Identification and Partial Characterization of Sepallata Genes in Coffea arabica L.

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SUMMARY

The SEPALATA genes play an important role in the flowering process being responsible for the determination of the four floral whorls. Among the factors that affect coffee quality, the sequential flowering found in this species plays a central role, leads to an asynchronous ripening process and consequently a lower cup quality. In order to get a better understanding coffee (Coffea Arabica) flowering process, this study aimed to identify and characterize the putative coffee SEPALLATA (SEP) genes present in the coffee expressed sequence tag (CAFEST) database. The phylogeny of the sequences found was assessed by phylogenetic trees and their expression profile was assessed by in silico Northern. The putative coffee SEP genes were cloned, sequenced and then compared to the sequences obtained in the CAFEST. Three putative SEP genes (C1, C8, C14) were identified, and the in silico expression profile showed that they’re expressed in different flower development stages and also during fruit development, which is in accordance with the function displayed by SEP genes in reproductive tissues. The comparison of the sequenced sequences with those found in CAFEST, allowed the observation of a great similarity between these sequences and confirmed the importance of previous bioinformatic studies in molecular analysis.