

## MITOGENOME ANNOUNCEMENT

**Complete mitochondrial genome of the Algerian honeybee,  
*Apis mellifera intermissa* (Hymenoptera: Apidae)**Peng Hu<sup>1\*</sup>, Zhi-Xiang Lu<sup>1\*</sup>, Nizar Haddad<sup>2</sup>, Adjlane Nouredine<sup>3</sup>, Wahida Loucif-Ayad<sup>4</sup>, Yong-Zhi Wang<sup>5</sup>, Ren-Bin Zhao<sup>1</sup>, Ai-Ling Zhang<sup>1</sup>, Xin Guan<sup>1</sup>, Hai-Xi Zhang<sup>1</sup>, and Hua Niu<sup>6</sup>

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**Abstract**

In this study, the complete mitochondrial genome sequence of Algerian honeybee, *Apis mellifera intermissa*, is analyzed for the first time. The results show that this genome is 16,336 bp in length, and contains 13 protein-coding genes, 22 transfer RNA genes, 2 ribosomal RNA genes, and 1 control region (D-loop). The overall base composition is A (43.2%), C (9.8%), G (5.6%), and T (41.4%), so the percentage of A and T (84.6%) is considerably higher than that of G and C. All the genes are encoded on H-strand, except for four subunit genes (ND1, ND4, ND4L, and ND5), two rRNA genes (12S and 16S rRNA), and eight tRNA genes. The complete mitochondrial genome sequence reported here would be useful for further phylogenetic analysis and conservation genetic studies in *A. m. intermissa*.

**Keywords**Algerian honeybee, *Apis mellifera intermissa*, mitochondrial genome**History**

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The Algerian honeybee, *Apis mellifera intermissa*, is one of the most successful species in the animal kingdom with regard to its ability to adapt to great variations in climatic conditions (Barour et al., 2011). It is a native subspecies of Algeria, and historically found in Tunisia, Algeria and Morocco, between the Atlas and the Mediterranean and Atlantic coasts (Garnery et al., 1992; Ruttner, 1988; Wagner, 1990). Based on the extensive morphometric, allozymic and molecular analyses, there are nearly 26 different subspecies currently recognized in the species of *A. mellifera* (Cornuet & Garnery, 1991; Ruttner, 1988). However, none of the mitochondrial genome for this species was reported previously. Here, using the sequencing data released by National Center for Agricultural Research and Extension (Amman, Jordan), we assembled and analyzed the mitochondrial genome of Algerian honeybee, *A. m. intermissa*, and deposited it into the GenBank database with the accession number of KM458618. This mitochondrial sequence reported here will contribute to address the phylogenetic placement of the Algerian honeybee, and enhance our understanding of honeybee's biology.

The complete mitochondrial genome sequence of *A. m. intermissa* (16,336 bp in length) harbored a total of 13 protein-coding genes, 22 tRNA genes, 2 rRNA genes (12S rRNA and 16S rRNA), and 1 non-coding control region (D-loop). The gene composition and arrangement were the same as the typical mitogenome structure of other honeybees (Crozier & Crozier, 1993; Tan et al., 2011; Wang et al., 2013). Most of these genes were located on the H-strand except for four subunit genes (ND1, ND4, ND4L, and ND5), two rRNA genes (12S and 16S rRNA), and eight tRNA genes (Table 1). The overall base composition was A (43.2%)4T (41.4%)4C (9.8%)4G (5.6%), and a significant A-T bias (84.6%) was observed.

All the 13 protein-coding genes (11,061 bp in length) of *A. m. intermissa* mitochondrial genome were annotated by comparing with the published sequences of other honeybees. They encoded 3674 amino acids in all. Of them, three (COX3, ATP6 and COX3) regarded ATG as the start codon, while ND3, ND4 and COX1 utilized ATA, ND1, ND4L, ND5, ND6, COX2 and ATP8 started with ATT, and ND2 initiated with ATC. All of the 13 protein-coding genes were terminated with TAA stop codon.

The 22 tRNA genes of *A. m. intermissa* range in size from 63 bp (tRNA<sup>Ser</sup>) to 78 bp (tRNA<sup>Thr</sup>). Of them, 21 could fold into typical cloverleaf secondary structure except for tRNA<sup>Thr</sup> whose dihydrouridine (DHU) arm was lost. The 2 rRNA genes, 12S and 16S rRNA, were 785 bp and 1369 bp in length, respectively. They were located between the tRNA<sup>Leu</sup> and tRNA<sup>Glu</sup> genes and further separated by tRNA<sup>Val</sup>. The control region of *A. m. intermissa* mtDNA was 821 bp long and located between tRNA<sup>Val</sup> and tRNA<sup>Glu</sup>.

