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The First Step of ABA Perception and Signal Transduction in Coffee: Evolutionary and Expression of PYR/PYL/RCARs, PP2Cs and SnRK2s Genes In *C. canephora* under Drought.

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Abscisic acid (ABA) pathway is aphytohormoneuniversally conserved in land plants which coordinates several aspects of the plant response to water deficit such as root architecture, seed dormancy and regulation of stomatal closure. A mechanism of ABA signal transduction has been proposed, evolving intracellular ABA receptors (PYR/PYL/RCARs) interacting with PP2Cs phosphatases and SnRK2 protein kinases regulating this tripartite protein system.

Rationale

The goal of this study was to identify and characterizefor the first time theorthologs genes of this tripartite system in*Coffea canephora*.

Methods

For this purpose, protein sequences from *Arabidopsis*, citrus, rice, grape, tomato and potatowere chosen as query to search orthologous genes in the Coffee Genome Hub (http://coffee-genome.org/). Differential expression in tissues as leaves, seeds, roots and floral organs was checked through *in silico* analyses.*In vivo* gene expression analyses were also performed by RT-qPCR in leaves and rootsofdrought-tolerant(D^T 14, 73 and 120) anddrought-susceptible (D^S 22) *C. canephora*Coniloncclones submitted (or not) to drought.

Results

This approach allowed the identification and characterization of 17 candidate genes (9 PYL/RCARs, 6 PP2Cs and 2 SnRK2s) in *C. canephora* genome. The protein motifs identified in predict coffee sequences enabled characterize these genes as family's members of PYL/RCARsreceptors,PP2Csphosphatases or SnRK2kinasesof the ABA response pathway. These families were functionally annotated in the *C. canephora* genome. *In vivo* analyses revealed that eight genes are up-regulated under drought conditions in both leaves and roots tissues. Among them, three genes coding phosphatases were expressed in all (D^T and D^S) clones therefore suggesting that they were activated as a general response to cope with drought stress. However, two other phosphatase coding genes were up-regulated only in the D^T clones, suggesting that they constituted key-genes for drought tolerance in these clones. The D^T clones also showed differential gene expression profiles for five other genes therefore reinforcing the idea that multiple biological mechanisms are involved drought tolerance in *C. canephora*.

Conclusions & Perspectives:

All these evidences will help us to identify the genetic determinism of drought tolerance through ABA pathway essential to obtain molecular markers that could be used in coffee breeding programs.