

Mitochondrial DNA Part A

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MITOGENOME ANNOUNCEMENT

Complete mitochondrial genome of *Spiniphilus spinicornis* (Coleoptera: Vesperidae: Philinae) and phylogenetic analysis among Cerambycoidea

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Abstract

Spiniphilus spinicornis belongs to subfamily Philinae of family Vesperidae from cerambycoid assemblage. The first complete mitogenome of *Spiniphilus spinicornis* was reported. The genome is 15 707 bp in length and contains the typical 37 genes that are arranged in the same order as that of the putative ancestor of beetles. The total base composition of the mitogenome is 30.9% for A, 11.1% for C, 19.3% for G, and 38.6% for T. The genome organization, nucleotide composition, and codon usage do not differ significantly from other members. The percentage of A+T is 69.5%. The first complete mitogenome of subfamily Philinae could be used in studies of molecular systematics, phylogenetic, and conservation genetics. Phylogenetic analysis showed that Cerambycoidea was monophyly with high support value. Lamiinae, Cerambycinae, and Philinae were monophyly too, respectively.

KeywordsCerambycoidea, mitogenome, phylogeny, *Spiniphilus spinicornis***History**

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Spiniphilus spinicornis (Lin & Bi, 2011) belongs to Philinae of Vesperidae, a family that is perhaps the most problematic family of the cerambycoid assemblage, whose monophyly requires further testing (Švácha & Lawrence, 2014). Philinae consists of five described genera and approximately 20 species (Švácha & Lawrence, 2014), while the genus *Spiniphilus* contains two species known exclusively from Yunnan of China (Bi & Lin, 2015; Lin & Bi, 2011). By adult morphology, Philinae were associated with Prioninae, Cerambycinae, and Lepturinae (Švácha & Lawrence, 2014). Molecular data should be used to test its monophyly.

Mitochondrial genome has been used to explore the phylogeny, molecular evolution and biological diversity of beetles (Nie & Yang, 2014). So far, seven mt genomes from seven species of Cerambycidae were submitted to Genbank. In this study, we sequenced the mt genome of *S. spinicornis* by the next-generation sequence technology. The complete mitogenome of *S. spinicornis* was the first mitogenome of subfamily Philinae. The sequencing of mtDNA will greatly contribute to the phylogenetic and systematic analyses within the family Vesperidae and also the cerambycoid assemblage.

The sample of *S. spinicornis* (male) was collected from Laifengshan (25.019°N, 98.485°E; altitude, 1700 m), Tengchong city, Yunnan province, China, on 6th May 2011. Voucher specimens for sampled taxa were deposited in the Institute of Zoology, Chinese Academy of Sciences. Genomic DNA was extracted by TIANGEN Midi Plasmid kit (TIANGEN, Beijing, China) and then sequenced using Illumina's HiSeq2000 platform (Illumina, San Diego, CA) with 200 bp insert size and a pair-end

100 bp sequencing strategy. The sequence reads were first filtered by the programs following Zhou et al. (2013) and then the remaining high-quality reads were assembled using SOAPdenovo-Trans (Xie et al., 2014). The annotations of genes were done by geneious 8.0.5 software (Kearse et al., 2012) and tRNAscan-SE 1.21 (Schattner et al., 2005).

The phylogenetic inference was done based on all available mitogenomes of Cerambycoidea (JX987292, NC_008221, NC_013070, NC_022671, NC_024652, NC_023937, AB703463, and KT781589) and two mitogenomes from Chrysomelidae (AF467886 and KT781589) as outgroups. TransAlign methods were used to align all genes (Bininda-Emonds, 2005). The aligned data from each locus were concatenated with Sequence Matrix v.1.7.8 (Vaidya et al., 2011). Bayesian inference was performed using MrBayes v.3.2 (Ronquist et al., 2012). Data were partitioned according to loci of 13 PCGs. The MCMC search was conducted for 50 000 000 generations, and sampling was done every 1000 generations until the average standard deviation of split frequencies was below 0.01. The first 25% of trees were discarded as 'burn-in' and posterior probabilities were estimated for each node.

The mt genome of *S. spinicornis* was a double-stranded circular molecule of 15 707 bp in length (GenBank accession no. KT781589), and it contained the entire set of 37 genes usually present in most insect mtDNAs (13 PCGs, 22 tRNA genes, and two rRNA genes), and a large non-coding region (control region). Twenty-three genes were transcribed on the majority strand (J-strand), whereas the others were oriented on the minority strand (N-strand). The overall organization of the mitogenome of *S. spinicornis* is very compact, and the overlaps between genes are often been found. There is a non-coding region of about 18 bp between *ND1* and *tRNA-Ser* (AGN).

Most PCGs begin with an ATT start codon, except for *ATP6*, *COX3*, *ND4*, *ND4L*, and *CYTB* (ATG). Eight PCGs terminate with

