

## Mitochondrial DNA Part B Resources

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## The complete mitochondrial genome of *Xystrocera globosa* (Coleoptera: Cerambycidae) and its phylogeny

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### ABSTRACT

The complete mitochondrial genome of *Xystrocera globosa* is 15,706 bp in length, containing 13 protein-coding genes, 22 transfer RNAs, two ribosomal RNAs and the A + T-rich region. The overall base composition is 72.7% AT and 27.3% GC, and the AT content of the control region is 79.3%. In ML and BI phylogenetic trees, *X. globosa* was a sister clade to *X. grayii*. The monophyly of Lamiinae and Prioninae were supported in ML analyses, but nevertheless, the monophyly of Cerambycinae was not recovered.

### ARTICLE HISTORY

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Beetles are the most varied of insect groups and include more than 360,000 species (Sheffield et al. 2008). Researchers are widely interested in beetle species because of their broad economic significance (Hunt et al. 2007). *Xystrocera globosa* is a beetle of the Cerambycinae subfamily of the family Cerambycidae, a group that is responsible for extensive damage to ornamental trees, reducing the ornamental effects of these trees, the value and utilization of their timber, and even causing death (Kim et al. 2009). Although a study of population genetics and molecular phylogenetics of *X. globosa* was previously reported (Hurst and Jiggins 2005), information on the mitochondrial genome was unknown. Hence, we sequenced the mitochondrial genome of *X. globosa* to discuss its phylogenetic relationship within Cerambycidae.

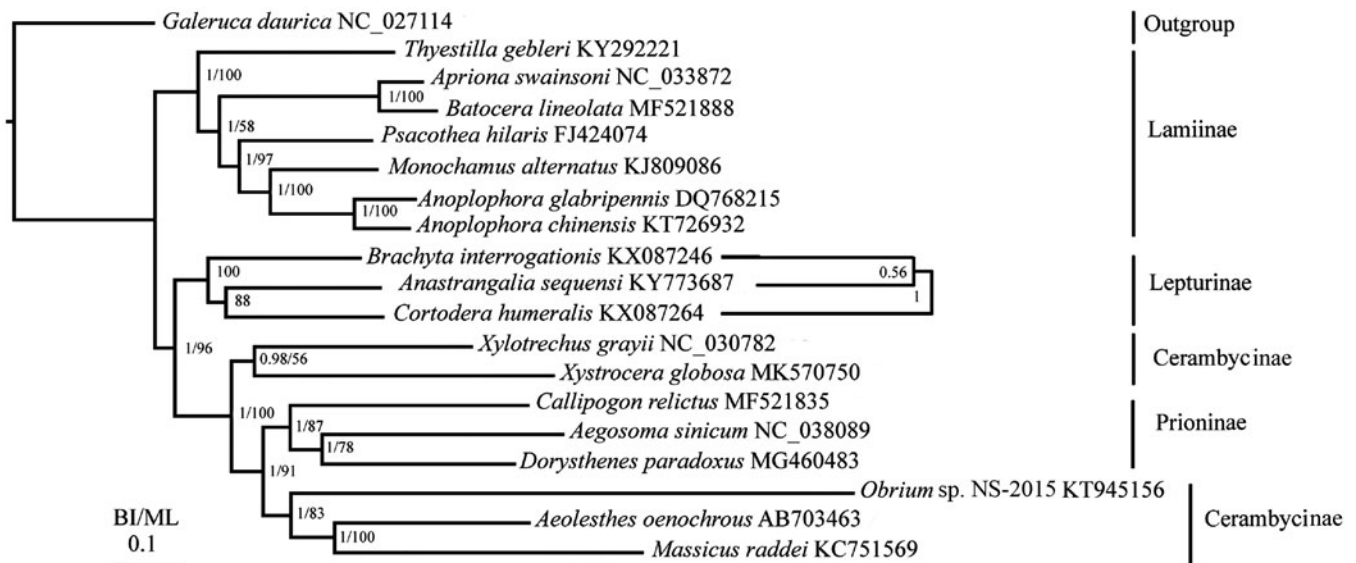
Samples of *X. globosa* were collected from Jinxiu, Guangxi province, China on 10 August 2016 by JY Zhang. Total genomic DNA was extracted from leg muscle tissue using an Ezup Column Animal Genomic DNA Purification Kit (Sangon Biotech Company, Shanghai, China). Remaining samples of *X. globosa* were stored in the lab of Dr JY Zhang, College of Chemistry and Life Science, Zhejiang Normal University. We used 8 universal insect primers (Simon et al. 2006; Zhang et al. 2008; Zhang, Cai, et al. 2018; Zhang, Yu, et al. 2018) and 10 specific primers to amplify the DNA fragments. The PCR products were sequenced by Sangon Biotech Company (Shanghai, China). The genomic sequence has been deposited in GenBank with an accession number MK570750.

The mitochondrial genome of *X. globosa* is 15,707 bp in length, containing 13 protein-coding genes, 22 transfer RNAs, two ribosomal RNAs, and the A + T-rich region. The mitogenome arrangement is identical to the typical coleopteran insect format, with the ancestral gene order of tRNA<sup>Ile</sup>-tRNA<sup>Gln</sup>-tRNA<sup>Met</sup> located between the A + T-rich region and ND2 (Liu et al. 2018). The initiation codon of the 12 protein-coding genes excluding ND1 (that uses TTG) is the typical ATN form (ATA, ATG, ATC, ATT), whereas 10 protein-coding genes (excluding ND3, ND4, and ND5 that end with a single T) have termination codons of TAA or TAG. The entire A + T content of the complete mitogenome is 72.7% (A = 38.4%, T = 34.3%, C = 15.5%, G = 11.8%), and the length of the control region is 1058 bp with 79.3% AT content (A = 40.8%, T = 38.5%, C = 11.3%, and G = 9.4%).

To reconstruct the phylogenetic relationships of Cerambycidae, 13 protein-coding genes of 19 species including *Galeruca daurica* as the outgroup were analyzed (Kim et al. 2009; Guo et al. 2014; Chiu et al. 2016; Fang et al. 2016; Li et al. 2016; Wang et al. 2016; Lim et al. 2017; Liu et al. 2017, 2018). Bayesian inference (BI) and maximum likelihood (ML) methods used MrBayes version 3.2 (Ronquist et al. 2012) and the RAXML version 8 programs, respectively (Stamatakis 2014). These established maximum likelihood (ML) and Bayesian inference (BI) trees (Figure 1). The results show that *X. globosa* is a sister clade to *Xylotrechus grayii*. The monophyly of Lamiinae, Lepturinae and Prioninae were supported by both BI and ML analyses, whereas the monophyly of

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**Figure 1.** Phylogenetic tree of the relationships among 19 species of Coleoptera, including *Xystrocera globosa* based on the nucleotide dataset of the 13 mitochondrial protein-coding genes. Numbers above branches specify posterior probabilities from Bayesian inference (BI) and bootstrap percentages from maximum likelihood (ML, 1000 replications) analyses. The GenBank accession numbers of all species are also shown.

Cerambycinae was not recovered. So, the monophyly of Cerambycinae needs to be further studied in the future.

## Disclosure statement

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

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