Insect tea is a traditional health beverage in China. They were made by faeces obtained from caterpillars after feeding on special plant leaves (Bai 2010). So far, a total of seven species in Lepidoptera were documented as insect-tea producers (Shang et al. 2011; Liu et al. 2013). Among them, Pyralis farinalis and Orthopygia glaucinalis were popular in South China.

In August 2012, the samples of P. farinalis were collected in tea garden of Chishui County, Guizhou Province, China (E 105°12’00”, N 28°10’9”) while O. glaucinalis were gathered in Congjiang County, Guizhou Province, China (E 108°15’14”, N 25°13’2”). Then all the insects were fed in the Institute of Entomology, Guizhou University, Guiyang, China (E 108°16’14”, N 25°13’2”). Both the voucher of P. farinalis and O. glaucinalis with their genomic DNA were deposited in the Institute of Entomology, Guizhou University, Guiyang, China (GUGC), accession number of them were GUGC-IPP-01801, GUGC-IPP-01901, respectively. Total DNA was extracted from the entire body of larva with Qiagen DNeasy kit (Venlo, the Netherlands) as the manufacture instruction. Raw data were outputted on an Illumina Novaseq 6000 platform at Berry Genomics (Beijing, China) for 150 bp paired-end reads. The reads were assembled de novo to draft mitogenome with NOVOPlasty version 2.7.2 (Dierckxsens et al. 2017). COI sequence of Pyralidae sp. (MK559413) was used as seed sequence for assembly. Then, Genes were annotated on mitogenome with Mitoz function in Mitoz version 2.4 (Meng et al. 2019). The results exhibited that 37 typical invertebrate mitochondrial genes (13 PCGs, 22 tRNAs, and 2 rRNAs) and the AT-rich region (D-loop) were identified from both mitochondrial genomes. Annotated sequences were submitted to Genbank with accession number MN442120 for P. farinalis and MN461479 for O. glaucinalis.

The circular mitogenome of P. farinalis was 15,204 bp in size, including 13 protein-coding genes (PCGs), 22 transfer RNAs (tRNAs), and 2 ribosomal RNAs (rRNAs). The nucleotide composition of the P. farinalis was obviously biased towards A + T (78.4%). There was 11,234 bp for the total length of 13 PCGs, which was used for encoding 3732 amino acids. The most common initiation codon was ATN within 13 PCGs. All PCGs of both mitogenome used TAN as stop codon, except for ND4 and NDS of O. glaucinalis. Phylogenetic relationship of both species was also shown with 13 references.

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Geneious Prime 2019.1.3 (Biomatters Ltd., Auckland, New Zealand). Results characterized that both species were clustered with family Pyralidae, along with other nine species. Species from family Crambidae were clustered separately (Figure 1). As a result, mitogenome data could provide more information on identification of insect tea producers.

**Disclosure statement**

No potential conflict of interest was reported by the authors.

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