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INTEGRATING GWAS AND GENE COEXPRESSION NETWORKS REVEALS CANDIDATE RESISTANCE GENES FOR COMMON FUNGAL DISEASES IN SOYBEAN (GLYCINE MAX)

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RESUMO

Soybean is one the most important legume crops worldwide, and it is used as food, feed and for industrial applications. Soybean crops are widely affected by fungal diseases that reduce yield significantly. Here, we identified high-confidence candidate genes involved in resistance to common fungal diseases. By curating the scientific literature, we built a database of single nucleotide polymorphisms (SNPs) associated to resistance to 5 fungi species: *Cadophora gregata*, *Fusarium graminearum, Fusarium virguliforme, Macrophomina phaseolina,* e *Phakopsora pachyrhizi* (*n*=70, 12, 91, 16, 2, respectively). 150 transcriptome samples comprising soybean tissues infected with the pathogens aforementioned were downloaded from the Soybean Expression Atlas (*n*=27, 12, 40, 4, 20, respectively). Coexpression network inference and selection of high-confidence candidate genes were performed with the R packages BioNERO and cageminer, both developed by our group. Genes that are known to be associated to resistance to fungi were retrieved from PLAZA Dicots 4.0 using MapMan annotations. Using a sliding window of 2 Mbp relative to each SNP, we obtained 407, 88, 31, and 18 genes potentially involved in resistance to *F. virguliforme, F. graminearum, C. gregata, M. phaseolina* , respectively. Overall, the candidate genes are not shared among species, revealing high host-pathogen specificity in this defense mechanism. The top 10 genes associated to resistance to each fungal species comprise both known (e.g., LRR-RK) and novel candidates. The set of candidate genes is enriched in genes related to transcriptional regulation, response to stress-related phytohormones (abscisic acid, salicylic acid and ethylene), hypersensitive reaction, phytoalexin production, stress signaling, and innate immunity. Finally, we highlighted the accessions from the USDA germplasm that contain the highest number of favorable alleles, which can be used to start breeding programs. These genes are promising targets for developing soybean lines with increased resistance to major fungal phytopathogens in crops worldwide.

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PALAVRAS-CHAVE: QTL, population genomics, bioinformatics

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