

P0821 Differentially expressed genes and proteins upon drought stress in tolerant and sensitive genotypes of *Coffea canephora*

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The molecular mechanisms underlying the response to drought stress in coffee plants were investigated by the identification of candidate genes (CGs) using different approaches. The first used the data generated during the Brazilian Coffee EST project to select thirteen CGs by an *in silico* analysis (electronic Northern). The second was based on screening macroarrays spotted with plasmid DNA (coffee ESTs) with separate hybridizations using leaf cDNA probes from drought-tolerant and susceptible clones of *Coffea canephora* var. Conilon, grown under different water regimes. This allowed the isolation of seven additional CGs. The third used two-dimensional gel electrophoresis to identify proteins displaying differential accumulation in leaves of drought tolerant and susceptible clones of *C. canephora*. Six of them were characterized by MALDI-TOF-MS/MS and the corresponding proteins were identified. Finally, additional CGs were selected from literature and the quantitative real-time polymerase chain reaction (qPCR) was performed to analyze the expression of all identified CGs. Altogether, more than forty genes presenting differential gene expression with drought stress were identified, some of them showing different expression profiles between drought-tolerant and susceptible clones. Our results led us to conclude that a complex network of responses certainly involving the ABA signaling pathway and Nitric oxide are major molecular determinants to explain the better efficiency in controlling stomatal closure and transpiration, displayed by clone 14 of *C. canephora*. In order to investigate CG genetic polymorphism, corresponding gene sequences of several of them were also amplified from different coffee accessions covering the coffee genetic diversity for drought tolerance.

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