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DISCRIMINATION OF VIETNAMESE SPECIES OF THE GENUS *Rhynocoris* (Hemiptera: Heteroptera: Reduviidae) WITH THE UTILIZATION OF INTEGRATIVE TAXONOMY

Truong Xuan Lam[1,2], Ha Ngoc Linh[1,*], Truong Thanh Truc[2,3], Nguyen Dac Dai[1,2], Nguyen Quang Cuong[1,2], Katsuyuki Eguchi[4]

[1]Institute of Ecology and Biological Resources, Vietnam Academy of Science and Technology, 18 Hoang Quoc Viet, Ha Noi, Vietnam
[2]Graduate University of Science and Technology, Vietnam Academy of Science and Technology, 18 Hoang Quoc Viet, Ha Noi, Vietnam
[3]Phan Dinh Phung High School, 30 Phan Dinh Phung, Ha Noi, Vietnam
[4]Graduate School of Science, Tokyo Metropolitan University, Minami-Osawa 1-1, Hachioji, Tokyo 192-0397, Japan

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ABSTRACT

The genus *Rhynocoris* Hahn, 1834 is one of the largest genera of the subfamily Harpactorinae. This genus consists of 144 described species widely distributed in the Afrotropical, Palearctic, Sino-Japanese, Oriental, and Nearctic Realms. There are three species, *Rhynocoris fuscipes* (Fabricius, 1787), *Rhynocoris marginellus* (Fabricius, 1803), *Rhynocoris mendicus* (Stål, 1867) recorded in Vietnam. In this study, we attempted to re-examine the *Rhynocoris* species collected from Vietnam based on external morphology, genital morphology, and COI phylogeny to reveal the species delimitation of this genus in Vietnam. As a result, the independence of the three *Rhynocoris* species from Vietnam was confirmed. Moreover, *R. mendicus* was revealed as being a polymorphic species with two intraspecific morphological phenotypes.

Keywords: Morphology, molecular phylogeny, taxonomy assassin bug, Reduviidae, Vietnam.

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[*]*Corresponding author email*: linh.hangoc02@gmail.com

INTRODUCTION

Rhynocoris Hahn, 1834 was established with *Cimex iracundus* Poda, 1761 (syn. *Reduvius cruentus* Fabricius, 1787) as the type species of the genus. The genus has been allocated currently to the tribe Harpactorini, subfamily Harpactorinae of the family Reduviidae (Fabricius, 1787; Hahn, 1834; Maldonado, 1990). The following definition of the genus *Rhynocoris* which was slightly revised by Ishikawa (2003) and the present study was herein used as the initial working hypothesis: body elongated, elliptic; head elongated and elliptic, nearly as long as pronotum; anteocular area of head as long as or shorter than postocular area; postocular area of head gradually narrowed posteriorly; scape longer than head; first visible labial segment shorter than second segment, reaching level of middle of eye; compound eye prominent; pronotum shorter than humeral width, prominent at anterolateral angles; anterior pronotal lobe shorter than posterior pronotal lobe, with median sulcus posteriorly; median sulcus not reaching posterior lobe; posterior lobe rounded at humeral angles, with reflexed posterolateral margins; scutellum triangular, reflexed in apical part, triangularly elevated discally; hemelytra reaching or exceeding apex of abdomen; abdomen elliptic, wider than hemelytra, with gently curved lateral margins; genital capsule with a process dorsoapically; parameres rod-shaped.

The genus currently comprises 144 described species distributed widely in Afrotropical, Palearctic, Sino-Japanese, Oriental, and Nearctic Realms (Stål, 1867; Distant, 1903; Ambrose & Livingstone, 1986; Maldonado, 1990; Truong et al., 2015). Among them, three species have been recorded and described from Vietnam, i.e., *Rhynocoris fuscipes* (Fabricius, 1787), *Rhynocoris marginellus* (Fabricius, 1803), *Rhynocoris mendicus* (Stål, 1867).

Similar to other congeners of the subfamily Harpactorinae as well as the family Reduviidae, *Rhynocoris* species, i.e., *R. fuscipes* (Fabricius, 1787), *Rhynocoris kumarii* Ambrose et Livingstone, 1986 and *R. marginatus* (Fabricius, 1794), usually exhibit a broad habitat preference and prey on a wide range of animals. Some species are also dominant in cultivated lands of rice, soybean, peanut, coffee, tea, etc., and thus, have the potential to be used as native natural enemies of agricultural pests (Ambrose, 1999, 2003). Besides, some "species" are known to exhibit remarkable variations or flexibilities in biological features relevant to their potential uses as biological control agents (Ambrose, 2003). For example, the brownish orange form of *Rhynocoris marginatus* (Fabricius, 1794) has more hunting efficiency and a higher ability to be insecticide-resisting than the sanguineous and the blackish red form (Sahayaraj & Ambrose, 1996; Ambrose, 1999, 2003; George, 1999a, 1999b, 2000a, 2000b). However, the conspecificity of such forms or the existence of unnoticed species currently assigned to a single valid species name needs to be confirmed by further studies.

