

## The complete mitochondrial genome of *Poecilocoris druræi* (Linnaeus, 1771) (Hemiptera: Scutelleridae) and its phylogenetic implications

Yi Liu<sup>a</sup>, Zhihang Zhuo<sup>b</sup>, Rui Fang<sup>c</sup>, Baoxin Wang<sup>d</sup>, Zhaolong Wang<sup>e</sup>, Guyue Xiao<sup>f</sup>, Shengxia Xiang<sup>g</sup> and Danping Xu<sup>b</sup>

<sup>a</sup>Chengdu Qingyang Maternal and Child Health and Family Planning Service Center, Chengdu, China; <sup>b</sup>College of Life Science, China West Normal University, Nanchong, China; <sup>c</sup>College of Forestry, Sichuan Agricultural University, Chengdu, China; <sup>d</sup>Chengdu Academy of Agricultural and Forestry Sciences, Chengdu, China; <sup>e</sup>College of Plant Protection, Gansu Agricultural University, Lanzhou, China; <sup>f</sup>No. 1 Orthopedics Hospital of Chengdu, Chengdu, China; <sup>g</sup>Department of Oncology, Sichuan Integrative Medicine Hospital, Chengdu, China

### ABSTRACT

The complete mitochondrial genome sequence of *Poecilocoris druræi* was sequenced and analyzed. The 16,524 bp mitogenome of *P. druræi* contained 21 tRNA genes, two rRNA genes, 13 protein-coding genes (PCGs), and a control region. Most PCGs used standard ATG start codons and complete TAA termination codons. Phylogenetic analysis indicated that *P. druræi* is closed related with *P. nepalensis*.

### ARTICLE HISTORY

Received 1 June 2021  
Accepted 27 July 2021

### KEYWORDS

Mitochondrial genome;  
Hemiptera; phylogeny;  
*Poecilocoris druræi*

*Poecilocoris druræi* (Linnaeus, 1771) (Hemiptera: Scutelleridae) is equipped with well-developed stinky glands and widely distributed all over the world, especially in the tropics and subtropics (Xu et al. 2019). Elucidating the structure and sequence of *P. druræi* mitogenome is important for understanding its phylogeny and evolution. Adult *P. druræi* was sampled from Nada County, Hainan Province, China (N 19°31'46.85" and E 109°29'39.04"). The specimen was deposited in College of Forestry, Hainan University (Zhihang Zhuo and [zhuozhihang@foxmail.com](mailto:zhuozhihang@foxmail.com); Voucher No. CFHU-PD-202006307), Haikou.

The complete mitochondrial genome of *P. druræi* was 16,524 bp in length (GenBank accession numbers: MZ269306), containing 13 protein-coding genes (PCGs), two rRNA genes, 21 tRNA genes, and a control region. Among them, 23 genes were encoded on the majority strand (N-strand) while another eight tRNA genes, four PCGs, and two rRNA genes were encoded on the minority strand (J-strand). The nucleotide composition was significantly biased (A, C, G, and T was 42.27%, 18.05%, 10.66%, and 31.99%, respectively), with A + T contents of 74.26%. Thirteen PCGs were identified, with a total length of 11,100 bp and distributed from 159 bp (*atp8*) to 1,713 bp (*nad5*). The shortest and longest PCGs are generally consistent with those found in other insects (Huang et al.

2019; Sun et al. 2021). Six types of start codons (ATA, TTG, ATA, ATG, ATT, and GTG) and three stop codons (TAA, TAG, T(AA)) were identified in PCGs.

