

Prediction of the secretome and effectors candidates of *Phakopsora pachyrhizi* during the course of infection in soybean

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(Predição do secretoma e de candidatos a efetores de *Phakopsora pachyrhizi* durante o curso da infecção em soja)

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Resumo

Soybean rust, caused by *Phakopsora pachyrhizi*, has been causing losses that vary from 10% to 80%. The success of infection relies on the production of virulence and avirulence proteins that facilitate host colonization, enhance the ability of parasite to survive and multiply in the host environment, and suppress host defense responses. In this study, we used ab initio strategies and sample enrichment combined with a deep sequencing methodology to access a catalogue of *P. pachyrhizi* expressed genes and its potential secretome, and to identify a set of potential effectors. The final secreted protein dataset was used to identify possible candidates to avirulence factors. Some criteria were evaluated to identify pathogenicity proteins: small ORF size <200bp, no intracellular function described, number of cystein residues >3%, the presence of previously described Y/F/WxC/FxC motifs in the N-terminal sequences of secreted protein and the similarity to PHI-base. To validate these candidates, we used RT-qPCR to assess the level of expression during the course of infection. Some of these effectors candidates showed up regulated in the early days of infection. Functional analyses are in progress to confirm our approach. To our knowledge this is the first study to predict a secretome dataset for *P. pachyrhizi* and to point out a set of effector candidates.

Apoio: Embrapa, Capes