

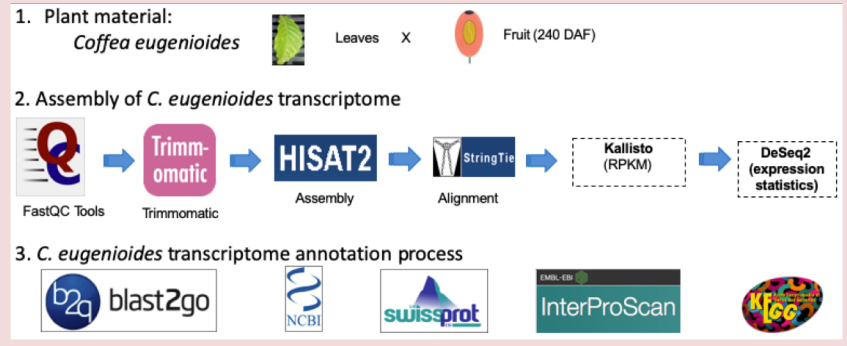
# Transcriptome of *C. eugenoides* reveals diterpene related genes differentially expressed in leaves and fruits

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## Introduction

Coffee is one of the main agricultural commodities in tropical countries. *Coffea arabica* represent 70% of coffee worldwide production and was originated from a recent and natural hybridization between *C. canephora* and *C. eugenoides*. The majority of coffee genetic studies have been focusing on the specie with greater economic importance, the allotetraploid *C. arabica* and its diploid ancestral *C. canephora*. However, *C. eugenoides* is still poorly studied. One way to improve our knowledge on *C. eugenoides* is to perform RNA-seq analysis. In this study we re-analyzed a previous RNA-seq data using a reference genome to improve transcriptome assembly and analysis.

## Materials/Methods



## Conclusion/Perspectives

Our results increase our knowledge about the genetic basis of one *C. arabica* ancestor, *C. eugenoides*, and can help future coffee breeding program to develop new cultivars with desirable diterpene content.

## Results/Discussion

Our transcriptome assembly using a reference genome resulted in a total of 16,743 transcripts (Tab. 1). More than 56 thousand GO terms were annotated in our transcriptome (Fig. 1). We observed 416 and 507 genes up-regulated in leaves and fruits, respectively. Six genes possibly related to diterpene biosynthesis had their expression profile validated by RT-qPCR analysis and all genes showed high transcriptional activity in the fruit compared to leaves (Fig. 2).

Table 1. Summary of *C. eugenoides* transcriptome assembly

Assembly information	Data
High quality reads	8,275,660
Reads aligned 1 time	6,781,345
Reads not aligned	1,494,315
Number of transcripts	16,743
Transcripts average size	1,284 bp
Size of the shortest transcript	200 bp
Size of the longest transcript	5,884 bp

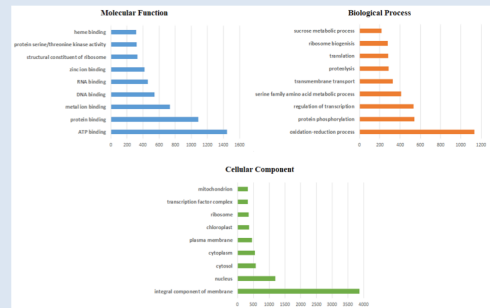


Figure 1: The most representative GO terms identified in *C. eugenoides* transcriptome

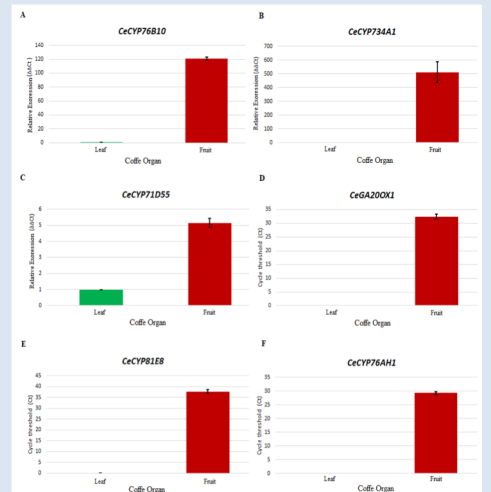


Figure 2: RT-qPCR analysis of *C. eugenoides* diterpene-related candidate genes.

## References:

1. Denoeud F., et al. 2014. *Science*. DOI: 10.1126/science.1255274.
2. Yuyama P. M. et al. 2016. *Molecular Genetics and Genomics*. DOI: 10.1007/s00438-015-1111-x.