

The mitochondrial genome of the Jeju ground beetle *Carabus smaragdinus monilifer* (Coleoptera, Carabidae)

Dae-Ju Oh , Kyoung-Sik Yang and Yong-Hwan Jung

Biodiversity Research Institute, Jeju Technopark, Seogwipo, Republic of Korea

ABSTRACT

The complete mitochondrial genome of the Jeju ground beetle *Carabus smaragdinus monilifer* was analyzed to determine its structure, morphology, and other characteristics. The 16,737-bp long mitochondrial genome consisted of 37 genes, including 13 protein-coding genes, two rRNAs, and 22 tRNAs. The order, encoding direction, and the initiation and termination codons of the 37 genes of *C. smaragdinus monilifer* were identical to those of other species in the family Carabidae. Phylogenetic analysis revealed that *C. smaragdinus monilifer* is clustered with *Carabus lafossei*. Herein, we have provided the complete mitochondrial genome sequence of *C. smaragdinus monilifer* to understand the phylogeny of Carabidae.

ARTICLE HISTORY

Received 2 October 2019
Accepted 9 November 2019

KEYWORDS

Carabus; mitochondrial genome; phylogeny

The carabid beetles belong to the family Coleoptera, which is one of the most diverse taxa. The ground beetle *Carabus smaragdinus* is classified into 11 subspecies in Korea. *C. smaragdinus monilifer* is the first recorded species from the Korean peninsula, and was found in Jeju Island by Tatum in 1847.

Despite the vast diversity of insect species, information about their phylogeny is lacking. Several researchers have used mitochondrial (mt) genomes to study molecular phylogeny (Wan et al. 2012; Cameron 2014; Kim et al. 2017).

Of the 39,819 species of the family Carabidae that have been reported (<http://carabidae.org>), only 8 mt genome sequences have been deposited in the GenBank database. Thus, we sequenced the mt genome of *C. smaragdinus monilifer* (Specimen num. JBRI-INSCT-0122) of the Jeju Island (geospatial coordinates: 33°18'N 126°38'E) and analyzed its structure, morphology, and other characteristics. Total DNA was extracted and stored in deep freezer in the Jeju Biodiversity Research Institute.

The 16,737-base pairs long mt genome of *C. smaragdinus monilifer* was deposited in GenBank (accession no. MN480425), and consisted of 37 genes, including 13 protein-coding genes (PCGs), two rRNAs, and 22 tRNAs. The mt gene order of *C. smaragdinus monilifer* was identical to that of other ground beetles. Moreover, similar to other ground beetles, most protein-coding genes and tRNAs were encoded on the H-strand, and four PCGs (NADH dehydrogenase subunit 1, 4, 4L, and 5) and eight tRNAs (G, C, Y, P, H, P, L, and V) were encoded on the L-strand. The 16S and 12S ribosomal RNA were also encoded on the L-strand.

All PCGs were initiated by ATT and ATG except NADH dehydrogenase subunit 1, which was initiated by TTG. All PCGs were terminated by TAA, TAG, and the incomplete termination codon T.

The mt genome of *C. smaragdinus monilifer* contained three tRNA clusters (IQM, WCY, and ARNSEF) that were conserved in the mt genome of other ground beetles (Song et al. 2010; Wan et al. 2012; Liu et al. 2018; Wang et al. 2018).

The phylogenetic relationship between *C. smaragdinus monilifer* and eight other Carabidae species previously reported in the GenBank database was determined using the newly determined mt genome sequences of *C. smaragdinus monilifer*. The maximum likelihood (ML) tree was constructed with 13 PCG sequences (Figure 1).

The ML tree revealed that *C. smaragdinus monilifer* is clustered together with *Carabus lafossei*. However, phylogenetic analysis could not provide much information because only eight mt genomes in the Carabidae have been reported in the GenBank database.

Several studies have been conducted to investigate the phylogenetic status and evolutionary history of the Coleoptera mt genes (Juan et al. 1996; Clark et al. 2001; Sota and Ishikawa 2004; Ribera et al. 2004; Andújar et al. 2012; Deuve et al. 2012; Yuan et al. 2016; Linard et al. 2018). Although Carabidae is one of the largest insect families, the mt genome sequences of its species are poorly reported. Thus, in this study, we have provided the mt genome of *C. smaragdinus monilifer* to understand the molecular phylogeny of the family Carabidae.

