MITOCHONDRIAL DNA PART B
2020, VOL. 5, NO. 1, 780–781
https://doi.org/10.1080/23802359.2020.1715882

Taylor & Francis
Taylor & Francis Group

MITOGENOME ANNOUNCEMENT

Sequencing and analysis of the complete mitochondrial genome of *Bactrocera cheni* from China and its phylogenetic analysis

Tao Wang[a,b], Yan-ling Ren[b], Yong Zhong[c] and Mao-fa Yang[a]

[a]Institute of Entomology, Guizhou University, Guiyang, P.R. China; [b]Guizhou Light Industry Technical College, Guiyang, P. R. China; [c]State key laboratory of tropical and subtropical fruit quarantine, Pingxiang Customs, Pingxiang, P. R. China

ABSTRACT

The complete mitochondrial genome (mitogenome) of the *Bactrocera cheni* (Diptera: Tephritidae: Dacinae) are sequenced and annotated. The mitochondrial genome is 15,945 bp (GenBank No. MN883026), with A + T% for the whole sequence = 73.0% (38.9% A, 16.4% C, 10.6% G, and 34.1% T), which is the classical structure for insect mitogenome. All PCGs started with ATN except ATP8; 9 PCGs use TAA as the stop codon, and others use TAG as the stop codon. The phylogenetic tree confirms that *B. cheni* and *B. tsuneonis* are not clade into one branch with strongly supported. And Pairwise Identity is 80.0% between *B. cheni* and *B. tsuneonis*. Based this study, we supported that *B. cheni* and *B. tsuneonis* are two different species clearly.

ARTICLE HISTORY
Received 3 January 2020
Accepted 7 January 2020

KEYWORDS
Mitogenome; Dacinae; *Bactrocera cheni*; phylogeny

Orange fly is considered to be one of the most serious pests damaging oranges and grapefruit, which is distributed in Japan, China and Vietnam, due to its prevention and control worldwide, people should pay substantial attention to them (Wang 1996). *Bactrocera cheni* was named and described by Zhao from a male holotype, plus 33 male and 25 female paratypes, from Guangxi, Hunan, Jiangsu and Sichuan (Zhao 1987). White and Wang had studied types of *B. cheni* from Guangxi and found them to be identical to *Bactrocera tsuneonis* (White and Wang, 1992), and it has been recognized by most studies. But according to *16S* rRNA and *COI-COII* gene sequences, Li et al believed that *B. cheni* and *B. tsuneonis* are very closed different species (Li et al. 2009). In this study, we sequenced and determined the complete mitochondrial genome (mitogenome) of *B. cheni*.

Total genome DNA was extracted from a male adult of *B. cheni* which was collected in Chongzuo City, Guangxi Zhuang Autonomous Region, China (E 106°50′49″, N 22°3′37″), in May 2019. The genome DNA and specimen are deposited in Specimen storage room of Guizhou Light Industry Technical College, label number of them is GLI-IDT-00130. Mitogenome sequences were assembled and annotated using Geneious Primer (Kearse et al. 2012), additionally, tRNAs were found by MITOS server (Bernt et al. 2013) and tRNA scan-SE server (Lowe and Chan 2016). The ML (Maximum Likelihood) tree was constructed using the nucleotide of 13 protein-coding genes and 2 RNA genes sequences by IQ-TREE v1.6.3 (Nguyen et al. 2015).

The complete mitogenome of *B. cheni* is 15,945 bp (GenBank No. MN883026), contained a typical set of 37 mitochondrial genes and one control region (951 bp). The mitogenome of *B. cheni* exhibited heavy AT nucleotide bias, with A + T% for the whole sequence = 73.0%. All PCGs started with ATN (ATA/ATG/ATT/ATC), except ATP8 which started with TTG; 9 PCGs use TAA as the stop codon, and others (*ND3, ND5, ND4* and *Cytb*) use TAG as the stop codon.

