

## Nearly Complete Nucleotide Sequence of the Mitochondrial Genome of the Bumblebee, *Bombus ignitus* (Hymenoptera: Apidae)

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*Bombus ignitus* is distributed in Korea, China, Russia, and Japan. The species is under extensive study for green house pollination in Korea. We have sequenced nearly complete mitochondrial (mt) genome of the bumblebee, *Bombus ignitus* (Hymenoptera: Apidae). The circular genome is 15,975-bp long, excluding unfinished "AT dinucleotide repeat region", located between two protein-coding genes, ND5 and ND3, which is believed to span ~300 bp. Although typical metazoan mt genome contains 13 protein-coding genes, 22 tRNAs, and 2 rRNAs plus A+T-rich region, but our data is peculiar in some aspects. The genome is lacking for six tRNAs, i.g., tRNA<sup>Met</sup>, tRNA<sup>Arg</sup>, tRNA<sup>Asn</sup>, tRNA<sup>Ser</sup>(AGN), tRNA<sup>Glu</sup>, and tRNA<sup>Phe</sup>. Among these tRNA<sup>Phe</sup> might be located between ND5 and ND4, but this region is overlapping by more than two-third of the gene with reversibly encoded tRNA<sup>His</sup>. Considering the size of unfinished "AT dinucleotide repeat region", the undiscovered six tRNAs may not be located in such a short stretch. Another possible location for those tRNAs in the mt genome can be a 982-bp long non-coding A+T-rich region, located between tRNA<sup>Gly</sup> and tRNA<sup>Ala</sup>, but an extensive effort to locate those tRNAs turned out to be failure. Comparison of gene arrangement of the *B. ignitus* mt genome with other insects, particularly to other bee species (Apidae) showed translocation in several tRNAs to each other, resulting in a unique gene arrangement in the *B. ignitus* mt genome, although protein-coding genes, rRNAs, and A+T-rich region are placed at the homologous region of the other insect mt genomes. Further scrutinized examination of the genomic organization and arrangement may provide interesting aspects of mt genome evolution in insects.