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Data Article

Transcriptomic data of the *Musa balbisiana* cultivar Kepok inoculated with *Ralstonia syzigii* subsp. *celebesensis* and *Ralstonia solanacearum*

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A R T I C L E I N F O

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A B S T R A C T

The increasing production of banana is hampered by the spread of banana plant diseases, one of which is caused by a group of bacteria, including those of causing wilt diseases. In Indonesia, blood disease is one of the important banana wilt diseases since loss due to the infection can reach up to 50%. There are numerous publications on the pathogen identification causing banana blood disease based on the molecular approach, however to date, no detailed molecular data are available for the interaction of banana host plant against the pathogen. Here, we present three raw data sets of the total RNA-seq from the inoculated *Musa balbisiana* cutivar kepok (ABB genome) inoculated with *Ralstonia syzigii* subsp. *celebesensis*, *Ralstonia solanacearum* and mock. The data provide essential knowledge for differentiating the banana response against pathogen, reveal pathogenesis-related genes and gene functions in the plant system, and research development to design blood disease-resistance of banana as one of the management strategies. Raw reads of RNA-seq data can be found in NCBI's Sequence Read Archive (SRA) database with the accession number

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of SRR10547839 (RSC), SRR10547840 (RS), and SRR10547841 (Mock).

Specifications Table

Subject	Biology
Specific subject area	Transcriptomics of inoculated banana plant with pathogenic and non-pathogenic bacteria
Type of data	Transcriptome sequences (RNA-seq raw reads)
How data were acquired	Total RNA sequencing using BGISEQ 500-Platform
Data format	Raw sequences (FASTQ)
Parameters for data collection	*Musa balbisiana* cultivar Kepok inoculated with *Ralstonia syzygii* subsp. *celebesensis* (RSC), *Musa balbisiana* cultivar Kepok inoculated with *Ralstonia solanacearum* (RS), and *Musa balbisiana* cultivar Kepok non-inoculated (Mock)
Description of data collection	Banana leaf from the treatment were collected from 3, 5 and 7 days after inoculation. Total RNA was isolated followed by cDNA library preparation for RNA sequencing. The result of RNAseq has been analyzed to get the clean reads and saved in FASTQ format.
Data source location	Bacteriology Laboratory, Department of Entomology and Plant Pathology, Faculty of Agriculture, Universitas Gadjah Mada Sleman/Yogyakarta, Indonesia (geo-coordinates: 7.768652, 110.381493)
Data accessibility	NCBI's Sequence Read Archive (SRA) database with the accession number SRR10547841 (https://www.ncbi.nlm.nih.gov/sra/SRX7230104) SRR10547840 (https://www.ncbi.nlm.nih.gov/sra/SRX7230105) SRR10547839 (https://www.ncbi.nlm.nih.gov/sra/SRX7230106)

Value of the Data

- The transcriptomic data of banana plant inoculated by *Ralstonia syzygii* subsp. *celebesensis*, *Ralstonia solanacearum* and mock reported here may provide essential knowledge for differentiating the banana response against pathogen.
- These bacterial pathogen treated-banana plant transcriptomes may reveal pathogenesis-related genes and gene functions in the plant system.
- By using bioinformatics approaches and functional studies, identification of candidate genes useful for research development to design blood disease-resistance of banana as one of the management strategies.

1. Data description

Raw data (FASTQ) was generated from *Musa balbisiana* cultivar Kepok inoculated with *Ralstonia syzygii* subsp. *celebesensis* (RSC), *Musa balbisiana* cultivar Kepok inoculated with *Ralstonia solanacearum* (RS) and Mock transcriptome has been deposited in NCBI-SRA database with accession SRR10547839 (RSC), SRR10547840 (RS), and SRR10547841 (Mock). Description on the isolate preparation, on the plant, total RNA extraction, sequencing and transcriptome data analysis is given in the next section. The statistics on the RNAseq data of the three set treatment are given in Table 1.

