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Integrated Analysis Of Drought Stress Responses In Coffee Plants

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Coffee is an important commodity worldwide with about 125 million people depending on this crop for their livelihoods. Drought stress significantly affects coffee yield with losses estimates in Brazil, varying from 10 to 15 % in recent years. Therefore, the development of molecular tools for rapid generation of drought-tolerant coffee varieties is amongst the priorities of the Brazilian Research Program on Coffee Genomics. The principal aim of this study was to investigate the molecular mechanisms underlying the response to drought stress in coffee plants by an integrated approach. As part of the Brazilian Coffee EST project, two EST libraries from leaves of drought-stressed plants of *Coffea arabica* cv. Rubi (drought sensitive) and *C. canephora* clone 14 (drought tolerant), were generated. The plant material of *C. arabica* and *C. canephora* were obtained from field and pot trials, respectively. More than 15,000 clones were sequenced and, after trimming and clustering, resulted in 10,924 reads grouped on 6,141 unigenes (1,779 contigs and 4,362 singlets). The approaches used to identify candidate genes (ESTs) underlying stress responses in coffee consisted of an in silico analysis of ESTs generated from drought-stressed and control libraries, physiological characterization, transcription profiling of drought-stressed and control tissues and protein profiling by 2-DE coupled with tryptic peptide identification by MALDI-TOF-MS/MS. These integrated analysis resulted in the identification of several candidate drought-responsive genes. In addition, a mapping population from crosses of *C. canephora* clones contrasting for this trait is also under way for future association studies and QTL mapping.