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

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Abstract
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* cultivar kepok (ABB genome) inoculated with *Ralstonia syzygii* 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...
of SRR10547839 (RSC), SRR10547840 (RS), and SRR10547841 (Mock).
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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 *Musa balbisiana* cultivar Kepok non-inoculated (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.
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 × 10⁹ CFU/mL (CFU: colony forming unit) using a spectrophotometer and previously constructed calibration curve.

For an infectivity titration technique, 10⁸ 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 10⁸ CFU/mL:CFU colon 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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