



## Mitochondrial DNA Part B Resources

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## The complete mitochondrial genome of the seed-borer weevil, *Bruchidius uberatus* (Coleoptera: Chrysomelidae: Bruchinae)

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### ABSTRACT

In this study, the complete 15,892 bp mitochondrial genome of *Bruchidius uberatus* (Fåhraeus) was sequenced using Illumina NovaSeq6000 platform. The mitogenome is a double-stranded circular molecule of 15,892 bp in length with 22 transfer RNA genes, 13 protein-coding genes and two ribosomal RNA genes as in other insects. Twenty-five species from 8 subfamilies of Chrysomelidae were selected as ingroups and 3 species of Lamiinae as outgroups for phylogenetic analysis based on mitogenome. The results showed that the subfamily Bruchinae was monophyly. Genus *Bruchidius* had more closed relationship with *Acanthoscelides* than *Callosobruchus* in Bruchinae with high support values.

### ARTICLE HISTORY

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Mitochondrial genome; phylogeny; *Bruchidius uberatus*; Bruchinae

*Bruchidius uberatus* (Fåhraeus) (Coleoptera: Chrysomelidae: Bruchinae) is a serious pest of *Vachellia nilotica* seeds (including *V. n. tomentosa* and *V. n. adansonii*), a far-spread tree species in African savannas with important economic and ecological value. In addition to the main host plant, this bruchid is also listed from *Senegalia senegal*, *Vachellia sieberiana*, *V. flava*, *V. tortilis*, *V. kirkii*, *V. seyal* and *Acacia ehrenbergiana* (Ernst et al. 1990; Delobel et al. 2015).

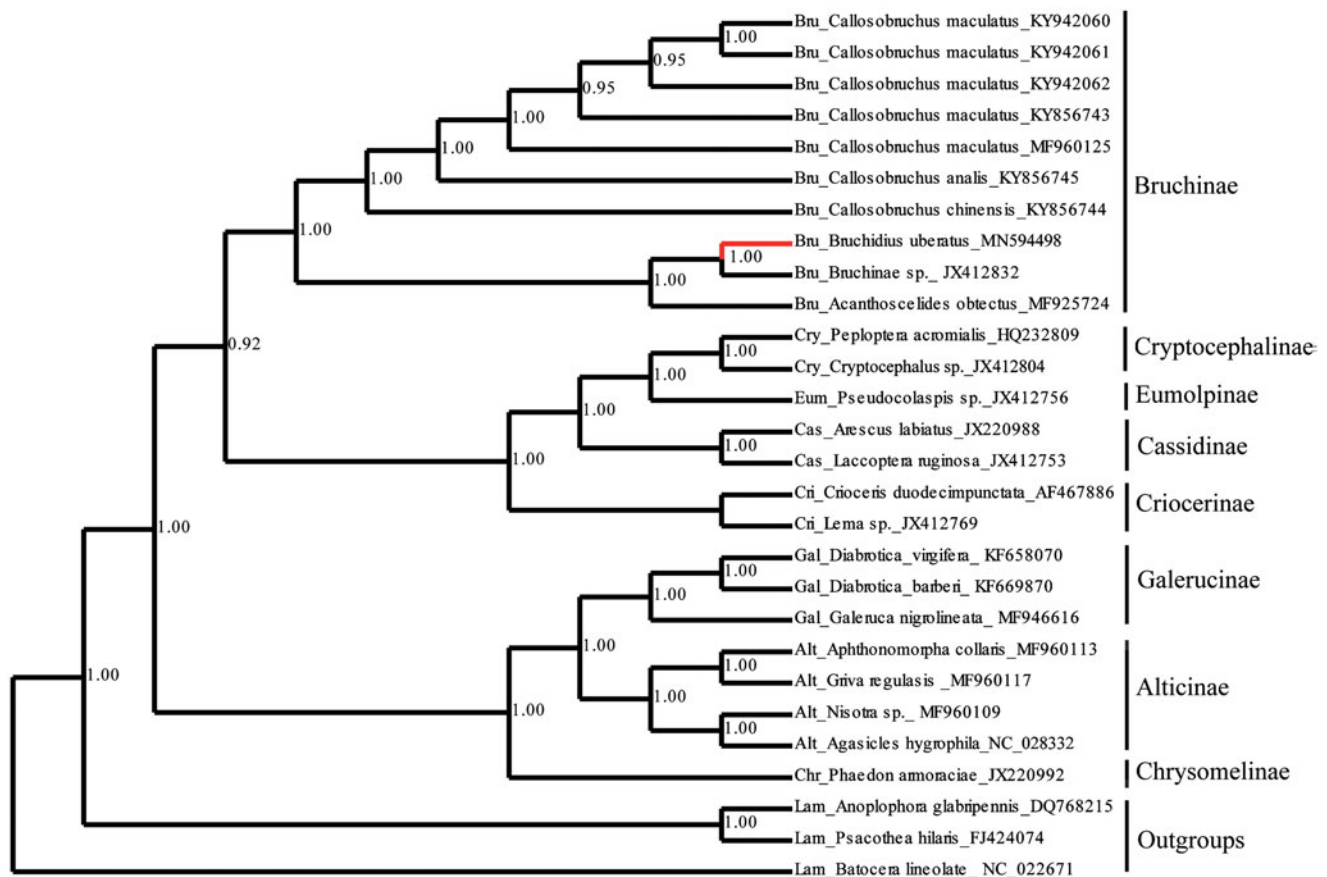
The specimens used in this study were intercepted in imported *Vachellia* sp. from Nigeria (N9°3'14.24"E7°29'17.57"). The sequenced DNA was kept at the National Zoological Museum of China, Institute of Zoology, Chinese Academy of Sciences, Beijing, China (NZMC, the DNA accession number: DX104). The species was identified by Dr. You Li. The complete mitogenome of *B. uberatus* was sequenced by Illumina's HiSeq6000 platform (Illumina, San Diego, CA, USA) with 350 bp insert size and a pair-end 150 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 IDBA-UD (Peng et al. 2012). 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 complete mitochondrial genome (mitogenome) of *B. uberatus* is a double-stranded circular molecule of 15,892 bp in length (GenBank accession number: MN594498), with 22 transfer RNA genes, 13 protein-coding genes and two ribosomal RNA genes as in other insects. The overall base composition is A: 39.3%, T: 38.2%, C: 13.4%, and G: 9.1%, with a much higher A + T content.