Despite the usefulness and fascination of Reduviidae and Harpactorinae as potential biological control agents in agriculture and forestry, the less-developed species-level and higher classifications are a significant obstacle to basic and applied research of reduviids. The current classification of Reduviidae species is still largely morphology-based and poorly and less comprehensively revised by modern approaches such as phylogenetics and species delimitation analyses using DNA sequence data. Thus, taxonomic obscurities and confusions in species recognition have been caused by cases of the cryptic species complex (Panzera et al., 2015; Zhao et al., 2021), male-female dimorphism in a single species (Kwadjo et al., 2010; Forthman, 2017; Gil-Santana, 2017; Weirauch et al., 2017; Chen et al., 2021), and remarkable morphological polymorphism or variation among conspecific populations or seasonal generations (Stål, 1867; Distant, 1903; Moreno et al., 2006; Rivas et al., 2021; Vilaseca et al., 2021). Moreover, recent studies using molecular phylogenetic analyses have provided phylogenetic hypotheses or

presumptions that claim the necessity of reexaminations of the boundaries of many genera and subfamilies in the current classification of the family (Weirauch & Munro, 2009; Hwang & Weirauch, 2012). Therefore, future studies with more representatives of subfamilies and genera might recognize more issues of the current taxonomy of Reduviidae.

Therefore, as one of the first case studies of re-examining the classification of species and higher levels of the family Reduviidae from Vietnam, the present study aimed to revise the classification and the phylogenetic relationship of Vietnamese species of the genus *Rhynocoris* using the integrative approach.

MATERIALS AND METHODS

Material examined and specimen depository

Rhynocoris specimens were collected by sweeping along trails in the shrubs and plants in both agricultural habitats (farming fields of vegetable, soybean, corn, rice, pepper, coffee, tea, etc.) and forestry habitats (evergreen and restoration forests) in Vietnam.

This study included 34 *Rhynocoris* specimens from Vietnam as ingroups and specimens of *Biasticus luteicollis* Ha, Truong & Ishikawa, 2022, *Sphedanolestes pubinotus* Reuter, 1881, and *Coranus* sp. collected from Vietnam as outgroups in molecular phylogenetic analyses (Table 1).

Table 1. The data of the specimens used in this study. All specimens were deposited at the Institute of Ecology and Biological Resources, Vietnam Academy of Science and Technology, tentatively held by HNL (corresponding author). Abbreviations and symbols: n/a: no data; M: male; F: female

No.	Morpho-species/Species	Specimen code	Collecting date	Locality	Sex	Accession numbers
						COI
Ingroups						
1	*Rhynocoris fuscipes* (Fabricius, 1787) (= *R.* sp. HNL001)	TXL2018-127	10. vi. 2018	Vietnam, Lang Son	M	PP647799
2	*Rhynocoris fuscipes* (Fabricius, 1787) (= *R.* sp. HNL001)	TXL2023-692	14. vi. 2023	Vietnam, Hoa Binh	M	PP647801
3	*Rhynocoris fuscipes* (Fabricius, 1787) (= *R.* sp. HNL001)	TXL2023-693	14. vi. 2023	Vietnam, Hoa Binh	M	PP647802
4	*Rhynocoris fuscipes* (Fabricius, 1787) (= *R.* sp. HNL001)	AD2020-041	29. x. 2020	Vietnam, Vung Tau	M	PP647771
5	*Rhynocoris fuscipes* (Fabricius, 1787) (=*R.* sp. HNL001)	AD2020-040	29. x. 2020	Vietnam, Vung Tau	F	PP647770
6	*Rhynocoris marginellus* (Fabricius, 1803) (= *R.* sp. HNL002)	TXL2018-129	10. vi. 2018	Vietnam, Son La	M	PP647800
7	*Rhynocoris marginellus* (Fabricius, 1803) (= *R.* sp. HNL002)	TXL2016-627	12. vi. 2016	Vietnam, Thanh Hoa	M	PP647793
8	*Rhynocoris marginellus* (Fabricius, 1803) (= *R.* sp. HNL002)	TXL2016-629	12. vi. 2016	Vietnam, Thanh Hoa	M	PP647794