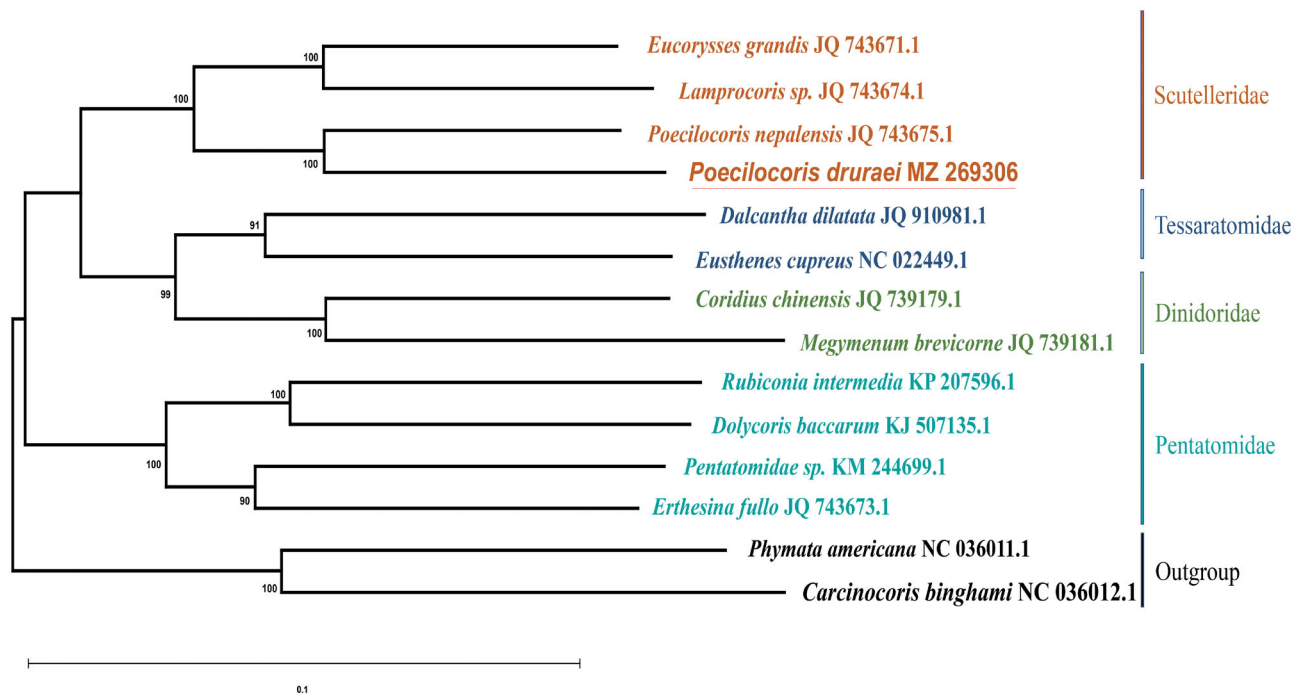
To perform a comparative mitochondrial genome analysis, twelve mitochondrial genomes of Hemiptera insects were downloaded from GenBank database. Multiple sequence alignment was conducted by MAFFT v7 (Katoh and Standley 2013). Phylogenetic analyses were performed with maximum-likelihood in MEGA X with 1000 bootstraps (Kumar et al. 2018). The phylogenetic tree revealed that *P. druræi* is closed related with *P. nepalensis* (Figure 1).

### Disclosure statement

No potential conflict of interest was reported by the author(s).

### Funding

This work was supported by Key Laboratory of Genetic Resources Utilization of Spice and Beverage Crops, Ministry of Agriculture and Rural Affairs, Hainan Provincial Key Laboratory of Genetic Improvement and Quality Regulation for Tropical Spice and Beverage Crops, or Hainan Provincial Engineering Research Center for Tropical Spice and Beverage Crops under Grant [2019xys008].



**Figure 1.** The phylogenetic relationship of 12 species within the Hemiptera species based on neighbour-joining analysis of complete mitochondrial genomes. *Phymata americana* and *Carcinocoris binghami* were served as the out-group.

### Data availability statement

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at (<https://www.ncbi.nlm.nih.gov/>) under the accession number MZ269306. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA 733298, SRR 15094403, and SAMN 20119651 respectively.

### References

Huang Y, Liu Y, Zhu X-Y, Xin Z-Z, Zhang H-B, Zhang D-Z, Wang J-L, Tang B-P, Zhou C-L, Liu Q-N, et al. 2019. Comparative mitochondrial genome analysis of *Grammodes geometrica* and other noctuid insects

reveals conserved mitochondrial genome organization and phylogeny. *Int J Biol Macromol.* 125:1257–1265.

Katoh K, Standley DM. 2013. MAFFT multiple sequence alignment software version 7: improvements in performance and usability. *Mol Biol Evol.* 30(4):772–780.

Kumar S, Stecher G, Li M, Knyaz C, Tamura K. 2018. MEGA X: molecular evolutionary genetics analysis across computing platforms. *Mol Biol Evol.* 35(6):1547–1549.

Sun Y, Huang H, Liu Y, Liu S, Xia J, Zhang K, Geng J. 2021. Organization and phylogenetic relationships of the mitochondrial genomes of *Speiredonia retorta* and other lepidopteran insects. *Sci Rep.* 11(1):2957.

Xu H, Bao X, Wang H, Li D, Cao X. 2019. Analysis on the faunal structure of Heteropter (Hemiptera) from Gansu Province. *J Lanzhou Univ Nat Sci.* 55(6):789–796.