RNA-seq data of *Ganoderma boninense* at axenic culture condition and under *in planta* pathogen-oil palm (*Elaeis guineensis* Jacq.) interaction

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Abstract

**Objective:** Basal stem rot disease causes severe economic losses to oil palm production in South-east Asia and little is known on the pathogenicity of the pathogen, the basidiomyceteous *Ganoderma boninense*. Our data presented here aims to identify both the house-keeping and pathogenicity genes of *G. boninense* using Illumina sequencing reads.

**Description:** The hemibiotroph *G. boninense* establishes via root contact during early stage of colonization and subsequently kills the host tissue as the disease progresses. Information on the pathogenicity factors/genes that causes BSR remain poorly understood. In addition, the molecular expressions corresponding to *G. boninense* growth and pathogenicity are not reported. Here, six transcriptome datasets of *G. boninense* from two contrasting conditions (three biological replicates per condition) are presented. The first datasets, collected from a 7-day-old axenic condition provide an insight onto genes responsible for sustenance, growth and development of *G. boninense* while datasets of the infecting *G. boninense* collected from oil palm-*G. boninense* pathosystem (*in planta* condition) at 1 month post-inoculation offer a comprehensive avenue to understand *G. boninense* pathogenesis and infection especially in regard to molecular mechanisms and pathways. Raw sequences deposited in Sequence Read Archive (SRA) are available at NCBI SRA portal with PRJNA514399, bioproject ID.

**Keywords:** *Ganoderma boninense*, Basidiomycete, Transcriptome, Basal stem rot, Pathogenicity factors

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understand the molecular events underpinning growth and BSR disease development; effectors for microhyphae, regulatory network of LME production and pathogenesis factor for penetration and colonization.

Data description

**Ganoderma boninense** axenic culture

The *Ganoderma boninense* PER71 culture was obtained from Malaysian Palm Oil Board (MPOB), Malaysia and was maintained on malt extract agar (MEA). From the peripheral region of a 7-day-old primary culture, cubes of \( 0.5 \times 0.5 \) mm were excised and inoculated onto fresh agar plates (three biological replicates). The Petri dish over-turned and placed in a dark chamber was incubated at 25 °C, 16/8 h day/night period. To represent *G. boninense* at axenic condition, the mycelium at 7 days after inoculation were scraped gently from the agar surface and flash frozen in liquid nitrogen for RNA isolation.

**Ganoderma boninense in planta**

For plant-pathogen *in planta* condition, rubberwood blocks (RWBs) were used to prepare *Ganoderma boninense* inoculum according to Govender et al. [6]. The 3-month-old oil palm seedlings (*Elaeis guineensis* Jacq. *Dura X Psifera*) were obtained from Sime Darby Sdn. Bhd., Malaysia. The seedlings (three biological replicates) were transplanted into pots (40 × 30 cm) of soil mixture. The planting medium preparation and artificial infection was performed according to Govender et al. [7]. Briefly, each pot received about 2 kg of planting medium. Transplanted seedlings were acclimatized at room temperature for 4 weeks prior to artificial infection with *G. boninense* colonized RWB (RWB-inocula). Each seedling was artificially infected with one RWB-inoculum. Oil palm seedlings were carefully pulled from the soil mixture and the RWB-inoculum was attached below the bole and root tissues were arranged randomly to cover the RWB surface. The RWB-inoculum together with the oil palm seedlings were re-planted into pots of soil mixture. All seedlings were regularly watered and maintained under glasshouse condition. At 1 month post-inoculation, root tissues from the artificially infected oil palm seedlings were collected for RNA isolation.

RNA isolation

RNA was extracted from 0.1 g (fine powder) samples using the TRIzol method. The quality of the RNA was determined by Agilent 2100 bioanalyzer and only RNA samples fulfilling the minimal requirements (RIN ≥ 6.5, concentration ≥ 20 ng/µL, OD260/280 ≥ 1.8, and OD260/230 ≥ 1.8) were used for library preparation.

