

Description of *Rhinocypha taiwana* sp. nov. from Taiwan, with a preliminary molecular phylogenetic analysis of the *Rhinocypha drusilla*-group (Odonata: Chlorocyphidae)

Liang-Jong Wang^{a*}, Jyh-Jong Cherng^b, Yung-Jen Chang^c and Jin-Li Jiang^b

^aDivision of Forest Protection, Taiwan Forestry Research Institute, Taipei, Taiwan, ROC; ^bWild Bird Society of Keelung, Keelung, Taiwan, ROC; ^cFormosa Ecological Company, New Taipei City, Taiwan, ROC

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Rhinocypha taiwana Wang & Chang, sp. nov. is described and illustrated for both sexes. The genetic distance of the cytochrome c oxidase I (COI) gene in *R. taiwana* and related species ranges from 4.2% to 10.4%. *R. taiwana* is shown to be a good species based on morphological and genetic criteria. It also is clearly retrieved as a distinct species based on COI phylogenetic analysis. The *R. drusilla* group is proposed and defined by a combination of characteristics which distinguish them from all other *Rhinocypha* species: male abdomen with reddish orange markings and S2 with a unique dorsal spade-shaped or similar marking. A key to the males of the six species of the *R. drusilla* group is provided. Two morphologically distinct continental species, *R. drusilla* and *R. arguta*, are shown to have a rather small genetic distance, only 1.2–1.7%. More material from the continental populations of this group is needed for further morphological and molecular studies.

Keywords: Odonata; dragonfly; *Rhinocypha taiwana*; new species; Taiwan; DNA barcoding; molecular phylogeny

Introduction

To date only three species of Chlorocyphidae have been recorded in Taiwan: *Libellago lineata* (Burmeister, 1839), *Aristocypha baibarana* (Matsumura, 1931) and *Heliocypha p. perforata* (Percheron, 1835) (eg Chang & Wang, 1997; Lieftinck et al., 1984; Wang, 2000). Recently, a new chlorocyphid species, with predominantly bright reddish orange markings on the dorsum of the abdomen, was discovered in Taiwan. The discovery of this species reopened an old discussion about the existence of a “red-bodied *Rhinocypha* from Formosa”. Discussing *Rhinocypha ogasawarensis* Oguma, 1913, Lieftinck (1962) wrote that he had examined a red-bodied species of *Rhinocypha* from “Formosa” in the University of Michigan Museum of Zoology, Ann Arbor (UMMZ). However Lieftinck believed that this specimen might have originated from the Ryukyu Islands rather than from Formosa as the label indicated. Two years later, in connection with the description of *R. uenoi* from Ryukyu Islands, Asahina (1964) wrote that he had failed to find this specimen during his visit to UMMZ in 1963. Subsequently he (Asahina, 1970) found this specimen in Leiden Museum, where Lieftinck had taken it on loan. Asahina identified it as *R. ogasawarensis*, and assumed that the specimen was collected in Ogasawara islands by H.J.S. Pryer, and that the specimen was sold and sent to Germany, ending up in the collection of F. Förster, a collection

*Corresponding author. Email: ljwang23@ms17.hinet.net

which was later acquired by the UMMZ. Whether or not this old specimen (because it was found neither in the UMMZ collections nor in the NMNS collections in November 2012) really came from Ogasawara Island rather than Taiwan, still requires confirmation. In any case, the recent discovery proves that there is also a red-bodied *Rhinocypha* species in Taiwan, which may or may not be the same as that discussed by Lieftinck (1962) and Asahina (1964, 1970). We describe this new find as *Rhinocypha taiwana* sp. nov. and describe both sexes of the adult stage. It is placed in the east-Asian *Rhinocypha drusilla* group, which we define by morphological characters. Characters distinguishing the species in this group are discussed and a key to the males is presented.

In addition to morphological studies, the 648-bp region of the mitochondrial cytochrome c oxidase I (COI) gene that is commonly used in barcoding studies (Hebert et al., 2003; Savolainen et al., 2005) was sequenced and used for species confirmation of the Taiwanese taxon, and a preliminary interspecific phylogeny of the *R. drusilla* group was constructed.

