MITOGENOME ANNOUNCEMENT

Complete mitochondrial genome and phylogenetic analysis of *Diaphania perspectalis*

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**ABSTRACT**

To explore the evolutionary relationships of Pyralidae, the complete mitochondrial genome of *Diaphania perspectalis* (Walker) was sequenced and annotated. The genome is found to be 15,232 bp in length and has a base composition of A (39.8%), G (7.7%), C (11.4%), and T (41.1%). Similar to other Pyralidae species, it contains a typically conserved structure including 13 protein-coding genes, 2 RNA genes, 1 control region (D-loop), and 22 transfer RNA genes. The proportion of coding sequences with a total length of 11,433 bp is 75.06%, which encodes 3787 amino acids. Most of the protein-coding genes are initiated by typical ATN codons. Ten are terminated with TAA, whereas three genes, cox1, cox2, and nad4, harbor incomplete termination codons of a single T. The lengths of 12S ribosomal RNA and 16S ribosomal RNA are 779 bp and 1338 bp, respectively. The length of control region is 317 bp, ranging from 14,916 bp to 15,232 bp. The complete mitochondrial genome sequence provided here would be useful for further understanding the evolution of ratite and conservation genetics of *D. perspectalis*.

Mitochondrial DNA (mtDNA) of insect is a circular DNA molecule 14–20 kb in size, containing a remarkably conserved set of 37 genes [13 protein-coding genes (PCGs), two ribosomal RNA genes (rRNA), and 22 transfer RNA genes (tRNA)]. In addition, it contains an adenine and thymine rich region (A+T-rich region) (Zhang et al. 1995; Taanman 1999). MtDNA have been widely used as informative molecular markers for the reconstruction of phylogenetic relationships owing to its maternal inheritance, conserved sequences and rare recombination events (Cameron and Whiting 2008; Yang et al. 2013).

Lepidoptera is the second largest order of insects, more than 160,000 species (Heppner 2008). Pyralidae is a major family in Lepidoptera (Wang 1980). Many species are important agricultural pests, such as *Ostrinia furnacalis*, *Cnaphalocrocis medinalis*, *Conogethes punctiferalis*, and so on. *Diaphania perspectalis* (Walker) is widely distributed in China. *D. perspectalis* mainly damages Buxaceae family, such as *Buxus bodinieri*, *Buxus sinica*, *Ilex chinensis*, and so on (Tang et al. 1990). The insects were collected on *Sophora japonica* from Fengxin, Jiangxi Province, China (located at E115°29’25”, N28°37’23”). Specimens were then stored in −80°C refrigerators of the laboratory in Jiangxi Academy of Forestry.

*D. perspectalis* can cause complete defoliation when reproducing on a large scale, even destroy the host a great quantity. It has two types of body colour: white-black and holo-black. It has four generations during a year and hibernates as a larva in the hibernaculum with leaves and resume eating in warm spring the next year, respectively. The adults of the first, second, third, and hibernated generations emerge in mid June, late July, early September of the first year and late April of the next year, respectively. The larva has 6–8 instar, whose first, second, and third generations has diapause on a part of them. Many natural enemies of the pest were reared. Protecting the natural enemies of *D. perspectalis* is a significant method for the pest control (Chen et al. 2005; Wang 2008; Leuthardt et al. 2010).

Whole mitochondrial genome of *D. perspectalis* has a circular genome of 15,232 bp, containing 13 protein-coding genes, 2 rRNA genes, 1 control region, and 22 tRNA genes. The contents of A, G, T, and C are 39.8, 7.7, 41.1, and 11.4%, respectively. AT and GC contents of mtgenome are 80.9 and 19.1%, respectively. The proportion of coding sequences with a total length of 11,433 bp is 75.06%, which encodes 3787 amino acids. Most of the protein-coding genes are initiated by typical ATN codons. Ten are terminated with TAA, whereas three genes, cox1, cox2, and nad4, harbor incomplete termination codons of a single T. The lengths of 12S ribosomal RNA and 16S ribosomal RNA are 779 bp and 1338 bp, respectively. The length of control region is 317 bp, ranging from 14,916 bp to 15,232 bp. The complete mitochondrial genome sequence provided here would be useful for further understanding the evolution of ratite and conservation genetics of *D. perspectalis*.
Disclosure statement

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper.

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