Acta Veterinaria Hungarica 66 (4), pp. 607–612 (2018)
DOI: 10.1556/004.2018.053

DESCRIPTION OF A NEW BAT-ASSOCIATED BUG SPECIES OF THE *CIMEX LECTULARIUS* GROUP FROM VIETNAM

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(Received 3 August 2018; accepted 20 November 2018)

Cimex lectularius, the common bedbug is an important, emerging pest of both veterinary and medical importance. Here a recently discovered, genetically distinct new species of the *C. lectularius* group is described morphologically, as *Cimex pulveratus* Hornok sp. nov.

Key words: *Cimex*, bedbug, Chiroptera, *Hypsugo pulveratus*, Vietnam

The common bedbug, *Cimex lectularius* Linnaeus, 1758 is a cosmopolitan blood-sucking ectoparasite, primarily infesting humans, but also frequently found on or near chickens and vespertilionid bats (Usinger, 1966). Bat-associated bugs of the *Cimex lectularius* group are not only important as pests, but also significant in an evolutionary context (Balvín et al., 2012*a*). Recently, two highly divergent novel genotypes have been reported in this species complex (Hornok et al., 2017). The purpose of the present study was to morphologically describe and illustrate that novel *Cimex* genotype which was the most different from other members of the *C. lectularius* group. In particular, the degree of barcoding sequence similarity between this novel genotype and *C. lectularius* was lower than between well-established *Cimex* species (Hornok et al., 2017), justifying the status of this novel genotype as a new species.

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Materials and methods

Two bugs were collected from a male and a female Chinese pipistrelle (*Hypsugo pulveratus* Peters, 1870) at Ngoc Khe, Ngoc Lac, Thanh Hoa in Vietnam, 2011. DNA was extracted and two genetic markers were amplified, sequenced from the whole body of one male and from four legs of a female specimen, as reported (Hornok et al., 2017). Pictures were taken and measurements were performed with a VHX-5000 digital microscope (Keyence Co., Osaka, Japan). Sizes below are provided in mm.

Cimex pulveratus Hornok sp. nov.

Taxonomic summary. Phylum Arthropoda, class Insecta, order Hemiptera, family Cimicidae, genus *Cimex*.

Diagnosis. Small-sized (3.8 mm) bug species with dense, short pubescence. Head and body brown, hemelytral pads golden yellow. Area around the paragenital sinus with bristles. Head broad, 2nd to 4th antennal segments long. Pronotum width to length ratio above 2.5 and hind margins of the hemelytral pads broadly rounded on inner halves (lectularius group). Paragenital sinus broadly rounded. Bristles anteriorly (on the pronotum and hemelytral pads), as well as posteriorly (last abdominal segment) exceed 100 µm.

Type material and locality

Holotype: female, collected at Hang Oc cave, Ngoc Khe, Ngoc Lac Secondary Forest after logging, surrounded by cultivated land (province: Thanh Hoa, geographic coordinates: N20.04,1860' – E105.23,2904', altitude: 37 m) in Vietnam, from the bat species *Hypsugo pulveratus*. The holotype is deposited at the Institute of Ecology and Biological Resources, Vietnam Academy of Science and Technology, Hanoi, Vietnam (code: VN11-0422).

Description

Female. Head brown, considerably broader (0.77, including eyes) than long (0.45). Interocular space 0.55, eyes 0.1. Antennae 1.51 long, segments I–IV 0.16, 0.43, 0.55, 0.37. Second antennal segment shorter than interocular space. Ratio of head width to 2nd and 3rd antennal segments 1.77 and 1.27, respectively (Fig. 1a). Rostrum ventrally reaching coxae I, segments I–III 0.23, 0.16, 0.23 (Fig. 1b).

Pronotum brown, 1.16 wide, 0.4 long, width to length ratio 2.9. (Fig. 1a). Lateral margins rounded, with bristles up to 0.14 (anteriorly).

