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Original article

Molecular identification of *Reesa vespulae* (Milliron) (Coleoptera: Dermestidae), a newly recorded species from Korea

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ABSTRACT

A museum pest belonging to the family Dermestidae was found in the Museum of Sunchon National University, Sunchon, Korea and identified using its morphological characteristics and a DNA-based analysis of the mitochondrial cytochrome *c* oxidase I (COI) gene. This marks the first recorded appearance of this pest, which is identified as *Reesa vespulae* (Milliron), in the Korean Peninsula. We provide the details of the morphological diagnosis with the habitus of its adult and larva and its COI barcode data, and introduce historical data about its invasion around the world.

Introduction

The family Dermestidae is one of the pest groups found in museums worldwide, with about 1,200 species, subdivided into 55 genera in 14 tribes belonging to six subfamilies: Dermestinae, Thorictinae, Trinodinae, Orphilinae, Attageninae, and Megatominae (Kiselyova and McHugh, 2006; Háva, 2014). Most genera are scavengers that feed on dry animal or plant material such as skin or pollen, animal hair, feathers, dead insects, and natural fibers. They are primarily involved with animal carcasses, and mammal, bird, bee, or wasp nests. This family is also known for the great propensity of its many species for introduction into and occurrence in new areas (Bunalski and Przewoźny, 2009).

We report the genus *Reesa* Beal, a museum pest new to Korea, which was found during the survey of specimens from the insect collections of the Department of Plant Medicine, Sunchon National University (SCNU), Suncheon, Korea. The genus *Reesa* Beal is a synanthropic Nearctic species that has become widespread in northern Europe and is now established elsewhere. In particular, this species had been breeding in the fluff under furniture and had damaged a small number of dried insects (Peacock, 1993). Although adults have been collected in the grounds of the museum, it was not known whether they had been breeding outdoors. This species also are known to be parthenogenetic, which leads to difficulty in the control of populations.

In this study, we report on the first recorded appearance of the dermestid genus *Reesa* in the Korean Peninsula. Morphological information (with illustrations and new data) is provided to help establish its identification.

Materials and methods

Taxon sampling and image data

We were able to examine the morphological characteristics and acquire the DNA barcode [cytochrome *c* oxidase I (COI)] sequence from adult and larval specimens, which were found among the insect collections of the Department of Plant Medicine in SCNU. At that time, we moved the damaged insect specimens to rearing containers. In 2014, the larvae of this species have been also observed in the rearing containers. The morphological images were

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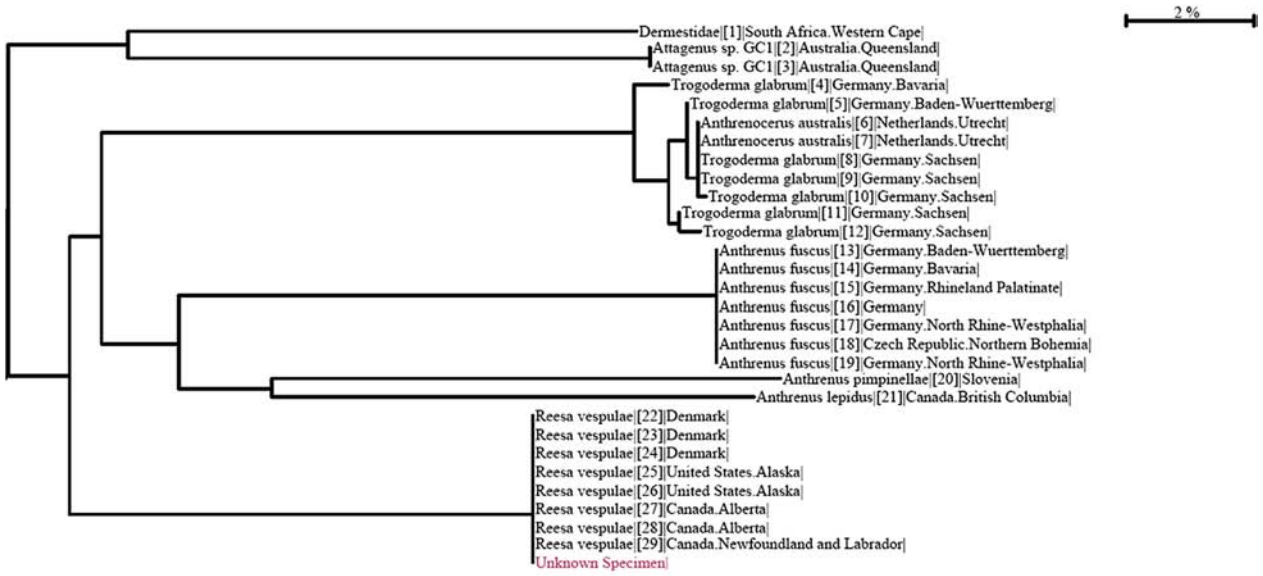

