




RESEARCH PAPER

Insight on kleptoparasitic bee, *Melecta chinensis* (hymenoptera: Apidae), in the Republic of Korea: Morphology, biology and molecular characteristics

Sora KIM^{1,2} , Kayun LIM³, Duk-Young PARK⁴, Jinsung PARK^{1,2}, In-Won JEONG^{1,2} and Seunghwan LEE⁴

¹ Lab. of Insect phylogenetics and evolution, Department of Plant Protection & Quarantine, Jeonbuk National University, Jeonju, Republic of Korea

² Department of Agricultural Convergence Technology, Jeonbuk National University, Jeonju, Republic of Korea

³ Department of Biology, Utah State University, Logan, Utah, USA

⁴ Lab. of Insect systematics, Research Institute for Agriculture and Life Sciences, Seoul National University, Seoul, Republic of Korea

Correspondence

Sora Kim, Department of Agricultural Convergence Technology, Jeonbuk National University, Jeonju, 54896, Republic of Korea.
Email: skim01@jnu.ac.kr

Received 2 November 2023;
accepted 6 March 2024.

doi: 10.1111/1748-5967.12723

Abstract

This study focused on a kleptoparasitic bee, *Melecta chinensis*, which is not well-known in the Republic of Korea. We provided a detailed morphological illustration of the adult bees and their nesting biological characteristics with distributional data. Additionally, the complete mitochondrial genome of the species is presented for the first time, and its phylogenetic position within the family Apidae is estimated.

As a result, we could suggest a full redescription of *M. chinensis* for identification and a newly reported potential flower host for it. In addition, the mitochondrial DNA (mtDNA) of *M. chinensis* is revealed as 15,489 base pairs (bp) long, with 35 eukaryotic mitochondrial genes (13PCGs, 2 rRNAs, and 20 tRNAs) and a 706 bp AT-rich region. The overall base composition is 75.82% AT and 24.18% GC. The 13 protein-coding genes (PCGs) started with a typical ATN codon (ATA in nine genes and ATG in four genes) and terminated with TNN (TAN in 10 genes and TTT in one gene) or ANN (AAC in one gene and ATT in one gene). The phylogenetic results based on 13 PCGs showed that *M. chinensis* is distantly positioned to bumble bees (*Bombus*) and honey bees (*Apis*) but closely related to a stingless bee, *Friesomelitta varia*, within the family.

Key words: Apidae, biology, complete mitochondrial genome, kleptoparasitic bee, *Melecta chinensis*, morphology, phylogeny

Introduction

Kleptoparasitic bees, also known as cuckoo bees, are a group of bees that exhibit a parasitic lifestyle. Rather than building their own nests and collecting pollen and nectar, they rely on the nests of other bees for reproduction. While they do not actively collect pollen and nectar themselves, they indirectly contribute to pollination by ensuring the survival and reproduction of the host bee species whose nests they exploit. Also, the kleptoparasitic bees contribute to the overall biodiversity of bee species within an ecosystem. Their presence adds to the complexity of interactions among bees

and other organisms, enriching the diversity of species and ecological processes. There are several kleptoparasitic bee genera found in many parts of the world. For example, *Nomada* bees are the most well-known group, with over 850 species that often parasitize the nests of mining bees, *Andrena* species (Litman 2019). *Sphecodes* bees, which comprise approximately 120 species, target the nests of both solitary and social bee hosts (Sick *et al.* 1994; Bogusch *et al.* 2006; Polidori *et al.* 2020), whereas *Epeolus* bees, with about 100 species, are kleptoparasites of the *Colletes* in North America and Europe (Onuferko 2018). The genus *Melecta*, established

by Latreille, is a relatively unknown kleptoparasitic bee genus that is mainly distributed in the Palearctic and Nearctic regions (Falk 2019). The *Melecta* belongs to the subfamily Nomadinae, which is the biggest kleptoparasitic group among bees. All the species in this subfamily exhibit a unique brood parasitism behavior called kleptoparasitism, indicating that they usurp the host nests and lay their eggs in closed host cells through small circular openings (Danforth *et al.* 2019; Rozen & Ding 2012). All *Melecta* species are kleptoparasites of the tribe Anthophorini, mainly associated with the *Anthophora* (Lieftinck 1972), which is a large genus of robust, fast-flying, pollen-collecting bees occurring on every continent except Australia and South America (Michener 2007; Stone 1993). *Melecta* has a single generation per year and is active in either spring or summer, depending on the species (Amiet *et al.* 2007). So far, there is only one *Melecta* in the Republic of Korea, which is *M. chinensis*. However, this Korean species has only a name (Korean Society of Applied Entomology & The Entomological Society of Korea 2021) and no information is available about its morphology, biology, distribution, or even what it looks like. In this study, we provide a morphological description, along with distribution and biological information of the Korean *M. chinensis*. We also propose the complete mitochondrial genome of *M. chinensis* with its phylogenetic relationship within the family Apidae.

