

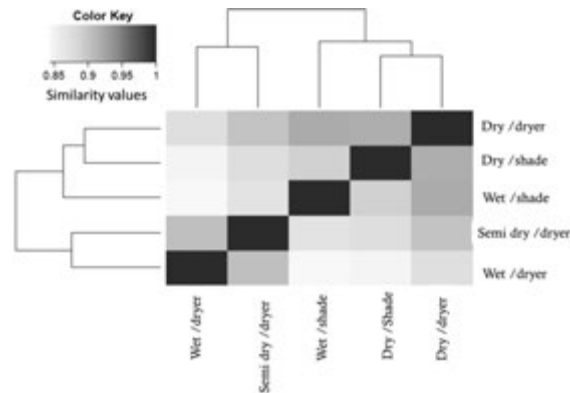
**PB241****DIFFERENTIAL EXPRESSION IN *Coffea arabica*  
SEEDS DURING THE PROCESSING AND  
DRYING**

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Coffee is one of the most important agricultural products in the world market. The mode of coffee processing, whether wet or dry, determines the characteristic flavor and also the seed quality. In recent years, high-throughput RNA-sequencing (RNA-Seq) has emerged as a powerful and cost-efficient tool for transcriptome analysis. RNA-Seq has proven useful for the detection of gene expression, the discovery of novel transcripts, and the identification of differentially expressed genes. In this study, we applied Illumina sequencing technology and the Heat Map

analysis for differential expression. Coffee seeds were processed by three different methods, dry, semi-dry or wet, and were dried under shade or dryer conditions. The samples were used to prepare a cDNA library for sequence analysis via Illumina (HiSeq 2000). After removal of low-quality reads, a total of 125,829,579 high-quality 50 bp reads were identified. As can be seen in the Heat Map graphic representation, semi-dry/dryer methods are separated from wet/dryer methods, with high differential expression. This representation indicates they have much differential expression in different metabolic pathways. However, semi-dry/shade and wet/shade have similar differential expression. These results provide information on how the processing and drying methods influences gene expression, and suggest that that more detailed analyzes in metabolic pathway studies are required.



*Heat Map of differential expression Coffea arabica seeds during the processing and drying.*