

Genome-wide Identification and Analysis of *Late Embryogenesis Abundant (LEA) Genes in Musa acuminata*

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Abstract

Key Message

Eighty four *MaLEA* genes were found coding for eighty five proteins, most of which are small and hydrophilic, and show ubiquitous distribution in the cell. *MaLEA* genes, having few introns, are distributed on all chromosomes, associated with abiotic stress-related cis-acting elements, and are differentially expressed under abiotic stress conditions.

Musa acuminata (Banana) is a major fruit crop grown worldwide. *M. acuminata* production is often threatened by abiotic environmental stresses. Late Embryogenesis Abundant (LEA) proteins play significant roles in plant growth, development, and responses to stresses. However, no studies have been carried out to elucidate the number, location, structure, molecular phylogenetics, and expression of *LEA* genes in *M. acuminata*. In this study, a genomic census of *LEA* genes in *M. acuminata* was carried out. A total of 84 *LEA* genes were identified and grouped in to eight sub-families. The *LEA_2* subfamily was the largest and most diverse, including 57 members. Repeated motifs corresponding to *LEA* groups were present in the *M. acuminata* *LEA* proteins. The majority of *MaLEA* proteins was hydrophilic, and contained amino acids such as alanine, glycine and serine in abundance. Various functions were predicted for these proteins including response to stress, binding, structural components, and embryo development. The majority of *MaLEA* proteins are associated with the cytoplasm and chloroplast, while others are present in different subcellular compartments. *MaLEAs* have few introns (< 3) and are distributed unevenly across all chromosomes indicating that a significant portion of these genes originated by tandem or segmental duplications. The upstream sequences of these genes contain cis-acting elements associated with stress responses. The large number and diversity of *LEA* genes found in banana indicates that they are important in abiotic stress tolerance. This investigation provides valuable insights for future functional studies of *MaLEA* genes which may be useful for developing drought-tolerant banana varieties.