Materials and Methods

Morphological analyses

All specimens for morphological examination were deposited in Seoul National University (SNU) in the Republic of Korea. In the collecting site, *M. chinensis* was found in a large aggregation of *Anthophora villosula*. After collecting both hosts and kleptoparasitic bees, we transported them to the laboratory for rearing to observe potential mating behaviors. Photographs of the nests of *A. villosula* and the mating behavior of *M. chinensis* were taken using a Nikon digital camera (D850, equipped with an AF-S Micro Nikkor 60 mm f/2.8G ED lens), and the dried specimens were photographed using a DMC 5400 digital camera attached to a Leica Z16 APO motorized microscope. Serial images were merged using Zerene Stacker, and the images were minimally edited and assembled into figure plates in Adobe Photoshop CS6 2012 software.

For morphologic description, all specimens were preserved in a dry state. The kleptoparasitic bees were identified at the species level following Lieftinck's (1980) and Brooks's (1988) references. The abbreviations used here, including the taxonomical terminologies, are as follows: OOL, minimal distance between posterior ocellus and inner orbit; POL,

distance between posterior ocelli; LOL, distance between anterior and posterior ocellus; MPOD, maximum diameter of posterior ocellus; UID, upper interocular distance; LID, lower interocular distance.

Molecular analysis

Specimens for molecular analysis were collected by the second author from Gimcheon-si, Gyeongsangbuk-do, Republic of Korea, on April 17, 2021.

Genomic DNA was extracted using an Exgene Tissue SV kit (GeneAll, Republic of Korea). The DNA were provided and deposited at the Laboratory of Insect Phylogenetics and Evolution, Jeonbuk National University (JBNU IPE), Republic of Korea, under the voucher number IPE ComG01.

Illumina DNA libraries were constructed using the Caliper Labchip GX HT DNA HiSeq chip and Bioo DNA Library kit (Bioo Scientific Cor. Austin, TX, USA). High-throughput sequencing was conducted using the Illumina NovaSeq 6000 (Illumina Inc., Sang Diego, CA, USA) at the Genome Analysis Center of the National Instrumentation Center for Environmental Management, Republic of Korea. The run mode was Rapid Pair End 250 cycles. A total of 4,533,422 reads were analyzed to generate 1,160,871,879 base pairs of sequence and assembled in a CLC genome assembler (ver. 4.010.83348, CLC Inc., Aarhus, Denmark). Annotation of protein-coding genes (PCGs), ribosomal RNAs (rRNAs), and transfer RNA (tRNA) genes was conducted using Ge-seq (Tillich *et al.* 2017). For phylogenetics, we used one species, *Vespa mandarinia*, of Vespidae as an outgroup and 11 species of Apidae, including *M. chinensis* as an ingroup. We reconstructed based on nucleotide sequences data of 13 PCGs (ND1, ND2, ND3, ND4L, ND5, COI, COII, CYTB, ATP8, ATP6, ND4, ND6, and COIII) with maximum likelihood analysis through IQ-Tree web server (Trifinopoulos *et al.* 2016; <http://iqtree.cibiv.univie.ac.at>). Branch support values were produced by ultrafast bootstrap pseudoreplicates (UFB) and maximum likelihood analysis with best-fit model, GTR + F + G4, according to the Bayesian information criterion.

Results

Morphological results

Taxonomic accounts.

Melecta (Melecta) chinensis Cockerell, 1931 (Figs. 1–4)

Melecta (Melecta) chinensis Cockerell, 1931, Amer. Mus. Novit. 466: 6.

