Comparison of the Expression profile between embryogenic and non-embryogenic *Coffea arabica L.* calli through RNA-Seq data analyses using combination of DE algorithms

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Coffea arabica L. is the main source of one of the most important beverages worldwide; more than 2 billion cups of coffee are consumed every day. Coffee trees are grown on more than 10 million hectares of tropical land, and Brazil is the world leader producer and exporter. Traditionally, coffee seedlings are produced from seeds, and undesirable traits can arise during the process of seed formation due to genetic recombination. On the other hand, the use of seedlings regenerated from somatic embryogenesis (SE) can be a more effective method for growing coffee once every new plant generated will be essentially a clone of the mother plant. Thus, in this work, we sequenced and compared the transcriptomic profiles of embryogenic and non-embryogenic calli from Coffea arabica. After a quality control, approximately 92% of the remaining 59,405,225 Illumina single-end reads were successfully mapped on the Coffea canephora genome using STAR aligner version 2.4.2a. Then, Cufflinks package was used to assemble the transcriptome and to identify new putative genes and isoforms. Differential expression analyses were carried out using a combination of the programs cuffDiff, edgeR and DESeq2. Those genes that showed at least a 2-fold expression change between the conditions, false discovery rate (FDR) bellow 5% of significance and meet the previous two conditions in at least two of the three programs were considered differentially expressed. We found 3,882 novel loci in the assembled transcriptome and 6,986 differentially expressed genes (DEG) between the two calli types, being 2,170 of those genes transcriptionally more active in embryogenic calli. The investigation and experimental validation of the role of those DEG will be the foundation for future research on the molecular control of SE in Coffea arabica, guiding us toward the understanding of the mechanisms involved in the transition between non-embryogenic calli to embryogenic ones.

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