Complete mitochondrial genome of *Anarta trifolii* (Lepidoptera: Noctuidae)

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**ABSTRACT**

The *Anarta trifolii* belongs to Noctuidae in Lepidoptera. The complete mitogenome of *A. trifolii* was described in this study, which is typical circular duplex molecules and 15,281 bp in length, containing the standard metazoan set of 13 protein-coding genes, 22 transfer RNA genes, 2 ribosomal RNA genes, and an A+T-rich region. The gene order is same with other lepidopterans. Except for *cox1* started with CGA, all other PCGs started with the standard ATN codons. Most of the PCGs terminated with the stop codon TAA, whereas *nad3* is TAG, *nad4* has the incomplete stop codon T. The phylogenetic tree showed that *A. trifolii* and other three species belong to Hadeninae, which are clustered into a clade.

*Anarta trifolii* Hufnagel [1766] is widely distributed in drier, open habitats throughout much of the northern hemisphere, and is often a major agricultural pest. The species is a generalist, feeding on many kinds of herbaceous vegetation, which include peas, lettuce, and cabbage. It belongs to Noctuidae of Lepidoptera. We sequenced the complete mitogenome of *A. trifolii* in this study, which would facilitate the researches of the phylogeography and phylogenetic relationship of Lepidoptera.

In this study, the samples were collected by light trapping in Taiyuan City of China (37°83′33″N, 112°66′61″E) in July 2019, some of these specimens were immediately frozen at −80°C for mitogenome analysis, and others were preserved by spreading wings in the Herbarium of Institute of Plant Protection, Shanxi Academy of Agricultural Sciences, and their numbers are 2019TYKD1722–1727. Total genomic DNA was extracted from tail tip using the Ezup pillar genomic DNA extraction kit (Sangon Biotech, Shanghai, China). The mitogenome was sequenced by Illumina Hiseq 4000. Gene annotation was performed and circularity was checked using the MITOS2 webserver (Bernt et al. 2013; http://mitos.bioinf.uni-leipzig.de/).

The mitochondrial genome of *A. trifolii* has a total length of 15,281 bp (GenBank accession No. MN715147), consisting of 13 protein-coding genes (PCGs), 22 tRNA, 2 rRNA genes, and an A+T-rich region. The major strand encodes a larger number of genes (9 PCGs and 14 tRNAs) than the minor strand (4 PCGs, 8 tRNAs, and 2 rRNA genes). Gene content and arrangement are highly conserved and typical of Lepidoptera (Wu, Zhao, Su, He et al. 2016, Wu, Zhao, SU, Luo et al. 2016). The mitogenome is highly biased toward A/T, contains 41.33% T, 40.23% A, 10.72% C, and 7.73% G, which is a feature commonly present in insects (Boore 1999).

All PCGs have ATN as the start codon except for *cox1*, which starts with CGA. Eleven PCGs have the common stop codon TAA. However, *nad3* have the stop codon TAG, and *nad4* has the incomplete stop codon T. All tRNAs exhibit typical clover-leaf secondary structure, except for tRNA-Ser(AGN) lacking the DHU arm, which is common in Lepidoptera insects (Garey and Wolstenholme 1989). The 16S rRNA is 1259 bp in length, and the 12S rRNA is 735 bp in length. The A+T-rich region is 278 bp long located between 12S rRNA and tRNA-Met. There is a motif ATAGA in downstream of 12S rRNA followed by an 19 bp Poly-T stretch.

The phylogenetic position of *A. trifolii* was inferred using sequences of the 13 PCGs of 24 species. Twenty-three of them belong to Noctuidae, and *Idaea effusaria* from Geometridae (which is used as outgroup) (Figure 1). The sequences were aligned with MAFFT v7.2 software (Katoh and Standley 2013), the evolutionary analyses were conducted with RAxML v8.2.10 (Stamatakis 2014) on the CIPRES Science Gateway (Miller et al. 2010). The result showed that *A. trifolii* and other three species *Mythimna pallidicosta*, *Protegira songi*, *Mythimna separata* belong to Hadeninae, which are clustered into a clade. Other species of the same tribes form a monophyly.

**Nucleotide sequence accession number**

The complete mitochondrial genome sequence of *A. trifolii* was deposited in GenBank under the accession number MN715147.

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Disclosure statement
No potential conflict of interest was reported by the author(s).

Funding
This work was supported by the National Key Research and Development Program of China [2018YFD0200404-9], the Key R & D projects of Shanxi Province (Social Development) [201903D321058], the Open fund of Shanxi Key Laboratory of Integrated Pest Management in Agriculture [YHSW2019001] and the Special Fund for Outstanding Research Group in Shanxi Academy of Agricultural Sciences [No.YCX2018D2Y508].

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