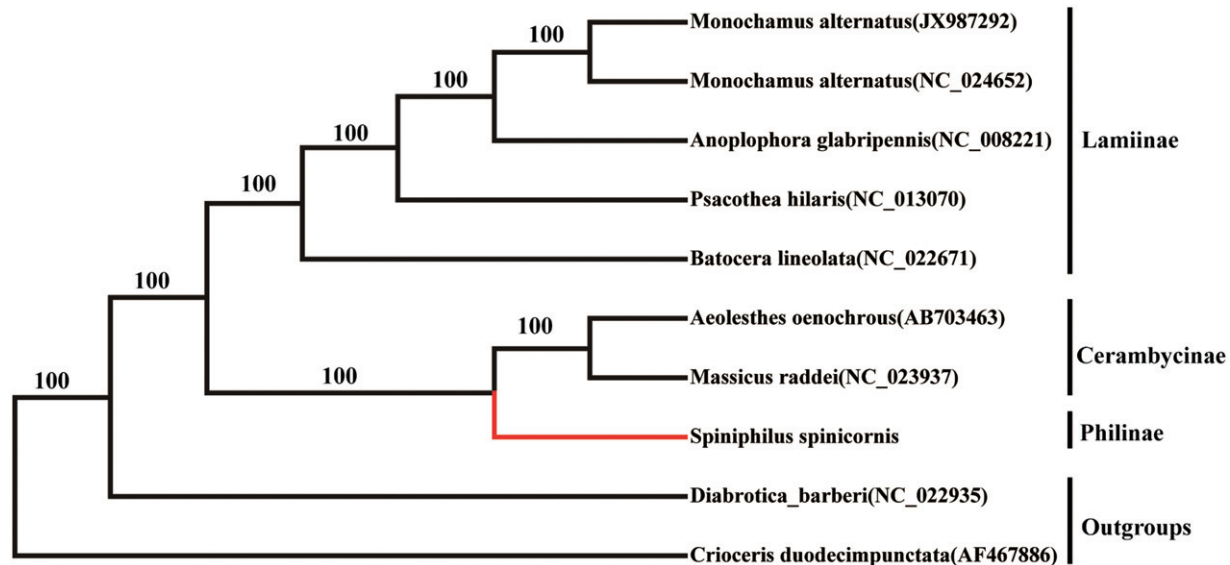


Figure 1. The Bayesian tree based on 13 PPGs combined data sets. Numbers on nodes indicate Bayesian posterior probabilities. Red clade is the new added one in this study.

a TAN (TAA or TAG) stop codon, whereas some genes such as *ND5* and *ND4* genes terminates with incomplete stop codons (T— or TA—), which was frequent in mt genomes of beetles (Sheffield et al., 2008). The genome contains two subunits of rRNA (srRNA and lrRNA) with lengths of 812 and 1297 bp, respectively. Twenty-two tRNA genes are detected based on their respective anticodons range in size from 63 (*tRNA-His*) to 70 (*tRNA-Val*) bp. The control region (AT rich region) is 1066 bp in length. The percentage of A+T of control region is 79.5%, which was consistently higher than that of the coding region.

The Bayesian tree (Figure 1) based on the concatenated 13 PCGs showed that Cerambycoidea were recovered monophyletic clade with 100% posterior probabilities. The available subfamily rank of Cerambycidae was resolved with high value support (all clades with 100% posterior probabilities). Lamiinae, Cerambycinae, and Philinae were monophyly, and the last two families have the nearest relationship, which is consistent with the morphological results.

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Declaration of interest

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References

Bi WX, Lin MY. (2015). Discovery of second new species of the genus *Spiniphilus* Lin & Bi, and female of *Heterophilus scabricollis* Pu with

its biological notes (Coleoptera: Vesperidae: Philinae: Philini). Zootaxa 3949:575–83.

Bininda-Emonds O. (2005). TransAlign: Using amino acids to facilitate the multiple alignment of protein-coding DNA sequences. BMC Bioinf 6:156.

Kearse M, Moir R, Wilson A, Stones HS, Cheung M, Sturrock S, Buxton S, et al. (2012). Geneious Basic: An integrated and extendable desktop software platform for the organization and analysis of sequence data. Bioinformatics 28:1647–9.

Lin MY, Bi WX. (2011). A new genus and species of the subfamily Philinae (Coleoptera: Vesperidae). Zootaxa 2777:54–60.

Nie RE, Yang XK. (2014). The progress on researches of mitochondrial genome of Coleoptera. Acta Entomol Sin 57: 860–8.

Ronquist F, et al. (2012). MrBayes 3.2: Efficient Bayesian phylogenetic inference and model choice across a large model space. Syst Biol 61: 539–42.

Schattner P, Brooks AN, Lowe TM. (2005). The tRNAscan-SE, snoscan and snoGPS web servers for the detection of tRNAs and snoRNAs. Nucleic Acids Res 33:686–9.

Sheffield NC, Song H, Cameron SL, Whiting MF. (2008). A comparative analysis of mitochondrial genomes in Coleoptera (Arthropoda: Insecta) and genome descriptions of six new beetles. Mol Biol Evol 25: 2499–509.

Švácha P, Lawrence JF. (2014). 2.1 Vesperidae Mulsant, 1839. In: Leschen RAB, Beutel RG, editors, Handbook of Zoology, Arthropoda: Insecta; Coleoptera, Beetles, Volume 3: Morphology and systematics (Phytophaga). Berlin, Boston: Walter de Gruyter. p 16–49.

Xie YL, Wu GX, Tang JB, Luo RB, Patterson J, Liu SL, Huang WH, et al. (2014). SOAPdenovo-Trans: De novo transcriptome assembly with short RNA-Seq reads. Bioinformatics 30:1660–6.

Vaidya G, Lohman DJ, Meier R. (2011). SequenceMatrix: Concatenation software for the fast assembly of multi-gene datasets with character set and codon information. Cladistics 27:171–80.

Zhou X, Li YY, Liu SL, Yang Q, Su X, Zhou LL, Tang M, et al. (2013). Ultra-deep sequencing enables high-fidelity recovery of biodiversity for bulk arthropod samples without PCR amplification. Gigascience 2:4.