



W077

Evolution Of Gene Families Involved In Banana Fruit Development and Ripening

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Cyril Jourda , CIRAD, Montpellier, France

Didier Mbéguié-A-Mbéguié , CIRAD, Capesterre-Belle-Eau, Guadeloupe

Corinne DaSilva , Commissariat à l'Energie Atomique (CEA), Evry, France

Karine Labadie , CEA - Genoscope, France

Céline Cardi , CIRAD, Montpellier, France

Angelique D'Hont , CIRAD, Montpellier, France

Nabila Yahiaoui , CIRAD, Montpellier, France

A reference genome sequence of banana was recently obtained from a *Musa acuminata* doubled-haploid accession (DH-Pahang, 523 Mb) and organized into eleven pseudomolecules. This genome opens brand new perspectives for the identification of genes underlying key physiological processes and agricultural traits in this economically important species.

To identify genes involved in banana fruit development and ripening, we used a whole genome-scale approach combining phylogenomic analyses and gene expression profiling. Global analysis of gene expression in banana fruits in response to ethylenic treatment was performed using RNA-seq. In parallel, gene families involved in core ethylene biosynthesis/signaling pathways and starch/sucrose metabolism were identified in the *Musa* genome using comparative genomics and phylogenomic analyses with eleven plant species. Our results showed a progressive global reprogramming of banana fruits during ripening characterized by an inhibition of the downstream ethylene signaling pathway. In addition, we identified expansions of gene families encoding transcriptional regulation elements of the ethylene signaling pathway in *Musa*. These expansions are currently analyzed in relation to *Musa* whole genome duplications. Finally, the combined structural and gene expression analyses led to the identification of candidate genes and gene family members involved in banana fruit ripening.