Diagnosis. This species is easily distinguished from *M. albifrons*, which has the same host of *M. chinensis*, by the

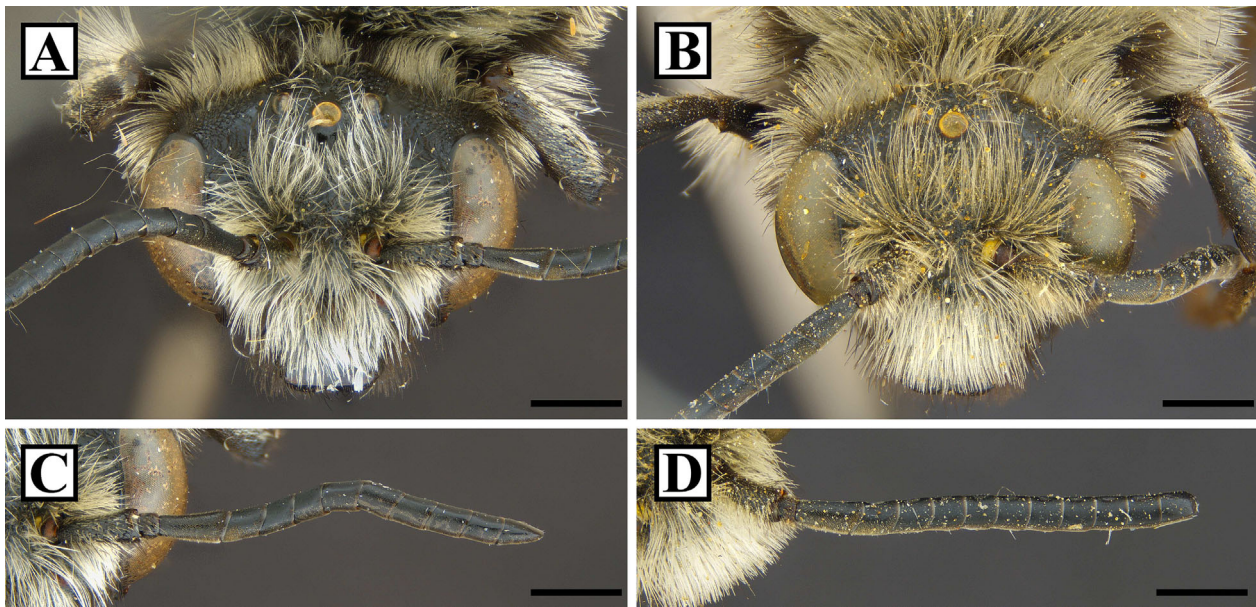


Figure 1 *Melecta (Melecta) chinensis* (A,C) female and (B,D) male: (A,B) head in frontal view; (C,D) antenna. Scale bar 1 mm for (A–D).

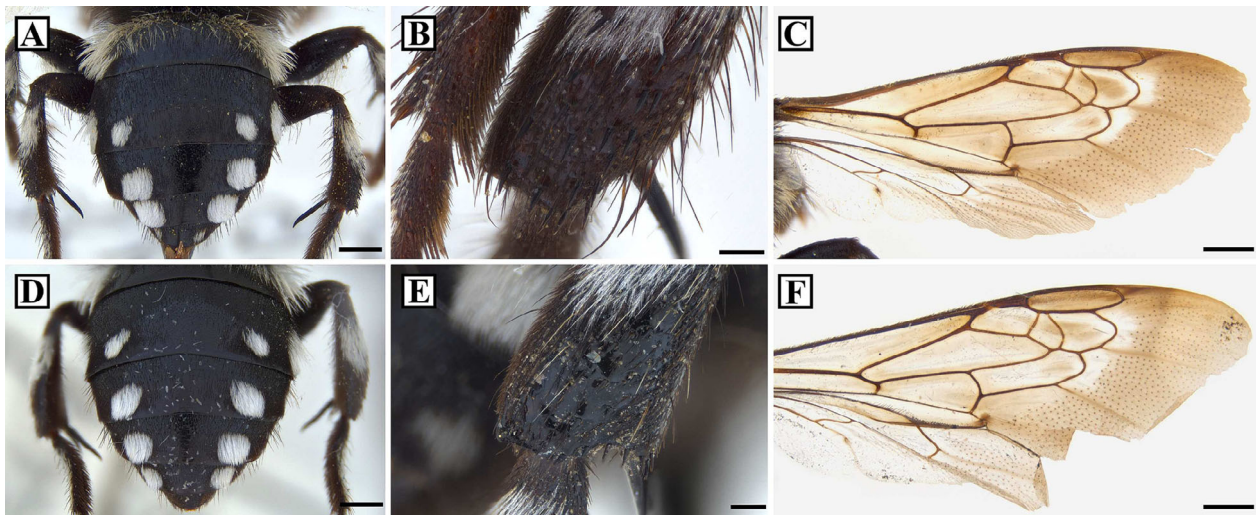


Figure 2 *Melecta (Melecta) chinensis* (A–C) female and (D–F) male: (A,D) abdomen in dorsal view; (B,E) apex of hind tibia; (C,F) wings. Scale bar 0.25 mm for (A,B,D,E), 1 mm for (C,F).

