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The Journal of DNA Mapping, Sequencing, and Analysis

Volume 24, 2013 - Issue 6

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Mitogenome Announcement

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

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Pages 622-624 | Received 24 Jan 2013, Accepted 25 Jan 2013, Published online: 01 Mar 2013

**66** Cite this article https://doi.org/10.3109/19401736.2013.772155



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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 noncoding A+T-rich region, with the typical arrangement found in Lepidoptera. The 316-bplong A+T-rich region located between srRNA and tRNA<sup>Met</sup> 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

Declaration of interest: This research was supported by the Basic Science Research Program through the National Research Foundation of Korea (NRF) funded by the Ministry of Education, Science and Technology (2012R1A1A4A01003465). The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper.

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