Complete mitochondrial genome of *Polyphaga plancyi* (Blattaria: Polyphagidae)

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**ABSTRACT**

The complete mitochondrial genome of *Polyphaga plancyi* is a 15,547 bp circular molecule, which contains 37 typical mitochondrial genes (13 protein-coding genes, 2 rRNAs and 22 tRNAs) and a 854 bp D-loop. Its gene arrangement pattern is identical with typical other cockroaches. All protein-coding genes start with an ATG codon except COI, ND3, ND5, ND4, ND4L ND6 and ND1. TAA is the most frequent stop codon, and TAG, GCA, TA- and T- are also occurred very common. The mtDNA sequence contains 12S RNA and 16S RNA of rRNA. Except for trNA\(^{\text{Ser(AGN)}}\) and trNA\(^{\text{Leu(CUN)}}\) without the dihydroxyuridine (DHU) arm, all tRNAs could be folded into canonical cloverleaf secondary structures. The phylogenetic trees from the ML and BI analyses based on the complete mtDNA of nine cockroaches species, share similar topologies and high node support values. *Polyphaga plancyi* has close relative with *Eupolyphaga sinensis*.

*Polyphaga plancyi* is endemic species belongs to the family Polyphagidae and the order Blattaria, distributed in North China of Hebei and Shanxi Province, and Beijing City. This species is used to be a traditional Chinese medicine, which play an important role in dealing with thrombi (He et al. 2004; Zhang et al. 2010). As an important traditional Chinese medicine, it has been widely artificial feeding in China. Despite a lot of studies about morphological, physiological and biological features were reported, few researches on molecular biology have been done yet.

The samples of *Polyphaga plancyi* was collected from Hejian City, Hebei Province in August, 2015. The samples were stored at medical animals room, in the School of Life Science, Anhui Medical University, P. R. China (Sample codes are AMHU-YXDW20150822). In this study, we determined the complete mtDNA sequence of *Polyphaga plancyi* with the hope of providing more useful molecular information for further studies of traditional Chinese medicine. The complete mtDNA sequence of *Polyphaga plancyi* has been assigned GenBank accession number KU157228.

The length of the complete mtDNA sequence is 15,547 bp, is similar to other Blattaria species (Yamauchi et al. 2004; Xiao et al. 2012). The overall base composition for the mtDNA contains 37 typical mitochondrial genes (13 protein-coding genes, 2 rRNAs and 22 tRNAs) and a 854 bp D-loop. Its gene arrangement pattern is identical with typical other cockroaches. All protein-coding genes start with an ATG codon except COI, ND3, ND5, ND4, ND4L ND6 and ND1. TAA is the most frequent stop codon, and TAG, GCA, TA- and T- are also occurred very common. The mtDNA sequence contains 12S RNA and 16S RNA of rRNA. Except for trNA\(^{\text{Ser(AGN)}}\) and trNA\(^{\text{Leu(CUN)}}\) without the dihydroxyuridine (DHU) arm, all tRNAs could be folded into canonical cloverleaf secondary structures. The phylogenetic trees from the ML and BI analyses based on the complete mtDNA of nine cockroaches species, share similar topologies and high node support values. *Polyphaga plancyi* has close relative with *Eupolyphaga sinensis*.

Through the 13 PCGs, the longest one is ND5, and the shortest is ATP8, similar with the other species (Zhang et al. 2010; Xiao et al. 2012). All protein-coding genes start with an ATG codon except COI, ND3, ND5, ND4, ND4L ND6 and ND1. TAA is the most frequent stop codon, although ND3, ND4L and ND1 end with TAG, and COI and ATP8 end with TA-, COII end with GCA, and ND4 stop with the single nucleotide T-.

The new mtDNA sequence contains a small subunit (12S RNA) and a large subunit (16S RNA) of rRNA, which are located between tRNA\(^{\text{Phe}}\) and D-loop, separated by tRNA\(^{\text{Val}}\). The 12S RNA is 711 bp long and the 16S RNA is 1 295 bp in length. All tRNA genes possess the typical clover leaf secondary structure except for tRNA\(^{\text{Ser(AGN)}}\) and tRNA\(^{\text{Leu(CUN)}}\), which lacks a dihydroxyuridine (DHU) arm. The non-coding regions include a control region (D-loop) and a few intergenic spacers. The D-loop is located between 12S RNA and tRNA\(^{\text{Val}}\), and is 854 bp long.

Phylogenetic trees were estimated using ML and BI methods, based on the complete mtDNA of 9 Blattaria species, and corresponding *Ctenoptilum vasava* (NC_016704) sequence was used as outgroup, sharing similar topologies and high node support values (Figure 1). *Polyphaga plancyi* has close relative with *Eupolyphaga sinensis*. The result indicates that these two species have close relationship, which is consistent with the traditional classification (Xiao et al. 2012).
The complete mtDNA sequence of *Polyphaga plancyi* has been assigned GenBank accession number KU157228.

**Disclosure statement**

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

**Funding**

This work was supported by Grants for Scientific Research of BSKY (XJ201419) from Anhui Medical University, The Scientific Research Project from College of Life Science, Anhui Medical University, The Natural Science Research Project of Anhui Province Colleges and Universities (KJ2015A002) and The National Training Program of Innovation and Entrepreneurship for Undergraduates (201510366037).

**References**

He WH, Cheng XH, Xu AL. 2004. An experimental study on the anticoagulant effect of extract from *Eupolyphage sinesis* walker on rabbits. J TCM Univ Hunan. 23:7–9.

Xiao B, Chen AH, Zhang YY, Jiang GF, Hu CC, Zhu CD. 2012. Complete mitochondrial genomes of two cockroaches, *Blattella germanica* and *Periplaneta americana*, and the phylogenetic position of termites. Curr Genet. 58:65–77.

Yamauchi MM, Miyaf MU, Nishida M. 2004. Use of a PCR based approach for sequencing whole mitochondrial genomes of insects: two examples (cockroach and dragonfly) based on the method developed for decapod crustaceans. Insect Mol Biol. 13:435–442.

Zhang YY, Xuan WJ, Zhao JL, Zhu CD, Jiang GF. 2010. The complete mitochondrial genome of the cockroach *Eupolyphaga sinensis* (Blattaria: Polyphagidae) and the phylogenetic relationships within the Dictyoptera. Mol Biol Rep. 37:3509–3516.