M-10

Dissecting the genetic basis of resistance to soybean cyst nematode for soybean breeding

Ying-hui Li *, NFCRI, Institute of Crop Science, Chinese Academy of Agricultural Sciences, Beijing, China
Xue-hui Shi, NFCRI, Institute of Crop Science, Chinese Academy of Agricultural Sciences, Beijing, China
Bo Liu, NFCRI, Institute of Crop Science, Chinese Academy of Agricultural Sciences, Beijing, China
Yu-lin Liu, NFCRI, Institute of Crop Science, Chinese Academy of Agricultural Sciences, Beijing, China
Yu Tian, NFCRI, Institute of Crop Science, Chinese Academy of Agricultural Sciences, Beijing, China
Jia-jun Wang, Soybean Research Institute, Heilongjiang Academy of Agricultural Sciences, Harbin, China
Bai-shuang Yu, Soybean Research Institute, Heilongjiang Academy of Agricultural Sciences, Harbin, China
Li-juan Qiu, NFCRI, Institute of Crop Science, Chinese Academy of Agricultural Sciences, Beijing, China

Soybean cyst nematode (SCN, *Heterodera glycines* Ichinohe) is a highly destructive pathogen of soybean. To bred superior resistant cultivars with more horizontal or broad-spectrum resistances by pyramiding major and minor genes for protecting soybean production, 585 SNPs was used to genotype both a panel of diverse accessions (mainly from Chinese SCN applied core-collection) and a set of RILs bred from the cross Zhongpin03-5373 (resistant) x Zhonghuang13 (susceptible). The SNP loci are mostly sited within genic sequence in regions of the soybean genome thought to harbor genes determining resistance to SCN. The three strongest quantitative trait nucleotides identified by association mapping corresponded to two QTL (multigene locus *rhg1-b* and its closest paralog *SCN3-11*) and involved the genes *Glyma18g02590 (*a component of the), *Glyma11g35820* and*Glyma11g35810 (*the closest paralog of *rhg1-b*). These two putative QTL were validated by the linkage mapping analysis, *rhg1-b* explained 25.5% of the phenotypic variance for SCN resistance and the latter 5.8%. In combination, the two major loci acted non-additively, providing a high level of SCN resistance. To further mining more new resistant genes, a SCN resistance-related family-based population with a clear breeding pedigree and the above-mentioned RILs were whole-genome re-sequenced more than 15× depth and 1× depth respectively. Interestingly we found several novel loci which have not been found previously by comparing genetic variation among resistant and susceptible cultivars and tracing their inheritance during breeding process. Based on these functional SNPs, labor/time-saving and cost-effective CAPS markers were exploited for assisted selection of desirable SCN resistance and pyramiding breeding. Our results would reveal the genetic basis of SCN resistance more thoroughly and provide useful information for bringing more desirable alleles from different sources into breeding program to develop super-resistant modern cultivars.