Materials and methods

Molecular studies

DNA extraction, sequencing and alignment

Total genomic DNA was extracted from one or two legs of each specimen studied using the QuickExtract™ DNA Extraction Solution kit (Epicentre, Madison, WI, USA) following the supplier's instructions. The DNA barcode region of the mitochondrial COI gene was amplified using primer set LCO-1490-HCO-2198 (Folmer et al., 1994). PCR reactions contained a total volume of 25 µl, composed of 10× reaction buffer, 0.25 mM dNTPs, 2.0 mM MgCl₂, 0.4 µM of each primer, 0.2 µl of Super-Therm polymerase (5 u µl⁻¹, Hoffman-La-Roche, Nutley, NJ, USA), 12.8 µl ddH₂O and 3 µl of DNA template and were performed in an GeneAmp PCR System 9700 (Applied Biosystems, Foster City, CA, USA). The PCR profile was: denaturing at 94°C for 5 min, 35 cycles of amplification at 94°C for 50 s followed by 50°C for 50 s and 72°C for 50 s, and a final extension at 72°C for 7 min. PCR products were stained with ethidium bromide and visualized by ultraviolet light on a 1.0% agarose gel after electrophoresis. Samples were sequenced in both directions on an ABI PRISM™ 3730 automatic sequencer (Perkin Elmer, Foster City, CA, USA) at the Genomics BioSci & Tech, Taiwan. COI sequences from raw chromatograph data were aligned without gaps using Clustal W (Thompson et al., 1994).

Phylogenetic analyses

Phylogenetic reconstruction was performed by maximum likelihood (ML) using Mega 5.0 (Tamura et al., 2011). The best-fitting model of nucleotide substitution was selected using the Bayesian Information Criterion (BIC) (Alfaro & Huelsenbeck, 2006) and ML branch supports were calculated with 1000 bootstrap replications (Felsenstein, 1985).

Description

Rhinocypha taiwana Wang & Chang, sp. nov.
(Figures 1–11)

Diagnosis

A medium sized *Rhinocypha* with yellow markings on head and thorax, a predominately red abdomen dorsally in the male (Figure 2), female abdomen mainly dark above with fine pale



Figure 1. *Rhinocypha taiwana* sp. nov., male photographed in Pinglin, New Taipei on 21 September 2012 by Jyh-Jong Cherng.



Figure 2. *Rhinocypha taiwana* sp. nov., holotype male, general habitus.

lateral markings except on distal segments (Figure 3). Wings in both sexes hyaline but hind wing tinted amber with distinct brown tinted area in outer one-third, clearing at tip which bears a small whitish patch.

Specimens examined

Holotype ♂, “DNA L.J.Wang 1002” [blue printed label], “site 1, Pinling, New Taipei, Taiwan, alt. 380 m, 22.IX.2012, leg. L.J. Wang”, “Holotype *Rhinocypha taiwana* n. sp. Wang et Chang des. 2012” [red label]. Deposited in Taiwan Forestry Research Institute, Taipei, Taiwan (TFRI).

Paratypes (a total of 12 ♂, 3 ♀). 1 ♂, same locality, date and collector as for holotype; 2♂, 1♀, “site 2, Pinling, New Taipei, Taiwan, alt. 360 m, 29.IX.2012, leg. L. J. Wang & Y. Z. Chang”;



Figure 3. *Rhinocypha taiwana* sp. nov., paratype female, general habitus.

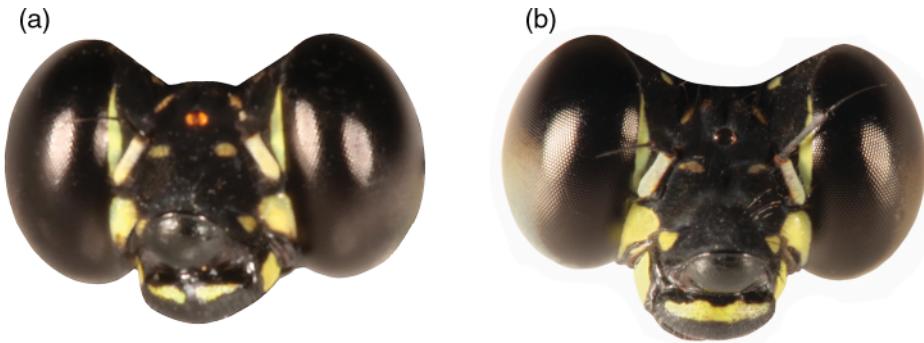


Figure 4. *Rhinocypha taiwana* sp. nov., head, frontal view: (a) holotype male; (b) paratype female.

