

Presence of Duplicated tRNA^{Ser}(AGN) in
the Complete Mitochondrial Genome of the Korean
Hairstreak, *Coreana raphaelis* (Lepidoptera: Lycaenidae)

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We determined the complete nucleotide sequences of the mitochondrial genome (mitogenome) of the Korean hairstreak, *Coreana raphaelis* (Lepidoptera: Lycaenidae). The entire mitochondrial DNA (mtDNA) molecule was 15,314-bp long. The *C. raphaelis* genes were in the same order and orientation as the completely sequenced mitogenomes of other lepidopteran species, except for the presence of an extra copy of tRNA^{Ser}(AGN). High similarity in primary sequence and secondary structure between the two tandemly located copies of the tRNA^{Ser}(AGN) suggest a recent duplication of an original single tRNA^{Ser}(AGN). The DHU arm of the two copies of tRNA^{Ser}(AGN) formed a simple loop as seen in many other metazoan mt tRNA^{Ser}(AGN). The putative initiation codon for the *C. raphaelis* COI gene appears to be a tetranucleotide, TTAG, found commonly in the sequenced lepidopterans. ATPase8, ATPase6, ND4L, and ND6 genes, which are neighboring to another protein-coding gene at their 3' end all had the sequences potential to form hairpin structure, suggesting the importance of such structure for precise cleavage of the mature protein-coding genes.