Figure 1. Neighbor-joining (NJ) tree based on the mitochondrial cytochrome *c* oxidase I (COI) gene sequence of the dermestid specimen in this study.

observed under a stereoscopic microscope (Leica EZ4 HD, X8-20). We used a Canon EOS 60D Camera, Canon Macro Photo lens MP-E 65 mm, and Auto montage program (Helicon Focus 6) to take photographs of the specimens. The specimens examined in this study are deposited in the insect collections of the Department of Plant Medicine in SCNU.

DNA extraction, amplification, and sequencing

Total genomic DNA was extracted from the leg of one of the dried specimens using a DNeasy Blood & Tissue Kit (Qiagen, Inc., Dusseldorf, Germany) following the manufacturer's protocol, except that the final elution step was performed with 60 μL of distilled water instead of 200 μL buffer. All of the vouchers used this study are deposited in the insect collections of SCNU. A 658-bp segment of the barcode region was amplified from specimens using the primer LepF1 and LepR1 (Hajibabaei et al., 2006). Polymerase chain reactions (PCRs) were performed using a Maxime PCRPreMix (iNtRON Biotechnology, Seongnam, Korea) with 2.0 pmol of each primer and 2–50 ng template DNA in a 20-μL reaction. PCR thermocycling was done as described in a previous report (Park et al., 2010). PCR products were visualized in a 2% agarose gel stained with ethidium bromide and bidirectionally sequenced using a BigDye Terminator version 3.1 Cycle Sequencing Kit (Applied Biosystems Inc., Foster, CA, USA) on an ABI 3730XL capillary sequencer. Contigs were assembled using CodonCode Aligner version 3.5.6 (CodonCode Co., Dedham, MA, USA). The DNA barcode sequences were deposited in GenBank (accession no. KJ909793). Sequence divergences were calculated using the Kimura 2-parameter (K2P) model (Kimura, 1980), and a neighbor-joining tree was generated by BOLD systems.

Results

Molecular identification using DNA barcode

PCR amplification and sequencing of the mitochondrial COI DNA barcode region for unknown dermestid larvae and adult specimens generated 624 bp of partial barcodes with 100% homogeneity. A BLAST search of the barcode in GenBank did not show a closely related species (the highest match was found with an Elateridae species with a sequence homology of 84%). However, we found that the barcode was identical to that of eight *Reesa vespulae* specimens collected in Denmark, the USA, and Canada in the BOLD system (www.boldsystems.org; Figure 1). The barcode sequence of the *R. vespulae* specimens has not been released yet in the BOLD system, and this study marks the first report of the COI barcode for the species.

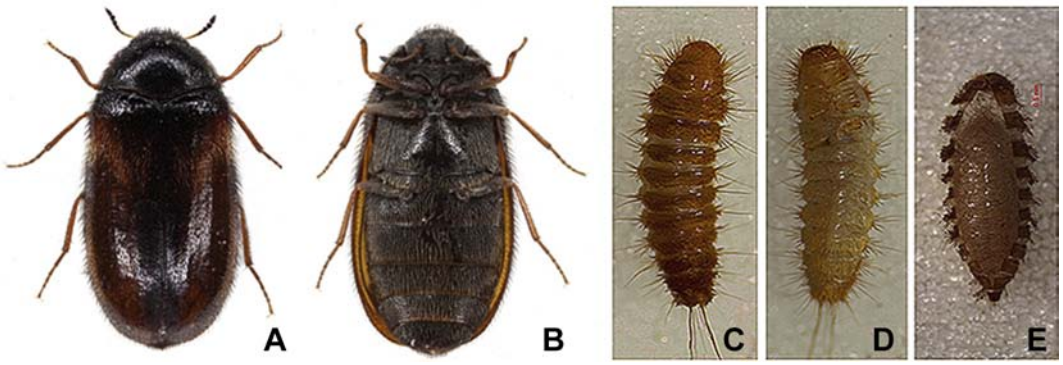

Figure 2. Habitus of *Reesa vespulae* (Milliron). A: Dorsal side and B: ventral side of adult; C: dorsal side, and D: ventral side of larva; E: pupa.

