

**DIFFERENTIAL TRANSCRIPTIONAL PROFILING OF *PHAKOPSORA PACHYRHIZI*-INFECTED SOYBEAN REVEALED BY HIGH-THROUGHPUT SUPERSAGE**

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To unravel important gene candidates in soybean accessions resistant and susceptible to Asian rust infection (*Phakopsora pachyrhizi*), the SuperSAGE methodology was applied allowing the identification of 104,725 unique tags (26 bp) of which 17,267 were differentially expressed (9,061 up-regulated and 8,206 down-regulated,  $p \leq 0.05$ ). Tags were estimated to cover twice the transcripts expected to have only one copy per cell. BlastN alignments with several EST databases enabled the analysis of the individual contribution of each bank for tag annotation. Also, tag alignments with soybean transcripts and genomes from the Phytozome database allowed tag mapping over gene models. Furthermore, the tag annotation and the similar EST categorization by Gene Ontology enabled a soybean expression profile generation in response to *P. pachyrhizi* revealing many differentially expressed tags related to biotic and abiotic stress responses, including categories like “oxidation reduction”, “response to biotic stimulus”, “response to abiotic stimulus”, “photosynthesis” and “regulation of transcription”. Into the top 100 most up-regulated tags were enzymes and proteins involved in plant secondary metabolism, members implicated in the signal transduction, regulatory mechanism, cellular signaling and some others involved in plant disease resistance, and candidates with unknown function (not yet categorized). Transcripts with a relevant expression profile are being validated by RTq-PCR and may be useful in soybean breeding programs.