Hemelytral pads golden yellow, 0.9 wide, 0.55 long, broadly rounded on inner halves, at its sides long bristles up to 0.14 (Fig. 1a). Scutellum triangular, with short (0.03) bristles in its posterior half, posterior edge close to midline slightly concave. Abdomen dorsally brown, ventrally segments golden yellowish posteriorly and towards midline, bristles usually below 0.1. Paragenital sinus on 5th abdominal segment broadly rounded, with bristles (Figs 1b, d and e). Ectospermalege transverse, as shown in Figs 1b and d.

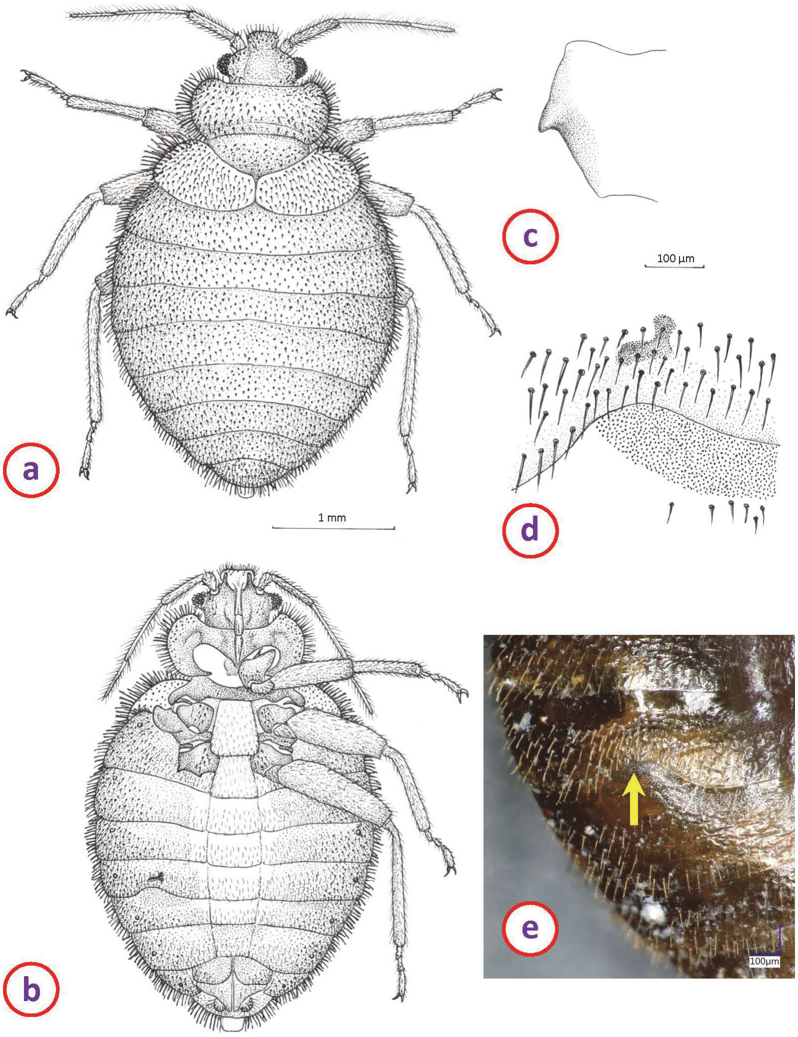

Fig. 1. Morphology of *Cimex pulveratus* sp. nov. female: (a) drawing of habitus: dorsal view; (b) drawing of habitus: ventral view; (c) drawing of spur on coxa III; (d) drawing of paragenital sinus; (e) picture of paragenital sinus (arrow)

Legs slender, except femur. Length of segments (3rd leg) from femur to tarsus: 1, 1, 0.1, 0.1, 0.2. Coxae trapezoid (Fig. 1b), coxa III with pointed, broad-based medial spur (Fig. 1c).

Gene sequences

Mitochondrial cytochrome oxidase subunit I (*cox*1) gene sequence deposited in the GenBank is MF415647. The internal transcribed spacer 2 (ITS2) sequence is MF161540. The phylogenetic relationships of the new species have been reported (Hornok et al., 2017).

Differential diagnosis

Bristles around the paragenital sinus and width to length ratio of the pronotum distinguish the new species from members of the *C. pipistrelli* group.

