Data Article

RNA-seq data of banana bunchy top virus (BBTV) viruliferous and non-viruliferous banana aphid (*Pentalonia nigronervosa*)

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**A R T I C L E  I N F O**

**Article history:**  
Received 29 September 2019  
Received in revised form 12 November 2019  
Accepted 13 November 2019  
Available online 21 November 2019

**Keywords:**  
Banana aphid  
BBTV  
RNA-Seq  
Transcriptomic analysis

**A B S T R A C T**

Banana bunchy top disease (BBT) is one of the most economically serious viral diseases of banana caused by banana bunchy top virus (BBTV: Nanoviridae: Babuvirus). BBTV is a circular, ssDNA virus which is suitable in the phloem tissue and currently only being transmitted by the banana aphid (*Pentalonia nigronervosa*) in a persistent, non-propagative, circulative manner. Interaction of BBTV and banana aphid had been studied in several ways, such as transmission and translocation of BBTV inside the banana aphid body at cellular level. However, the molecular mechanism underlying the interaction between BBTV and banana aphid have been poorly understood. Therefore, this transcriptomic study was conducted to obtain the raw data for differential genes expression study in BBTV viruliferous (Vr) and non-viruliferous (NVr) banana aphid. Here, we present two data sets of RNA seq raw reads which is available in GenBank Sequence Read Archive (SRA) database with accession number of SRX6918251 and SRX6918252 for the Vr and NVr banana aphid respectively.

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1. Data

FASTQ raw data file which was generated from two sets of Vr and NVr banana aphid transcriptome has been deposited to NCBI-SRA data base with the accession number SRX6918251 and SRX6918252 respectively. Methods of insect rearing and collection, total RNA extraction, sequencing and generating clean transcriptome data is presented in the following section.

2. Experimental design, materials, and methods

2.1. Insect rearing, sample collection and BBTV detection

Initial colony of banana aphids were obtained from banana plantation grown in Bantul, Yogyakarta, Indonesia, and further transferred to the greenhouse facilities in Universitas Gadjah Mada, Yogyakarta. BBTV infected and non-infected banana were utilized for the rearing of BBTV Vr and NVr banana aphid respectively. New banana seedlings were continuously provided to replace old banana seedling to keep banana aphid population exist. Pool of 40 individuals banana aphid at different instars were collected and immersed on RNA later (Ambion) for RNA extraction. Confirmation of the BBTV viruliferous banana aphid population was conducted by amplifying the BBTV primers BBT1: 5’-CTCGTCATGTGCAAGGT-TATGTCG-3’ and BBT 2: 5’-GAAGTTCTCCAGCTATTCATCGCC-3’, on pool of 10 adult aphid DNA (Geneaid DNA extraction kit) targeting 250–350 bp PCR product [5].

2.2. RNA isolation, library preparation and RNA-seq

Both Vr and NVr banana aphid samples (whole body) were RNA extracted using RNeasy Plus kit (Qiagen, MD, USA) according to the manufacturer’s instructions. The quantity and quality of the total RNA were validated using NanoDrop spectrophotometer (Thermos, USA) for the purity of the RNA samples, and Agilent 2100 Bioanalyzer (Agilent RNA 6000 Nano Kit) for the RNA integrity (RIN value), 28S/18S and
the fragment length distribution. The samples were further sequenced using BGISEQ-500 platform following the steps as follow; 1) mRNA enrichment, 2) RNA fragment and reverse transcription: 3) End repair, 4) PCR amplification, 5) Denature and cyclization, 6) Sequencing on BGISEQ-500 platform.

2.3. RNA-seq data workflow

Filtering step was first performed on the raw sequencing reads generated by RNA-seq., mainly by removing those raw reads with adaptors and reads with more than 5% of unknown bases (N). After filtering, the remaining reads are called “Clean Reads” and stored in FASTQ file. Those clean read then ready for further assembly process. Descriptive statistics on the RNA-seq data of the two set of both Vr and NVr banana aphid samples are given in Table 1.

Acknowledgments

We gratefully thank the support from the Ministry of Research, Technology and Higher Education (KEMENRISTEKDIKTI) of the Republic of Indonesia through the World Class Professor Program (No.168.A10/D2/KP/2017), and the Bill and Melinda Gates Foundation, project no: OPP1130226, entitle “BBTV mitigation: community management in Nigeria and screening wild banana progenitors for resistance”.

Conflict of interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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