

Gene expression analysis and phenolic accumulation in the soybean – *Phakopsora pachyrhizi* interaction

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(Análise da expressão gênica e acúmulo de compostos fenólicos na interação soja – *Phakopsora pachyrhizi*)

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Resumo

Asian soybean rust, caused by *Phakopsora pachyrhizi*, is a major disease affecting the soybean crop and causing damage levels that can reduce the potential of production. In order to obtain information about the soybean defense response against this fungus, transcriptomic and metabolomic analysis were performed. RNA and soybean extracts of rust-infected and non-infected leaves were analyzed by quantitative PCR and high performance liquid chromatography (HPLC) using tolerant (BRS 231), resistant (PI561356) and susceptible (BRS 184) genotypes. From 16 genes evaluated, 10 were involved in the synthesis of phenylpropanoids. For most of these genes, the expression profiles were similar among genotypes and activation was higher at 192 hours after inoculation (hai) indicating their involvement in the basal defense response. On the other hand, some genes such HDzip (Homeobox-leucine zipper), serine/threonine kinase with LRR domain (Leucine rich repeat) and CHS (chalcone synthase) were intensely activated earlier in the resistant plants suggesting a greater involvement in the resistance. In addition, HPLC analysis showed accumulation of the isoflavones genistein and daidzein in all genotypes in response to the infection, particularly at 192 hai, suggesting also a basal response to the fungal attack. In contrast, early intense accumulation of free aglycone in the resistant genotype suggest a direct involvement in the resistance response on soybean plants.

Apoio: CAPES