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

BOOK OF ABSTRACTS

6 to 8 • NOVEMBER • 2013

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

Cana Brava Resort • Ilhéus-Bahia, Brazil • 6th-8th November 2013

POSTER SESSION

S01P01

***In silico* characterization and expression analysis of a Selenium-Binding Protein gene from cacao**

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Witches' broom disease, caused by the fungus *Moniliophthora perniciosa*, is one of the main diseases of cacao (*Theobroma cacao* L.) and is responsible to severe economic losses in the production areas. Recently, expressed sequence tags (ESTs) from cacao-*M. perniciosa* interaction were obtained and differentially defense-related genes expressed during the cacao-*M. perniciosa* interaction were identified. Among them, a Selenium-Binding Protein (*TcSBP*) was found. In other organisms, *SBP* genes are related to the increase of plant defenses against abiotic and biotic stresses; in rice the *SBP* gene was successfully used to increase the plant resistance to *Magnaporthe grisea* by plant transformation. Here, *in silico* characterization and expression analysis of *TcSBP* were developed. Search on the Cacao Genome Database revealed the presence of only one *SBP* sequence of 4774 pb in length located on the chromosome 4. The *TcSBP* ORF is 1431 bp in length and encodes a protein of 476 amino acids which does not contain any signal peptide. Prediction of possible post-translational events allowed the identification of several glycosylation, phosphorylation and acetylation sites. The comparison of *TcSBP* sequence with *SBP* from other organisms using the BLASTP tool revealed identity from 62% to 91% and allowed the identification of specific conserved regions. The expression analysis of *TcSBP* in meristems of cacao plantlets varieties Catongo (susceptible) and TSH1188 (resistant to *M. perniciosa*), inoculated or not with *M. perniciosa*, was obtained by RT-qPCR using 3 biological and 3 experimental replicates. qPCR analysis of *TcSBP* gene was conducted using the standard settings of the ABI PRISM 7500 and the System of Sequence Detection software. The *TcSBP* relative expression was analyzed with the comparative Ct method ($2^{-\Delta\Delta Ct}$) using malate dehydrogenase and actin as endogenous reference genes, and non-inoculated plants (control) as calibrator. The relative expression of *TcSBP* was significantly increased 8 and 15 days after inoculation in the resistant variety TSH1188 compared to susceptible Catongo. These data suggest the possible role of *TcSBP* in cacao resistance to *M. perniciosa*. This study is the first step to better understand the role of *TcSBP* in cacao resistance as well as for the development of control strategies of the witches' broom disease (e.g. using plant transformation).

Work supported by FAPESB, CAPES, EMBRAPA, CNPq, FINEP/Renorbio and CIRAD

S01P02

Identification, classification and phylogenetic analysis of bZIP proteins from *Theobroma cacao* for subsequent studies of resistance to witches' broom disease

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Biotic and abiotic stresses are a major factor in decreased production of various cultures around the world. The culture of cacao (*Theobroma cacao*) has been suffering for many years with one of the diseases that most affect their crops, the witches' broom caused by the fungus *Moniliophthora perniciosa*. Studies have identified several transcription factors as promising candidates for developed roles in the regulation and signaling via various stresses in plants. bZIP family proteins are transcription factors (TF) that regulate various physiological and development processes, such as seed maturation, vascular development, and responses to biotic and abiotic stresses. Here, we performed an *in silico* analysis of the bZIP family from *Theobroma cacao* to subsequently develop a comprehensive phylogenetic analysis in four angiosperms species. For this, bZIP protein sequences of *Arabidopsis thaliana* were downloaded from the Phytozome database. BLASTP search was performed to identify