3♂, same locality as above, 6.X.2012, leg. L.J. Wang; 2♂, 2♀, same locality as above, 20.X.2012, leg. J. J. Cherng; 2 ♂ same locality as above, 21.X.2012, leg. J. J. Cherng; 2 ♂, “Site 3, Pinling, New Taipei, Taiwan, alt. 280 m, 27.X.2012, leg. J. J. Cherng”. All paratypes furnished with label “*Rhinocypha taiwana* n. sp. Wang et Chang des. 2012” Paratypes are deposited in National Museum of Nature and Science, Tokyo, Japan (NMNS), Department of Entomology, National Taiwan University, Taipei, Taiwan (NTUE), Naturalis Biodiversity Centre, Leiden, The Netherlands (RNMH), Museum of Zoology, University of Michigan, Ann Arbor, USA (UMMZ), and in the private collection of the first author.

Etymology

The specific name of this species is derived from the name of the type locality, Taiwan.



Figure 5. *Rhinocypha taiwana* sp. nov., holotype male; head, prothorax and mesothorax in dorsal view.

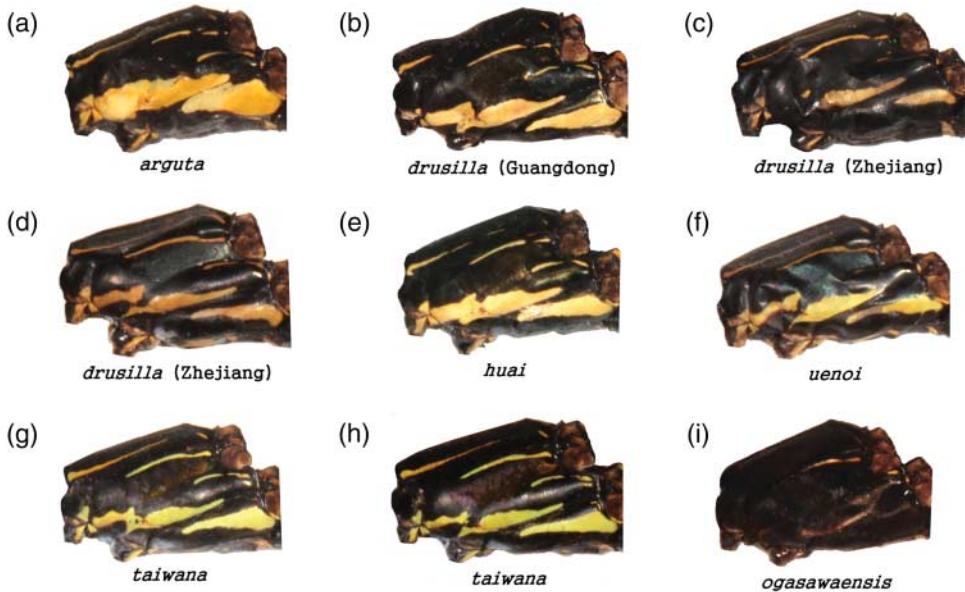


Figure 6. Synthorax of male in lateral view: (a) *Rhinocypha arguta* (Thailand); (b) *R. drusilla* (Guangdong, China); (c) *R. drusilla* (Zhejiang, China); (d) *R. drusilla* (Zhejiang, China); (e) *R. huai* (Hainan, China); (f) *R. uenoi* (Iriomote Island, Japan); (g) *R. taiwana* sp. nov., holotype; (h) *R. taiwana* sp. nov., paratype; (i) *R. ogasawaensis* (Ogasawara Islands, Japan).

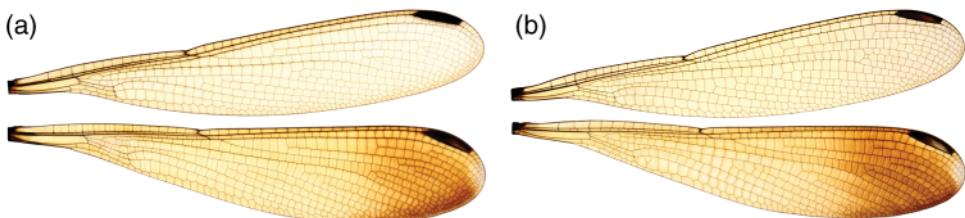


Figure 7. *Rhinocypha taiwana* sp. nov., wings: (a) holotype male; (b) paratype female.

