Transcriptomic analysis in banana during an early drought stress

Cenci A.1, Zorrilla-Fontanesi J.2, Kissel E.2, Hueber Y.1, Dubois E.3, Parrinello H.1, Swennen R.1,2,4, Roux N.1, Rouard M.1, Carpentier S.2

Introduction

Bananas (Musa spp.) are a major staple food crop for hundreds of millions of people in developing countries. Banana needs high amounts of water which is one of the most limiting abiotic stress factors in production. Climatic changes as well as expansion of banana cultivation in less humid areas drive the search for a better understanding of drought tolerance at the molecular and physiological levels. Different degrees of drought tolerance have been observed in different cultivars (Vanhove et al. 2012).

Most cultivated banana varieties are triploids with an AAA, AAB, or ABB genome constitution, where A and B genomes are contributed by *Musa acuminata* and *M. balbisiana*, respectively, both sequenced (D’Hont et al. 2012; Davey et al. 2013).

Three rounds of Whole Genome Duplication (WGD) have been inferred in its evolution (D’Hont et al. 2012); being the last two WGDs relatively recent, the fragmentation process is still in progress and several genes are present in multiple copies (paralogs).

Material and Methods

To explore the transcriptome global response to drought stress in banana and detect cultivar specific responses to counteract low water availability, three cultivars (one allo-triploid (Cachaco, ABB) and two auto-triploid (Grande Naine and Mbwazirume, AAA)) were sampled for RNAseq analyses under different water supply conditions (5% (W/W) PEG8000 was added to the in vitro medium of the stressed plants, equivalent to an osmotic pressure of 0.5 Bars).

Impact of the B genome

Several banana and plantain cultivars are allo-triploid with A and B genomes. Since the B genome is considered to provide higher drought tolerance to the hybrids (Simmonds 1966), the comparison between A and B derived homeoalleles is particularly interesting. The cultivar Cachaco has an ABB genome constitution and the expression pattern of A and B homeoalleles can be inferred with the help of the Musa A and B whole genome sequences.

Silencing of A homeoalleles or additive expression could be observed (Figure 4). The impact of the B genome in the physiological responses to the osmotic stress might be explained by the expression pattern of B homeoalleles.

Glycolysis-fermentation pathway

Genes coding for several enzymes involved in the energy production were up-regulated in stressed banana roots. All the *Musa* genes orthologous to the *Arabidopsis thaliana* genes coding for enzymes in the KEGG Glycolysis-fermentation pathway were identified and their expression checked in the roots of all three cultivars. Most of the genes up-regulated are involved in the transformation of Glucose into Pyruvate (Figure 3).

Musa paralogs may hamper result interpretation

Analysis of Differentially Expressed Genes (DEGs) was conducted by taking into account the paleo-polyploid nature of the *Musa* genome that often implies the presence of two or more paralogous genes with different patterns of gene expression. For each DEG, a genome wide analysis was performed in order to detect all its paralogs (i.e. *Musa* genes originated by duplication after the separation of Arabidopsis (dictot) and *Musa* lineages).

In several cases very different expression patterns between paralogs were observed, suggesting sub-functionalization of gene copies (an example in figure 2).

**References**

[2] Laboratory of Tropical Crop Improvement, Division of Crop Biotechnics, RU Leuven, B-3001 Leuven, Belgium
[3] AGRO-Montpellier GenomiX, Montpellier Genomics and Bioinformatics Facility, Montpellier F-34096, France
[4] ITA, P.O. Box 10, Dullut, Arusha, Tanzania