Complete mitochondrial genome of Ricana shantungensis Chou & Lu, 1977 (Hemiptera: Ricaniiidae)

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ABSTRACT

Ricana shantungensis Chou & Lu, 1977 (Hemiptera: Ricaniiidae), is an invasive pest that attacks forest as well as agricultural trees. We sequenced the 15,358 bp long complete mitochondrial genome (mitogenome) of this species; it consists of a typical set of genes (13 protein-coding genes, 2 rRNA genes, and 22 tRNA genes) and one major non-coding AT-rich region. The orientation and gene order of the R. shantungensis mitogenome are identical to that of the ancestral type found in majority of the insects. Bayesian inference (BI) phylogeny placed the R. shantungensis examined in our study, together with Ricana spp. in a group with the highest nodal support, forming the family Ricaniiidae to which R. shantungensis belongs.

Materials and methods

One wild male adult sample was collected on the tree of heaven (Ailanthus altissima) by Hyobin Lee with an insect net in the Haenam-gun, Jeollanam-do, Republic of Korea (34.6724270 N, 126.617252 E) and its DNA was extracted from one of the hind legs. Leftover DNA and the specimen were deposited at the Gyeongsang National University, Jinju, Republic of Korea; however, these specimens revealed that genetic difference was not associated with geographical distance, suggesting the need for variable markers for population genetics data (Kwon et al. 2017).

In previous studies, mitochondrial cytochrome c oxidase subunit I (COI) were analyzed from specimens collected from Korea; however, the specimens revealed that genetic difference was not associated with geographical distance, suggesting the need for variable markers for population genetics data (Kwon et al. 2017).

Results

The R. shantungensis mitogenome was found to be 15,358 bp in length, with typical gene sets – 2 rRNAs, 22 tRNAs, and 13 PCGs – and a major non-coding AT-rich region of 961 bp length (GenBank accession number MW036196). The gene arrangement of R. shantungensis was identical to that of the ancestral type found in majority of the insects (Boore 1999).

Phylogenetic analyses using a BI method, using 13 PCGs and 2 rRNAs, placed R. shantungensis from Korea, along with...
Ricania spp., into the genus Ricania, with the highest nodal support. The family Ricaniidae, to which R. shantungensis belongs, forms a cohesive monophyletic group with the highest nodal supports indicated by BI analysis.

Disclosure statement

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

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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 no. MW036196. The associated BioProject and BioSample numbers are PRJNA700097 and SAMN17823576, respectively.

References

Boore JL. 1999. Animal mitochondrial genomes. Nucleic Acids Res. 27(8): 1767–1780.

Chou I, Lu C. 1977. On the Chinese Ricanidae with descriptions of eight new species. Acta Entomologica Sinica. 20(3):314–322.

Kazutaka K. 2005. MAFFT version 5: improvement in accuracy of multiple sequence alignment. Nucleic Acids Res. 33(2):511–518.

Kim DE, Lee H, Kim MJ, Lee D-H, Department of Eco-safety, Bureau of Conservation Ecology, National Institute of Ecology, Seocheon 325-813, Korea. 2015. Predicting the potential habitat, host plants, and geographical distribution of Pochazia shantungensis (Hemiptera: Ricanidae) in Korea. Korean J Appl Entomol. 54(3):179–189.

Kwon DH, Kim S-J, Kang T-J, Lee JH, Kim DH. 2017. Analysis of the molecular phylogenetics and genetic structure of an invasive alien species, Ricania shantungensis, in Korea. J Asia Pac. Entomol. 20(3):901–906.

Rahman M, Kwon Y, Suh S, Youn Y, Jo S. 2012. The genus Pochazia Amyot and Serville (Hemiptera: Ricanidae) from Korea, with a newly recorded species. J of Entomology. 9(5):239–247.

Ronquist F, Teslenko M, van der Mark P, Ayres DL, Darling A, Hohna 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.