Proceedings of the 13th ISTRC Symposium, 2007
pp. 45 – 50

# Towards identifying the full set of genes involved in postharvest physiological deterioration in cassava

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**Abstract.** Cassava is the world's sixth most important crop in terms of production and is a vital staple food to over 500 million in the humid tropics. Unfortunately, it suffers from a rapid post-harvest physiological deterioration (PPD) that can render the roots uneatable and unmarketable within 24-72 hours of harvest. Increased urbanization has lengthened the distance and time between farmers' fields and markets and processors, thereby incurring losses, wastage and discounting of poor quality cassava. PPD is a major constraint to the development of cassava for farmers, processors and consumers alike, and the successful application of strategic research is necessary to solve this problem. With a view to fully understanding PPD and to ultimately producing the tools to control this problem, we have identified some of the key genes that play major roles during PPD and mapped these on the genetic map of cassava. Recently, we have embarked on a major programme employing massively parallel methods of gene analysis (cDNA microarrays) to identify the full set of genes involved in PPD. Screening 11,136 cDNA clones from early and late PPDrelated libraries using a series of character probes from a range of time points during the time course of deterioration has led to the identification of 114 clones whose expression is increased and 70 clones whose expression is decreased at least two-fold during PPD.