

an Innovative Agricultural Biotechnology Approachesto Understanding Physiological Disorder in Mangosteen (*Garcinia Mangostana L.*)

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ABSTRACT

Mangosteen is one of the most important Indonesian fruits and horticultural crops in the tropical region because it has high economic value for export as well as contain of high anti-oxidants known as xanthone. However, the fruit quality is affecting the occurrence of most two physiological disorders, gamboge disorder and translucent flesh disorder. Recently, high-throughput sequencing technology such as RNA sequencing is an advance technique to study the transcriptome under various conditions and can generate valuable treatment strategies. In this study, we analyzed through bioinformatics method to predict molecular mechanism from the quantitative expression values of differentially expressed genes based on RNA-Seq transcriptome data of tissues in different types and conditions in mangosteen. We provided our perspective on future developments in plant gene regulatory network to support sustainable agriculture in horticultural crops.

Keywords: fruits, horticultural and developments in plant

A REVIEW

Two major physiological disorders in mangosteen such as translucent flesh disorder (TFD) and gamboge disorder (GD), respectively have affected to fruit quality. Only 25 % of fruit have desirable criteria for export quality from mangosteen production total (Mansyah et al. 2013). TFD and GD symptoms are caused by several factors, such as agro climate conditions, mineral deficiency, and mechanical damage (Jacob and Tindall, 1995). Translucent flesh disorder is changing white flesh to firm and crisp as well as to be like water soaking or translucent. Therefore, the gamboge disorder is broken yellow resin duct and flooding the resin into aril surface as well as the white flesh tastes bitter and yellowish. Our objective of this study was to investigate causes of occurrences of physiological disorders in mangosteen using an innovative agricultural biotechnology approaches.

The experiment was conducted to sequence mRNA from two types of tissues, named normal dan disorder-affected tissue, respectively using Ion Proton™ System. The high-quality reads were produced by trimming and filtering with specific parameters. The de novo assembly was performed with optimized reads normalization by 30x coverage and 300 bp in minimum length (Haas et al. 2013). The high quality of reads was aligned individually into the assembled-transcripts by Bowtie2 and estimated by eXpress software to be further analyzed in the differential gene expression (DGE).

The functional annotation of unigenes with blast hits was further classified by Gene Ontology (GO) analysis and KEGG pathway. Furthermore, the DEG of transcripts will validate through RT-PCR in the future work. Matra et al. (2016) reported 268,851 transcripts as well as 155,850 unigenes as mangosteen genes. They were annotated with two main databases from NCBI and UniProtKB, respectively having annotated-sequences of 73,287 and 73,107, respectively. From this gene, the library was selected to be potential genes related to occurrences of physiological disorders in mangosteen using DEG analysis.

In this study, we analyzed through bioinformatics method to predict gene control mechanism from the quantitative expression values of differentially expressed genes based on RNA-Seq transcriptome data of fruit tissues in different types. The selected genes were annotated using EnsemblePlant database. We identified best candidate genes to be further analyzed in the differential gene expression (DGE). These results provide a starting information to further discovering and understanding the regulating genes involved in the physiological disorders of mangosteen. We also provided our perspective on future developments in plant gene regulatory network related to under various environmental condition in horticultural crops.

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