

ESTs Microarray Gene Expression Analysis of Postharvest Physiological Deterioration in *Manihot esculenta* roots

Upon harvesting, the starchy roots of *Manihot esculenta* Crantz suffer a rapid deterioration that renders them unpalatable within 24–72 hours. This deterioration is a purely physiological process, though microbial deterioration can set in subsequently, and is known as post-harvest physiological deterioration (PPD). The objective of this project is to identify the full set of major genes involved in PPD by exploiting the powerful high-throughput analysis of cDNA microarrays. Over 11,000 cDNA clones from cassava PPD-related libraries were spotted onto microarray slides and hybridised with cassava roots mRNA samples ranging over a deterioration time course, in order to identify clones corresponding to genes that were regulated during PPD. Strict selection criteria enabled the selection of 114 up- and 70 down-regulated clones. These have all been partially sequenced and compared to sequence databases in order to establish their putative identity. These clones include genes with roles in: cell wall strengthening; glucosinolate biosynthesis; programmed cell death; control of transcription and translation; oxidative stress; signal transduction or perception; ion, water and metabolite transport; and of unknown function. This will not only help understand the process, but also provide the tools (clones) that could serve as components of gene constructs to modulate PPD.

Keywords: *Manihot esculenta*, post-harvest physiological deterioration, microarrays, gene expression.

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