The phylogenetic relationships of *B. cheni* were reconstructed with IQ-TREE using an ultrafast bootstrap approximation approach with 10,000 replicates based on concatenated the nucleotides of the 13 PCGs and 2 rRNAs with 13,101 bp (Figure 1). Each PCG and rRNA sequence was aligned using the MAFFT algorithm in TranslatorX and MAFFT v7.0 online serve with the G-INS-i strategy respectively, and aligned sequences were eliminated using Gblocks 9.1 b (Abascal et al. 2010; Katoh et al. 2017). Within phylogenetic tree, *B. cheni* as the sister group of *Bactrocera tryoni* with strongly supported (bootstrap support value = 100). *B. cheni* and *B. tsuneonis* are not clade into one branch with strongly supported. And compared two sequences, the pairwise Identity is 80.0% between *B. cheni* and *B. tsuneonis*. Thus, based this study, we supported that *B. cheni* and *B. tsuneonis* are clearly two different species which different from traditional ideas, and we hope that our data can useful for further study.

CONTACT Mao-fa Yang wjchuzhou@sina.com, gdgdly@126.com Institute of Entomology, Guizhou University, Guiyang 550025, P.R. China

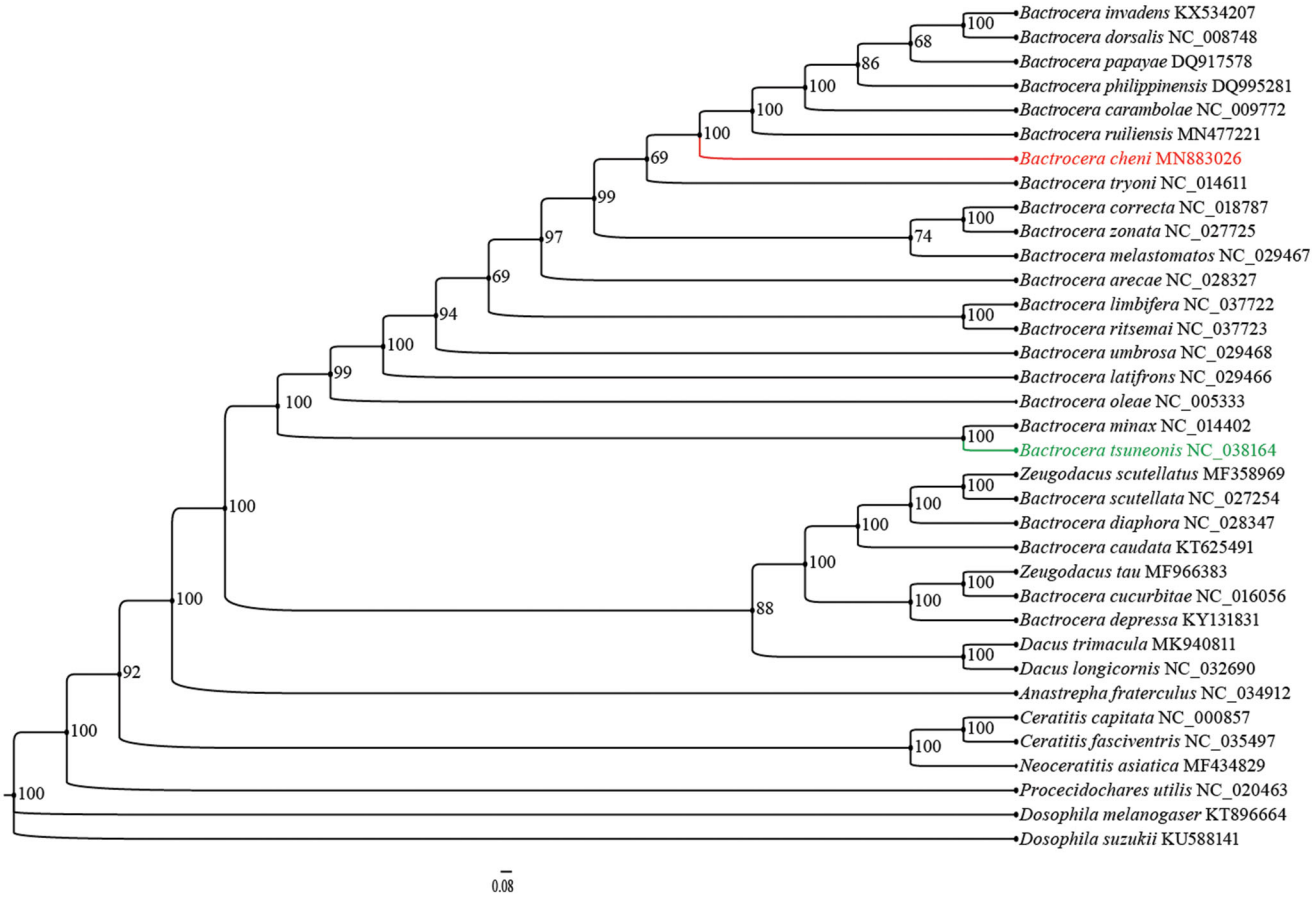

Figure 1. Phylogenetic analyses of *Bactrocera cheni* based upon the concatenated the nucleotides of the 13 PCGs and 2 rRNAs of 32 ingroup species by IQ-TREE. Numbers at nodes are bootstrap values. The accession number for each species is indicated after the scientific name.

Disclosure statement

No potential conflict of interest was reported by the authors.

Funding

This study was supported by the Science and Technology Foundation of General Administration of Quality Supervision, Inspection and Quarantine of the People's Republic of China [2017IK257, 2017IK261]; Guizhou Province Quality Development Project [(2019)10]; China Tobacco Corporation Guizhou Provincial Company Technology Project [201918].

