

Title Identification of differentially expressed genes in postharvest ripening banana by suppression subtract hybridization 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. The identified cDNAs 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). To establish the connection between differentially expressed cDNAs in the SSH library and the onset and peak of ripening ethylene biosynthesis, we conducted cDNA microarray analysis on 10 and 14 DPH banana fruit, which was characterized as the time of onset and peak of ethylene biosynthesis in the postharvest banana. A total of 16 cDNAs were found to be upregulated and six cDNAs were found to be downregulated at 10 DPH and 23 cDNAs were found to be upregulated and one cDNA was found to be downregulated. These results were confirmed by using RT-PCR. The cDNAs identified are involved in signal transduction, amino acid metabolism, lipid metabolism, proteolysis, citrate biosynthesis and metabolism, and the uptake and transport of potassium.