

Phenotypic and molecular analysis of an incompatible interaction between soybean and the fungus *Uromyces appendiculatus*

Romero, CCT^{1,2*}; Stolf-Moreira, R¹; Brito Junior, SL^{1,2}; Nascimento, LC³; Carazzolle, MF³; Marcelino-Guimaraes, FC¹; Abdelnoor, RV¹

¹Embrapa Soja, Londrina, PR, 86001-970;

²Programa de Pós-Graduação em Genética e Biologia Molecular, Univ. Est. de Londrina, Londrina, PR, 86051-980;

³Dep. de Genética e Evolução, Lab. de Genômica e Bioinformática, Univ. Est. de Campinas, Campinas, SP, 13083-970.

*E-mail: cyromero@gmail.com

Keywords: Glycine max, non-host resistance, subtractive library, biotic stress, Asian Soybean Rust

Plants are immune to the majority of potentially pathogenic microorganisms, a phenomenon known as non-host resistance. This defense mechanism is the most durable and common type of resistance, involving pre-formed and inducible barriers. Due to its complex nature, non-host resistance has been less studied over the years than specific resistance, mediated by *R* genes. Understanding the molecular basis of non-host resistance is important to help develop alternative strategies for crop plant disease control. Soybean is the main Brazilian agricultural commodity, but this crop suffers annually losses of million dollars because of Asian Soybean Rust (ASR), caused by the biotrophic fungus *Phakopsora pachyrhizi*. The current study aimed to investigate phenotypically and molecularly the non-host interaction between soybean and another rust fungus: *Uromyces appendiculatus*, causer of common bean rust. Phenotypic analyses, by optical and scanning electron microscopy, suggests the unsuccessful attempt to fungal penetration in soybean leaf, and classify this incompatible interaction as “type I” non-host resistance. For molecular studies, we proposed the analysis of differentially expressed transcripts, generated by the construction of cDNA subtractive libraries. In addition to important genes involved in defense against pathogens, we also detected the expression of genes related to non-host resistance. Analysis by qRT-PCR showed overexpression of *PEN2* and *PEN3* at 72 hours after inoculation. Apparently both genes work in co-operation in a pre-invasion defense mechanism which involves traffic of toxic compounds to the plasma membrane at sites of attempted invasion. Another gene, *BI-1*, showed to play an important role in the conserved endoplasmic reticulum stress response pathway to modulate cell death, and it was demonstrated to be overexpressed in the initial hours of infection.

Financial support: CNPq, Embrapa Soja.