



CoffeebEST: an integrated resource for *Coffea* spp expressed sequence tags

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ABSTRACT. Coffee is one of the most important commodities in the world, and its production relies mainly on two species, *Coffea arabica* and *Coffea canephora*. Although there are diverse transcriptome datasets available for coffee trees, few research groups have exploited the potential knowledge contained in these data, especially with respect to fruit and seed development. Here, we present a comparative analysis of the transcriptomes of *Coffea arabica* and *Coffea canephora* with a focus on fruit development using publicly available expressed sequence tags (ESTs). Most of the fruit and seed EST data has been obtained from *C. canephora*. Therefore, we performed a fruit EST analysis of the 5 developmental stages of this species (18, 22, 30, 42, and 46 weeks after flowering) comprising 29,009 sequences. We compared *C. canephora* fruit ESTs to reference unigenes of *C. canephora* (7710 contigs and 8955 singletons) and *C. arabica* (15,656 contigs and 16,351 singletons). Additional analyses included functional annotation based on Gene Ontology, as well as an annotation using PlantCyc, a curated plant protein database. The Coffee Bean EST (CoffeebEST) is a public database available at <http://bioinfo-02.cp.utfpr.edu.br/>. This database

represents an additional resource for the coffee scientific community, offering a user-friendly collection of information for non-specialists in coffee molecular biology to support experimental research on comparative and functional genomics.

Key words: Fruit; *Coffea arabica*; *Coffea canephora*; Bioinformatics; Transcriptome; Expressed sequence tag