

The complete mitochondrial genome of *Stegobium paniceum* (Coleoptera: Anobiidae)

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ABSTRACT

The complete mitochondrial genome of *Stegobium paniceum* (Coleoptera: Anobiidae) is a circular DNA molecule of 15,271 bp (GenBank accession number XK819317), and its nucleotide composition is biased towards A + T nucleotides (78.32%). This genome comprises 13 protein-coding genes, 2 ribosomal RNA genes, 22 transfer RNA (tRNA) genes, and an A + T-rich region. The gene order of *S. paniceum* was similar to those found in other known Coleoptera species. Sixteen reading frame overlaps and six intergenic regions were found in the mitochondrial genome of *S. paniceum*. All 22 tRNA genes have the typical cloverleaf secondary structure, with an exception for *trnS*₁ (AGN). The phylogenetic relationships based on neighbour-joining method revealed that *S. paniceum* is closely related to *Apatides fortis*, which is consistent with the traditional morphological classification.

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The drugstore beetle, *Stegobium paniceum* (Linnaeus) (Coleoptera: Anobiidae), is a major pest that cause tremendous damage to stored grains and seeds, packaged food products, animal-, and plant-derived products, including more than 300 drug materials (Li et al. 2009; Abdelghany et al. 2010). In this study, the *S. paniceum* samples were collected from medicinal materials company in Guizhou province of China (N26°31', E106°43'). The specimen was deposited in Insect Collection (Accession Number GYU-Col-20090001-2), College of Biology and Environmental Engineering, Guiyang University, Guiyang, China.

The complete mitochondrial genome of *S. paniceum* (GenBank accession number XK819317) has been sequenced and annotated. It is a typical circular DNA molecule of 15,271 bp in length, larger than *Eucryptorhynchus brandti* (15,122 bp) and smaller than *Tribolium castaneum* (15,883 bp), *Dastarcus helophoroides* (15,878 bp), and *Hycleus chodschanticus* (16,257 bp) (Liu et al. 2014; Zhang et al., 2014; Nan et al. 2016; Yuan et al. 2016). The nucleotide composition of mitochondrial genome of *S. paniceum* is heavily biased towards A + T nucleotides, accounting for A (41.62%), T (36.70%), G (9.06%), and C (12.62%). The AT-skew and GC-skew of this genome were 0.063 and -0.164, respectively.

The mitochondrial genome of *S. paniceum* contains 37 genes, including 13 protein-coding genes (PCGs), 2 ribosomal RNA (rRNA) genes, and 22 transfer RNA (tRNA) genes. The gene order of *S. paniceum* was similar to those found in other known Coleoptera species. Gene overlaps 39 bp that have been found at 16 gene junctions, the longest 8 bp

overlapping exists between *trnW* and *trnC*. The *S. paniceum* mitochondrial genome harbours six intergenic regions (*trnS*₂ and *nad1* share 20 nucleotides, *trnM* and *nad2* share three nucleotides, *nad4L* and *trnT* share two nucleotide, *trnY* and *cox1* share a nucleotide, *trnP* and *nad6* share a nucleotide, and *nad1* and *trnL*₁ share a nucleotide). With an exception for *trnS*₁ (AGN), all tRNAs have the typical cloverleaf secondary structure, which are common in most animal mitochondrial genome (Wolstenholme 1992). The length of these tRNAs vary from 62 bp for *trnI*, *trnL*₁, *trnY* to 70 bp for *trnM*, A + T content ranged from 70.31% (*trnF*) to 90.48% (*trnE*).

Two rRNA genes (*rnl* and *rns*) are located between *trnL*₁ and *trnV*, and between *trnV* and the A + T-rich region, respectively. The size of *rnl* and *rns* of *S. paniceum* is 1254 bp and 755 bp long, respectively. Of the 13 PCGs, 11 genes start with ATN codons, including five ATAs (*cox2*, *nad3*, *nad4*, *nad6*, and *nad2*), four ATGs (*atp6*, *cox3*, *nad4L*, and *cob*), two ATTs (*atp8* and *nad5*). However, *cox1* and *nad1* used AAA and TTG as start codon, respectively. Eight PCGs terminate with the conventional stop codons TAA (*atp6*, *atp8*, *nad4L*, *nad6*, and *nad2*) or TAG (*nad3*, *cob*, and *nad1*), the remaining PCGs including *cox1*, *cox2*, *cox3*, *nad4*, and *nad5* use a single T as stop codon. The major A + T-rich region was located between *rns* and *trnI* genes with a length of 795 bp long, and the A + T content was 90.69%. Based on the concatenated amino acid sequences of 13 PCGs, the neighbour-joining method was used to construct the phylogenetic relationship of *S. paniceum* with 13 other representative beetles. The mitochondrial genome of neuropteran *Ascalohybris subjacens*

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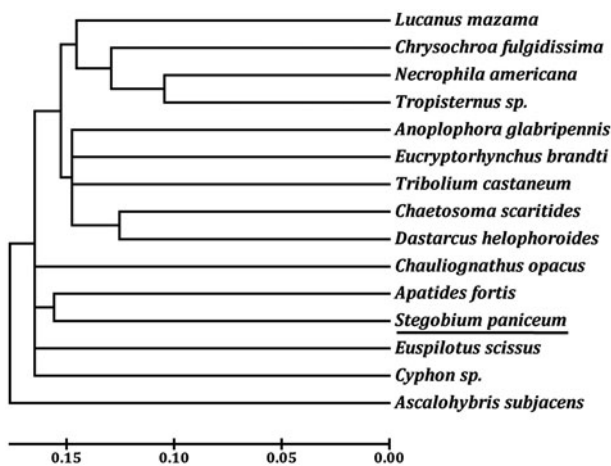


Figure 1. The neighbour-joining phylogenetic tree of *S. paniceum* and other beetles was constructed based on 13 mitochondrial protein-coding genes. The GenBank accession numbers used for tree constructed are as follows: *A. fortis* (NC_013582), *Anoplophora glabripennis* (NC_008221), *Chaetosoma scaritides* (NC_011324), *Chrysochroa fulgidissima* (NC_012765), *Chauliognathus opacus* (NC_013576), *Cyphon* sp. (NC_011320), *D. helophoroides* (NC_024271), *E. brandti* (NC_025945), *Euspilotus scissus* (NC_018353), *Lucanus mazama* (NC_80 013578), *Necrophila americana* (NC_018352), *T. castaneum* (NC_003081), and *Tropisternus* sp. (NC_018349).

(NC_011277) was used as an outgroup. The results demonstrated that *S. paniceum* is more closely related to *Apatides fortis* than other beetles (Figure 1), which is consistent with the traditional morphological classification.

Disclosure statement

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

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