following morphological characters: white rectangular spots, three in number, on dorsal area of abdomen of female *M. chinensis* (Fig. 2A), while smaller and rounder white spots, zero (uncommon form) to three in number, in female *M. albifrons*; white square-formed spots, four in number, on dorsal area of abdomen of male *M. chinensis* (Fig. 2D), whereas the spots are absent or two in number in male *M. albifrons*.

Sexes are not easily distinguishable in the field. The third submarginal cell is longer and apically pointed in male than

female bees (Fig. 2C,F); sharp and thick spines are evenly distributed in the hind tibia in female, while blunt, short spines are mainly concentrated at the distal area of the hind tibia (Fig. 2B,E).

Description. FEMALE: body length 12.58–12.96 mm. Body entirely black.

Head. In frontal view (Fig. 1A), 1.17–1.16× as wide as long; OOL: POL: LOL: MPOD = 3.12–3.24: 2.75–2.84: 0.92–0.98: 1.0; UID 1.10–1.16× as long as LID;

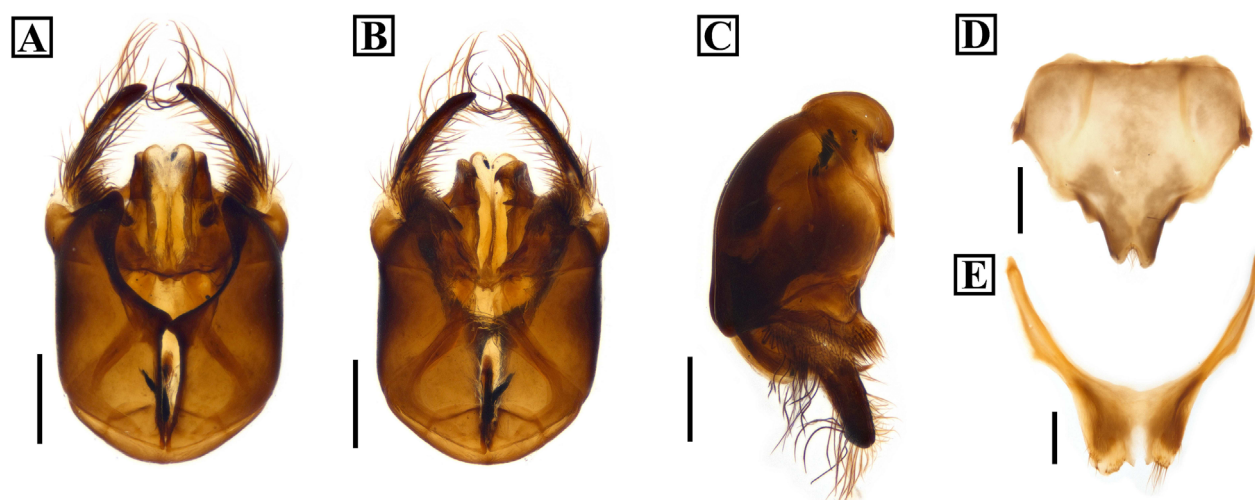


Figure 3 (A–C) Male genitalia of *Melecta (Melecta) chinensis* and (D, E) metasomal sternum of the same. (A) in ventral view; (B) in dorsal view; (C) in lateral view; (D) eighth metasomal sternum in dorsal view; (E) seventh metasomal sternum in dorsal view. Scale bar 0.5 mm for (A–C), 0.25 mm for (D, E).

