IDENTIFICATION AND FUNCTIONAL CHARACTERIZATION OF GENES INVOLVED IN DROUGHT STRESS RESPONSES IN COFFEE PLANTS

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Abiotic stresses, such as drought, salinity and extreme temperatures, are serious threats to agriculture due to severe climate changes, observed in the last decades around the globe. Therefore, identification of the molecular mechanisms involved in abiotic stress responses aiming at improving breeding for abiotic-stress tolerance in crop plants is considered priority in current plant biotechnology programs. Supported by the Consórcio Brasileiro de Pesquisa e Desenvolvimento do Café (CBP&D-Café), it was recently concluded the Brazilian Coffee EST-project. The project resulted in the identification of more than 30 thousand genes from a large-scale sequencing effort (200.000 EST), obtained from several coffee-cDNA libraries, including those made from plants submitted to abiotic stresses. The conclusion of this project provided coffee researchers a resourceful database, containing a large set of transcribed genes associated with the diverse stress conditions applied before the construction of the cDNA libraries.

The aim of the present work was to identify and characterize genes potentially involved in the response to drought stress. The analysis consisted initially on the identification of coffee genes displaying high degree of sequence similarity to well characterized genes described as to be involved in the abiotic stress responses (IASR) from other plant species and by electronically characterizing its expression. Furthermore, transcriptional profiling on cDNA arrays associated with tryptic peptide MS/MS analysis of extracts from controls and coffee plants submitted to drought, revealed a large set of candidate genes involved in abiotic-stress responses in coffee. These identified genes were classified in four different categories: 1. Sensing and signal transduction; 2. Transcription Factors; 3. Structural genes and, 4. Unknown Function. Results indicate that the approach used provided a fast and efficient way to identify and select novel candidate genes involved in abiotic-stress responses in coffee. Some of these pre-selected genes are currently being further studied and characterized.