



Complete mitochondrial genomes of the Bright Sunbeam *Curetis bulis* and the Small Copper *Lycaena phlaeas* (Lepidoptera: Lycaenidae) and their phylogenetic implications

L.L. Zhang¹, J.S. Hao^{1,2}, D.Y. Huang¹, X.Y. Sun², J.J. Hao¹, C.M. Peng¹ and Q. Yang²

¹Laboratory of Molecular Evolution and Biodiversity, College of Life Sciences, Anhui Normal University, Wuhu, China

²State Key Laboratory of Palaeobiology and Stratigraphy, Nanjing Institute of Geology and Palaeontology, Chinese Academy of Sciences, Nanjing, China

Corresponding author: J.S. Hao / Q. Yang
E-mail: jshaonigpas@sina.com / qunyang@nigpas.ac.cn

Genet. Mol. Res. 12 (4): 4434-4445 (2013)

Received September 28, 2012

Accepted January 31, 2013

Published October 10, 2013

DOI <http://dx.doi.org/10.4238/2013.October.10.9>

ABSTRACT. In this study, the complete mitochondrial genomes of *Curetis bulis* and *Lycaena phlaeas* were determined and analyzed. The circular genomes are 15,162 bp long for *C. bulis* and 15,280 bp long for *L. phlaeas*, with a total A+T content of 82.6 and 83.1%, respectively. Both mitogenomes contain 37 genes, and their gene orders are similar to those of other lepidopterans. All protein-coding genes (PCGs) are initiated by ATN codons, except for *cox1*, which is started with the CGA codon; all PCGs terminate in the typical stop codon TAA, except for *cox1*, *cox2*, and *nad4*, which end with a single T. The codons TTA (Leu), ATT (Ile), TTT (Phe), ATA (Met), and AAT (Asn) appear the most frequently. Both of the mitogenome A+T-rich regions harbor the motif ATAGA, followed by a 19-bp

poly(T) stretch, with *C. bulis* containing a microsatellite-like (AT)₅ element next to the ATTTA motif, and *L. phlaeas* containing a microsatellite-like (TA)₆ (AT) element next to the ATTTA motif. The phylogenetic trees of the 17 representative butterfly species, including the two species of this study, were reconstructed with the maximum likelihood and Bayesian inference methods, based on the 13 PCG nucleotide sequence data. The results of the phylogenetic analyses strongly supported the relationships of (((Lycaenidae + Pieridae) + Nymphalidae) + Hesperidae) + Papilionidae, which was markedly different from the traditional morphological view of the Lycaenidae and Nymphalidae considered to be sisters of each other.

Key words: Mitochondrial genome; Lepidoptera; Lycaenidae; *Curetis bulis*; *Lycaena phlaeas*; Phylogenetic analysis