

**PB234****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 a phytohormone universally 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, involving 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 characterize for the first time the orthologous genes of this tripartite system in *Coffea canephora*.

**Methods**

For this purpose, protein sequences from *Arabidopsis*, citrus, rice, grape, tomato and potato were 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 roots of drought-tolerant (D<sup>T</sup> 14, 73 and 120) and drought-susceptible (D<sup>S</sup> 22) *C. canephora* clones 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 predicted coffee sequences enabled characterizing these genes as family members of PYL/RCAR receptors, PP2C phosphatases or SnRK2 kinases of 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<sup>T</sup> and D<sup>S</sup>) 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<sup>T</sup> clones, suggesting that they constituted key-genes for drought tolerance in these clones. The D<sup>T</sup> clones also showed differential gene expression profiles for five other genes therefore reinforcing the idea that multiple biological mechanisms are involved in 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.