2. Experimental design, materials, and methods

2.1. Plant material

Three individual aclimated banana seedling from in vitro propagation (*Musa balbisiana* cultivar Kepok) with 3–5 leaves of 3 biological replications for each treatment were selected from banana nursery. Each plant was screened for healthy plants, without any symptom either other damage.

Table 1
RNA-seq statistics data of the *Musa balbisiana* cultivar Kepok inoculated with *Ralstonia syzigii* subsp. *celebesensis* (RSC), *Ralstonia solanacearum* (RS), or Mock.

Attributes	Values		
	RSC	RS	Mock
Total raw reads (Mb)	70.24	70.24	65.22
Total clean reads (Mb)	64.47	70.24	65.22
Total clean bases (Gb)	6.45	6.73	6.29
Clean reads Q20 (%)	97.52	97.34	97.17
Clean reads Q30 (%)	90.32	89.88	89.38
Clean reads ratio (%)	91.79	95.78	96.51
Biosample ID	SAMN13155832	SAMN13155833	SAMN13155834

Total raw reads (Mb): The reads amount before filtering.
Total clean reads (Mb): The reads amount after filtering.
Total clean bases (Gb): The total base amount after filtering.
Clean reads Q20(%): The Q20 value for the clean reads.
Clean reads Q30(%): The Q30 value for the clean reads.
Clean reads ratio(%): The ratio of the amount of clean reads.

2.2. Pathogen and inoculation

The pathogen was isolated from infected banana fruit for RSC (geo-coordinates: -7.835059, 110.388721), tomato plant for RS (geo-coordinates: -7.538688, 110.337296). The pathogen was identified using Gram-test, Kovac's Oxidation Test and PCR confirmation method [1–5]. Cultures maintained as a suspension in 5 mL sterile water in plastic-capped glass culture tubes and stored at 20 °C. Culture streaked onto Casein Peptone Glucose + 500 ppm of triphenyl tetrazolium chloride (TZC) agar plates [6] to check for purity and virulent colony type. Typical colonies were chosen to streak onto CPG agar plates and then incubated at 30 °C for 48–72 hours for further preparation. Bacterial growth on CPG was suspended using 10 mL sterile distilled water. The suspension was mixed thoroughly and the concentration was adjusted for the concentration approximately at 5×10^9 CFU/mL (CFU: colony forming unit) using a spectrophotometer and previously constructed calibration curve. For an infectivity titration technique, 10^8 CFU/mL (CFU: colony forming unit) concentration was prepared by dilution. The suspension was inoculated into aclimated banana seedling from in vitro propagation (*Musa balbisiana* cultivar Kepok) with 3–5 leaves. Each seedling was inoculated by inserting 2 yellow tips into the axils each tip containing 200 µl bacterial pathogen suspension at 10^8 CFU/mL(CFU: colony forming unit). The tip at leaf axil kept standing until the bacterial suspension has been completely taken by the plant in few hours.

2.3. RNA isolation, library preparation and RNA-seq data workflow

Samples were taken on 3, 5, and 7 days after inoculation. Total RNA was extracted from the banana leaf (0.5 cm square, 3 replicates) using Rneasy plant mini kit (Qiagen, Hilden, Germany) with minor modification. Total RNA quantity and quality were validated using the NanoDrop ND-1000 Spectrophotometer (NanoDrop Technologies, USA), respectively for the purify of the RNA. Quality control of the total RNA sample was performed using Agilent 2100 Bio analyzer (Agilent RNA 6000 Nano Kit) including RNA concentration, RIN value, 28S/18S and the fragment length distribution. Sequencing was performed using the BGISEQ- 500 platform [7]. Clean reads obtained from removing reads with adaptors, removing reads in unknown bases (N) are more than 10% and removing low quality reads then stored in FASTQ format. Those data then ready for further bioinformatics process. The statistics on the RNA-seq data of the set are given in Table 1.

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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.

Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.dib.2020.105366.

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