Poster: Plant-pathogen interactions

Abs # P16037: Construction of a subtracted library and a macroarray to identify defense response genes from rice plants upon infection with a native *Magnaporthe grisea* isolate

Presenter: Salerno, Graciela G *Contact Presenter*

Authors Consolo, Fabiana (A) Giarrocco, Laura E (A) Corsetti Purcino, Antonio A (B) Salerno, Graciela G (A)

Affiliations: (A): FIBA (Fund. Inv. Biol. Aplic.)
(B): EMBRAPA Milho e Sorgho, Sete Lagoas, Brazil

Magnaporthe grisea is a heterothallic ascomycete pathogenic to a large number of graminea species. It causes the most important rice disease worldwide and consequently, severe yield losses. The development of new strategies for disease control based on the understanding of plant-pathogen interaction mechanisms may offer the promise of sustainable agricultural production. Suppression Subtractive Hybridization (SSH) is an efficient tool to selectively amplify target cDNA fragments. The objective of this work was to identify differentially expressed genes in a compatible interaction between a rice line (CT13432-6) carrying a *M. grisea* resistance gene (*Pi33*) and a native *M. grisea* isolate (FCC40, native from Argentina), using the SSH technique. Three-weeks-old plants were inoculated with a spore suspension, or sprayed with water. Leaf tissues, harvested at three times after inoculation, were pooled and mRNA was extracted. A library was constructed using a PCR Select cDNA Subtraction Kit. The resistant rice line inoculated with fungi was used as tester and the same cultivar inoculated with water, as driver. The final PCR products were cloned, resulting in a 200 clones-subtractive library. The average insert size ranged from 200 to 800 bp. The nucleotide sequences were analyzed (E-value below 10^5) and grouped according to potential functions in pathogenesis, or biotic and abiotic stress responses. Some clones (88) were selected by their biological function for macroarray screening. This technique allowed us the identification of six induced and four repressed genes. Some of those genes may be useful for the development of new strategies towards durable-resistance rice cultivars. Supported by CABBIO-ANPCyT (N^o 64), CONICET, FIBA and UNMdP.

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