RNA-sequencing

We used Illumina HiSeq1000 platform to sequence the high quality RNA samples obtained from *G. boninense* axenic and *in planta* *G. boninense*-oil palm (root tissues) interaction. All raw reads obtained were subjected to quality check and a subsequent filtering; sequence reads were (Q > 30) “trimmed” to remove low quality bases using Skewer version 0.1.120 [8]. For *in planta* samples, the good quality reads were aligned against the oil palm reference genome (ASJS0000000.1). Aligned reads were removed to knock out the presence of host RNA using HISAT2 [9]. Next, the filtered reads together with reads obtained from the axenic sample were subjected to de novo assembly using the Trinity pipeline (Trinity version 2.8.4); a set of contiguous sequences (contigs) comprised of full and partial fragments of fungal transcripts were generated [10]. Descriptive information on the *Ganoderma boninense* data sets are presented in Table 1. Samples with a SRA label of SRS4243090–SRS4243092 are *in planta* *G. boninense* and SRS4243093–SRS4243095 represent the fungus in an axenic condition.

Data

See Table 1.

Limitations

The transcriptome data of *G. boninense* strain PER71 represents a moderate virulence. There are different strains of *G. boninense* described with variable degree of

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**Table 1 Overview of Ganoderma boninense data sets available at [https://www.ncbi.nlm.nih.gov/bioproject/PRJNA514399](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA514399)**

| File link | Description of data set | File name | BioSample ID |
|-----------|--------------------------|-----------|--------------|
| [https://www.ncbi.nlm.nih.gov/sra/SRX5240215](https://www.ncbi.nlm.nih.gov/sra/SRX5240215) | Axenic *Ganoderma boninense* BR1 | SRX5240215 | SAMN10724118 |
| [https://www.ncbi.nlm.nih.gov/sra/SRX5240214](https://www.ncbi.nlm.nih.gov/sra/SRX5240214) | Axenic *Ganoderma boninense* BR2 | SRX5240214 | SAMN10724119 |
| [https://www.ncbi.nlm.nih.gov/sra/SRX5240213](https://www.ncbi.nlm.nih.gov/sra/SRX5240213) | Axenic *Ganoderma boninense* BR3 | SRX5240213 | SAMN10724120 |
| [https://www.ncbi.nlm.nih.gov/sra/SRX5240212](https://www.ncbi.nlm.nih.gov/sra/SRX5240212) | In planta *Ganoderma boninense* BR1 | SRX5240212 | SAMN10724121 |
| [https://www.ncbi.nlm.nih.gov/sra/SRX5240211](https://www.ncbi.nlm.nih.gov/sra/SRX5240211) | In planta *Ganoderma boninense* BR2 | SRX5240211 | SAMN10724122 |
| [https://www.ncbi.nlm.nih.gov/sra/SRX5240210](https://www.ncbi.nlm.nih.gov/sra/SRX5240210) | In planta *Ganoderma boninense* BR3 | SRX5240210 | SAMN10724123 |

BR biological replicate
virulence and any other similar transcriptomic comparisons to *G. boninense* strain PER71 may result to variation at the expression levels of the pathogenicity genes. In addition, other environmental variables may also affect the pathogenicity gene expression; temperature, moisture, osmotic stress, host genotypes and presence/absence of commensal microbes.

Abbreviations

BSR: basal stem rot; OPs: oil palms; LME: lignin modifying enzyme; SRA: Sequence Read Archive.

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Authors’ contributions

WMY conceived the study and secured funding. OCS performed the experiment. NG performed the bioinformatics analyses and wrote the manuscript. All authors read and approved the final manuscript.

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Availability of data materials

The data presented here are available in the Sequence Read Archive, National Centre for Biotechnology Institute (https://www.ncbi.nlm.nih.gov/bioproject/PRJNA514399).

Ethics approval and consent to participate

Not applicable.

Consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

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