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Biotic and Abiotic Stress Tolerance in Plants: the Challenge for the 21st Century

BOOK OF ABSTRACTS

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among them, 460 were common to both treatments, 144 were present only in the non infected sample, and 158 present only in the infected one. In the "Pera C21" variety, 394 and 328 spots were detected in infected and non infected samples, respectively; among them, 266 were common to both treatments, 128 were present only in the non infected sample, and 62 present only in the infected one. The differences of protein profiles between varieties as well as between infected and non infected sample for the same variety revealed probable differential variety-dependant biochemical responses that may be explore for further development of Citrus Tristeza control strategies.
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S01P11

In silico characterization of a pathogenesis-related protein PR-1 from _Theobroma grandiflorum_

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The cupuassu (*Theobroma grandiflorum* [Wild. Ex Sperg.] K. Schum) is a native species of Brazil with a large industrial potential related to the use of the fruit pulp and seeds. In particular, the cupuassu presents a great economic value for the Pará State, which invested in cupuassu sweet (e.g. ice-cream) and cupulate (chocolate obtained from cupuassu seeds) production and commercialization. *Theobroma grandiflorum* belongs to the same genus than cacao (*Theobroma cacao*), and, unfortunately, both suffer from the attack of the fungus *Moniliophtora perniciosa* responsible for the witches' broom disease. Several molecular studies of the interaction between cacao and *M. perniciosa* were previously developed, while little is still known in regards to cupuassu resistance to witches' broom disease. Among the well known genes involved in plant-pathogen interactions, the pathogenesis-related proteins (PR proteins) could be highlighted. In particular, the PR-1 family proteins presented several functions that vary according to the organism and that may be involved in different ways in defense to pathogen infection. Recently Next Generation Sequencing of cupuassu expressed sequences tags allowed the identification of several PR proteins, and here we developed an *in silico* analysis of a TgPR-1 sequence. The TgPR-1 ORF encoded a 161 amino acid protein that showed homology with the PR-1 proteins belonging to the serine-carboxyl proteinase superfamily. A multiple alignment using the ClustalW program allowed the identification of domains conserved between the TgPR-1 and its homologs from other organisms. The TgPR-1 protein presented a peptide signal (24 amino acids identified by the SignalP 4.1 software), and had an isoelectric point and a molecular weight of about 8.75 and 17.3 kDa, respectively. The protein presented possible post-translational modification sites such as 10 phosphorylation sites (encountered using the NetPhos 2.0 software) – but no glycolsylation sites were found. The systems biology analysis of TgPR-1 was performed using the BLASTO and OMA browser to find a corresponding ortholog. The best score protein was found for the PRB1 from *Arabidopsis thaliana*. The network was set up using the software Cytoscape 2.8.2. The protein showed direct interaction with other proteins involved in responses to biotic stimuli, fungus, bacteria and stress as well as involved in mechanisms of resistance and plant defense. The *in silico* characterization of TgPR-1 constitute the first steps towards understanding the mechanisms of *T. grandiflorum* defense.
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Systems biology of proteins expressed during the _Moniliophthora perniciosa_ necrotrophic phase

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The fungus *Moniliophthora perniciosa*, the etiologic agent of witches' broom disease of cacao (*Theobroma cacao* L.) has a hemibiotrophic life cycle, with a biotrophic and a necrotrophic phase. The biotrophic phase, initiating the disease, is characterized by a monokaryotic mycelium, while the