

Title Molecular analysis of differentially expressed genes during postharvest deterioration in cassava (*Manihot esculenta* Crantz) tuberous roots

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Abstract

One of the major problems for cassava is the rapid deterioration after harvesting cassava tuberous roots, which limits the possibilities for production and distribution of cassava in the world. Postharvest deterioration is an inherent problem for cassava since wounding and mechanical damage of the tuberous roots cannot be prevented during harvesting, which includes postharvest physiological deterioration (PPD) and secondary deterioration. To date, the molecular mechanism and biochemical pathways of PPD are poorly understood. The aim of this project, which is focusing on the early stages (first 72 hrs), is to gain molecular insight and identify important metabolic pathways during the process of PPD in cassava tuberous roots. Finally by reverse genetic approaches to delay or even prevent the process of PPD in cassava tuberous roots. By using a new RNA fingerprinting method, called cDNA-AFLP, we have screened more than 6,000 TDFs (Transcript Derived Fragments) via up to 100 primer combinations during the early process of PPD in cassava. Only 10% of the TDFs are developmentally regulated, while the other 90% are expressed throughout the process of PPD in cassava tuberous roots. Furthermore, in order to set up a functional catalogue of differentially expressed genes during PPD, 70 TDFs were selected and isolated based on their expression patterns, which were either up-regulated, down-regulated or transiently induced. Around 40 of these TDFs were found to be similar with known genes in databases. The other 30 TDFs were present mostly genes without known function. Through data analysis, it is shown that important biochemical and physiological processes, such as notably oxygen stress, carbohydrate metabolism, protein metabolism and phenolic compounds synthesis, are involved in PPD in cassava tuberous roots.