No.	Morpho-species/Species	Specimen code	Collecting date	Locality	Sex	Accession numbers
9	*Rhynocoris marginellus* (Fabricius, 1803) (= *R.* sp. HNL002)	TXL2016-641	14. vi. 2016	Vietnam, Thanh Hoa	M	PP647795
10	*Rhynocoris marginellus* (Fabricius, 1803) (= *R.* sp. HNL002)	TXL2017-665	16. ix. 2017	Vietnam, Lang Son	M	PP647796
11	*Rhynocoris marginellus* (Fabricius, 1803) (= *R.* sp. HNL002)	TTN2020-003	30. viii. 2023	Vietnam, Nghe An	M	PP647783
12	*Rhynocoris marginellus* (Fabricius, 1803) (= *R.* sp. HNL002)	TXLBX15	13. vi. 2016	Vietnam, Thanh Hoa	F	PP647803
13	*Rhynocoris mendicus* (Stål, 1867) (= *R.* sp. HNL003)	TXL2018-040	09. v. 2018	Vietnam, Gia Lai	M	PP647797
14	*Rhynocoris mendicus* (Stål, 1867) (= *R.* sp. HNL003)	TXL2016-592	04. v. 2016	Vietnam, Dak Lak	M	PP647785
15	*Rhynocoris mendicus* (Stål, 1867) (= *R.* sp. HNL003)	TXL2016-593	04. v. 2016	Vietnam, Dak Lak	M	PP647786
16	*Rhynocoris mendicus* (Stål, 1867) (= *R.* sp. HNL003)	TXL2016-594	04. v. 2016	Vietnam, Dak Lak	M	PP647787
17	*Rhynocoris mendicus* (Stål, 1867) (= *R.* sp. HNL003)	TXL2016-595	04. v. 2016	Vietnam, Dak Lak	M	PP647788
18	*Rhynocoris mendicus* (Stål, 1867) (= *R.* sp. HNL003)	TXL2016-596	04. v. 2016	Vietnam, Dak Lak	M	PP647789
19	*Rhynocoris mendicus* (Stål, 1867) (= *R.* sp. HNL003)	TXL2016-597	04. v. 2016	Vietnam, Dak Lak	M	PP647790
20	*Rhynocoris mendicus* (Stål, 1867) (= *R.* sp. HNL003)	TXL2016-598	04. v. 2016	Vietnam, Dak Lak	M	PP647791
21	*Rhynocoris mendicus* (Stål, 1867) (= *R.* sp. HNL003)	TXL2016-599	04. v. 2016	Vietnam, Dak Lak	M	PP647792
22	*Rhynocoris mendicus* (Stål, 1867) (= *R.* sp. HNL003)	AD2019-001	iii. 2019	Vietnam, Kon Tum	M	n/a
23	*Rhynocoris mendicus* (Stål, 1867) (= *R.* sp. HNL003)	TXL2018-041	09. v. 2018	Vietnam, Gia Lai	F	PP647798
24	*Rhynocoris mendicus* (Stål, 1867) (= *R.* sp. HNL003)	TXL2011-663	03. vii. 2011	Vietnam, Dong Nai	M	PP647784

No.	Morpho-species/Species	Specimen code	Collecting date	Locality	Sex	Accession numbers
25	*Rhynocoris mendicus* (Stål, 1867) (= *R.* sp. HNL003)	HNL2019-174	12. xi. 2019	Vietnam, Dong Nai	M	PP647774
26	*Rhynocoris mendicus* (Stål, 1867) (= *R.* sp. HNL003)	NDD2019-229	13. ix. 2019	Vietnam, Gia Lai	M	PP647775
27	*Rhynocoris mendicus* (Stål, 1867) (= *R.* sp. HNL003)	NDD2019-233	13. ix. 2019	Vietnam, Gia Lai	M	PP647777
28	*Rhynocoris mendicus* (Stål, 1867) (= *R.* sp. HNL003)	NDD2019-234	13. ix. 2019	Vietnam, Gia Lai	M	PP647778
29	*Rhynocoris mendicus* (Stål, 1867) (= *R.* sp. HNL003)	NDD2019-239	13. ix. 2019	Vietnam, Gia Lai	M	PP647779
30	*Rhynocoris mendicus* (Stål, 1867) (= *R.* sp. HNL003)	NDD2019-244	13. ix. 2019	Vietnam, Gia Lai	M	PP647780
32	*Rhynocoris mendicus* (Stål, 1867) (= *R.* sp. HNL003)	NDD2019-245	13. ix. 2019	Vietnam, Gia Lai	M	PP647781
33	*Rhynocoris mendicus* (Stål, 1867) (= *R.* sp. HNL003)	NDD2019-246	13. ix. 2019	Vietnam, Gia Lai	M	PP647782
34	*Rhynocoris mendicus* (Stål, 1867) (= *R.* sp. HNL003)	TXLBX23	19. ix. 2021	Vietnam, Dak Lak	F	PP647804
Outgroups						
1	*Sphedanolestes pubinotus* Reuter, 1881	HNL2019-002	11. iii. 2019	Vietnam, Quang Tri	F	PP647772
2	*Coranus* sp.	HNL2023-059	21. iii. 2023	Vietnam, Thua Thien - Hue	M	PP647773
3	*Biasticus luteicollis* Ha, Truong et Ishikawa, 2022	HNL2018-025	09. v. 2018	Vietnam, Dak Lak	M	OM868187

