Fifth International Conference of the Peanut Research Community

Book of Abstracts

5th AAGB
Advances in Arachis through
Genomics & Biotechnology
2011

Brasília, DF - Brazil
June 13th to 15th, 2011

Notes	

Large scale transcriptome analysis of wild peanut (*Arachis stenosperma*) inoculated with *Passalora personata*, the causal agent of Late Leaf Spot

ACQ Martins[1,2*], CV Morgante[3], AK Silva[2], IC Galhardo[1], GJ Pappas Jr[2], OB Silva Jr[2], SCM Leal-Bertioli[2], DJ Bertioli[1], RNG Miller[1], ACM Brasileiro[2] & PM Guimarães[2].

[1]UnB – University of Brasília, Campus Darcy Ribeiro, Brasília, Brazil. [2]Embrapa Genetic Resources and Biotechnology, PqEB, W5 Norte Final, Brasília, Brazil. [3]Embrapa Semi-Arid, Petrolina, Brazil.

Peanut (*Arachis hypogaea*) is one of the most important oilseed in the world due to its high energy value and nutrition. However, peanut has a low genetic variability, especially for agronomical traits, which differs from its wild species, which are sources of disease resistance and adaptation to various environments. *Arachis stenosperma* is a wild species resistant to some pests and diseases, among them, the Late Leaf Spot, caused by the fungus *Passalora personata*. Aiming to identify genes associated with response to resistance, the transcriptome of *A. stenosperma* V10309, challenged with the fungus *P. personata* and its control was analyzed by large scale pyrosequencing (http://www.454.com – Roche). For this, leaves of plants inoculated with 5×10^5 spores/ml were collected 24, 48 and 72 hours after inoculation. A pool of total RNA comprising equal amounts of the three collection points was formed for cDNA synthesis and construction of two cDNA libraries (Creator SMART cDNA library construction kit, Clontech).The libraries were sequenced by pyrosequencing454 technology (GS-FLX Titanium Fragment Series Kits, Roche Applied Science) resulting in 194.076 reads from the infected sample and 168.555 from the control, covering respectively 51.609.348bp and 48.784.925bp. After analysis by bioinformatics, 39,620unigenes were identified and primers were designed for validation of candidate genes by quantitative real-time PCR. This dataset will be an important tool for identifying differentially expressed genes, characterization of wild alleles and development of molecular markers for peanut.

*andressa.cqm@gmail.com