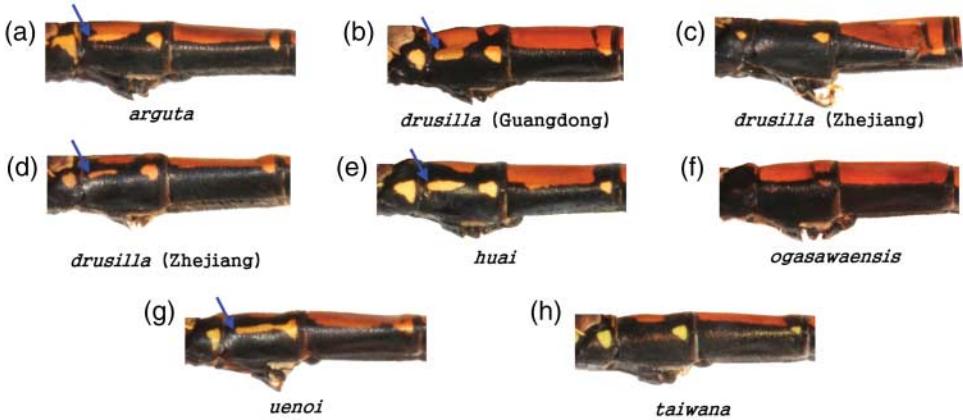


Figure 8. Abdomen S1–S3 of male in lateral view (arrow indicates the laterobasal stripe on S2): (a) *Rhinocypha arguta* (Thailand); (b) *R. drusilla* (Guangdong, China); (c) *R. drusilla* (Zhejiang, China); (d) *R. drusilla* (Zhejiang, China); (e) *R. huai* (Hainan, China); (f) *R. ogasawarensis* (Ogasawara Islands, Japan); (g) *R. uenoi* (Iriomote Island, Japan); (h) *Rhinocypha taiwana* sp. nov., holotype.

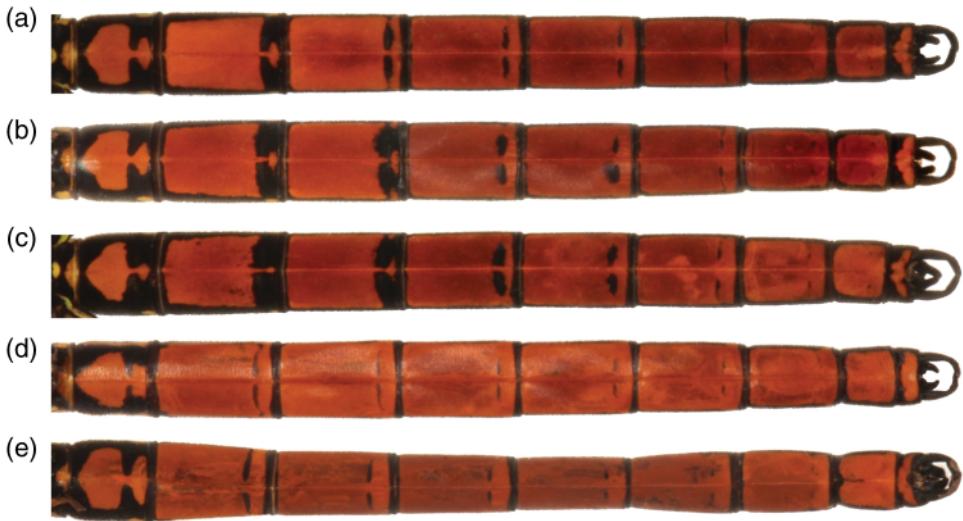


Figure 9. Abdomen of male in dorsal view: (a) *Rhinocypha taiwana* sp. nov., holotype; (b) *R. taiwana* sp. nov., paratype; (c) *R. taiwana* sp. nov., paratype; (d) *R. uenoi* (Iriomote Island, Japan); (e) *R. drusilla* (Zhejiang, China) (shrinkage caused by drying).

