



Mitochondrial DNA Part B Resources

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The complete mitochondrial genome of an edible wasp *Vespula flaviceps* (Hymenoptera, Vespidae)

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ABSTRACT

In this study, the complete mitogenome sequence of *Vespula flaviceps* (Hymenoptera, Vespidae) has been sequenced. The mitogenome, 17,489 bp, includes 13 protein-coding, 22 transfer RNAs, two ribosomal RNAs genes and a noncoding D-loop region. The D-loop of 1302 bp length is located between rRNA-S and tRNA^{Tyr}. The overall base composition of *V. flaviceps* is 39.34% for A, 13.62% for C, 40.99% for T, and 6.05% for G, with a high AT bias of 80.33%. This mitogenome data might be useful for further phylogeography analyses and other related studies in Hymenoptera.

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Vespula flaviceps (Hymenoptera, Vespidae, Vespula) is a species of social wasp, mainly distributed in Eastern and Southern Asia. This wasp is popular as food in Southern China, Central Japan, and Korea, and its larvae are considered as a special delicacy. Elucidating the structure of *V. flaviceps* mitogenome is important for understanding its diversity and evolution.

The specimen of *V. flaviceps* was obtained from Kunming, Yunnan, P.R. China and kept in the Insect Collection of Research Institute of Resource Insects, Chinese Academy of Forestry. Total genomic DNA was extracted from its chest muscle with SDS-phenol chloroform method. Sequencing work of the complete mitogenome of *V. flaviceps* was performed by Illumina Nextseq500 in Beijing Microread Genetics Co., Ltd., with a total data volume 4G (150 bp Reads), and high-quality reads were assembled from scratch using IDBA-UD and SPAdes (Gurevich et al. 2013).

The complete mitogenome of *V. flaviceps* was found to be bigger than most other invertebrates. The gene order and orientation are also different from the most common type suggested as ancestral for insects (Boore et al. 1998; Taanman 1999). It was 17,489 bp in size (GenBank accession number MK248830), including 13 typical invertebrate protein-coding genes (PCGs), 22 transfer RNA genes, two ribosomal RNA genes and a noncoding control region (D-loop). The A+T content of the whole *V. flaviceps* mitogenome is 80.33%, showing an obvious AT mutation bias (Eyre-Walker 1997). The D-loop region exhibits the highest A+T content (88.33%) in the *V. flaviceps* mitogenome. This region has

been shown to harbor the origin sites for the transcription and replication for both strands of insect mitogenomes (Yukuhiro et al. 2002).

All the 13 PCGs use standard ATN (Met) start codon (ATG in *ND2*, *ATP6*, *COX3*, *ND4*, *ND6*, *CytB*; ATT in *COX1*, *COX2*, *ATP8*; ATA in *ND3*, *ND5*, *ND4L*, *ND1*) All the PCGs, except *COX3*, had the common stop codon TAA, whereas *COX3* terminated with incomplete stop codon T. Similar cases could be found in other insect mitogenomes (Yin et al. 2012). It has been demonstrated that the incomplete stop codons could produce functional stop codons 'TAA' in polycistronic transcription cleavage and polyadenylation processes by the addition of 3'A residues (Ojala et al. 1981).

All the tRNAs except tRNA^{Ser}(AGN) could be folded into the typical cloverleaf secondary structures. The unusual tRNA^{Ser}(AGN) lacks dihydrouridine (DHU) arm. The rRNA-S gene is located between tRNA^{Val} and the D-loop region, while rRNA-L is located between *ND1* and tRNA^{Val}. In other insects, the rRNA-L gene is usually located between tRNA^{Leu} (CUN) and tRNA^{Val} (Boore et al. 1998; Kim et al. 2009), this demonstrated that in *V. flaviceps* mitogenome the positions of *ND1* and tRNA^{Leu} (CUN) were interchanged.

Based on the concatenated amino acid sequences of 13 PCGs, the neighbour-joining method was used to construct the phylogenetic relationship of *V. flaviceps* with 11 other wasps (Figure 1). The result showed that *V. flaviceps* is closely related to *V. germanica*, which is in accordance with the traditional morphological classification (Carpenter and Nguyen 2003).

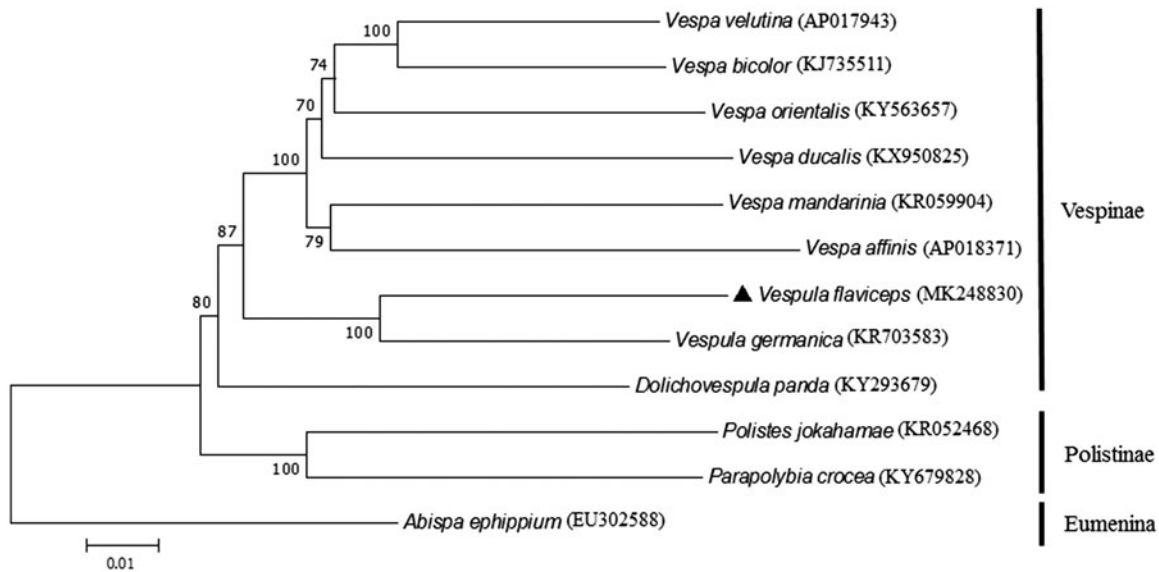


Figure 1. Phylogenetic tree showing the relationship between *V. flaviceps* and 11 other wasps based on neighbour-joining method. *Abispa ephippium* was used as an outgroup. GenBank accession numbers of each species were listed in the tree.

Disclosure statement

The authors declare no competing materials in the preparation and execution of this manuscript. The authors are responsible for the content and writing of this paper.

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