Morphological examination of the validly named species of the genus was conducted by referring to the original descriptions, other taxonomic publications, and type specimens where available (Fabricius, 1794, 1803; Stål, 1867, 1874; Reuter, 1881; Distant, 1903, 1904, 1909; Schouteden, 1910; Bergroth, 1915; Miller, 1941, 1948, 1954; Ambrose & Livingstone, 1986; Dioli, 1990).

Morphological examination and imaging

External morphological characteristics were examined for dry-mounted specimens using a Nikon SMZ1270 stereomicroscope. The genitalia were prepared for examination as described below. Firstly, each male specimen was relaxed by soaking for 3 days in 70 % ethanol. After that, the male genitalia

was detached from the body and then soaked in hot 10 % KOH for five minutes until body fat and muscle were released. The endosoma was pulled out of the phallosoma by fine tweezers after removing the phallus from the pygophore. All parts of the male genitalia were preserved in a genitalia vial filled with propylene glycol and subsequently associated with the pinned specimens. Next, the female genitalia were inspected without being detached from the body. A Nikon SMZ1270 stereomicroscope was used to examine the male and female genital morphology.

Focus stacking was executed using Helicon Focus Pro 8.2.0 software (Helicon Soft Ltd., Ukraine) based on a sequence of the source pictures photographed by a Canon EOS Kiss X10 digital camera connected to a Nikon AZ100 stereomicroscope, and artifacts were removed using the retouch function of the software. After that, the contrast, brightness, color balance, and intensity were adjusted using Adobe Photoshop Elements 10.0 software (Adobe Systems Incorporated, San Jose, CA, USA) using a color corresponding sticker (CASMATCH, Bear Medic Corporation, Japan).

Molecular data preparation

DNA was isolated from each specimen's left leg/legs using the Chelex-TE-ProK protocol (Satria et al., 2015). The mitochondrial COI gene fragments were examined using the primer set, LCO1490m (5'-TAC TCA ACA AAT CAC AAA GAT ATT GG-3') and COI-E (5'-TAT ACT TCT GGG TGT CCG AAG AAT CA-3') (Shekhovtsov et al., 2013). Polymerase chain reaction (PCR) amplification, cycle sequencing reaction, sequencing using ABI PRISM 3130xl (Applied Biosystems), and sequence assembly using ChromasPro 1.7.6 (Technelysium Pty Ltd., Australia) were executed using the methods of Satria et al. (2015) and Shekhovtsov et al. (2013). The PCR thermal situation for the COI gene fragment, comprised of initial denaturation at 94 ^{o}C (2 min), denaturation at 94 ^{o}C (30 s), annealing at 48.5 ^{o}C (30 s), and extension at 72 ^{o}C (45 s) for 35 cycles, with final extension at 72 ^{o}C (7 min). COI sequences were effectively obtained from 34 of the 34 *Rhynocoris* samples.

Test for association was performed using MUSCLE implemented in MEGA X (Kumar et al., 2018) with default setting (Gap Open = -400.00; Gap Extend = 0.00; Cluster Method [Iterations 1,2 and Other iterations] = UPGMA; Min Diag Length [Lambda] = 24) for COI sequences while including and excluding outgroups (OG+ or OG−): $COI^{(OG+)}$ (606 bp) and $COI^{(OG-)}$ (606 bp) datasets. The FASTA-configured files derived from MEGA X were then converted to NEXUS layout or PHYLIP design, which were suitable input layouts for molecular phylogenetic examination and estimation of genetic distances and species delimitation analysis by ClustalX 2.0.11 (Larkin et al., 2007).

