Genetic diversity of rhg1 and Rhg4 loci in wild soybeans resistant to soybean cyst nematode race 3

C.P. Yuan¹, Y.J. Wang², H.K. Zhao³, L. Zhang³, Y.M. Wang¹, X.D. Liu¹, X.F. Zhong⁴ and Y.S. Dong⁴

¹Soybean Research Institute, Jilin Academy of Agricultural Sciences, Changchun, Jilin, China
²Institute of Agricultural Resources and Environment, Jilin Academy of Agricultural Sciences, Changchun, Jilin, China
³Crop Germplasm Institute, Jilin Academy of Agricultural Sciences, Changchun, Jilin, China
⁴Agro-Biotechnology Research Institute, Jilin Academy of Agricultural Sciences, Changchun, Jilin, China

Corresponding author: Y.S. Dong
E-mail: yingshan.dong@yahoo.com

Received August 6, 2015
Accepted December 9, 2015
Published June 10, 2016
DOI http://dx.doi.org/10.4238/gmr.15027386

ABSTRACT. Over-utilization of germplasms that are resistant to the soybean cyst nematode (SCN) in soybean breeding programs can lead to genetic vulnerability in resistant cultivars. Resistant wild soybean (Glycine soja) is considered an invaluable gene source for increasing the genetic diversity of SCN resistance. In this study, we genotyped 23 G. soja accessions that are resistant to SCN race 3 for polymorphisms in the resistance genes, rhg1, Rhg4, and SHMT, and investigated their genetic relationship with eight Glycine max resistant cultivars. We identified 89 single nucleotide polymorphisms (SNPs) and 11 DNA insertion-deletions (InDels), of which 70 SNPs and 8 InDels were found
in rhg1, 9 SNPs were found in Rhg4, and 10 SNPs and 3 InDels were found in SHMT. Nucleotide diversity was $\pi = 0.00238$ and $\theta = 0.00235$, and haplotype diversity was 1.000. A phylogenetic tree comprising four clusters was constructed using sequence variations of the 23 G. soja and 8 G. max resistant accessions. Five G. soja accessions in subcluster A2, and four G. soja accessions in cluster B were genetically distant from G. max genotypes. Eight resistance-associated SNPs in the three resistance genes formed nine haplotypes in total. G. soja resistant accessions had different haplotypes (H2, H4, H5, H6, H7, and H8) compared with those of G. max (H1, H3, and H9). These results provide vital information on the use of wild soybeans for broadening the genetic base of SCN resistance.

**Key words:** Wild soybean; Genetic diversity; Soybean cyst nematode; Resistance gene