

Functional Characterization of Five Coffee Homeobox Genes Involved in Drought Stress Responses

Cruz, F.P.¹; Arongaus, A.B.¹; Romano, E.³; Almeida, J.³; Carvalho, A.³; Vaslin, M.F.S.² & Alves-Ferreira, M¹.

1- Genetic Department, Biology Institute, UFRJ, Rio de Janeiro; 2-Virology Department, Microbiology Institute, UFRJ; Rio de Janeiro 3- CENARGEN, EMBRAPA, Brasília.

Plant transcriptional factors containing homeodomain are frequently involved in developmental processes, and can be divided into eight sub-families according to sequence conservation and structure in and outside the homeodomain: Zinc-finger homeobox, Bell, Knox, Wuschel-like, HD-ZipI, HD-ZipII, HD-ZipIII, e HD-ZipIV. Recent studies have shown that homeobox genes are also involved in transcriptional regulation of stress response in plants. Expression analysis of *Arabidopsis thaliana* genes Athb5, -6, -7, -12 (HD-ZipI sub-family) and the sunflower orthologue Hahb-4, suggest that these genes may regulate growth in response to the abscisic acid (ABA) hormone in water deficit conditions and also enhance tolerance to drought.

In this work, we searched for potential homeobox genes in the "Genoma Café" Sequencing Project Consortium database, and used phylogenetic methods to classify those among the well-established groups in *Arabidopsis thaliana*. We were able to identify 29 high quality assemblies of homeobox genes after an extensive search on the "Genoma Café" database. To better understand homeobox gene expression at plant system level, and to identify genes differentially expressed and also tissue-specific, we conducted a digital expression analysis. By clustering genes according to their relative abundance in the various EST libraries, expression patterns of genes across various tissues were generated, and genes with similar patterns were grouped. Five contigs with expression patterns apparently influenced by water stress were chosen for further analysis: Contig6827 (homologue of HAT22/HD-ZipII of *A. thaliana*), Contig11116 (Athb12/HD-ZipI), Contig11933 (Athb1/HD-ZipI), Contig12072 (Athb1/HD-ZipI), and Contig14161 (BELL1). Expression levels of these five homeobox genes were analyzed by real-time PCR, in coffee plants submitted to 2, 7, and 10 days of drought. Preliminary results were in agreement with the digital northern data, showing that all coffee homeobox genes have their expression modulated under water deficit conditions.

The data supported by the "Genoma Café" project can be very helpful in developing strategies for the biotechnological improvement of coffee. Understanding the molecular mechanisms underlying stress tolerance mediate by homeoboxes genes can provide new ways for the improvement of drought tolerance in coffee.

M. Alves-Ferreira is recipient of research fellowship from CNPq (307219/20046).
Financial support: CBAB (CNPq)