Taxonomic account

Family DermestidaeLatreille, 1807
Subfamily Megatominae Leach, 1815
Tribe MegatominiGanglbauer, 1904
Genus *Reesa* Beal, 1967

Reesa Beal, 1967, Miscell. Pub. Entomol. Am. 5: 310. [Type species: *Perimegatoma vespulae* Milliron, 1939]

Reesave spulae (**Milliron, 1939**) Pyo-bon-su-si-reong-i

Perimegatoma vespulae Milliron, 1939, Ann. Entomol. Soc. Am. 32: 570. [Type locality: MN, USA].

Megatoma vespula Spencer, 1948: 6–9.

Diagnosis. The habitus of this species has characteristic features (Figure 2) that make it fairly easy to distinguish this species from other species of Dermestidae in Korea. This species is distinguished by the following characteristics: (1) antennae club with four segments (this feature also occurs in Korean Dermestidae, but only in females of the genus *Trogoderma* DeJean); (2) body covered with strong black setae (absence of scales like setae forming a color band pattern differentiates this genus from *Trogoderma* DeJean); (3) characteristic coloration of the body, forming two light red bands in the front half of elytra. Determination of this species can be carried out by following the key of Háva (2004) for the adult stage and the key of Peacock (1993) for the larval stage.

Specimen examined. 2♀ (adult), 7.x.2013; 2♀ (larva), 22.v.2014 (in the insect collections of SCNU); 9♀ (adult), 5–8.vi.2014 (specimens reared in insect specimens).

Distribution. Korea (new record), Japan, Europe (Austria, Czech Republic, Denmark, Finland, Great Britain, Germany, Hungary, Holland, Norway, Russia, Slovakia, Sweden, and Switzerland), Africa (Algeria, Egypt, Morocco, and Tunisia), Canada, Mexico, USA, Chile, Afghanistan, Asiatic part of Russia, Australia, and New Zealand.

Remarks. This genus is placed in the tribe Megatomini in subfamily Megatominae (Háva, 2003). Information on this species has been obtained from female specimens only, so it is considered parthenogenetic (Milliron, 1939). This study marks the first confirmation of this species in Korea. In 2013, dead adult specimens of this species were first observed in the unprotected insect collections of the SCNU. At that time, we moved the dermestid beetles from the damaged insect specimens into rearing containers. The larvae of this species were also observed in the rearing containers with a co-occurrence species, *Trogoderma varium* (Matsumura & Yokoyama) of 2014.

Discussion

This species was described as *Perimegatoma vesuplae* Milliron and obtained from wasp nests in St. Paul, MN, USA (Milliron, 1939). Beal (1967) revised the classification of this species to a new genus, *Reesa* (Háva, 2004). Shortly thereafter, reports of its occurrence outside the United States territory followed; this species was also found in Canada (Spencer, 1948). In Europe, *R. vespulae* (Milliron) was recorded for the first time in the beginning of the 1970s (Zhantiev, 1973); however, Bunalski and Przewoźny (2009) suggested that this species was actually introduced in Europe earlier, in the beginning of the 1960s. In recent decades, this species has been recorded in many European countries, and was also introduced in Australia, New Zealand, South America, and North Africa (Háva, 2003).

Very similar to what Bunalski and Przewoźny (2009) have reported in Poland, *R. vespulae* (Milliron) has been recorded only in this one locality (SCNU) in Korea, so it is difficult to evaluate if this species is already invasive in Korea or will disperse eventually. It could be also a possible danger to other insect collections within Korea, but because of its small range in the country, its importance is rather low for now.

Acknowledgments

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