MITOCHONDRIAL DNA PART B: RESOURCES, 2018
VOL. 3, NO. 1, 88–89
https://doi.org/10.1080/23802359.2017.1422411

Taylor & Francis
Taylor & Francis Group

MITOGENOME ANNOUNCEMENT

Complete mitochondrial genome of the bamboo snout beetle, *Cyrotrachelus buqueti* (Coleoptera: Curculionidae)

Wen-Jia Yang*, Da-Xing Yang*, Kang-Kang Xu, Yu Cao, Yong-Lu Meng, Yan Wu, Guo-Yong Li, Guo-Zhou Zhang, Ya-Wei Wang and Can Li

Guizhou Provincial Key Laboratory for Rare Animal and Economic Insects of the Mountainous Region, College of Biology and Environmental Engineering, Guiyang University, Guiyang, China

ABSTRACT

The bamboo snout beetle *Cyrotrachelus buqueti* (Coleoptera: Curculionidae) is a destructive forest pest and distributed widely in Southeast Asia. The 15,035 bp complete mitochondrial genome of the species consists of 13 protein-coding genes (PCGs), two ribosomal RNA genes (rRNAs), 21 transfer RNA genes (tRNAs) and a control region (GenBank accession no. MG674390). The *trnI* gene was not found in the *C. buqueti* mitogenome. The gene order and the orientation of *C. buqueti* were similar to those found in other Coleoptera species. The nucleotide composition was significantly biased (A, G, C, and T was 38.18%, 10.10%, 16.16%, and 35.56%, respectively) with A + T contents of 73.74%. ATG, ATA, ATT, AAT, and TTG were initiation codons and TAA, TAG, and T were termination codons. All the 21 tRNAs displayed a typical cloverleaf secondary structure, except for $trnS_1$ which lacked the dihydrouridine arm. Phylogenetic analysis was performed using 13 PCGs with 14 other beetles showed that *C. buqueti* is closely related to *Eucryptorhynchus brandti*, which agree with the traditional classification.

ARTICLE HISTORY
Received 21 December 2017
Accepted 26 December 2017

KEYWORDS
Cyrotrachelus buqueti; bamboo snout beetle; mitochondrial genome

The bamboo snout beetle, *Cyrtotrachelus buqueti* Guerin-Meneville (Coleoptera: Curculionidae), is a highly destructive forest pest and distributed widely in Southeast Asia (Yang et al. 2017). The larvae of *C. buqueti* bore into the shoots of clumping bamboo species, causing serious damage to bamboo production (Yang et al. 2009). Adult specimens of *C. buqueti* were collected from Nanming District, Guiyang City, Guizhou Province, China (N26°33′, E106°46′). Samples have been deposited in the insect specimen room of Guiyang University with an accession number GYU-Col-20170001).

The circular mitochondrial genome of *C. buqueti* was 15,035 bp in length (GenBank accession no. MG674390) and included sets of genes, including 13 protein-coding genes (PCGs), two ribosomal RNA genes (*rrnL* and *rrnS*), 21 transfer RNA genes (tRNAs), and a large non-coding region (putative control region). The *trnI* was not found in the *C. buqueti* mitogenome, as observed in *Sympiezomias velatus* (Tang et al. 2017), another completely sequenced species in Coleoptera. The gene order and the orientation of *C. buqueti* were similar to those of putative ancestor of insects (Boore 1999). The nucleotide composition of was significantly biased (A, G, C, and T was 38.18%, 10.10%, 16.16%, and 35.56%, respectively) with A + T contents of 73.74%. The AT-skew and GC-skew of this genome were 0.036 and −0.231, respectively. Twenty-two genes were transcribed on the J-strand, whereas the others were oriented on the N-strand. Gene overlaps were present at eight gene junctions and involved a total of 20 bp; the longest overlap (7 bp) existed between *atp8* and *atp6*. A total of 59 bp intergenic spacers were found in 10 positions, ranging in size from 1 to 21 bp. The largest intergenic spacer sequence of 21 bp was located between $trnS_2$ and *nad1*. The control region was located between *rrnS* and *trnQ* gene with a length of 430 bp, and the A + T content was 81.16%.

All the 21 tRNAs were predicted to have typical cloverleaf secondary structures, except the gene $trnS_1$ (AGN) lacking a stable dihydrouridine arm, which were consistent with those reported in other animal mitogenomes (Wolstenholme 1992; Yuan et al. 2016). The length of these tRNAs ranged from 63 bp (*trnC* and *trnE*) to 71 bp (*trnK*), A + T content ranged from 58.46% (*trnN*) to 86.15% (*trnD*). The *rrnL* was located between $trnL_1$ and *trnV*, and *rrnS* resided between *trnV* and the control region. The *rrnL* was 1298 bp in length with A + T content of 78.43%, and the *rrnS* was 788 bp in length with A + T content of 75.13%.