Description of male holotype

Head (Figures 4a, 5). Eyes of living specimens blackish brown above, yellowish grey below (see Figure 1). Labium black with setae; lateral lobes with 1/2 basal margins pale blue; middle lobe yellowish blue at base. Labrum black, near the upper margin with a yellow transverse band interrupted medially. Anteclypeus black, postclypeus black with 2 oval yellow spots laterally. Mandibles black with the basal part yellow. Genae and eye margin black with yellow markings. Second segment of antennae yellowish white, the apical segments black. Between the antennae a pair of yellow round spots. Frons and vertex black, with a pair of narrow yellow stripes beside the lateral ocelli and a pair of yellow round spots beyond. Along the margin of occiput a short yellow transverse stripe.

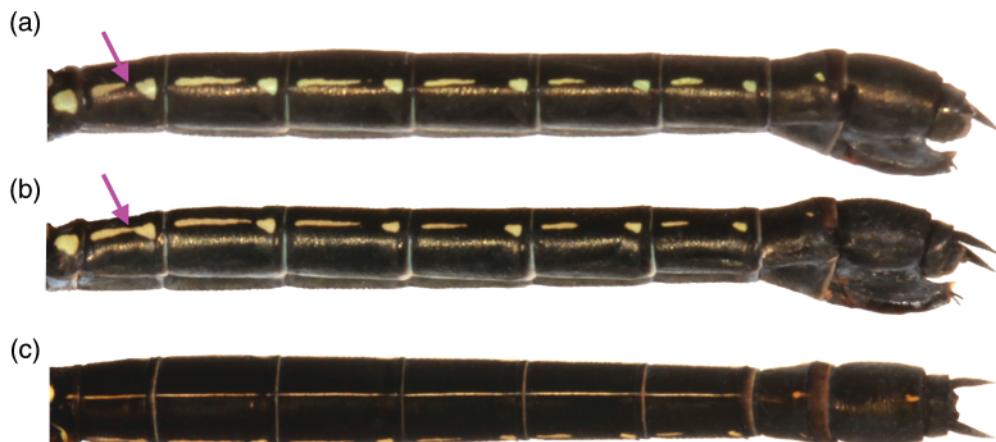


Figure 10. *Rhinocypha taiwana* sp. nov., two paratype females, abdomen: (a) lateral view; (b) lateral view; (c) dorsal view. Photos (b) and (c) show the same female specimen.

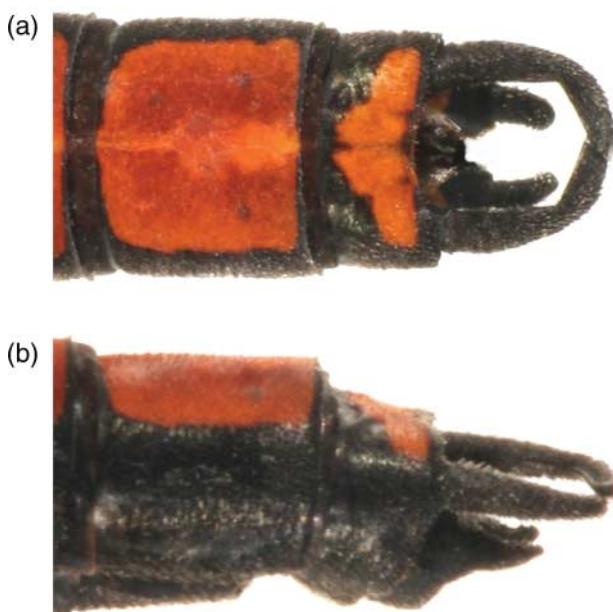


Figure 11. *Rhinocypha taiwana* sp. nov., holotype male, anal appendages: (a) dorsal view; (b) lateral view.

Thorax. Prothorax (Figure 5) black; anterior lobe with a transverse olive yellow stripe along anterior margin; median lobe with a pair of yellow triangular markings on either side, and with a pair of small yellow spots in the centre; posterior lobe with a pair of yellow markings at side, and a yellow median longitudinal stripe reaching the apical margin. Synthorax (Figure 6g) metallic black, with olive yellow stripes, bands and markings as follows. Mesothoracic triangle not enlarged, black. Mesepisternum with a long yellowish antehumeral stripe narrowing posteriorly; a separate small yellow oblique spot near the antealar ridge. Mesepimeron with a long yellow distal stripe just below the humeral suture, tapering toward antealar ridge. Metepisternum with a posterior narrow stripe below the first lateral suture, disconnected from a shorter narrow stripe distally; a broad irregular patch from lower part of metepisternum covering the stigma, reaching