Molecular phylogenetic analyses

The mitochondrial COI dataset (603 bp; 33 ingroup OTUs, 3 outgroup OTUs) was successfully obtained (as listed in Table 1). Molecular phylogenetic analyses were done based on the COI dataset. The generalized time-reversible (GTR) + Gamma model was chosen for the COI dataset using Model Finder (Kalyaanamoorthy et al., 2017) under the Bayesian information criterion. The Bayesian inference (BI) evaluations were then executed for the data using MrBayes v.3.2.7 (Ronquist & Huelsenbeck, 2003) with 20,000,000 production and statutory parameter configuration (examining every 500 generations and tuning constraints every 100 generations, with a burn-in of 25%). The effective sampling size (ESS) of each constraint was verified to be > 200 using Tracer 1.7.2 (Rambaut et al., 2018). The nodes were designated as "well supported" when posterior probability (PP) ≥ 0.95.

Pairwise p-distances and Kimura-two-parameter (K2P) distances were calculated for the COI dataset of *Rhynocoris* using MEGA X (Kumar et al., 2018) under "pairwise deletion".

Species delimitation analyses

To create species partitions, two different protocols, i.e., Assemble Species by Automatic Partitioning (**ASAP**) (Puillandre et al., 2021) and Bayesian implementation of the Poisson Tree Processes model (**bPTP**) for species delimitation (Zhang et al., 2013), were used with pairwise genetic distances. For ASAP, the FASTA-configured file of the $COI^{(OG-)}$ dataset was used and executed on the ASAP website (https://bioinfo.mnhn.fr/abi/public/asap), with two replacement samples to estimate the distances, i.e., simple p-distance model and K2P model. The bPTP were executed in the bPTP online server (https://species.h-its.org) based on the NEXUS formatted BI tree of the $COI^{(OG-)}$ dataset, with default values (100,000 Markov chain Monte Carlo [**MCMC**] generations, thinning = 100, burn-in = 0.1, and Seed = 123). The NEXUS formatted BI tree used in bPTP was converted from TREE formatted by TreeGraph 2.15.0-887 (Stöver & Müller, 2010).

RESULTS

Morphological examination in the male and female adults

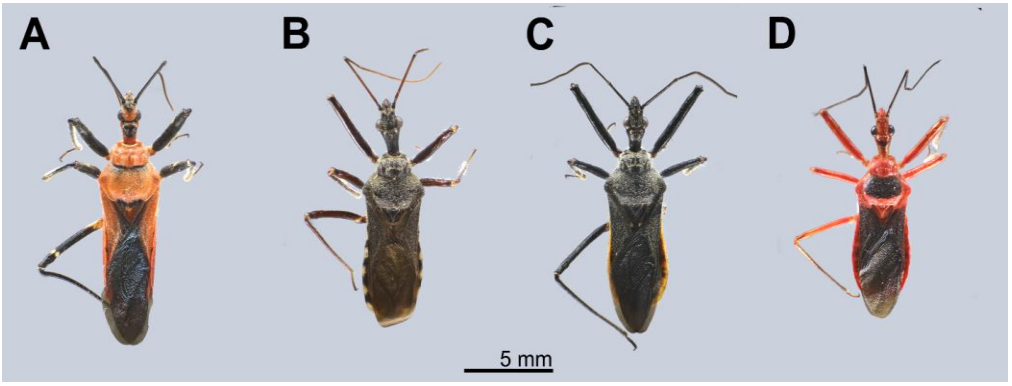

Figure 1. Body in dorsal view of four morphospecies (*Rhynocoris* sp. M1–M4). A, TXL2019-692, ♂, *R.* sp. M1; B, TXL2016-625, ♂, *R.* sp. M2; C, NDD2019-245, ♂, *R.* sp. M3; D, AD2019-001, ♂, *R.* sp. M4

