The complete mitochondrial genome of *Pericapritermes nitobei* (Isoptera: Termitidae)

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**ABSTRACT**

The complete circular mitochondrial genome of a higher termite *Pericapritermes nitobei* has a length of 15,224bp and encodes 37 genes including 13 protein-coding genes (PCGs), 22 transfer RNA (tRNA), 2 ribosomal RNA (rRNA) and a non-coding control region (D-loop). Protein coding genes (PCGs) in this circular mitogenome start with standard ATN initiation codons and end with complete termination codons TAN except for *cox2* and *nad5* genes with an incomplete stop codon T. The percentage of A and T (67.49%) is higher than that of G and C (32.51%). The phylogenetic tree revealed that mitogenomes of *Pericapritermes* formed one clade. The tree also revealed that *Pericapritermes dolichocephalus* and *Pericapritermes latignathus* constituted a sister group to *P. nitobei*. The date here provide a resource for genetics and evolution analysis within termites especially *Pericapritermes* genus.

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Pericapritermes genus contains 33 species and mainly distributes in tropical and subtropical regions (Tan and Yan, 2013). As typical species of higher termites, the mitochondrial genomes of *Pericapritermes* are applied for termites evolutionary analysis (Bourguignon et al. 2015, 2017). *Pericapritermes nitobei* was first described as *Eutermes nitobei* and Krishna revised the species to *P. nitobei* (Krishna et al. 1968). Although there are some studies on the mitochondrial genes of *P. nitobei* such as *rml*, *rms* and *cox2* (Ohkuma et al. 1999, 2004; Bujang et al. 2014), there is no available information about its complete mitochondrial genome. The present study was the first report on the complete mitochondrial genome sequences of *P. nitobei*.

Specimens were collected from Ningbo city, China and kept in the insect lab at Zhejiang A & F University with Accession number NB0024-TT-4. The entire mitochondrial genome sequence of *P. nitobei* was 15,224 bp in length, including 13 protein-coding genes, 22 tRNA genes (*rml* and *rms*) and 1 non-coding control region (D-loop). Most of these genes were located on the H-strand except for *nad1*, *nad4*, *nad4l*, *nad5* and 8 tRNA genes (*trnQ*, *trnC*, *trnY*, *trnF*, *trnH*, *trnP*, *trnL1* and *trnV*). The genetic compositions and coding sequences are similar to other termites (Zhao et al. 2016; Hervé and Brune 2017).

The overall base compositions of *P. nitobei* mitochondrial genome had a high A+T tendency. The A+T content of *P. nitobei* was 67.49%, higher than that of G+C (32.51%). The mitochondrial genome of *P. nitobei* included intergenic spacers and overlapping regions. The intergenic spacer sequences were on 22 regions ranging in size from 1 to 17 bp. The overlapping sequences varied from 1 to 44 bp in five areas.

The mitochondrial genome of the *P. nitobei* contained 13 protein-encoding genes, with the total length of 11,144 bp. All protein-coding genes (PCGs) start with standard ATN initiation codons and end with complete termination codons TAN except for *cox2* and *nad5* genes with an incomplete stop codon T. There were 22 tRNA genes in the mitochondrial genome of *P. nitobei*. Except for the tRNA-Ser, which lacked the dihydrorubamide (DHU) arm, the other tRNAs have the classical cloverleaf structures.

The control region (D-loop) with 336 bp in size is located between *rms* and *trnL* gene. The content of A+T in control region was 70.54%, and its content was significantly higher than that of the whole mitochondrial genome.

*Pericapritermes nitobei* mitochondrial genome has two ribosomal RNAs, *rml* and *rms*. *rml* is located between *trnL* and *trnV* with the length of 1368 bp and *rms* is located between *trnV* and the control region with 806 bp in size.

A phylogenetic tree among Pericapritermes was constructed using a dataset which contained all the nucleotide sequences of PCGs of *Pericapritermes* mitochondrial genes. *Microcerotermes crassus* and *Termes fatalis* (Termitidae) were set as outgroups. Two major clades were formed, one was *M. crassus* and *T. fatalis*, the other was the remaining species (Pericapritermes) (Figure 1). The tree also revealed that *P. dolichocephalus* was closest to *P. latignathus* and constituted a sister group to *P. nitobei*. 
The complete genome sequence of \textit{P. nitobei} has been assigned GenBank accession number (MH194575).

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**Disclosure statement**

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

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