs. Likewise, the identified putative QTLs and the candidate genes could help to facilitate efficient marker-assisted selection, gene pyramiding and/or genetic transformation for the future development of durable resistance to SBR. As a recommendation, genomic regions associated with SBR resistance should further be identified and mapped from the highly resistant parental genotypes. The identified QTLs in line UG-5 need to be further screened on larger population size and increased number of markers from each linkage group. The structural and functional roles of the putative genes need to be determined.