

Genomics of Tree-fungi interaction: Witches' broom disease on cacao and SALB  
on rubber.

Júlio Cascardo, Fátima Alvim, Carlos Pirovani, Abelmon Gesteira, Paulo Monzani,  
Fabienne Micheli, Dominique Garcia

Centro de Biotecnologia e Genética, UESC/DCB, Ilhéus-Bahia  
[cascardo@uesc.br](mailto:cascardo@uesc.br)

The interaction of *Moniliophthora perniciosa* with *Theobroma cacao* was evaluated at the genomic and proteomic level. The partial sequencing of the fungus genome, together with two interaction cDNA libraries sequenced, and the proteome project of this organism and its interaction with its host cacao allowed the identification of several genes involved in this complex interaction. *M. perniciosa* possesses a hemibiotrophic life system. High density macroarrays and candidate gene approach allowed the identification of some genes possibly involved in these processes. The analyses of the fungus genome allowed the identification of key genes. Mass spectrometry of fungus secreted proteins in different medium culture and proteins of the apoplastic fluid allowed the identification of important proteins. Heterologous protein expression of diverse fungus and plant proteins followed by bioassays allowed the understanding of some biological processes in the colonization and resistance process. Protein structures of some possible targets were resolved and we currently are testing possible ligands that block its function. South American Leaf Blight (SALB) caused by the Ascomycota, *Microcyclus ulei*, is the most severe disease affecting *Hevea* spp. Susceptible and resistant cultivars were chosen for comparative analysis and identification of candidate genes. A partially resistant (MDF180) and the susceptible (PB314) were used. Five SSH libraries allowed the cloning of genes differentially expressed during the interaction between rubber tree and *Microcyclus ulei*. Two MDF180 cDNA libraries and three PB314 cDNA libraries (infected leaves vs. control leaves), highly enriched for *M. ulei*-induced genes were prepared. The sequences were annotated and their function assessed in order to identify genes associated to resistance or susceptibility.

Keywords: Witches' broom disease, SALB, genomics.