Data Article

RNA-seq data of tea mosquito bugs, *Helopeltis bradyi*, antennae

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\textbf{A R T I C L E  I N F O}

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\textbf{A B S T R A C T}

Tea Mosquito Bug (TMB), *Helopeltis bradyi* (Hemiptera: Miridae) is one of the major pests infesting tea and cocoa plantations worldwide. Developing olfaction-based control methods was urged as an alternative to commonly used but non-environmentally friendly chemical pesticides. However, the molecular mechanisms underlying TMB reception mechanism are still lacking. Here, we collected a pooled male and female TMB antennae for RNA extraction followed by sequencing using the BGISEQ-500 platform and de novo assembly. TMB antennae RNA-seq data yielded 32,142 unigenes with N50 and GC (%) were 2322 and 40.25; subsequently. The RNA-seq data are available in GenBank Sequence Read Archive (SRA) database with accession number SRR13327229. De novo transcriptome analysis had identified several genes involved in TMB odorant reception includes; 39 OBPs (odorant binding proteins), 10 CSPs (chemosensory proteins), 81 Ors (odorant receptors), 1 Orcos (co-receptors), 9 SNMPs (sensory neuron membrane proteins), 3 GRs (gustatory receptors) and 4 IRs (ionotropic receptors). Our study presents the first RNA seq for TMB antennae, which serve the primary molecular resources data, which will facilitate further

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Specifications Table

| Subject area | Insect Science |
|--------------|----------------|
| Specific subject area | Transcriptomics |
| Type of data | Transcriptome sequences (RNA-Seq raw reads) |
| How data was acquired | BGISEQ-500 sequencing platform |
| Data format | Raw sequence (FASTQ) |
| Parameters for data collection | Antennae of tea mosquito bugs, *Helopeltis bradyi* |
| Description of data collection | RNA-seq data from Pooled antennae of *Helopeltis bradyii* male and female, complemented with Descriptive quality of RNA seq raw data (Table 1), De Novo assembly (Table 2) and Unigenes related to reception mechanism (Supplementary file) |
| Data source location | *Helopeltis bradyii* populations were collected from the infested cocoa plantation in Segayung [GPS data: -6.94383, 109.80328] and laboratory maintained with cucumber as their diet in Universitas Gadjah Mada, Yogyakarta, Indonesia |
| Data accessibility | NCBI’s Sequence Read Archive (SRA) database with the accession number SRR13327229. [https://www.ncbi.nlm.nih.gov/sra/?term=SRR13327229](https://www.ncbi.nlm.nih.gov/sra/?term=SRR13327229) and Suplementary file; [https://doi.org/10.17632/7hdjzw5hzd.1](https://doi.org/10.17632/7hdjzw5hzd.1) |

Value of the Data

- Tea Mosquito Bug (TMB), *Helopeltis bradyi* (Hemiptera: Miridae) is one of the major pests causing significant loss in tea and cocoa production [1–3]. The infestation area of TMB in a plantation may reach up to 80% coverage, with yield loss vary between 40-80% [4–7].
- The raw-FASTQ file of TMB antennal transcriptome data and the annotated olfaction genes were presented here to support the understanding of molecular mechanism underlying TMB reception system.
- The presented data can be further annotated for the discovery of another gene and perform the characterization, differential gene expression, and functional study to determine the gene of interest and reveal the TMB molecular reception mechanism, which finally may support TMB management.

1. Data Description

The antennae FASTQ raw data file of tea mosquito bugs (*Helopeltis bradyi*), has been deposited to NCBI’s Sequence Read Archive (SRA) database with the accession number SRR13327229. Additionally, de novo transcriptome analysis revealing the genes involved in TMB odorant reception were presented, includes; 39 OBPs (odorant binding proteins), 10 CSPs (chemosensory proteins), 81 Ors (odorant receptors), 1 Orcos (co-receptors), 9 SNMPs (sensory neuron membrane proteins), 3 GRs (gustatory receptors) and 4 IRs (ionotropic receptors) (Supplementary file 1: [https://doi.org/10.17632/7hdjzw5hzd.1](https://doi.org/10.17632/7hdjzw5hzd.1)).
2. Experimental Design, Materials and Methods

2.1. Insect rearing and antennal collection

TMB populations were collected from the infested cocoa plantation in Segayung, Yogyakarta, Indonesia, and maintained in cucumber as described previously [8]. Adult emergence was observed daily, and an equal number of both male and female were paired for rearing in a plastic cup. Antennal collection for RNA extraction was conducted by immobilizing the TMB in a short period of about 3–6 min in a freezer (-10°C) followed by cutting the insect's antennae from their base. Antenna dissection was performed under the simple light microscope then immersed in RNA later (Ambion).