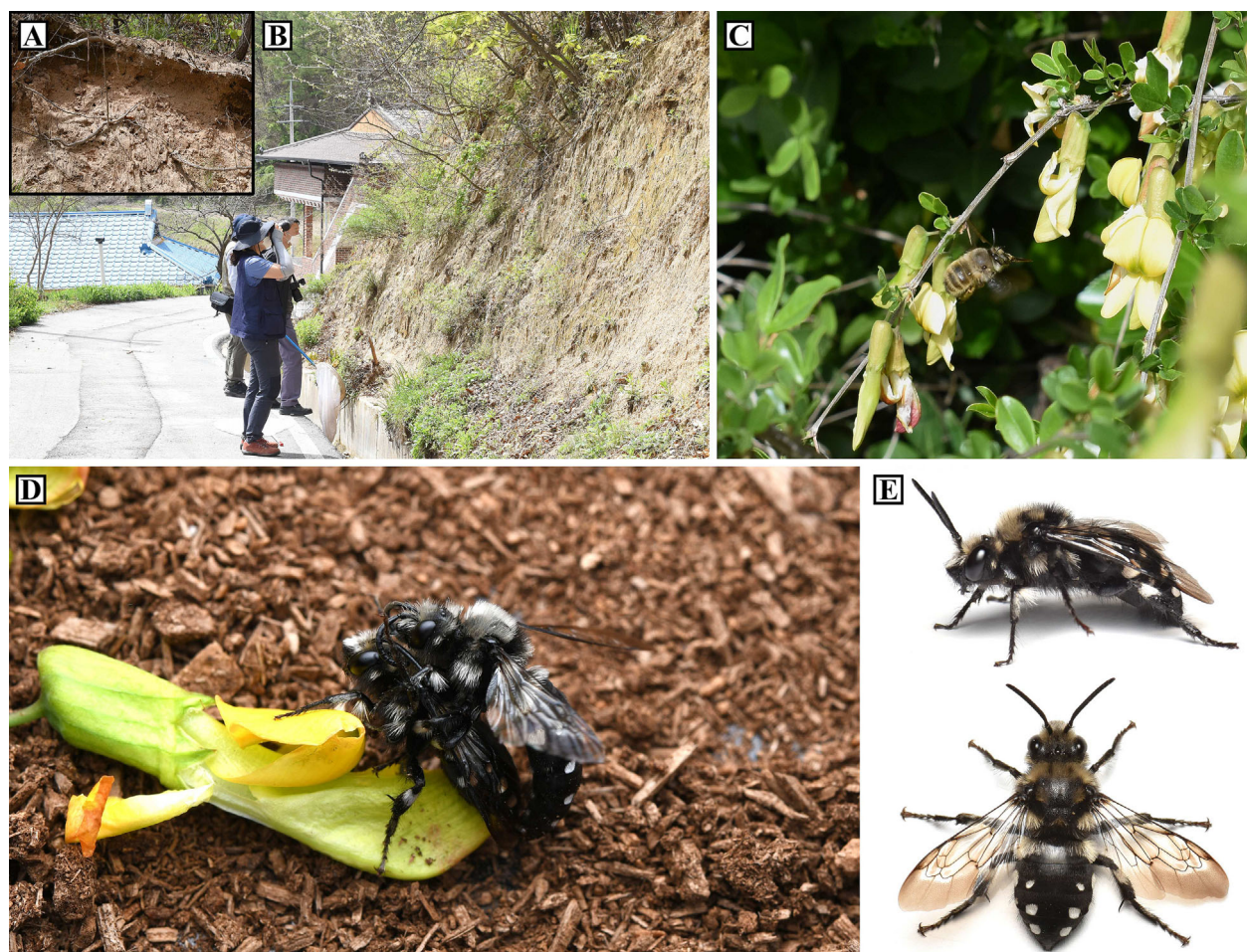


Figure 4 Photographic information for *Melecta (Melecta) chinensis*: (A, B) habitat; (C) host plant (*Caragana sinica*) and host species (*Anthophora villosula*); (D) mating female (left) and male (right); (E) habitus of alive female in lateral and dorsal view (Photo: C Soo Jeong Cho, E Wonwoong Kim).

imbricate-foveolate on vertex except confused with smooth and punctate surface around ocelli; covered with long whitish to light brown hair, except bare on vertex and dark brown hair on ventral margin of labrum. Eye $1.92\text{--}1.98\times$ as high as wide. Mandible triangular with apical tip acute. Antennae (Fig. 1C) with scape cylindrical having yellowish short white setae on upper side, but long dark brown setae on lower side; with 10 flagellar segments; 1st flagellar segment distinctly longer than wide, $1.89\text{--}1.99\times$ as long as wide; 2nd to 10th flagellar segment slightly longer than wide, $1.08\text{--}1.30\times$ as long as wide; pedicel to 2nd flagellar segment with erect dark brown setae on lower side, but 3rd–10th flagellar segments almost bare.

