The complete mitochondrial genome of *Anatrichus pygmaeus* Lamb, 1918 (Diptera, Chloropidae)

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**ABSTRACT**

The genus *Anatrichus* Loew, 1860 belongs to the subfamily Oscinellinae of the family Chloropidae. We report the complete mitogenome of *Anatrichus pygmaeus* as the new representative of the subfamily Oscinellinae. The complete mitochondrial genome was 17,125 bp in length. It consisted of 13 protein-coding genes, 22 transfer RNA genes, two ribosomal RNA genes, and a control region. The phylogenetic result showed that the family Chloropidae is monophyletic, and the subfamily Chloropinae is a sister group of the subfamily Oscinellinae.
GTG and COX1 started with TCG. TAA was used as the stop codon for nine protein-coding genes. However, the COX1, COX2, NAD4, and NAD5 used a single T as the incomplete stop codon.

The phylogeny analysis based on 18 Diptera species protein-coding genes was performed by the IQ-TREE web server (Trifinopoulos et al. 2016) with 1000 bootstrap replications (Figure 1). Three species of Chloropidae were included in the analysis, of which Anatrichus pygmaeus and Dicraeus orientalis Becker, 1911 belong to the subfamily Oscinellinae and Chlorops oryzae Matsumura, 1915 belongs to the subfamily Chloropinae. The phylogenetic result showed that the monophyly of Chloropidae was strongly supported (100%), which was consistent with previous phylogenetic results based on morphological characteristics (Griffiths 1972). The monophyly of the subfamily Oscinellinae was also strongly supported (100%), and the subfamily Chloropinae is a sister group of the subfamily Oscinellinae.

**Author contributions**

XDC, DY, and XYL contributed to the conception and design of the research. XDC performed experiments and analyzed the data. XDC drafted the manuscript. XYL and DY revised the manuscript. All authors have approved the manuscript for publication and agreed to be accountable for all aspects of the work.

**Ethical approval**

The specimen collection protocol was approved by the Ethics Committee of China Agricultural University. The studies did not involve endangered or protected species.

**Disclosure statement**

No potential conflict of interest was reported by the author(s).

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**Data availability statement**

Mitochondrial genome sequence can be accessed via accession number OM214541 in GenBank of NCBI at https://www.ncbi.nlm.nih.gov. The associated BioProject, Bio-Sample, and SRA, numbers are PRJNA795831, SAMN24781128, and SRR17640167, respectively.

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