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## Update on the search of candidate genes for drought-tolerance in coffee

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It is well known that drought periods affect coffee plant development, leading to plant death and abortion of developing fruits in case of severe drought. In relation to coffee genetic diversity, several works reported the identification of plants of *C. canephora* conilon susceptible or tolerant to drought which were analyzed at the physiological level and also used to identify candidate genes underlying stress responses. Even narrow, a genetic diversity for drought tolerance also exist in the species *C. arabica*. In addition to the identification of undiscovered transcripts, the recent development of low-cost, high throughput next-generation (NGS) sequencing technologies now opens the way to perform expression profiling and to identify gene presenting differential expression patterns by comparing the frequency of reads obtained after sequencing. In order to initiate such kind of approach in coffee, RNAseq approach was performed using (1) roots of *C. canephora* conilon susceptible (clone 22) or tolerant (clones 14, 73 and 120) to drought grown under greenhouse conditions with (I) or without (NI) irrigation and (2) meristematic tissues from Iapar59 (I59, drought tolerant) and Rubi (R, drought susceptible) cultivars of *C. arabica* grown under field-grown with (I) or without (NI) irrigation. These data were compared with those of *Coffea* transcriptome, including the EST sequences from both *C. arabica* and *C. canephora*. Electronic northern blots produced by these comparisons identified differentially expressed genes between drought-tolerant and -susceptible clones and cultivars. By qPCR experiments, more than 80 candidate genes, that could play a crucial role in the genetic determinism of drought tolerance in coffee plants, were selected. Based on these results, it can be concluded that the abscisic (ABA) signaling pathway (including ABA synthesis and perception) is one of the major molecular determinants that might explain the better efficiency in controlling stomata closure and transpiration displayed by drought-tolerant clones of *C. canephora*. The high up-regulation of genes encoding for dehydrins, detoxifying enzymes in drought-tolerant clones of *C. canephora* also suggests a strong induction of antioxidant and osmoprotection systems in these clones. On the other hand, the over-expression in the plagiotropic meristems of drought-tolerant cultivar IAPAR59 of *C. arabica* grown under NI of genes coding for proteins involved for example in the SAM (S-adenosyl-methionine) pathway and the wax biosynthesis (*i.e.* lipid transfer proteins) also suggested their involvement in the genetic determinism of drought tolerance in coffee. Interestingly, our work also led to the identification of several “unknown” (orphan) genes highly over-expressed mainly in drought-tolerant plants of both *C. canephora* and *C. arabica*. All these RNAseq data are now being analyzed with genomic sequences of drought-susceptible (clone 22) or tolerant (clone 14) of *C. canephora* for example to see if the differential expression profiles that were observed could be explained by the presence of nucleic polymorphisms (SNPs and/or Indels) in promoter regions of corresponding genes.

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