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Table 1. List of genes encoded by *A. m. intermissa* mitochondrial genome.

Gene	Position		Size (bp)	Base composition (%)				Start codon	Stop codon	Strand
	From	To		A	C	G	T			
tRNA <sup>Glu</sup>	1	66	66	53	3	1.5	42.4			H
tRNA <sup>Ser</sup>	116	178	63	41.3	14.3	6.3	38.1			H
tRNA <sup>Met</sup>	217	282	66	43.9	12.1	9.1	34.8			H
tRNA <sup>Gln</sup>	292	354	63	39.7	3.2	7.9	49.2			H
tRNA <sup>Ala</sup>	355	424	70	45.7	4.3	5.7	44.3			H
tRNA <sup>Ile</sup>	428	497	70	42.9	4.3	8.6	44.3			H
ND2	498	1499	1002	39.1	9	4.9	47	ATC	TAA	H
tRNA <sup>Cys</sup>	1499	1571	73	46.6	5.5	6.8	41.1			L
tRNA <sup>Tyr</sup>	1592	1659	68	50	4.4	7.4	38.2			L
tRNA <sup>Trp</sup>	1726	1797	72	50	5.6	2.8	41.7			H
COX1	1798	3363	1566	34.8	13.2	10.9	41.1	ATA	TAA	H
tRNA <sup>Leu</sup>	3359	3428	70	42.9	7.1	11.4	38.6			H
COX2	3620	4297	678	38.6	11.5	8.6	41.3	ATT	TAA	H
tRNA <sup>Asp</sup>	4296	4364	69	47.8	4.3	4.3	43.5			H
tRNA <sup>Thr</sup>	4372	4440	69	37.7	8.7	11.6	42			H
ATP8	4446	4604	159	46.5	8.8	3.1	41.5	ATT	TAA	H
ATP6	4586	5266	681	38.2	10	5.6	46.3	ATG	TAA	H
COX3	5287	6066	780	36.7	10.5	7.2	45.6	ATG	TAA	H
tRNA <sup>Gly</sup>	6121	6186	66	53	6.1	1.5	39.4			H
ND3	6187	6540	354	38.1	9.3	4.8	47.7	ATA	TAA	H
tRNA <sup>Arg</sup>	6574	6640	67	43.3	7.5	6	43.3			L
tRNA <sup>Asn</sup>	6737	6805	69	47.8	7.2	7.2	37.7			H
tRNA <sup>Phe</sup>	6813	6881	69	43.5	2.9	8.7	44.9			L
ND5	6894	8558	1665	37.5	5	9.7	47.7	ATT	TAA	L
tRNA <sup>His</sup>	8559	8626	68	41.2	2.9	11.8	44.1			L
ND4	8646	9983	1338	36.2	4.6	8.7	50.4	ATA	TAA	L
ND4L	9989	10,252	264	32.2	2.3	12.1	53.4	ATT	TAA	L
tRNA <sup>Thr</sup>	10,265	10,342	78	47.4	5.1	5.1	42.3			H
tRNA <sup>Pro</sup>	10,362	10,430	69	40.6	2.9	11.6	44.9			L
ND6	10,439	10,942	504	42.9	9.9	3	44.2	ATT	TAA	H
CytB	11,002	12,153	1152	36.6	11.5	8.3	43.6	ATG	TAA	H
tRNA <sup>Ser</sup>	12,199	12,265	67	46.3	4.5	9	40.3			H
ND1	12,300	13,217	918	33.9	5.6	11.7	48.9	ATT	TAA	L
tRNA <sup>Leu</sup>	13,218	13,288	71	42.3	4.2	8.5	45.1			L
16S rRNA	13,289	14,657	1369	40.5	5	10.4	44			L
tRNA <sup>Val</sup>	14,661	14,731	71	42.3	2.8	9.9	45.1			L
12S rRNA	14,731	15,515	785	41.9	6	12.9	39.2			L
D-loop	15,516	16,336	821	52.4	3.5	1.1	43			H

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## Declaration of interest

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper.

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