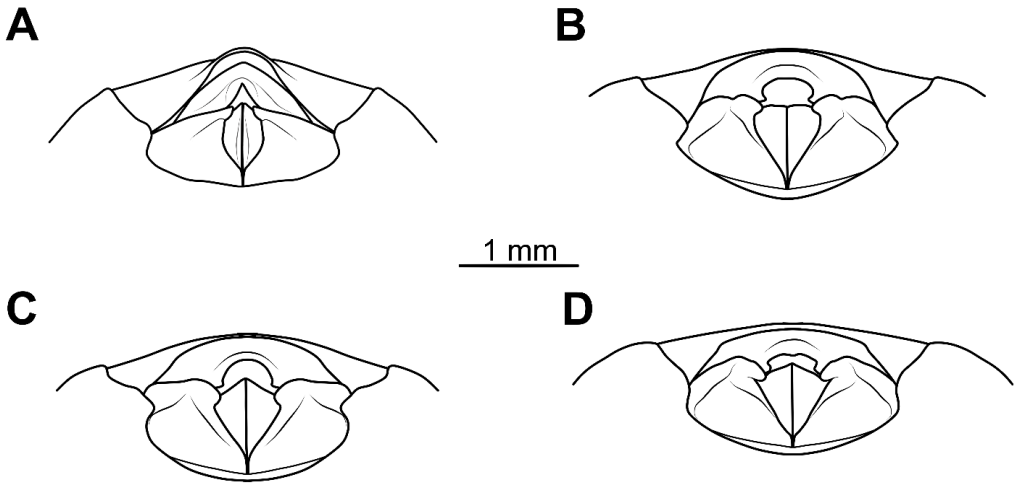

Figure 2. Female genitalia in ventral view of four morphospecies (*Rhynocoris* sp. M1–M4). A, AD2020-041, ♀, *R.* sp. M1; B, HNL2019-136, ♀, *R.* sp. M2; C, TXLBX23, ♀, *R.* sp. M3; D, TXL2018-041, ♀, *R.* sp. M4

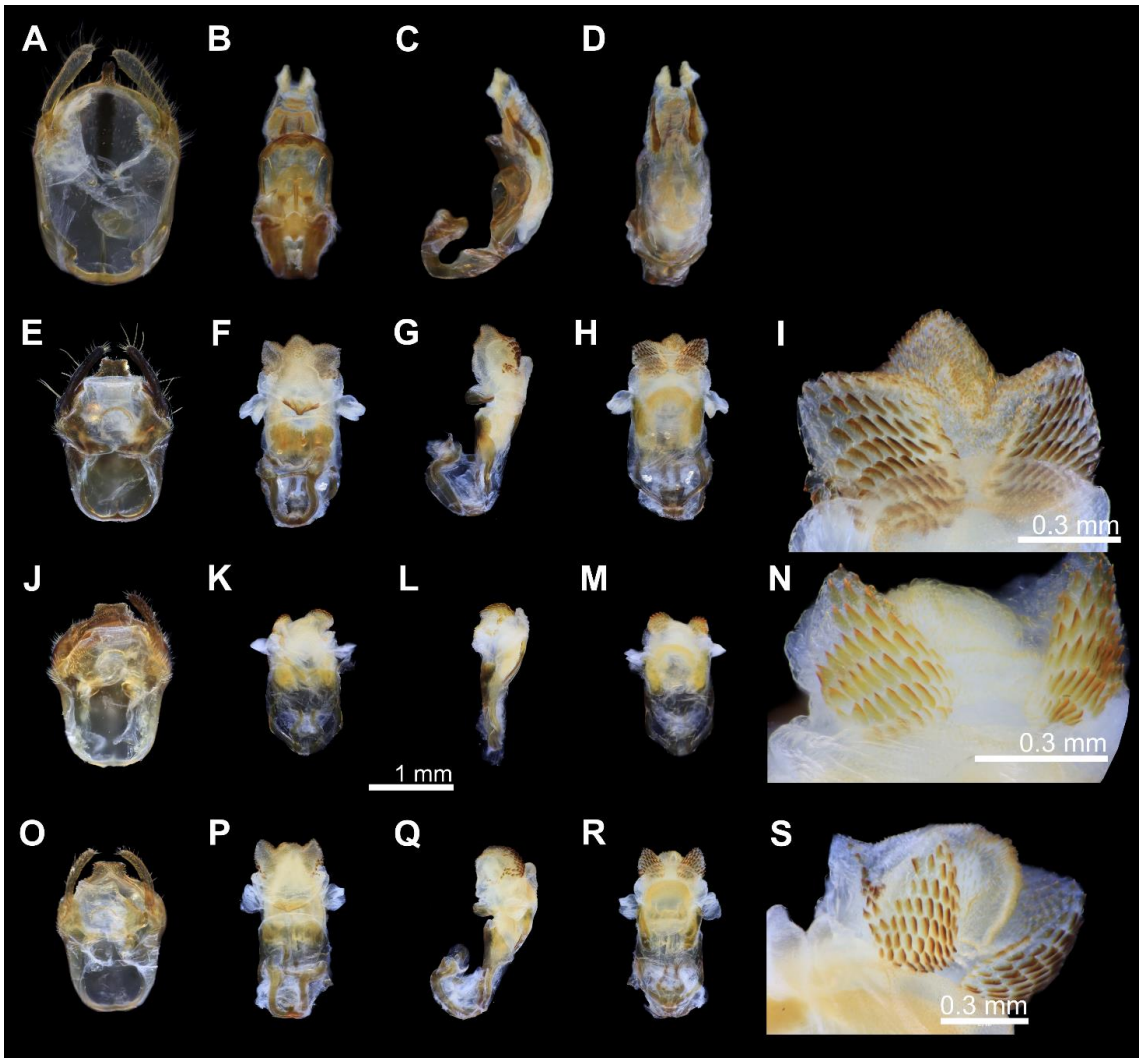

Figure 3. Male genitalia of four morphospecies (*Rhynocoris* sp. M1–M4). A–D, TXL2019-692, ♂, *R.* sp. M1; E–I, TXL2016-625, ♂, *R.* sp. M2; J–N, TXL2016-663, ♂, *R.* sp. M3; O–S, AD2019-001, ♂, *R.* sp. M4. A, E, J, O, pygophore in dorsal view; B, F, K, P, phallus in dorsal view; C, G, L, Q, phallus in lateral view; D, H, M, R, phallus in ventral view; I, N, S, distal dorsal lobe of endosoma (ddl)