the anterior margin of metepisternum and connected to a yellow stripe along the first lateral suture. Metepimeron with a broad triangular mark narrowing anteriorly, reaching the wing base. Poststernum largely black with 2 pairs of yellow spots. – Legs black with a yellow posterior stripe on each coxa. – Wings (Figure 7a) rather narrow. Fw hyaline with slightly yellow tinge anteriorly. Hw pale brown, beyond Px 16 heavily tinted brown with the extreme tip whitish. Fw with 13 Ax and 29 Px; Hw with 14 Ax and 22 Px. Arculus slightly distal to Ax 3; quadrangle with three crossveins in Fw and four in Hw. 1A arises proximal to the level of Ax 2. 1A meets wing margin at the level of Px 10 or 11 in Fw, Px 8 or 9 in Hw. CuP meets wing margin at the level of Px 13 in Fw, Px 11 in Hw. MA meets wing margin at the level of Px 18 or 19 in Fw, Px 13 in Hw. R3 arising between Px 2 and 3. Pterostigma covering 6–7 underlying cells, brown in Fw, obscurely bicoloured in Hw with largely brown and light brown posteroapically.

Abdomen (Figures 8h, 9a, 10). Black, with predominantly bright reddish orange markings on dorsum. S1 black with a dorsal apical orange marking connected to orange suture distally; laterally with a broad sub-triangular shaped olive yellow marking occupying the distal 2/3. S2 black with a reddish orange spade-shaped marking on dorsum; laterally with a triangle-shaped olive-yellow spot at the distal end. S3 with a predominantly large reddish orange patch, apically with black marking on each side of dorsal carina, broadly connected with the intersegmental black ring; laterally with a smaller triangle-shaped olive-yellow distal spot. S4–S10 without lateral spots. S4–S7 reddish orange with a pair of small distal black markings not connected to the intersegmental black ring, largest on S4 and smallest on S7. S8–S9 reddish orange. S10 with a sub-triangular-shaped reddish orange marking distally, intersegmental rings bordered black. Ventral side of abdomen black. Anal appendages (Figure 11) black; the superiors bending inwards in dorsal view. The inferior appendages bent inwards in dorsal view.

Measurements (mm). Hind wing 26, abdomen (including appendages) 23.

Variation in male paratypes

Labrum with variable coloration in paratypes: in five males the yellow transverse band near the upper margin not interrupted medially; in three males the yellow transverse band short and existing in left half of labrum; in two males the metepisternum has the broad irregular patch in its lower part disconnected from a short yellow stripe on the first lateral suture (Figure 6h). In two males the reddish orange spade-shaped marking on dorsum of S2 is weakly developed (Figure 9c). In three males S4 has a pair of broad distal black markings connected to the intersegmental black ring (Figure 9b, c). There is some variation in venational details; in the forewing the antenodals (Ax) number 12–15 and postnodals (Px) 20–29. In the hind wing the corresponding numbers are 12–14 and 20–24, respectively. Pterostigma bicoloured in Hw, with dark brown and light brown to whitish portions.

Measurements (mm). Hind wing 25.2–27, abdomen (including appendages) 21.5–24.

Description of female paratypes

Head. Marking generally similar to male (Figure 4b). Labrum black, near the upper margin with a yellow transverse band. Frons, vertex and occiput black, with two round yellow spots between the antennae, a pair of yellow narrow stripes beside the lateral ocelli and a pair of yellow spots on the side of the occiput. Along the margin of occiput a short yellow transverse stripe.



Figure 12. Habitats of *Rhinocypha taiwana* sp. nov.: (a) a shaded slow-flowing small rocky stream; (b) a well-shaded narrow rocky stream.

Thorax (Figure 3). Markings similar to those of male.

Wings (Figure 7b). Fw hyaline. Hw tinted pale brown, beyond Px 13 or 14 brown with extreme tip subhyaline. Fw with 14–15 Ax and 21–23 Px; Hw with 12–13 Ax and 19–22 Px. Arculus slightly distal to Ax 3. Quadrangle with 3–4 crossveins in Fw and 4 in Hw. 1A arises proximal to the level of Ax 2. 1A meets wing margin at the level of Px 4–5 or Px 6–7 in Fw, Px 6–7 in Hw. CuP meets wing margin at the level of Px 9 in Fw, Px 8 in Hw. MA meets wing margin at the level of Px 13 or 14 in Fw, Px 11 or 12 in Hw. R3 arising between Px 2 and Px 3. Pterostigma covering 4–5 or 5–6 underlying cells, brown in Fw with anterior margin dark brown, bicoloured with brown and whitish portions in Hw.