The initial codons for 11 PCGs of *C. buqueti* were the canonical putative start codons ATN (ATG for *atp6*, *nad4L*, and *cob*; ATT for *cox2*, *atp8*, and *nad5*; ATA for *cox3*, *nad3*, *nad1*, and *nad4*; ATC for *nad2*). However, *cox1* and *nad6* used AAT and TTG as start codon, respectively. Nine PCGs were terminated with TAA or TAG, and the remaining PCGs including *cox1*, *cox3*, *nad4*, and *nad5* use a single T as stop codon. We analyzed the amino acid sequences of 13 PCGs with neighbour-joining method to construct the phylogenetic

CONTACT Can Li lican790108@163.com Guizhou Provincial Key Laboratory for Rare Animal and Economic Insects of the Mountainous Region, College of Biology and Environmental Engineering, Guiyang University, Guiyang 550005, China
*These authors contributed equally to this work.

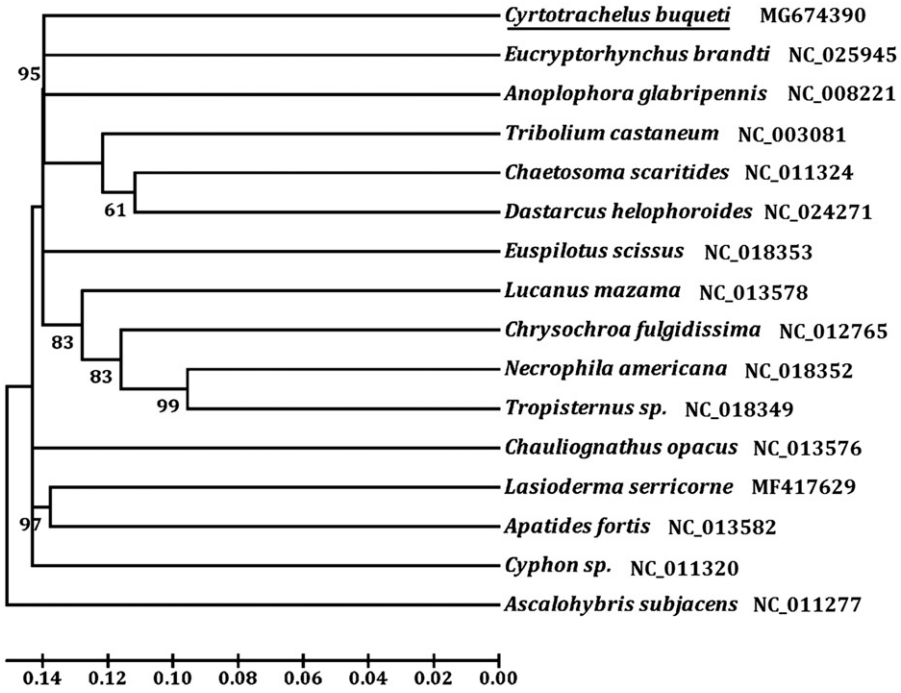

Figure 1. Phylogenetic tree showing the relationship between *C. buqueti* and 14 other beetles based on neighbour-joining method. *Ascalohybris subjacens* was used as an outgroup. GeneBank accession numbers of each species were listed in the tree.

relationship of *C. buqueti* with 14 other representative bettles. The result showed that *C. buqueti* is closely related to *Eucryptorhynchus brandti* (Figure 1), which agree with the traditional classification.

Disclosure statement

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

Funding

This work was supported in part by the Training Program for High-level Innovative Talents of Guizhou Province (QKHRC[2016]4020), the Program for First-class Discipline Construction in Guizhou Province (QJKYF[2017]85), the Science and Technology Foundation of Guizhou Province (QKHJZ[2014]2002), and the Engineering Research Center of Pest Ecological Management in Guizhou Province (1491).

References

Boore JL. 1999. Survey and summary: animal mitochondrial genomes. Nucleic Acids Res. 27:1767–1780.

Wolstenholme DR. 1992. Animal mitochondrial DNA: structure and evolution. Int Rev Cytol. 141:173–216.

Tang PA, Zhang L, Li XP, Li FF, Yuan ML. 2017. The complete mitogenome of *Sympiezomias velatus* (Coleoptera: Curculionidae). Mitochondrial DNA Part B. 2:449–450.

Yang H, Su T, Yang W, Yang C, Lu L, Chen Z. 2017. The developmental transcriptome of the bamboo snout beetle *Cyrtotrachelus buqueti* and insights into candidate pheromone-binding proteins. PLoS ONE. 12:e0179807.

Yang YJ, Wang SF, Gong JW, Liu C, Mu C, Qin H. 2009. Relationships among *Cytotrachelus buqueti* larval density and wormhole number and bamboo shoot damage degree. Chinese J Appl Ecol. 20: 1980–1985.

Yuan ML, Zhang QL, Zhang L, Guo ZL, Liu YJ, Shen YY, Shao RF. 2016. High-level phylogeny of the Coleoptera inferred with mitochondrial genome sequences. Mol Phylogenet Evol. 104:99–111.