


MITOGENOME ANNOUNCEMENT



## The complete mitochondrial genome of *Melanostoma orientale* (Diptera: Syrphidae)

Qianquan Chen , Xiaojuan Niu, Zheng Fang and Qingbei Weng

School of Life Sciences, Guizhou Normal University, Gui'an, China

### ABSTRACT

The mitochondrial genome of *Melanostoma orientale* has been decoded by Illumina sequencing. The mitogenomic size is 16,229 bp with 40.96% A, 40.29% T, 10.60% C, and 8.15% G. It is encoded with 13 protein-coding genes, 2 ribosomal RNA, and 22 transfer RNAs. The phylogenetic tree showed that 10 species of Syrphidae, belonging to six genera, were clustered into two clades. This is the first mitochondrial genome for the genus *Melanostoma*.

### ARTICLE HISTORY

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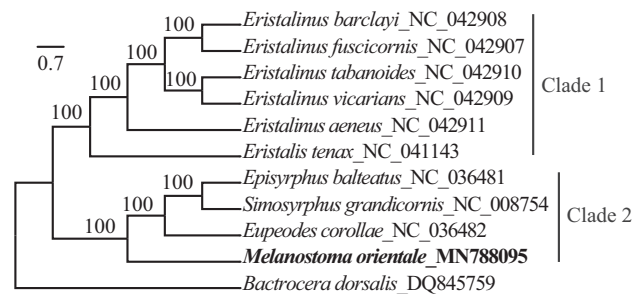
### KEYWORDS

Flower flies; pollinators; mitogenome; Diptera

Syrphidae is a large family of Diptera with more than 6200 species (Mengual et al. 2015; Young et al. 2016). They are known as hoverflies as their adults can pollinate for plants. Due to the lack of comprehensive identification keys, it is difficult to discriminate hoverflies by morphological characteristics (Jordaens et al. 2015; Adachi-Hagimori et al. 2018). Mitogenomic information could overcome the difficulty.

Specimens of *Melanostoma orientale* were collected from the campus of Guizhou Normal University (26°22'50.30"N, 106°38'11.72"E) on April 2019. The specimens (GZNU-cqq-10) were stored at the Museum of Guizhou Normal University. The mitogenome was sequenced using Illumina HiSeqXten, and assembled with SOAPdenovo2 (Luo et al. 2012). Gaps were filled by Sanger sequencing. Protein-coding genes (PCGs) were identified by blasting with mitogenomes of Syrphidae. tRNAs were identified with MITOS2 (Bernt et al. 2013), and rRNAs and A+T-rich region were determined by the boundary of tRNAs. Phylogenetic tree was constructed with the whole mitogenome sequence of Syrphidae using PhyloSuite (Zhang et al. 2019).

The mitogenomic size of *M. orientale* (MN788095) is 16,229 bp. *Melanostoma orientale* shared similar gene distribution pattern with other Syrphidae species (Li et al. 2017; Pu et al. 2017; Li and Li 2019). A total of 168 bp intergenic spacers were distributed in 20 locations. The shortest intergenic spacer was 1 bp and the longest intergenic spacer was 31 bp, which was located between trnS2 and *nad1*. The shortest overlap, located between trnF and *nad5*, was 1 bp;



**Figure 1.** Bayesian phylogenetic tree of 10 Syrphidae species. *Bactrocera dorsalis* (Diptera: Tephritidae) was selected as representative of the outgroup.

the longest overlap, located between *atp8* and *atp6*, *nad4* and *nad4l*, was 7 bp. The A+T-rich region, located between *rrnS* and *trnI*, was 1270 bp. Six PCGs (*cox2*, *atp6*, *cox3*, *nad4*, *nad4l* and *cob*), four PCGs (*nad2*, *nad3*, *nad5* and *nad6*), two PCGs (*cox1* and *nad1*) and *atp8* used ATG, ATT, ATA and ATC as start codon, respectively. Ten PCGs used TAA as stop codon. However, *nad2*, *cox1* and *nad3* used T as an incomplete stop codon.

At present, only 10 mitogenomic sequences of Syrphidae are available in NCBI. Phylogenetic tree showed that 10 species belonged to six genera (Figure 1). *Eristalinus* and *Eristalis* were clustered into one clade. The relationship of another clade was: *Melanostoma* + (*Eupeodes* + (*Simosyrphus* + *Episyrrhus*)).

## Disclosure statement

No potential conflict of interest was reported by the authors.

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## ORCID

Qianquan Chen  <http://orcid.org/0000-0002-6703-6273>

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