GENOME-WIDE IDENTIFICATION OF THE CIS-ELEMENTS IN PROMOTER REGION OF HEVEA BRASILIENSIS GENOME

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Abstract

Draft genome sequences of Hevea brasiliensis cultivar Reyan7-33-97 and RRIM 600 have been reported. Although the assembly only spans partial Hevea genome, over ninety percent known expressed sequence tags (ESTs) and transcriptome sequence reads could be aligned, indicating that the draft assembly represents a large proportion of the gene space. To better explore the Hevea genome, the Bioinformation of Hevea brasiliensis (BHB) website was developed (www.H-brasiliensis.com), in which a nucleotide sequence could be online blasted against either Reyan7-33-97 or RRIM 600 genome, the matched gene sequence would be indicated, including exon, intron and corresponding promoter sequence. Furthermore, an HCES (Hevea Cis-Elements Scanning) program was developed. JA and/or ET-responsive cis-elements were screened in genome wide using HCES, 18,073 potential JA and ET-responsive genes were identified. Clusters of Orthologous Groups (COG) classification reveal that biggest cluster is involved in “Signal transduction mechanisms”. To reveal the regulation of rubber biosynthesis, cis-elements in promoters of rubber biosynthesis related genes were analyzed. Statistical results revealed that Dof, MYB, MYC and WRKY were potentially the main transcription factor families regulating latex biosynthesis in H. brasiliensis. This work proves that global analysis of gene expression could be addressed by genome-wide screening of cis-elements using bioinformatics tools.

Keywords: Hevea brasiliensis, ethylene, jasmonic acid, cis-element, HCES, rubber, Signal transduction mechanisms, genome-wide screening, transcriptome, EST, transcription factor, latex, gene