RNA-seq analysis of mangosteen (Garcinia mangostana L.) fruit ripening

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ABSTRACT

Mangosteen (Garcinia mangostana L.) is known for its delectable taste and contains high amount of xanthones which have been reported to possess anti-cancer, anti-inflammatory and other bioactive properties. However, stage-specific regulation of mangosteen fruit ripening has never been studied in detail. We have performed a comparative transcriptomic analysis of three ripening stages (Stage 0, 2 and 6) of mangosteen. We have obtained a raw data from six libraries through Illumina HiSeq 4000. A total of ~40 Gb of raw data were generated. Clean reads of 650,887,650 (bp) were obtained from 656,913,570 (bp) raw reads. The raw transcriptome data were deposited to SRA database, with the BioProject accession number of PRJNA339916. These data will be beneficial for transcriptome profiling in order to study the regulation of mangosteen fruit ripening. The lack of a complete sequence database from this species impedes protein identification. These data sets provide a reference data for the exploration of novel genes or proteins to understand mangosteen fruit ripening behaviour.

Specifications

Organism/cell line/tissue: Garcinia mangostana L. (Pericarps)
Sex: N/A
Sequencer or array type: Illumina Hiseq™ 4000
Data format: Raw data: FASTQ file
Experimental factors: Ripening stages of mangosteen, stage 0 pericarp/aril, stage 2 pericarp, stage 6 pericarp
Experimental features: Two biological replicates for each stage
Consent: N/A
Sample source location: UKM Bangi, Malaysia (2°55′09.0″N 101°47′04.8″E)

1. Direct link to deposited data

The data is accessible via the following link https://www.ncbi.nlm.nih.gov/bioproject/PRJNA339916 and individual link for each sample are provided as follows:

2. Introduction

Mangosteen (Garcinia mangostana L.) is a tropical climacteric fruit from the family of Clusiaceae (Guttiferae) cultivated in Southeast Asian countries such as Malaysia, Thailand, Indonesia and Philippines [1,2]. Its extract is rich in beneficial metabolites particularly xanthones which are known to have anti-cancer, anti-inflammatory, anti-oxidant, anti-bacteria and anti-viral properties, among others [1,2]. The ripening of mangosteen fruit can be divided into seven stages, Stage 0 until Stage 6 [3]. Despite being classified as climacteric (ripening with a surge of ethylene production), mangosteen will only be fully ripen if harvested at the middle of ripening process (Stage 2 onwards), not at mature green stage (Stage 0). In contrast, other climacteric fruits such as tomato and banana will ripen off the plant once they reach mature green stage [4]. A recent study has been conducted which employed an ion proton sequencer for the de novo transcriptome analysis of mangosteen [5] yet this is only specific to one fully ripened stage. In this study, three mangosteen ripening stages (Stages 0, 2 and 6 corresponding to early, middle and late ripening stages) were analysed using RNA-seq, specifically Illumina Hiseq 4000 platform, to understand the ripening regulation. The short reads were trimmed, processed, assembled and analysed as described below. Raw reads for this project were deposited in the NCBI SRA database (Table 1). These data sets would be beneficial to reveal any novel genes or proteins in the mangosteen ripening process.

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3. Experimental design, materials and methods

3.1. Plant materials

Garcinia mangostana L. fruits were obtained from experimental plot at Universiti Kebangsaan Malaysia, Bangi (2°55′09.0″N 101°47′04.8″E). Mangosteen were harvested according to different stages (Stage 0, 2 and 6) of ripening process (May until September 2014) and their pericarps were separated and grounded in liquid nitrogen before being stored at −80 °C for analysis. Whole fruit of Stage 0 was used because pericarp and aril were inseparable at this stage [3]. Five biological replicates from each stage were used for RNA extraction and two replicates from each stage with the highest RIN number were chosen for RNA-seq analysis.

3.2. Total RNA extraction and quality control, library preparation and RNA-seq

Modified CTAB method was used to isolate pure RNA from the mangosteen fruit [6]. NanoDrop spectrophotometer (Thermo Fisher Scientific Inc., USA) and Agilent 2100 Bioanalyzer (Agilent Technologies, USA) were used to confirm the total RNA quantity and integrity (RIN > 8). Purified samples were then prepared using the standard polyA-enriched library preparation protocol implemented by Macrogen, South Korea. Sequencing was performed using the Illumina Hiseq 4000 platform that generates paired end reads of 100 bp.

3.3. Transcriptome de novo assembly

Adapter sequences were removed from the raw reads with Trimmomatic program [7]. Only high quality reads with phred score ≥ 25 were retained for de novo assembly using Trinity (V2.2.0) [8]. We obtained 250,682 and 181,646 of unique transcripts and unigenes respectively. Statistics of the assembly is shown in Table 2.

Conflict of interest

All the authors have approved the submissions and there are no conflicts of interest.

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