

MITOGENOME ANNOUNCEMENT



The complete mitochondrial genome of the wild silkmoth *Antheraea yamamai* from Heilongjiang, China (Lepidoptera: Saturniidae)

Shu-Wei Sun^{a*}, Jing-Chao Huang^{b*} and Yan-Qun Liu^b

^aCollege of Agronomy, Eastern Liaoning University, Dandong, China; ^bCollege of Bioscience and Biotechnology, Shenyang Agricultural University, Shenyang, China

ABSTRACT

Here, we reported the complete mitochondrial genome of *Antheraea yamamai* Guérin-Ménéville (1861) collected in Heilongjiang Province, China. The mitochondrial genome is 15,341 bp and encodes 13 protein-coding genes, two ribosomal RNA genes, and 22 transfer RNA genes. Sequence comparison identified 22 SNVs in the *A. yamamai* mitochondrial genomes between Chinese and Korean populations, indicating a low intraspecific variation between the two populations. Phylogenetic analyses with maximum-likelihood and Bayesian inference methods revealed a close relationship between *A. yamamai* and *Antheraea frithi* and supported the relationship among *Antheraea* species ((*A. yamamai* + *A. frithi*) + *A. pernyi*) + *A. assamensis*).

ARTICLE HISTORY

Received 23 April 2021
Accepted 16 June 2021

KEYWORDS



Antheraea yamamai;
mitochondrial genome;
phylogenetic relationship;
intraspecific variation

The wild silkmoth *Antheraea yamamai* Guérin-Ménéville (1861) is one of the most well-known wild silkmoths belonging to the family Saturniidae. This species is distributed throughout China, Korea, Japan, and Russia. *Antheraea yamamai* produces green silk called Tensan silk, which has been considered a new biomaterial and a useful product in human health research and economic fields (Kim et al. 2018). The pupae of this species are also considered to be potential insect-derived food resources with high nutritional value (Yue et al. 2017). To date, this insect is still a noncultivated silkmoth reared outdoors. To protect this economically important silkmoth resource as well as its living environment, the province-level Shuguang Nature Reserve (N45°47'40" ~ 45°35'27"; E131°03'20" ~ 131°11'17") was created in Heilongjiang Province, China (Hou et al. 2010). In the present study, we reported the complete mitochondrial genome of this wild silkmoth collected in the Shuguang Nature Reserve to provide basic genetic information.

The *A. yamamai* eggs collected in the Shuguang Nature Reserve were kindly provided by Tian-Mao Wang, Developmental Center of Heilongjiang Provincial Sericulture and Bee Industry (N45°54'; E126°39'), Harbin, China. After hatching, the larvae were fed with the leaves of *Salix viminalis* in the Silkmouth Experimental Field of Shenyang Agricultural University (N41°50'1.08"; E123°34'21.92"). An adult specimen was deposited at the Department of

Sericulture, Shenyang Agricultural University, China (<https://www.syau.edu.cn/>, Dr. Yan-Qun Liu, liuyanqun@syau.edu.cn) under voucher number SILKMOTH_YAMAMAI_01. A hind leg was used to extract the total genomic DNA, which was also deposited at the Department of Sericulture. Long PCR amplification was used to obtain the whole mitochondrial genome with two species-specific primer pairs. After purification by gel extraction, the amplification products were mixed equally with a sample from *Antheraea pernyi* Qing_6 and then sequenced on the Illumina PE 150 platform. The resulting clean reads were subjected to the Galaxy web server at usegalaxy.org (<https://usegalaxy.eu/>) to assemble the mitochondrial genome (Jalili et al. 2020).

The whole mitochondrial genome of *A. yamamai* presented here is 15,341 bp in length, thus exhibiting a highly similar size as the reference genome from the Korean population (15,338 bp; EU264055; Kim et al. 2009). This genome also encodes 37 mitochondrial genes, including 13 protein-coding genes, 2 ribosomal RNA genes, and 22 transfer RNA genes, showing an identical genomic component and gene order with known Saturniidae species. The length of the A + T-rich region for *A. yamamai* is 334 bp, which is similar to those of *Antheraea assamensis* and *Antheraea frithi* (328 ~ 334 bp) but much shorter than that of *A. pernyi* (516 ~ 552 bp). Further analysis revealed that the presence of a 38 bp tandem repeat unit (Arunkumar et al. 2006) in *A. pernyi* resulted in the size

CONTACT Yan-Qun Liu  liuyanqun@syau.edu.cn  College of Bioscience and Biotechnology, Shenyang Agricultural University, 120 Dongling Road, Shenyang 110866, China

*S.-W.S. and J.-C.H. contributed equally to this work.