Mesosoma. Mesoscutum densely foveolate; anterior and sublateral side covered with light brown to yellowish white long hair, but bare on median area. Scutellum similar to mesoscutum in sculpture, but entirely bare. Tegula smooth. Side of propodeum covered with long yellowish white hair. Hind tibia (Fig. 2B) with sharp and thick spines. Fore wing (Fig. 2C) $3.05\text{--}3.13\times$ as long as wide; hind wing $3.45\text{--}3.50\times$ as long as wide; fore and hind wings infusate except subbasal area; extreme basal area deep brown and apical margin with broad brown band. Leg with entirely dark brown hair, except as follows: white long hair on posterior side of pro- and mesofemur, white short setae on posterior side of protibial and basal one-third region of metatibia; hind tibia $3.85\text{--}3.97\times$ as long as wide, with evenly distributed sharp and thick spines; hind tarsus $5.65\text{--}5.78\times$ as long as wide; length of spur $0.62\text{--}0.68\times$ as long as length of hind tarsus.

Metasoma (Fig. 2A). Anterior half of 1st gastral tergite sparsely foveolate to posteriorly half finely strigulate; 2nd to 6th gastral tergites finely imbricate; sparsely covered with black short hair, except white long hair on anterolateral side of 1st gastral tergite; 4–6 pairs of white hair spot on 2nd to 5th gastral tergites; normally 2 pairs on 2nd gastral tergite and each 1 pair on 3rd to 5th gastral tergites.

Male. Body length $11.91\text{--}12.79$ mm. Color and sculpture of male similar to those of female, except as follows: head (Fig. 1B) $1.10\text{--}1.13\times$ as wide as long in frontal view; OOL: POL: LOL: MPOD = $3.08\text{--}3.16$: $2.80\text{--}2.97$: $0.89\text{--}0.95$: 1.0 ; UID $1.13\text{--}1.15\times$ as long as LID; eye $1.95\text{--}2.02\times$ as high as wide; antenna (Fig. 1D) composed of 11 flagellar segments; 3rd submarginal cell pointed apically and longer than that of female; hind tibia $2.87\text{--}2.95\times$ as long as wide; spines of hind tibia (Fig. 2E) more short and blunt than that of female; hind tarsus $5.95\text{--}6.01\times$ as long as wide; length of spur $0.42\text{--}0.47\times$ as long as length of hind tarsus. Male genitalia and sternites as in Figure 3.

Material examined. [Republic of Korea] Gangwon-do, 1♂, Chuncheon-si, April 23, 1985, G.M.H; Gyeonggi-do, 1♀, Songhyun-ri, Sanbuk-myeon, Yeosu-si, May 23, 2019, J. Hyun; 1♀, Suwon, April 07, 1994, H. Lee; 1♀, Mt. Gwanggyo, May 16, 1995, unknown; 1♂, Mt. Cheonggye, Gwacheon-si, April 11, 1977, unknown; Gyeongsang-do, 1♂, Andong-si, May 01, 1994, JY Lee; 1♂, Temple Dasol, 417, Dasolsa-gil, Gonmyeong-myeon, Sacheon-si, April 29, 1989, unknown; 2♀, 2♂, Gimcheon-si, April 17, 2021, K. Lim, H. Lee, and H. Lee; Jeollanam-do, 1♂, Mt. Baikun, Gwangyang-si, May 22, 1993, H. Lee.

Distribution. Republic of Korea, China.

Flower information. *Caragana sinica* (this study).

Host. *A. villosula* (Fig. 4C) (Orr & Koch 2023).

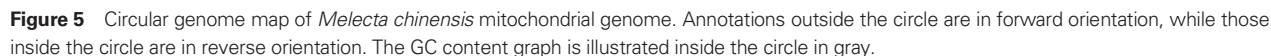
Biology. *M. chinensis* was found in a large aggregation of the *A. villosula* (Apidae) in the Republic of Korea. The nests were situated approximately 2 m above the ground and numerous host females and several *Melecta* females were observed at the location. Despite our efforts to excavate the nests, we faced challenges due to the soft soil and the elevated position of the nests. We also observed that the females of *M. chinensis* were patrolling *Caragana sinica* bushes and males of *M. chinensis* were more often chasing females at the same location (Fig. 4C–D).

