Title Proteomic analysis of banana fruit reveals proteins that are differentially accumulated during ripening

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Abstract

Bananas (*Musa* spp.) are highly perishable fruit of notable economic and nutritional relevance. Because the identification of proteins involved in metabolic pathways could help to extend green-life and improve the quality of the fruit, this study aimed to compare the proteins of banana pulp at the pre-climacteric and climacteric stages. The use of two-dimensional fluorescence difference gel electrophoresis (2D-DIGE) revealed 50 differentially expressed proteins, and comparing those proteins to the Mass Spectrometry Protein Sequence Database (MSDB) identified 26 known proteins. Chitinases were the most abundant types of proteins in unripe bananas, and two isoforms in the ripe fruit have been implicated in the stress/defense response. In this regard, three heat shock proteins and isoflavone reductase were also abundant at the climacteric stage. Concerning fruit quality, pectate lyase, malate dehydrogenase, and starch phosphorylase accumulated during ripening. In addition to the ethylene formation enzyme amino cyclo carboxylic acid oxidase, the accumulation of S-adenosyl-l-homocysteine hydrolase was needed because of the increased ethylene synthesis and DNA methylation that occurred in ripening bananas. Differential analysis provided information on the ripening-associated changes that occurred in proteins involved in banana flavor, texture, defense, synthesis of ethylene, regulation of expression, and protein folding, and this analysis validated previous data on the transcripts during ripening. In this regard, the differential proteomics of fruit pulp enlarged our understanding of the process of banana ripening.