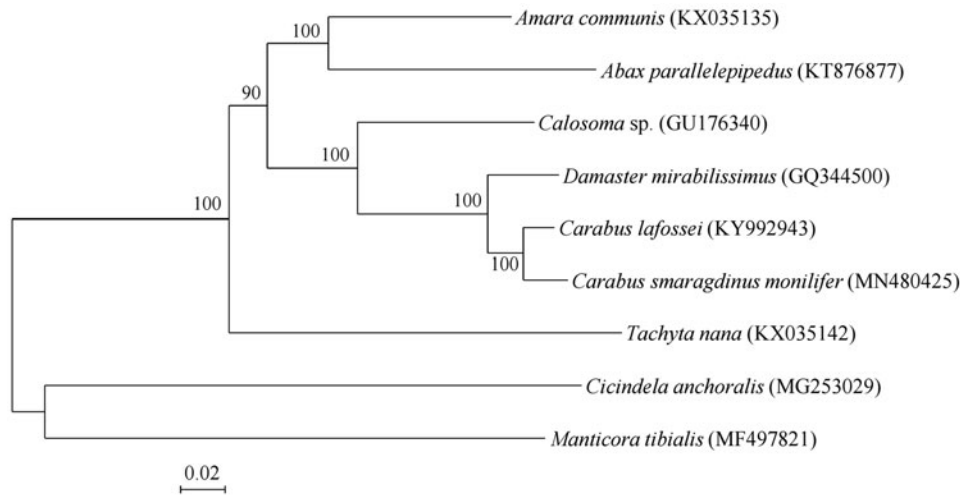


Figure 1. Molecular phylogenetic analysis of mitochondrial 13 protein-coding genes in 9 species of Carabidae. The phylogenetic tree was constructed using MEGA X software (Kumar et al. 2018) with maximum likelihood method using the GTR+G+I model. Percentages of trees where associated taxa were clustered together were shown next to branches.

Disclosure statement

The authors report no conflict of interest. The authors are responsible for the contents of this paper.

ORCID

Dae-Ju Oh  <http://orcid.org/0000-0003-2110-6341>

References

- Andújar C, Serrano J, Gómez-Zurita J. 2012. Winding up the molecular clock in the genus *Carabus* (Coleoptera: Carabidae): assessment of methodological decisions on rate and node age estimation. *BMC Evol Biol.* 12(1):40.
- Cameron SL. 2014. Insect mitochondrial genomics: implications for evolution and phylogeny. *Annu Rev Entomol.* 59(1):95–117.
- Clark TL, Meinke LJ, Foster JE. 2001. Molecular phylogeny of Diabrotica beetles (Coleoptera: Chrysomelidae) inferred from analysis of combined mitochondrial and nuclear DNA sequences. *Insect Mol Biol.* 10(4):303–314.
- Deuve T, Cruaud A, Genson G, Rasplus JY. 2012. Molecular systematics and evolutionary history of the genus *Carabus* (Col. Carabidae). *Mol Phylogenet Evol.* 65(1):259–275.
- Juan C, Oromi P, Hewitt GM. 1996. Phylogeny of the genus *Hegeter* (Tenebrionidae, Coleoptera) and its colonization of the Canary Islands deduced from cytochrome oxidase I mitochondrial DNA sequences. *Heredity.* 76(4):392.
- Kim SR, Kim JS, Kim KY, Kim MJ, Jeong JS, Kim I. 2017. Complete mitochondrial genome of the wild silkworm, *Saturnia boisduvalii* (Lepidoptera: Saturniidae). *Entomol Res.* 47(6):344–351.
- 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.
- Linard B, Crampton-Platt A, Moriniere J, Timmermans MJTN, Andújar C, Arribas P, Miller KE, Lipecki J, Favreau E, Hunter A, et al. 2018. The contribution of mitochondrial metagenomics to large-scale data mining and phylogenetic analysis of Coleoptera. *Mol Phylogenet Evol.* 128:1–11.
- Liu N, Wang S, Yang X, Song J, Wu J, Fang J. 2018. The complete mitochondrial genome of *Carabus (Damaster) lafossei* (Coleoptera: Carabidae). *Conservation Genet Resour.* 10(2):157–160.
- Ribera I, Nilsson AN, Vogler AP. 2004. Phylogeny and historical biogeography of Agabinae diving beetles (Coleoptera) inferred from mitochondrial DNA sequences. *Mol Phylogenet Evol.* 30(3):545–562.
- Song H, Sheffield NC, Cameron SL, Miller KB, Whiting MF. 2010. When phylogenetic assumptions are violated: base compositional heterogeneity and among-site rate variation in beetle mitochondrial phylogenomics. *Syst Entomol.* 35(3):429–448.
- Sota T, Ishikawa R. 2004. Phylogeny and life-history evolution in *Carabus* (subtribe Carabina: Coleoptera, Carabidae) based on sequences of two nuclear genes. *Biol J Linn Soc.* 81(1):135–149.
- Wan X, Hong MY, Liao A, Kim MI, Kim KG, Han YS, Kim I. 2012. Complete mitochondrial genome of a carabid beetle, *Damaster mirabilissimus* (Coleoptera: Carabidae). *Entomol Res.* 42(1):44–54.
- Wang AR, Kim MJ, Jeong SY, Kim I. 2018. Complete mitochondrial genome sequence of *Cicindela anchoralis* Chevrolat, 1845 (Coleoptera: Carabidae). *Mitochondrial DNA B.* 3(1):282–283.
- Yuan ML, Zhang QL, Zhang L, Guo ZL, Liu YJ, Shen YY, Shao R. 2016. High-level phylogeny of the Coleoptera inferred with mitochondrial genome sequences. *Mol Phylogenet Evol.* 104:99–111.