Cimex lectularius group: concerning the morphology of females, *C. pulveratus* sp. nov. is similar to *C. lectularius* based on its coxal spur and width to length ratio of pronotum (exceeding 2.5). However, the paragenital sinus of *C. pulveratus* sp. nov. is different from that in *C. lectularius* and other Palearctic members of its group, i.e. it is rounded, which is a character of Neotropical species of the genus *Cimex*, not reported previously from the Old World (Usinger, 1966).

Cimex hemipterus group: *C. pulveratus* sp. nov. is similar to *C. hemipterus* Fabricius, 1803 based on its head shape (wider than long). In addition, the 2nd antennal segment is shorter than the interocular space. However, the width to length ratio of the pronotum of *C. pulveratus* sp. nov. exceeds 2.5, unlike in the case of *C. hemipterus*. A further member of the *C. hemipterus* group, i.e. *C. insuetus* Ueshima, 1968 (indigenous in Thailand and India) can be distinguished from *C. pulveratus* sp. nov. by its width to length ratio of the pronotum (which is below 2), elongated head and 2nd antennal segment (which is longer than the interocular space) (Ueshima, 1968).

The above differences were confirmed by molecular and phylogenetic analyses (Hornok et al., 2017).

Host records and distribution

Known host species: *Hypsugo pulveratus* (of both bug specimens). Known distribution: Vietnam, Thanh Hoa, Ngoc Lac, Ngoc Khe.

Etymology

The new species was named after its host species, *Hypsugo pulveratus*.

General

In accordance with section 8.5 of the ICZN's International Code of Zoological Nomenclature, details of the new species have been submitted to ZooBank with the life science identifier (LSID) D64E4517-FF7C-48C4-9AAB-60156E82517E.

Discussion

In the family Cimicidae, the common bedbug (*C. lectularius*) can be regarded as the species with the highest historical, economical and veterinary-medical importance, also taking into account its worldwide occurrence and preference of human environment and body. Recently, high degrees of genetic differences have been reported between cimicid bugs, both within Europe and between specimens collected in Europe and Asia (Hornok et al., 2017). In particular, the sequence divergence between a newly discovered genotype (described here as *C. pulveratus* sp. nov.) and *C. lectularius* greatly exceed the limit of known intraspecific variation (Hornok et al., 2017), i.e. in the *cox*1 gene this difference was above 17% in comparison with *C. lectularius*, while this value is 5.8–6.4% between *C. lectularius* and members of the *C. hemipterus* or *C. pipistrelli* species groups. In line with this, the morphological characteristics of *C. pulveratus* sp. nov. described above justify its distinct species status.

The host species of *C. pulveratus* sp. nov., i.e. *Hypsugo pulveratus*, is closely related to the genus *Pipistrellus*, which contains important hosts of bat-associated bugs from both the lectularius and pipistrelli groups (Balvín et al., 2014). Host associations have been considered important drivers in the evolution/speciation of bat-associated bugs, as exemplified by *C. lectularius* (Balvín et al., 2012*b*; Booth et al., 2015). In the present case, to the best of our knowledge, no previous records and contemporaneous genetic/morphologic analyses of cimicid bugs from *H. pulveratus* are available. Thus, it can only be postulated that this host association may have contributed to the genetic and morphologic segregation of *C. pulveratus* sp. nov. Taking into account the geographic range of *H. pulveratus* (including China, Laos, Thailand and Vietnam), *C. pulveratus* sp. nov. most likely has a wide distribution in southeast Asia.

Acknowledgements

SH and VTT were supported by NKFIH 115854 and Rufford Foundation, respectively. Authorisation for bat capture was provided by the Vietnamese Ministry of Agriculture and Rural Development (Vietnam Administration of Forestry). The authors thank Alexandre Hassanin (Institute of Systematic Evolution and Biodiversity, Sorbonne University, Muséum National d'Histoire Naturelle, Paris, France) for providing the sample originally collected in Vietnam by Vuong Tan Tu. The publication of this research was supported by the 17896-4/2018/FEKUTSTRAT grant of the Hungarian Ministry of Human Capacities.

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