References

Abascal F, Zardoya R, Telford MJ. 2010. Translator X: multiple alignment of nucleotide sequences guided by amino acid translations. Nucleic Acids Res. 38(suppl_2):W7–W13.

Bernt M, Donath A, Jühling F, Externbrink F, Florentz C, Fritzsch G, Pütz J, Middendorf M, Stadler PF. 2013. MITOS: improved de novo metazoan mitochondrial genome annotation. Mol Phylogenet Evol. 69(2):313–319.

Katoh K, Rozewicki J, Yamada KD. 2017. MAFFT online service: multiple sequence alignment, interactive sequence choice and visualization. Brief Bioinform. 30:3059.

Kearse M, Moir R, Wilson A, Stones-Havas S, Cheung M, Sturrock S, Buxton S, Cooper A, Markowitz S, Duran C, et al. 2012. Geneious basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. Bioinformatics. 28(12): 1647–1649.

Li FW, Tang K, Wang Z.J, Tang S.Q. 2009. Comparison study of the *Bactrocera (Tetradacus) cheni* (Zhao) and *Bactrocera (Tetradacus) tsuneonis* (Miyake) (Diptera: Tephritidae) based on Nucleotide Sequences of the mitochondrial DNA. Biotechnol Bulletin. S1:320–325.

Lowe TM, Chan PP. 2016. Trna scan-SE On-line: integrating search and context for analysis of transfer RNA genes. Nucleic Acids Res. 44(W1): W54–W57.

Nguyen LT, Schmidt HA, von Haeseler A, Minh BQ. 2015. IQ-TREE: a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. Mol Biol Evol. 32(1):268–274.

Wang XJ. 1996. The fruit flies (Diptera: Tephritidae) of the East Asian region. Acta Zootaxon Sin. 21:1–338.

White I M, Wang X-j. 1992. Taxonomic notes on some dacine (Diptera: Tephritidae) fruit flies associated with citrus, olives and cucurbits. Bull Entomol Res. 82(2):275–279. doi:10.1017/S0007485300051828.

Zhao YX. 1987. The two species of fruit flies on oranges in China. Tech Bulletin Plant Quarantine Res. 5:1–10.