For the phylogenetic analysis, all available mitogenomes of the subfamilies of Chrysomelidae was downloaded and analyzed. The acceptable sequences including 13 protein-coding

genes and longer than 10K bp were kept. Total twenty-five species (accession numbers: KY856743, KY856744, KY856745, KY942060, KY942061, KY942062, MF960125, JX412832, MF925724, MN594498, AF467886, JX412769, KF669870, KF658070, MF946616, MF960113, MF960117, MF960109, NC\_028332, JX220992.1, HQ232809, JX412804, JX412756, JX220988, JX412753) from 8 subfamilies (Bruchinae, Criocerine, Cassidinae, Eumolpinae, Cryptocephalinae, Chrysomelinae, Galerucinae, Alticinae) were selected as ingroups and 3 species of Lamiinae (accession numbers: DQ768215, NC\_022671, FJ424074) were selected as outgroups. The phylogenetic inference was based on 13 Protein coding genes (PCGs). TransAlign methods were used to align all genes (Bininda-Emonds 2005). The aligned data from 13PCGs 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 1,000,000 generations, and sampling was done every 100 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.

Phylogenetic analyses (Figure 1) showed that the subfamily Bruchinae was monophyly. Genus *Bruchidius* had more closed relationship with *Acanthoscelides* than *Callosobruchus* in Bruchinae with high support values. The position of Bruchinae in Chrysomelidae was not stable by the results of Nie et al. (2019). In this study, 'chrysomeline' clade (Chrysomelinae, Galerucinae, Alticinae) formed a well supported basal branch, the 'sagrine' clade (Criocerine) and 'eumolpine' clade (Cassidinae, Eumolpinae, Cryptocephalinae) formed another branch, which was close to Bruchinae. Bruchinae was not



**Figure 1.** The Bayesian tree based on 13 PCGs combined data sets. Numbers on nodes indicate Bayesian posterior probabilities. Grey branch is the new data in this study.

nested into 'sagrine' clade, may be because the sampling of 'sagrine' clade is limited and the data type and tree building methods are different. More thorough taxon sampling and diversiform tree building methods will be needed to well understand the status of Bruchinae in Chrysomelidae.

## Disclosure statement

No potential conflict of interest was reported by the authors.

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## References

- Bininda-Emonds O. 2005. TransAlign: using amino acids to facilitate the multiple alignment of protein-coding DNA sequences. *BMC Bioinf.* 6(1):156.
- Delobel A, Ru BL, Genson G, Musyoka BK, Kergoat GJ. 2015. Molecular phylogenetics, systematics and host-plant associations of the *Bruchidius albosparsus* (Fähræus) species group (Coleoptera, Chrysomelidae, Bruchinae) with the description of four new species. *Zootaxa.* 3931(4): 451–482.
- Ernst WHO, Decelle JE, Tolsma DJ, Verweij RA. 1990. Lifecycle of the bruchid beetle *Bruchidius uberatus* and its predation of *Acacia nilotica* seeds in a tree savanna in Botswana. *Entomol Exp Appl.* 57(2):177–190.
- Kearse M, Moir R, Wilson A, Stones-Havas S, Cheung M, Sturrock S, Buxton S, Cooper A, Markowitz S, Duran C, et al. 2012. Geneious basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. *Bioinformatics.* 28(12):1647–1649.
- Nie RE, Andújar C, Gómez-Rodríguez C, Bai M, Xue HJ, Tang M, Yang CT, Tang P, Yang XK, Vogler AP. 2019. The phylogeny of leaf beetles (Chrysomelidae) inferred from mitochondrial genomes. *Syst Entomol.* DOI:10.1111/syen.12387
- Peng Y, Leung HCM, Yiu SM, Chin F. 2012. IDBA-UD: a de novo assembler for single-cell and metagenomic sequencing data with highly uneven depth. *Bioinformatics.* 28(11):1420–1428.
- Ronquist F, Teslenko M, van der Mark P, Ayres DL, Darling A, Höhna S, Larget B, Liu L, Suchard MA, Huelsenbeck JP. 2012. MrBayes 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. *Syst Biol.* 61(3):539–542.
- 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.* 33:686–689.
- 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(2):171–180.
- Zhou X, Li YY, Liu SL, Yang Q, Su X, Zhou LL, Tang M, Fu RB, Li JG, Huang QF. 2013. Ultra-deep sequencing enables high-fidelity recovery of biodiversity for bulk arthropod samples without PCR amplification. *GigaSci.* 2(1):4.