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Analyses of the Pineapple Watercore Transcriptome

Manuela Sarmento*

Department of New Sciences and Technologies, University of Tehran, Tehran, Iran

Abstract

Watercore is a pineapple physiological disorder that manifests as water-soaked tissue and fluid deposition in intercellular spaces. The pineapple industry in China is being hampered by this disorder, which has a negative impact on the quality of the fruit and shortens its shelf life. As a result, growers are losing a lot of money and the pineapple industry is being held back. Water core's molecular mechanism, on the other hand, is still a mystery. De novo RNA-sequence technology was used for the first time to conduct transcriptome analyses of water cored and normal pineapple fruits for the purpose of elucidating the molecular mechanism of pineapple water core. In the transcriptomes of normal and mildly water cored fruits, respectively, high-quality reads of 46.66 M were found. After filtering the initial data, clean reads of 45.50 and 42.79 M were obtained. In subsequent pineapple water core research, these genes will be useful resources.

Keywords: RNA-sequence • molecular mechanism • Watercore

Introduction

There were significant differences between normal and water cored fruits in fifty genes related to phenylpropanoid biosynthesis, glucose metabolism, calcium transport, cell wall metabolism and cell wall metabolism. AcPME, AcBGLU43, Ac4CL5, AcPER1 and AcPOD were all up regulated by 7–21 times in water cored fruit, while AcSUS7 was down regulated by 16.61 times and other differential genes were either up regulated or down regulated by more than 2 times. Screening resulted in the discovery of 38 transcription factors with differential expression. WRKY was the most prevalent transcription factor, followed by MYB. The procurement of these qualities is significant for the primary comprehension of the atomic system of this physiological problem. An agilent bioanalyzer was utilized for the assessment of the RNA's integrity. Tests with RNA honesty numbers were exposed to resulting examination. In accordance with the instructions provided by the manufacturer, libraries were constructed with a truSeq Stranded mRNA Sample Prep Kit. The constructed library was high-throughput sequenced with an Illumina Hiseq X Ten system to generate 125 or 150 bp double-ended data. OE Biotech completed the sequencing work.

Description

An enormous number of Crude information were sequenced and clean peruses were gotten by eliminating the joint succession, groundwork grouping and bad quality peruses in the crude information. Base mass value Q30 and GC content were used to determine the quality of the data. For the clean reads and alignment of the pineapple genome sequence, we used hisat2, its location in the reference genome or genetic data and the particular sequence characteristics of the sequencing samples. The parts per kilobase of exon model per million planned peruses esteem was utilized to quantify the overflow worth of quality articulation and the impact of quality length and sequencing volume contrasts on qualityarticulation was dispensed with. The calculated levels of gene expression could be directly used to compare the differences in gene expression between various samples. The p value and fold-change or fold-change was the screening criteria for differentially expressed genes. For the selected DEGs, the kyotoencyclopedia of genes and genomes pathway enrichment analysis and gene ontology gene function annotation were carried out. We selected 18 key DEGs related to phenylpropanoid biosynthesis and performed an expression analysis between CK and MS to confirm the repeatability and accuracy of the RNA-sequence analysis. Supplementary contains a list of the gene-specific primers used in the qRT-PCR analysis. Using a Light Cycler System and a fast start Essential DNA Green Master Kit, quantitative real-time PCR was carried out. Ac actin served as the standard gene. The method was used to look at the relative levels of expression.

Changes in monosaccharide content are depicted in Pineapple phenotype and physiological responses to water core.Compared to CK, MS contained more fructose and less sucrose and glucose. The items in sucrose and glucose in MS diminished by 30% and 15.87%.However, the fructose level did not differ significantly between CK and MS. Polysaccharides like pectin, cellulose and hemicellulose, along with a small amount of protein, make up the cell walls of higher plants. The items in complete gelatin, hemicellulose and cellulose in MS were 14.6%, 2.6% and 6.9% lower than those in CK, separately. The proportions of hemicellulose and cellulose in CK and MS were not significantly different. The findings demonstrated that the calcium content of MS was 16.38 percent lower than that of CK. The total phenolic content of MS was lower than that of CK, but the difference was not significant. Water cored and normal fruits express different TFs in different ways. At least seven similar protein genes have been found [1-5].

Conclusion

The regulation of secondary metabolite biosynthesis, participation in various stress responses and response to plant hormone responses are all important functions of transcription factor in plant growth and development. Motifs that can be used to predict water core symptoms before they appear could be found by identifying components affected by these genes. The event of pineapple water core is a mind boggling process including numerous qualities and different metabolic cycles. This study found that genes involved in phenylpropanoid biosynthesis, calcium transport, glucose metabolism, cell wall metabolism and incomplete cell wall structure were either increased or decreased, resulting in water core and accelerated cell wall degradation. The transcriptional level provides a reference for the molecular mechanism of pineapple water core and provides genetic resources for the study of water core's key functional genes.

***Address for Correspondence:** Manuela Sarmento, Department of New Sciences and Technologies, University of Tehran, Tehran, Iran, E-mail: sarmento@ut.ac.ir*

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Conflict of interest

No potential conflict of interest was reported by the authors.

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