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Complete mitochondrial genome of the larch hawk moth, ***Sphinx morio*** (Lepidoptera: Sphingidae)

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Abstract

The larch hawk moth, Sphinx morio, belongs to the lepidopteran family Sphingidae that has long been studied as a family of model insects in a diverse field. In this study, we describe the complete mitochondrial genome (mitogenome) sequences of the species in terms of general genomic features and characteristic short repetitive sequences found in the A+T-rich region. The 15,299-bp-long genome consisted of a typical set of genes (13 protein-coding genes, 2 rRNA genes, and 22 tRNA genes) and one major non-coding A+T-rich region, with the typical arrangement found in Lepidoptera. The 316-bp-long A+T-rich region located between srRNA and tRNA^{Met} harbored the conserved sequence blocks that are typically found in lepidopteran insects. Additionally, the A+T-rich region of S. morio contained three characteristic repeat sequences that are rarely found in Lepidoptera: two identical 12-bp repeat, three identical 5-bp-long tandem repeat, and six nearly identical 5–6 bp long repeat sequences.

Keywords::

Mitochondrial genome

Sphinx morio

repeat sequence

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