

Abundant tRNA Rearrangement and tRNA-like Structures in
the Mitochondrial Genome of the Bumblebee,
Bombus ignitus (Hymenoptera: Apidae)

Iksoo Kim^{1*}, So Young Cha¹, Hyung Joo Yoon¹, Eun Mee Lee¹,
Yong Soo Choi³, Myung Hee Yoon², Jae Sam Hwang¹ and Byung Rae Jin³

¹Department of Agricultural Biology, The National Institute of Agricultural
Science and Technology, Suwon 441-100, Korea; ²Department of Biology,
Kyungsung University, Busan 608-736, Korea; and ³College of Natural
Resources and Life Science, Dong-A University, Busan 604-714, Korea

The complete nucleotide sequence of the mitochondrial genome of the bumblebee, *Bombus ignitus* (Hymenoptera: Apidae), was determined. The entire *B. ignitus* mitochondrial genome (mitogenome) was sequenced by amplification in ten overlapping fragments. The circular genome was 16,434 bp and contains a typical base composition, and codon usage found in metazoan mt genome. However, in addition to the regular 22 tRNA genes the *B. ignitus* mitogenome contains five tRNA-like structures: each two tRNA^{Leu}(UUR)-like sequences and tRNA^{Ser}(AGN)-like sequences and one tRNA^{Phe}-like sequence. Their locations and possibility as genuine genes were discussed. In comparison with other insect mitogenomes sequenced in their entirety (e.g., *Drosophila*) the *B. ignitus* mitogenome has several translocations in tRNA genes, resulting in unique orientation and gene order among sequenced insect mitogenomes.