

CLONING AND CHARACTERIZATION OF RIPENING-RELATED cDNAs FROM BANANA FRUIT: FUNCTIONAL GENOMIC TOOLS FOR MOLECULAR-MECHANISM STUDIES OF FRUIT-QUALITY ELABORATION

D. MBEGUIE-A-MBEGUIE^{1*}, O. HUBERT¹, M. CHILLET¹, B. FILS-LYCAON², R.-M. GOMEZ², D. RINALDO², F.-C. BAURENS³.

¹CIRAD-FLHOR / UMR 1270 QUALITROP, Station de Neufchâteau, Sainte-Marie, 97130 Capesterre-Belle-Eau, Guadeloupe, French West Indies, mbeguie@cirad.fr, olivier.hubert@cirad.fr, chillet@cirad.fr

² UMR 1270 QUALITROP Domaine de Duclos, 97170 Petit-Bourg, Guadeloupe, French West Indies, Bernard.Fils-Lycaon@antilles.inra.fr, Dominique.Rinaldo@antilles.inra.fr, Rose-Marie.Gomez@antilles.inra.fr

³ CIRAD-AMIS /UMR PIA 1096 TA40/03 Avenue Agropolis 34098 Montpellier cedex5, France baurens@cirad.fr

*Corresponding Author, mbeguie@cirad.fr

It is now assumed that the quality of fruit is a complex trait in which a lot of mechanisms are involved, some of them being antagonistic. All of these mechanisms are the results the coercive action of differentially regulated genes. Understanding at molecular level of the mechanisms that control the target quality trait is an essential work beforehand to any plan of improvement of fruit quality trait using plant genetic strategies such as candidate-gene approach and or marker-assisted selection. Presently we investigate at molecular level the ethylene responsiveness, and sugar and phenylpropanoid metabolisms, three ripening aspects involved in functional, nutritional and organoleptic qualities of banana fruit. As a first part of this project, we report here the cloning and sequencing of genes that are differentially expressed during fruit ripening, as tools for functional genomic studies and putative molecular marker developments. Different molecular biology approaches have been used to isolate ripening these ripening related-genes. They include cDNA amplification (RT- and RACE-PCR) and, construction of complete and subtractive suppressive cDNA libraries (SSH). Sequencing and BLAST analysis of some of these isolated cDNA clones revealed that 205 of them presented a high homology with different genes in database. Many of the predicted proteins encoded by these genes are putatively involved in the regulation of gene expression, hormonal metabolism, hormonal-signal transduction, sugar metabolism and other ripening process. Among these 205 genes, 11 are still unclassified since presenting homology to unknown proteins of rice or *Arabidopsis*. Finally, thirteen additional clones were putatively novel, since they failed to match with database sequences. Expressions of a few of the matching clones have been followed in relation with ethylene responsiveness of fruit. Our results show that the expression of these genes is under ethylene and development (or both) control. These cDNA clones provide us with a basis for future work that will combine physiological, genomic and genetic approaches to identify key candidate-genes involved in the expression of banana quality trait.

Keywords: Banana, Ethylene, Fruit, Musa, Ripening, gene cloning