Remark. The host, *A. villosula*, of the *M. chinensis* was previously identified as *A. plumipes* in having a similar appearance, but distinguished through molecular analysis (Černá et al. 2017).

Molecular results

Complete MT genome of *M. chinensis*. The complete mitogenome of *M. chinensis* (15,489 bp) consisted of 35 individual genes, 13 PCGs, two rRNAs, 20 tRNA genes, and the A + T region (Fig. 5). Among the 13 PCGs, nine genes (ND1, ND2, ND3, ND4L, ND5, COI, COII, CYTB, and ATP8) started with the ATA codon, and four genes (ATP6, ND4, ND6, and COIII) began with ATG. Eleven genes harbored typical stop codons, TAN (TAA: ND2, ND3, ND4, ND6, ATP6, and ATP8; TAC: COIII) or TTT (COI). Two genes were terminated with ANN (AAC in COII and ATT in ND5). The mitogenome of *M. chinensis* was larger than those of other sequenced Apidae species, ranging from 14,862 bp in *Melipona scutellaris* to 17,693 bp in *Apis florea*. The 706 bp A + T rich region was located between 12S rRNA and rRNA¹⁶, and the overall base composition was 75.82% AT and 24.18% GC.

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. OQ465871.



Phylogenetic relationship based on 13 protein-coding genes. In the maximum likelihood tree based on 13 PCGs, all members of Apidae were positioned within the clade A (Fig. 6). The phylogenetic position of *M. chinensis* was clustered with a stingless bee, *Frieseomelitta varia* (Fig. 6,

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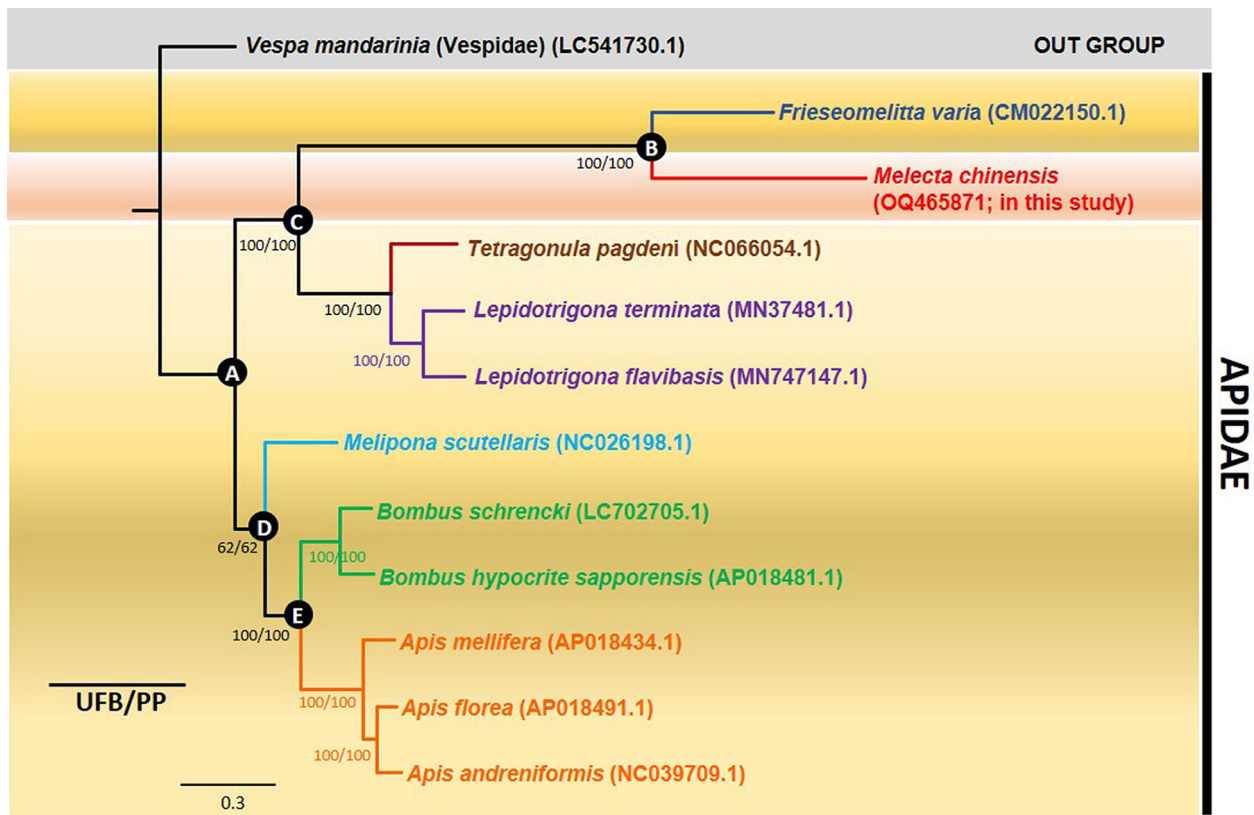