Thirty-four specimens were grouped into four morphospecies (*Rhynocoris* sp. M1–M4) based on characteristics presenting in external morphology, for example, body coloration, anterior and posterior pronotal lobes, and scutellum (Fig. 1) and features presenting in female genitalia, for instance, the posterior margin of abdominal sternite VII, the shape and structure of gonocoxa VIII, and the inner margin of abdominal laterotergite VIII (Fig. 2). However, except *R.* sp. M1, no remarkable distinct characteristics were found in the genital morphology of male-based morphospecies of the remaining three morphospecies, *R.* sp. M2, M3, and M4 (Fig. 3).

Identities of the morphospecies based on the COI phylogenetic trees

For four morphospecies, mitochondrial COI sequences were successfully obtained.

In the BI tree, three putative species, *R.* sp. M1, *R.* sp. M2, and (*R.* sp. M3 + *R.* sp. M4) were recovered as independent monophyletic lineages with a high supporting value (PP ≥ 0.99) and long basal branches (Fig. 4).

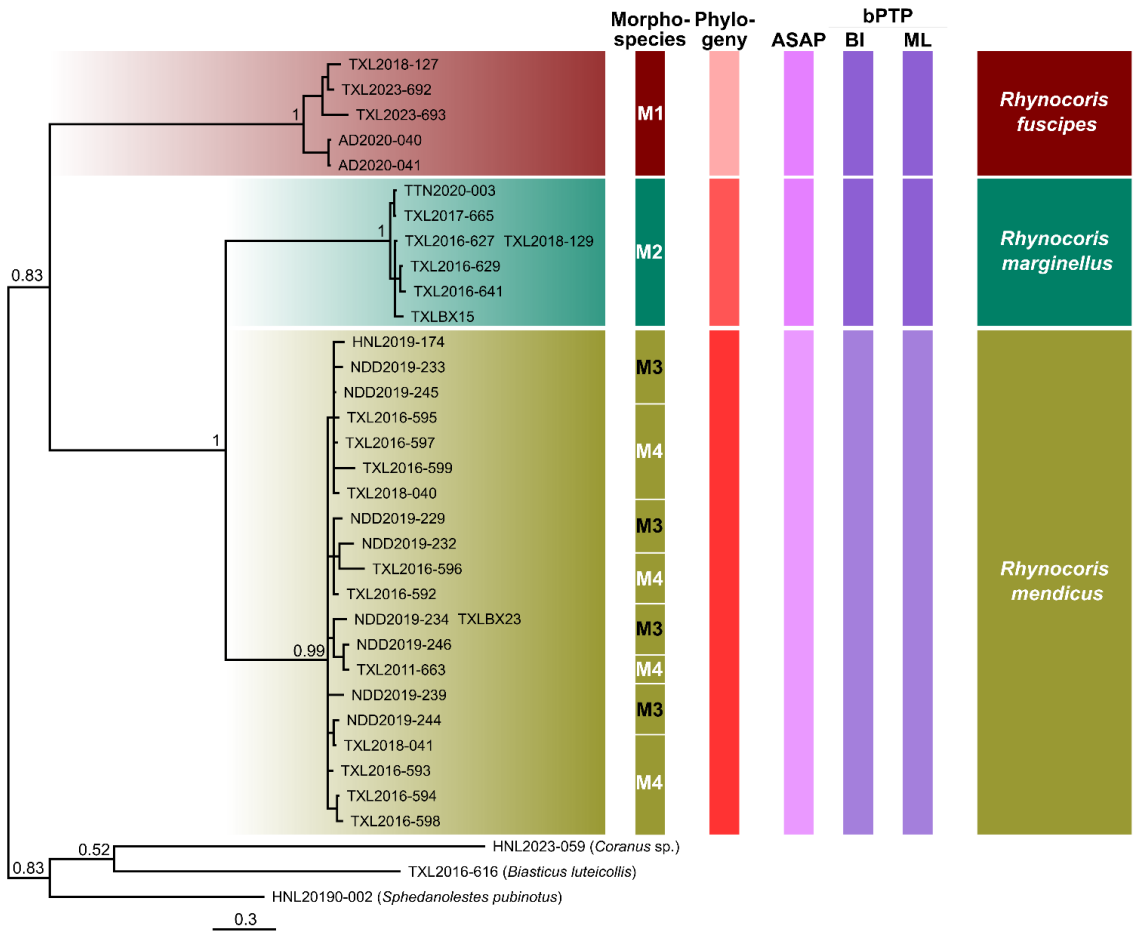

Figure 4. Bayesian inference phylogenetic trees based on the mitochondrial COI dataset (603 bp) of the genus *Rhynocoris.* Supports by posterior probability (PP) are indicated behind each node

