

FIRST ASSESSMENT OF GENE EXPRESSION IN THE SOYBEAN RUST
Phakopsora pachyrhizi

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Soybean rust is caused by the obligate fungal pathogen *Phakopsora pachyrhizi* Sydow. A unidirectional cDNA library was constructed in the plasmid pSPORT1 using mRNA isolated from *P. pachyrhizi* urediniospores germinating on a water surface. Single pass sequencing of 908 clones revealed that 404 sequences displayed significant similarities ($Evalue < 10^{-05}$) to sequences deposited in public databases. The remaining 504 sequences showed no significant or no similarities to protein database entries. 488 unique ESTs were identified. Among genes with assigned function, approximately 20% were involved in primary metabolism, 7.5% in gene/protein expression, 5.5% in cell structure and growth, 4.5% in cell division, 3.5% in cell/organism defense and 3% in cell signaling/cell communication. Approximately 56.5% of the identities found were to hypothetical proteins and proteins with unknown function.