The complete mitochondrial genome of *Reticulitermes periflaviceps* (Isoptera: Rhinotermitidae)

Xin Ye, Yin Hu, Haihong Chen, Yiyuan Liao, Tong Chen and Dayu Zhang

College of Agricultural and Food Science, Zhejiang A & F University, Hangzhou, P. R. China; National Termite Control Center, Hangzhou, P. R. China; Ningbo Housing Safety Management and Service Center, Ningbo, P. R. China

**ABSTRACT**

The mitochondrial genome of the *Reticulitermes periflaviceps* contains 15,925 bp of nucleotide in length including 13 protein-coding genes, 22 transport RNAs, 2 ribosomal RNAs, and a non-coding region. The overall A + T among the genome sequence is 65.64%. The start codons of all protein-coding genes are ATN and the stop codons are TAG except for Nad1 and incomplete T for COII and Nad5. The length of 12sRNA and 16sRNA genes are 743 and 1309 bp, respectively, and the control region was 1118 bp in length, with two repeating tandem regions. The phylogenetic tree revealed that *R. periflaviceps* and *Reticulitermes kanmonensis* constituted a sister group to *Reticulitermes flaviceps*. The mitochondrial genome here provides a resource for evolution analysis within termites especially *Reticulitermes*.

**CONTACT** Dayu Zhang

zhangdayu@zafu.edu.cn

College of Agricultural and Food Science, Zhejiang A & F University, Hangzhou, P. R. China

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Disclosure statement

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