



ELSEVIER

Contents lists available at ScienceDirect

Data in Brief

journal homepage: www.elsevier.com/locate/dib

Data Article

Data on RNA-seq analysis of *Garcinia mangostana* L. seed developmentOthman Mazlan, Azhani Abdul-Rahman, Hoe-Han Goh,
Wan Mohd Aizat, Normah Mohd Noor *

Institute of Systems Biology (INBIOSIS), Universiti Kebangsaan Malaysia (UKM), 43600 Bangi, Selangor, Malaysia

ARTICLE INFO

Article history:

Received 29 August 2017

Received in revised form

18 October 2017

Accepted 1 November 2017

Available online 7 November 2017

Keywords:

Mangosteen fruit
Seed development
Transcriptomics
RNA sequencing

ABSTRACT

Mangosteen (*Garcinia mangostana* L.) has exceptional potential for commercial and pharmaceutical applications due to its delicious fruit and medicinal properties. Nevertheless, the molecular mechanism of mangosteen seed development is poorly understood. In this study, we performed transcriptomic analysis of four seed developmental stages; eight, ten, twelve and fourteen weeks after anthesis. Illumina HiSeq™ 4000 sequencer was used to generate raw data of approximately 68 Gb in size. From 451,495,326 raw reads, 406,143,756 clean reads were obtained. The raw data were uploaded to SRA database and the BioProject ID is PRJNA395504. These data provide the basis for further exploration and understanding of the molecular mechanism in mangosteen seed development.

© 2017 Published by Elsevier Inc. This is an open access article under the CC BY license (<http://creativecommons.org/licenses/by/4.0/>).

Specifications Table

Subject area	Biology
More specific subject area	Transcriptomics
Type of data	Tables, text file
How data was acquired	Illumina HiSeq™ 4000

* Corresponding author.

E-mail addresses: profnormah@yahoo.com, normah@ukm.edu.my (N.o.s. Mohd Noor).<https://doi.org/10.1016/j.dib.2017.11.001>2352-3409/© 2017 Published by Elsevier Inc. This is an open access article under the CC BY license (<http://creativecommons.org/licenses/by/4.0/>).

Data format	Raw (FASTQ)
Experimental factors	Mangosteen seed development; eight, ten, twelve and fourteen weeks after anthesis.
Experimental features	Transcriptome of mangosteen seed development
Data source location	UKM Bangi, Malaysia (2°55'09.0"N 101°47'04.8"E)
Data accessibility	Data can be accessed from NCBI SRA (BioProject ID: PRJNA395504) (https://www.ncbi.nlm.nih.gov/bioproject/PRJNA395504)

Value of the data

- The data obtained using Illumina sequencer is the first report on RNA-seq of mangosteen seed at different developmental stages (eight, ten, twelve and fourteen weeks after anthesis).
 - This permits the identification of differentially expressed genes that may play an important role in mangosteen seed development.
 - Transcriptomics analysis provides the foundation in elucidating the molecular regulation during mangosteen seed development. Data obtained will be valuable for further investigation on putative genes and proteins discovery in mangosteen seed development.
-

1. Data

This dataset are raw reads for mangosteen seed at four different developmental stages; eight, ten, twelve and fourteen weeks after anthesis. Consequently, the data were *de novo* assembled into full-length transcriptome.

2. Experimental design, materials and methods

2.1. Plant materials

Mangosteen fruit were obtained from mangosteen plots at Universiti Kebangsaan Malaysia, Bangi (2°55'09.0"N 101°47'04.8"E). Flowers of mangosteen were labelled at anthesis during its flowering season (March – April 2014). During fruiting period (June – August 2014), fruits were harvested for seeds at eight, ten, twelve and fourteen weeks after anthesis denoting different developmental stages. Seed samples were stored at –80 °C and grounded to fine powder prior analysis.

2.2. Total RNA extraction and quality control, library preparation and transcriptomic service

Extraction of seed total RNA was done [1,2] via modifying the CTAB method [3]. For quality control, NanoDrop spectrophotometer (Thermo Fisher Scientific Inc., USA) and Agilent 2100 Bioanalyzer (Agilent Technologies, USA) were used to determine the total RNA quantity, quality and reliability. Samples with RNA integrity number (RIN) of around 8.0 or higher were selected for library preparation and sequencing. The mRNA library preparation employed was SureSelect Strand-Specific RNA Library Prep for Illumina Multiplexed Sequencing (protocol version E0, March 2017). Consequently, RNA-seq was performed using Illumina HiSeq™ 4000 (Theragene Etex, South Korea), generating 150 bp of paired end reads (Table 1).

2.3. De novo transcriptome assembly

Quality control of raw reads were tested via FastQC version 0.11.2 [4]. Then, high quality reads were obtained by trimming adapters and other unwanted sequences sequence using cutadapt version

Download English Version:

<https://daneshyari.com/en/article/6597348>

Download Persian Version:

<https://daneshyari.com/article/6597348>

[Daneshyari.com](https://daneshyari.com)