



# Distribution of mitochondrial DNA fragments in the nuclear genome of the honeybee

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**ABSTRACT.** Nuclear mitochondrial pseudogenes (numts), which originated from mitochondrial DNA (mtDNA) insertions in the nuclear genome, have been detected in many species. The distribution of numts in the honeybee nuclear genome has not yet been fully reported. By referring to the whole honeybee mtDNA sequence and to the recent version of the honeybee nuclear genome, 236 reference sequences were identified by BLAST, with 90 unmapped. The size of the numts ranged from 219 to 3788 bp, and the homologous identity between numts and their corresponding mtDNA fragments varied from 71 to 93%. Furthermore, identified honeybee numts covered nearly all mitochondrial genes and were distributed over all chromosomes. This study provides useful information for further research related to mitochondrial genes and the evolution of the honeybee.

**Key words:** Honeybee; Mitochondrial pseudogenes (numts)