Targeted Transcriptome Profiling during Seed Development in *C. arabica* cv. Laurina

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SUMMARY

Due to its economic importance, *Coffea* is receiving increasing attention with respect to genomic research. As a first approach on coffee seed development, we carried out a preliminary targeted transcriptomic study using carefully selected cDNAs. On the basis of EST libraries generated from mRNAs of *C. canephora* and *C. arabica* fruits and leaves we focused on cDNAs encoding enzymes potentially involved in seed development and/or in biosynthesis of precursors playing a role in beverage quality. We selected 266 candidate genes that were PCR-amplified and spotted onto a nylon membrane. So obtained cDNA arrays were used to screen the transcriptional status of the endosperm of *C. arabica* cv. Laurina grown in La Réunion Island, at seven different development stages (sampled between 60 and 250 days after flowering). Clustering analysis was performed using gene expression data and was used to highlight observed phenological changes. Analysis of variance sorted seventy five cDNAs differentially expressed during seed development. We classified these genes into five distinct groups of expression pattern through multivariate analysis.