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Study of genes related to the flowering process in coffee: toward genetic improvement in a climate change scenario

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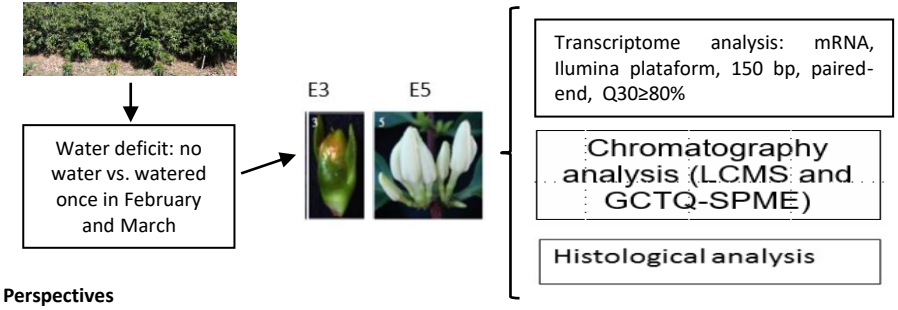
Introduction

In coffee, the effect of climate change has been observed for several years in the different producing regions. The increase in temperature and changes in rainfall behavior have affected coffee phenology in important processes such as flowering and fruit development, causing losses in productivity as well in coffee quality in many coffee regions. Coffee plants also have the important problem of floral asynchrony that causes uneven ripening of fruits and, therefore, affects product quality. Although the molecular mechanisms involved in the flowering process are well characterized in herbaceous species, from the molecular point of view, the mechanism involved in the perception of these stimuli and the activation of reproductive development in *C arabica* L is little known In this sense, analyzing the molecular process of flowering of coffee would provide useful information for agricultural practices, such as synchronization in flowering and, consequently, the ripening of the fruit with an improvement in both coffee quality and production.

Materials/Methods



Results/Discussion

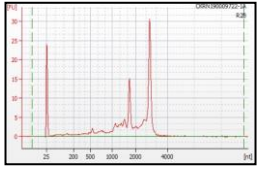


Figure 1. RNA quality

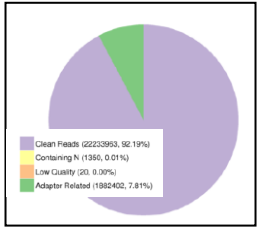


Figure 2. Composition of raw reads

Plant material (coffee leaves and flowers) has been collected. It was possible to establish an efficient protocol for RNA extraction from coffee leaves and flowers. This protocol allows to obtain RNA in a high concentration and of very good quality (according to the estimates of the A260 / 280 and RIN values) (Fig. 1). The mRNA was sequenced and there are approximately 128 GB of raw reads and 123 GB of clean reads . In total 823 335 992 clean reads were obtained. An example of the sequencing data filtration is shown in Figure 2.

Preliminary GCTQ/SPME analysis revealed 28 peaks and some compounds, such hexanal and caffeine, were identified (Fig. 3).

Figure 3 . Chromatography analysis representation of a coffee flower bud

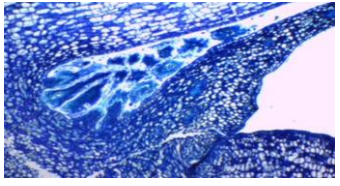


Figure 4. Histological representation of a coffee flower bud

Histological analysis showed the development of vegetative axillary buds into floral buds under drought conditions (Fig. 4)

Perspectives

We are going to analyse our RNA-seq data using available software (CLC Genomics Workbench software, Trinity, Geneious). Identification of genes differentially expressed in leaves and flowers under water deficit condition (edgeR, DEseq2, or other) will be performed. Digital gene expression profile of some genes are going to be validate using RT-qPCR technique.

References:

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Yuyama PM, Reis JO, Ivamoto ST, Domingues D, Carazzolle M, Guimarães Pereira GA, Pierre C, Leroy T, Pereira LFP (2016) Transcriptome analysis in *Coffea eugenioides*, an Arabica coffee ancestor, reveals differentially expressed genes in leaves and fruits. Mol Genet Genomics 291:323–336