Table 2. The minimal interspecific distance of species of genus E based on the COI dataset. The upper right diagonal shows the p-distance, and the lower left diagonal shows the distance in the K2P model

	Rhynocoris fuscipes	*Rhynocoris marginellus*	*Rhynocoris mendicus*
Rhynocoris fuscipes (N = 5) (Max K2P = 0.025; Max p = 2.5%)		15.8	14.4
Rhynocoris marginellus (N = 7) (Max K2P = 0.005; Max p = 0.5%)	0.18		9.3
Rhynocoris mendicus (N = 19) (Max K2P = 0.025; Max p = 2.5%)	0.16	0.10	

The minimum intraspecific diversity within a single lineage ranged from 0.5–2.5% in both p-distance and K2P models. On the other hand, the maximum interspecific divergences between the three lineages ranged from 9.3–15.8% in p-distance and 10.2–17.8% in the K2P model (Table 2).

The phylogenetic independencies of the three lineages were also supported consistently by ASAP and bPTP based on the $COI^{(OG-)}$ dataset (Fig. 4).

DISCUSSION

Full recognition of the species and identification

It is reasonable that the following three OTUs, which were consistently recovered by the integrative approach, are treated as fully recognized species (or herein simply referred to as species): *R.* sp. HNL001 (= *R.* sp. M1), *R.* sp. HNL002 (= *R.* sp. M2), and *R.* sp. HNL003 (= *R.* sp. M3 + *R.* sp. M4).

On the other hand, there is an incompatible case between morphological and molecular phylogenetic results. The color forms *R.* sp. M3 (Fig. 1C) and *R.* sp. M4 (Fig. 1D), which were discriminated from each other by the body coloration, were not discriminated by the present integrative approach, and so the two morphospecies are herein treated as intraspecific morphological phenotypes of a single species coded as *R.* sp. HNL003. It is noted that the two color forms were recorded exclusively in the Central Highlands of Vietnam, but the color form *R.* sp. M3 was recorded mainly in September, while the color form *R.* sp. M4 was recorded exclusively in May. The genetic divergence corresponding to the two color forms was, however, not observed (Fig. 4).

By examining type material and taxonomic articles (including the original descriptions) of the validly named species of the genus *Rhynocoris* and species of some closed related genera (*Sphedanolestes* and *Biasticus*), the following two species can be reasonably identified: *R.* sp. HNL001 = *Rhynocoris fuscipes* (Fabricius, 1787), *R.* sp. HNL002 = *Rhynocoris marginellus* (Fabricius, 1803), and *R.* sp. HNL003 = *Rhynocoris mendicus* (Stål, 1867).

The problem of using morphological examination in discrimination of the genus rhynocoris

Among the three species, a polymorphic species comprising two intraspecific morphological phenotypes has been recognized. Therefore, the morphological examination based on external and genital morphology might not be a reasonable approach for discriminating species of the genus *Rhynocoris*, even though the two morphological variations of *R. mendicus* were described in its original taxonomic articles (Stål, 1867).

CONCLUSION

In this study, integrative taxonomy, consisting of morphological examination, molecular phylogenetic analyses, and species delimitation analyses, was employed to discriminate Vietnamese species of the genus *Rhynocoris.* As a result, the independence of the three species of the genus *Rhynocoris*, *Rhynocoris fuscipes* (Fabricius, 1787), *Rhynocoris marginellus* (Fabricius, 1803), and *Rhynocoris mendicus* (Stål, 1867), from Vietnam was revealed. Moreover, three variations (color forms) of *R. mendicus* were recorded in Distant (1904), including *R.* sp. M3, *R.* sp. M4, and another variation of having sanguineous femora and black tibiae. However, in this study, the third variation was not found and there was no genetic divergence found between the two morphological phenotypes, *R.* sp. M3 and *R.* sp. M4. In summary, the three Vietnamese species of the genus *Rhynocoris* were revealed as being independent and consistent with historical studies based on external morphology (Fabricius, 1787, 1803; Stål, 1867, Distant, 1904).

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