Characterization of the complete mitochondrial genome of the tea leaf roller *Caloptilia theivora* (Insecta: Lepidoptera: Gracillariidae)

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**ABSTRACT**

The tea leaf roller, *Caloptilia theivora* (Walsingham), is a serious pest of tea plants. We have obtained and annotated the complete mitochondrial genome of *C. theivora* (GenBank accession No. MK541932). The entire mt genome is 15,297 bp long with an A+T content of 80.66%. The mt genome of *C. theivora* encodes all 37 genes that are typically found in animal mt genomes, consists of 13 protein-coding genes, 2 ribosomal RNA, and 22 transfer RNA genes. The gene order is consistent with other moths mt genome in Ditrysia. The control region of this genome is 192 bp long with a high A+T content of 96.35%, and located between the *rrnS* and *trnL* genes. Phylogenetic analysis was performed using 13 protein-coding genes among 19 moths showed that *C. theivora* is closely related to species of Gracillariidae.

The A+T content of this region is 96.35%, the highest level of each region in this mt genome. The gene arrangement of this mt genome is conserved as other moths mt genome in Ditrysia. Twenty-three of all 37 genes are encoded on the majority strand (U-strand) and the others encoded by the minority strand (N-strand). Twelve of the 13 PCGs start with ATN codons (ATG for *atp6*, *cox2*, *nad1*, *cob*, *nad4*, and *nad4L*; ATT for *atp8*, *nad2*, *nad5*, and *nad6*; ATA for *cox3* and *nad3*) and *cox1* used CGA as start codon, same situation exists in most Lepidoptera species (Chen et al. 2016). Three PCGs (*cox1*, *cox2*, and *nad4*) have incomplete terminal codons consisting of single T nucleotide, and the other PCGs stop with TAA and TAG. The nucleotide length of tRNA genes is ranging from 61 bp (*trnA*) to 80 bp (*trnS*)), and A+T content is ranging from 70.42% (*trnK*) to 89.39% (*trnD*). All of the 22 tRNA genes have the conventional cloverleaf-shaped secondary structure. The two rRNA genes have been identified on the N-strand in the *C. theivora* mt genome: the *rrnL* gene locates between *trnL* and *trnV* genes, and the *rrnS* gene between the *trnV* gene and the control region. The length of *rrnL* and *rrnS* genes was 1389 and 770 bp, and their A+T content was 85.46% and 85.84%, respectively.

We analyzed amino acid sequence of 13 PCGs with the maximum likelihood (ML) method to understand the phylogenetic relationship of *C. theivora* with other moths. The mt genome sequence of *Drosophila melanogaster* (GenBank accession no. DMU37541) was used as an outgroup. The tea leaf roller and other three moths in the Family Gracillariidae are clustered into a branch of the phylogenetic tree with 100% bootstrap value (Figure 1). It infers that *C. theivora* is...
closely related to species of Gracillariidae, and the complete mitochondrial genome of *C. theivora* can be used for further taxonomic analysis.

**Disclosure statement**

No potential conflict of interest was reported by the authors.

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**Figure 1.** The maximum likelihood (ML) phylogenetic tree of *Caloptilia theivora* and other moths. The GenBank accession numbers used for tree constructed are as follows: *Mahasena colona* (KY856825), *Tineola bisselliella* (KJ508045), *Cameraria ohridella* (KJ508042), *Phyllonorycter platanii* (KJ508044), *Phyllonorycter froelichiella* (KJ508048), *Buzura suppressaria* (KF278206), *Bombyx mori* (AF149768), *Antheraea pernyi* (HQ264055), *Manduca sexta* (EU286785), *Thitarodes renziensis* (HM746904), *Helicoverpa armigera* (GU188273), *Phalaena flavescens* (JF440342), *Hyphantria cunea* (GU592049), *Gynaephora menyuanensis* (KC185412), *Leucoptera malifoliella* (JN790955), *Adoxophyes honmai* (DQ073916), *Ostrinia furnacalis* (AF467260), and *Lista haraldusalis* (KF709449).