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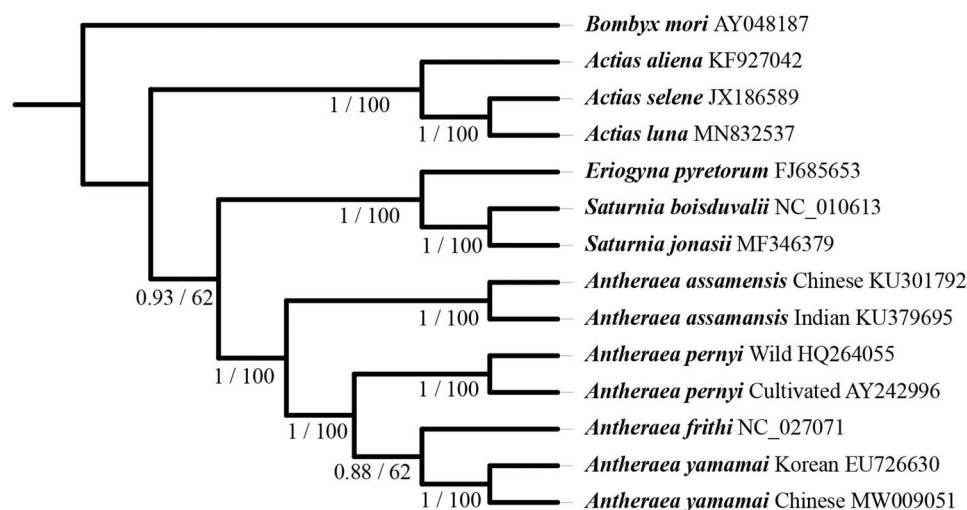


Figure 1. Phylogenetic tree inferred from the whole mitochondrial genome sequence using the maximum-likelihood method and Bayesian inference method with the GTR + F + R3 model. The numbers at each node are Bayesian posterior probabilities (first value) and bootstrap percentages of 1000 replicates (second value). GenBank accession numbers are listed following the scientific name.

variation of the A + T-rich region mentioned above, thus contributing to the length variation of whole mitochondrial genomes of the genus *Antheraea*.

By sequence comparison, we identified 22 SNVs (19 SNPs and three indels) between the two *A. yamamai* mitochondrial genomes. Three single-base deletion mutations occurred in the intergenic spacer region *ND4-ND4L*. Among these 19 SNPs, four were present in *rRNAs* and one was in the intergenic spacer region *ND2-tRNA^{trp}*; the remaining 14 occurred in protein-coding genes, resulting in five amino acid changes. The number of SNVs between the two *A. yamamai* mitochondrial genomes were smaller than those between the cultivated and noncultivated *A. pernyi* mitochondrial genomes [264 SNVs (213 SNPs and 51 indels)] and between the two *A. assamensis* mitochondrial genomes [246 SNVs (158 SNPs and 88 indels)], but similar to those between strains of *A. pernyi* (Li et al. 2021). These results indicated a low intraspecific variation between Chinese and Korean populations of *A. yamamai*, suggesting that they might be derived from a common population.

For phylogenetic analysis (Figure 1), seven whole mitochondrial genomes from *Antheraea* species were included (Kim et al. 2009; Shantibala et al. 2017; Singh et al. 2017; Zhong et al. 2017). Six mitochondrial genomes from non-*Antheraea* species were also included. *Bombyx mori* (Lu et al. 2002) served as an outgroup. A maximum-likelihood tree was constructed with IQ-TREE 1.6.12 (Nguyen et al. 2015), and a Bayesian inference tree was constructed with MrBayes v.3.2 (Ronquist et al. 2012). Our phylogenetic analyses revealed a close relationship between *A. yamamai* and *A. frithi* and supported the relationship of the genus *Antheraea* (((*A. yamamai* + *A. frithi*) + *A. pernyi*) + *A. assamensis*).

Disclosure statement

The authors declare no competing financial interest. The authors alone are responsible for the content and writing of the paper.

Funding

This work was supported by grants from the National Natural Science Foundation of China [31972617] and China Agriculture Research System of MOF and MARA [CARS-18].

Data availability statement

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at (<https://www.ncbi.nlm.nih.gov/>) under the accession No. MW009051. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA702206, SRS8270459, and SAMN17928658, respectively.

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