2.2. Total RNA extraction, cDNA library construction, and RNA sequencing

Total RNA was extracted from pooled 50 TMB antennae of both male and female. Their quantity and quality were measured using Agilent 2100 Bioanalyzer (Agilent RNA 6000 Nano Kit), including RNA concentration, RIN value, 28S/18S, and the fragment length distribution, followed by NanoDrop to identify the purity of the RNA samples. Qualified total RNA was prepared for RNA sequencing following the BGISEQ-500 transcriptome library workflow (Fig. 1).

Following total RNA extraction was mRNA purification from total RNA using oligo(dT)-attached magnetic beads. Once Ribosomal RNA (rRNA) was removed from total RNA, the mRNA was fragmented and reverse transcribed into double-strand cDNA (dscDNA) by N6
Table 1
Descriptive quality information for RNA seq raw data for tea mosquito bugs (TMB), Helopeltis bradyi Antennae.

| Descriptive                  | Helo1          |
|------------------------------|----------------|
| Total Raw Reads(M)           | 82.78          |
| Total Clean Reads(M)         | 79.5           |
| Total Clean Bases(Gb)        | 7.95           |
| Clean Reads Q20(%)           | 97.84          |
| Clean Reads Q30(%)           | 90.73          |
| Clean Reads Ratio(%)         | 96.03          |
| Biosample ID                 | SAMN17126627   |

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 rate of bases which quality is greater than 20 value in clean reads
Clean Reads Q30(%) The rate of bases which quality is greater than 30 value in clean reads
Clean Reads Ratio(%) The ratio of the amount of clean reads

Table 2
Descriptive quality information for De Novo assembly for tea mosquito bugs (TMB), Helopeltis bradyi Antennae.

| Descriptive  | Unigenes |
|--------------|----------|
| Total Number | 32,142   |
| Total Length | 38,692,350 |
| Mean Length  | 1203     |
| N50          | 2322     |
| GC(%)        | 40.25    |
| Annotation [Nr] | 17,209  |

N50: The N50 length is used to determine the assembly continuity, the higher the better. N50 is a weighted median statistic that 50% of the total length is contained in transcripts that are equal to or larger than this value

random primer. The cDNA then “A” tailed and ligated with the adaptor, followed by PCR amplification to enrich the purified cDNA, then purified with Ampure XP Beads (AGENCOURT). The final step before sequencing on BGISEQ-500 was denaturation of the PCR product by heat and the single strand DNA was cyclized by splint oligo and DNA ligase.

2.3. RNA-seq workflow and De novo transcriptome analysis

Sequence reads filtering was conducted by filtering from those reads with low quality (More than 20% of the bases qualities are lower than 10), reads with adaptors, and reads with unknown bases (N bases more than 5%). These clean reads was stored in FASTQ format, their descriptive statistics are presented in Table 1. Following the clean read is de novo assembly to get the Unigenes by using Trinity, which contains three independent software modules: Inchworm, Chrysalis, and Butterfly, which further followed by functional annotation by using NR database (ftp://ftp.ncbi.nlm.nih.gov/blast/db), their descriptive information is presented in Table 2.

Ethics Statement

This work does not contain any studies with humans. The original collections of tea mosquito bugs (TMB), Helopeltis bradyii were made with the direct permission of Cocoa plantation owner [Pagilaran Co.] in the Segayung area [GPS data: -6.94383, 109.80328], followed by TMB mass rearing on cucumber. We confirm that none of the TMB were collected from National Parks or protected wilderness areas. Additionally, these TMB are definitely not endangered species.
CRediT Author Statement

**Alan Soffan**: Conceptualization, Methodology, Writing – original draft; **Siti Subandiyah**: Conceptualization, Data curation, Validation; **Arman Wijonarko**: Writing – review & editing; **Widhi Dyah Sawitri**: Writing – review & editing, Data curation, validation.

Declaration of Competing 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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