# 56. The early steps of drought response mediated by ABA: evolutionary and molecular mechanism of *Coffea canephora* PYR/PYL/RCAR receptors

Michelle G. Cotta[1], Stéphanie Bocs[2], Érica C. S. Rêgo [3], Tatiana S. Costa[3], Sinara O. Aquino[3], Fernanda A. Carneiro[3], Dominique This[2], Pierre Marraccini[2], Alan C. Andrade[3]
*[1]University of Lavras, Lavras, 37200.000, Brazil /SupAgro, Montpellier, 34093, France; [2]CIRAD UMR AGAP, Montpellier, 34398, France; [3] Embrapa Genetic Resources and Biotechnology, Brasilia, Brazil*
Email: michellegcotta@gmail.com, alan.andrade@embrapa.br

The abscisic acid (ABA) is a vital phytohormone synthesized in roots and leaves, acting as central regulator involved in plant responses against abiotic stress, such as drought. It mediates stress-responsive gene expression by controlling stomatal closure, root growth modulation and seed dormancy, for example. Water deficit affects coffee plant development and production and consequently the biochemical composition of beans. It is also well known that genetic variability exists in the *Coffea* species for drought tolerance. Recently, novel intracellular ABA receptors (PYL/RCARs) involved in ABA sensing and signaling were identified. A mechanism of ABA transduction was proposed, involving PYR/PYL/RCARs ABA receptors interacting with PP2Cs phosphatases and SnRK2 protein kinases. The goal of this study was to identify and characterize orthologous genes of PYR/PYL/RCAR family in *C. canephora*. For this purpose, protein sequences from *Arabidopsis*, citrus, rice, grape and tomato species were chosen as query to search orthologous genes in coffee genome. This approach allowed the identification and characterization of 9 candidate genes for PYR/PYL/RCAR family in *C. canephora* genome. The protein domains identified in the predict coffee sequences enabled to characterize these genes as family's members of receptors of ABA response pathway. Phylogenetic analysis allowed classifying coffee polypeptides sequences in three subfamilies expected. These genes were functionally annotated in the Coffee Genome Hub (http://coffee-genome.org/). *In silico* analyses also revealed differential expression profiles of coffee PYR/PYL/RCAR genes in tissues such as leaves, seeds, and floral organs, although, the highest expression profiles were identified in roots. Regarding drought stress, *in silico* analyses from RNAseq data obtained from roots of tolerant (Cc14, Cc73, Cc120) and susceptible (Cc22) clones of *C. canephora* grown with (I) or without (NI) irrigation also confirmed differential expression profiles of PYR/PYL/RCAR genes, suggesting the existence of multiple biological mechanisms for drought tolerance in coffee. Among the 9 coffee candidate genes, only the PYR1, PYL6, PYL8-2, PYL8-8, PYL9 appeared expressed in roots. By qPCR analyses, we showed that the two copies of PYL8 gene present in *C. canephora* genome are co-expressed in root. Even members of the same subfamily, an in depth analysis of the coffee genome sequence revealed that these two genes were located in different chromosomes. As previously reported for several specific coffee gene families, such gene expansion could evidence a sequential tandem duplication followed by functional diversification. In order to understand the genetic determinism of drought tolerance in coffee, analyses are currently on going to identify the nucleic polymorphisms in promoter regions and coding sequences of PYR/PYL gene family.

Support: CAPES COFECUB, INCT-Café, CNPq and Consórcio Pesquisa Café