

Title Differentially expressed cDNAs at the early stage of banana ripening identified by suppression subtractive hybridization and cDNA microarray

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Abstract

The banana (*Musa acuminata* L. AAA group) fruit undergoes a postharvest ripening process, which plays an important role in improving the quality and extending the shelf life of bananas. To manipulate postharvest banana ripening, a better understanding of the mechanism of postharvest ripening is necessary. The isolation of mRNA transcripts encoding proteins associated with the ripening process is a powerful tool for this purpose. To isolate differentially expressed genes at the early stage of postharvest banana ripening, a forward suppression subtractive hybridization (SSH) cDNA library was constructed. SSH was performed with cDNA from banana fruit on the day of harvest as the “driver” and cDNA from banana fruit 2 days postharvest (DPH) as the “tester.” A total of 289 clones in the SSH library were sequenced. BLASTX results revealed that 191 cDNAs had significant sequence homologies with known sequences in the NCBI database. Of the 191 cDNAs, 138 were singletons, and 53 belonged to divergent clusters containing 2–8 sequences. The identified cDNAs encoded proteins involved in cellular processes such as: metabolism; protein destination and storage; protein synthesis; signal transduction; transport and intracellular traffic; cell structure, growth, and division; transcription and post-transcription; and disease and defense. To characterize differentially expressed cDNAs in the SSH library, cDNA microarray analysis was conducted. A total of 26 cDNAs in the 2-DPH banana fruit were found to be up-regulated and these results were confirmed by using reverse transcriptase-polymerase chain reaction (RT-PCR). The information generated in this study provides new clues to aid in the understanding of banana ripening.