

The Complete Nucleotide Sequence and Gene Organization  
of the Mitochondrial Genome of the Korean Hairstreak,  
*Coreana raphaelis* (Lepidoptera: Lycaenidae)

Iksoo Kim<sup>1</sup>, Eun-Mee Lee<sup>1</sup>, Kwang-Youl Seol<sup>1</sup>, Eun-Young Yun<sup>1</sup>, Jae-Sam Hwang<sup>1</sup> and Byng Rae Jin<sup>2</sup>

<sup>1</sup>*Department of Agricultural Science and Technology, Suwon 441-100, Korea*  
and <sup>2</sup>*College of Natural Resources and Life Science, Dong-A University,*  
*Busan 604-714, Korea*

The complete nucleotide sequences of the mitochondrial genome (mitogenome) of the *Coreana raphaelis* (Lepidoptera: Lycaenidae) was determined. The 15,314 bp long *C. raphaelis* mitogenome contains lepidopteran-specific gene order and arrangement, but has an extra tRNA<sup>Ser</sup>(AGN), which encodes an anticodon ACT, instead of the common TCT. The *C. raphaelis* is the first species of the lepidopteran insect with 23 tRNA genes instead of the usual 22. The anticodons of all lepidopteran tRNAs sequenced in their entire mitogenomes (including two nearly completed ones) are universally identical to their counterparts, except for *C. raphaelis* tRNA<sup>Ser</sup>(AGN), for which TCT, instead of GCT, was utilized. The tRNA<sup>Ser</sup>(AGN) could not form a stable stem-and-loop structure in the DHU arm as shown in many other insect tRNA<sup>Ser</sup>(AGN). Genes overlap in a total of 20 bp in 4 locations and contain a total of 178 bp of intergenic spaces spread over in 17 locations. The *C. raphaelis* A+T-rich region contains several short conserved sequence blocks (6 bp ~ 13 bp) scattered through the whole region, a poly-thymidine stretch, TA(A)<sub>n</sub>-like stretch downstream of the poly(T) stretch, and several inverted sequence blocks that have the potential to form stable stem-and-loop structure without conserved flanking sequences at each end. The initiation codon for *C. raphaelis* COI gene appears to be the tetranucleotide, TTAG, found commonly in the sequenced Lepidoptera. Only five of 13 protein-coding genes (PCGs) have a complete termination codon, and the remaining eight have incomplete T or TA. The PCGs neighboring to the 5' end region of

another PCG (ATPase8, ATPase6, ND4L, and ND6) have a potential to form hairpin structure. The complete nucleotide sequence of the *C. raphaelis* mtDNA described here will be useful sequence information to determine genetic relatedness of donor and donee populations of the rare *C. raphaelis*.