Figure 6 Maximum likelihood (ML) phylogenetic tree inferred from the nucleotide sequence data of mitogenomic 13 PCGs. *Melecta chinensis* newly reported by this study is colored in red with its Genbank accession No. OQ465871. The following sequences were used: *Vespa mandarinia* (LC541730.1), *Frieseomelitta varia* (CM022150.1), *M. chinensis* (OQ465871; in this study), *Tetragonula pagdeni* (NC066054.1), *Lepidotrigona terminata* (MN37481.1), *Lepidotrigona flavibasis* (MN747147.1), *Melipona scutellaris* (NC026198.1), *Bombus schrencki* (LC702705.1), *Bombus hypocrite sapporensis* (AP018481.1), *Apis mellifera* (AP018434.1), *Apis florea* (AP018491.1), *Apis andreniformis* (NC039709.1). The numbers under nodes represent the ultrafast bootstrap (UFB) support values and the posterior probabilities (PP) from the ML results.

Discussion

According to Rasmont (2016), *Melecta* species are nowhere abundant, and they are rare and occur in isolation. He also noted that these *Melecta* spp. do not seem to fly in circuits like *Anthophora*, which means that if you miss them at first sight, they are unlikely to fly back. He emphasized that *Melecta* species are very difficult to sample. Furthermore, species identification within the genus is very difficult, except for the most common species, *M. albifrons*.

This study focuses on the kleptoparasitic bee species, *M. chinensis*, which is relatively unknown in the Republic of Korea. We provide a taxonomic morphological diagnostic description by comparing the external morphology of *M. chinensis* with that of the well-known species, *M. albifrons*, enabling rapid species identification. Distinctions between sexes within the same species, detailed magnifications of male and female adults with full taxonomic descriptions, and distributional information on all specimens in domestic collections are provided. In addition, we newly found its host

flower, *Caragana sinica*, and addressed the nesting behavior with biological information, such as nest features and adult behavior. As a molecular approach, we implemented and analyzed the complete mitochondrial genome of the species for the first time. The mtDNA of *M. chinensis* is revealed as 15,489 bp and is consisted of 35 individual genes, 13 PCGs, 2rRNAs and 20 tRNA genes and A + T region. Compared to mtDNA of species of Apidae, it was larger than those of *M. scutellaris* (14,862 bp) and *Frieseomelitta varia* (15,144 bp) and had a similar length to those of *Lepidotrigona flavibasis* (15,408) and *L. terminata* (15,431 bp). The mtDNA of the other remaining species, *Apis mellifera*, *Apis andreniformis*, *A. florea*, *Bombus hypocrite sapporensis*, *B. schrencki* and *Tetragonula pagdeni*, were all in a range from 15,793 bp (*B. schrencki*) to 17,693 bp (*A. florea*), which is larger than that of *M. chinensis*. Lastly, we conducted the phylogenetic position of the species, *M. chinensis*, within the family Apidae. In the phylogenetic relationship based on 13 PCGs, we could confirm that *M. chinensis* is closer to stingless bee genera *Frieseomelitta*, *Tetragonula* and

Lepidotrigona, but distantly positioned to bumble bees and honey bees within the family. This study will provide a comprehensive understanding of kleptoparasitic bees and insights into understanding the overall bee diversity and its function in the ecosystem.

Acknowledgments

This work was supported by Basic Science Research Program through the National Research Foundation of Republic of Korea (NRF) funded by the Ministry of Education (2020R111A1A01069466 and NRF2020R111A2069484). Additionally, we would like to thank Dr. Heung-sik Lee (for providing the locality of *M. chinensis*), Soo Jeong Cho and Wonwoong Kim (for providing valuable pictures).

Funding

This work was supported by the Basic Science Research Program through the National Research Foundation of the Republic of Korea (NRF) funded by the Ministry of Education (2020R111A1A01069466 and NRF2020R111A2069484).

Conflict of interest statement

The authors have no conflict of interest regarding the content of this article.

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