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Genome-Wide Association Analysis of Disease Resistance Against *Phytophthora nicotianae* in Korean Sesame Germplasm Collection

Sovetgul Asekova^{1*}, Sungup Kim¹, Euyoung Oh¹, Myoung Hee Lee¹, Jung In Kim¹, Min Su Kim², Suk Bok Pae¹, Tae Jung Ha¹, Do Yeon Kwak¹

¹Department of Southern Area Crop Science, NICS, RDA, Miryang, Korea

²School of Applied Biosciences, Kyungpook National University, Daegu 41566, Korea

[Introduction]

Sesame (*Sesamum indicum* L.), from Pedaliaceae, is an ancient and important oil seed crop. Genome-wide association study (GWAS) based and linkage disequilibrium (LD) is a powerful and promising tool for the detection and fine mapping of quantitative trait loci (QTL) underlying complex agronomic traits. To investigate the disease resistance of sesame germplasm panel, GWAS of 8883 SNPs with genome-wide coverage was used to identify the candidate genes for four different *Phytophthora nicotianae* Breda de Haan dominant isolates from Korea provinces. The results of this study may provide a theoretical basis of *Phytophthora* disease resistance in sesame.

[Materials and Methods]

For the all 87 sesame accessions comprising the GWAS population, the screening of genotypes were screened against *Phytophthora* blight ('KACC48121', 'KACC48120', 'No.2526', and 'No.2040') in greenhouse as per modified 9-point scale of Oh *et al.* (2018). The disease score of 1–3 was considered as resistant and 4–9 as susceptible. We used GBS generated 8883 high-quality SNP markers. The GBS libraries were constructed using restriction enzyme *ApeK1*. Association analysis was performed with compressed mixed linear model implemented in the GAPIT R package. A marker trait association was considered when the marker main effect was significant at P -value < 0.01 and FDR adjustment < 0.08 .

[Results and Discussions]

Large phenotypic variation was observed for analyzed traits. Principal Coordinate Analysis (PCoA), conducted with five, clearly separated the population into five subgroups. Our results indicated a strong association between *phytophthora* isolates (strains) and the similar SNPs. In the optimal GWAS model (K+PCA), we found that 37 SNP loci significantly associated with disease resistance traits, and each locus explained phenotypic variations ranging from 34.9 to 56.5%. By analyzing the LD interval of the significant locus and the corresponding interval to reference genome of *Sesame indicum* (ver. 2.0), total of 75 genes were involved within the 570-kb flanking region. The most significant associations were corresponding to (PRR) pentatricopeptide repeat-containing protein, receptor-like protein kinase domains (NBS-LRR) and phosphatase (PERK3 and PP1), F-box protein (PP2-B5), cytochrome P450, defense response-NB-ARC gene analogs provided support for the hypothesized *phytophthora* resistance involving strong *R*-genes. Our result demonstrate that GBS-GWAS represent a powerful approach for the identification of loci controlling disease related traits.

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*Corresponding author: Tel. +82-55-350-1239, E-mail, asekovasovetgul@korea.kr