Abdomen (Figure 10). Black, without any reddish orange markings dorsally; S1–7 dorsally with a yellow line along carina. S8 and S9 dorsally each with a small yellow spot at distal end. S1 laterally with a broad oval yellow marking occupying the distal 2/3. S2–7 laterally with similar marking pattern. S2 laterally with a yellow longitudinal stripe in the anterior half and a triangular yellow spot at the distal end. One paratype with yellow longitudinal stripe connected to triangle-shaped yellow spot (Figure 10b). The yellow longitudinal stripe and distal triangle-shaped yellow spot becoming progressively shorter and smaller from S3–7.

Measurements (mm). Hind wing 28.5–30, abdomen (including appendages) 21.8–22.

Remarks on biology

So far this new species has been found only in North Taiwan. The habitats of *R. taiwana* vary from shaded slow-flowing small rocky streams (Figure 12a) to well-shaded narrow rocky streams (Figure 12b). These types of stream occur with thick canopy cover in dense lowland forest. Based on the collecting data and further observation made by Yung-Jen Chang we presume that the flight season is from September to early January. Both males and females were active on sunny days. The appearance of males was almost always dependent on sunshine. Exceptionally two males were collected by Liang-Jong Wang in rather cloudy weather. The altitudes of known habitats range from 280 to 380 m. Males perched on rocks in streams, or twigs or leaves of the plants above the streams at a height of 1–3 m. Females were found on twigs or leaves of the plants above the streams. These observations were made from 10:30 am to 2:40 pm. Syntopically occurring damselfly species included *Heliocypha perforata*, *Matrona cyanoptera* Hämäläinen & Yeh, 2000; *Psolodesmus mandarinus* McLachlan, 1870; *Euphaea formosa* Hagen, 1869; *Bayadera*

Table 1. List of species included in the *Rhinocypha drusilla* group with their distributions.

Species	Type locality	Distribution	Reference
<i>Rhinocypha arguta</i> Hämäläinen and Divasiri, 1997	Phu Kradung, Loei province, Thailand	North Thailand	Hämäläinen and Divasiri (1997)
<i>Rhinocypha drusilla</i> Needham, 1930	Ching Yuan, Chekiang (= Zhejiang), China	China (Zhejiang, Fujian, Guangdong, Guangxi, Guizhou)	Needham (1930); Wilson and Reels (2003); Wilson and Xu (2007); Zhang (2010, 2011)
<i>Rhinocypha huai</i> (Zhou & Zhou, 2006)	Jian Feng Ling, Hainan, China	China (Hainan)	Wilson et al. (2008); Zhang et al. (2010); Zhou and Zhou (2006)
<i>Rhinocypha ogasawarensis</i> Oguma, 1913	Ogasawara Islands, Japan	Japan (Ogasawara Islands)	Oguma (1913); Ozono et al. (2012)
<i>Rhinocypha taiwana</i> Wang & Chang, sp. nov.	Pinglin, New Taipei, Taiwan	North Taiwan	This paper
<i>Rhinocypha uenoi</i> Asahina, 1964	Urauchi-gawa Draniage, Iriomote, Japan	Japan (Iriomote island)	Asahina (1964); Ozono et al. (2012)

brevicauda Fraser, 1928 and *Coeliccia cyanomelas* Ris, 1912. Interspecific aggression between *R. taiwana* males was not observed by us. However, in one occasion Jyh-Jong Cherng observed a male *R. taiwana* chasing a male *Euphaea formosa* from its perch.

Rhinocypha drusilla group

Laidlaw (1950) first introduced the *R. drusilla* and *R. ogasawarensis* groups, belonging to “Grade II” in his survey of Chlorocyphidae, but no diagnostic characters were proposed for the definition of these two groups. There has been no further discussion of these species groups. So far, there has been no comprehensive published study of the genus *Rhinocypha* and the related genera based on morphology or DNA data. However, in the present paper we prefer to use a preliminary “group-name” – *Rhinocypha drusilla* group – for the six related, similarly patterned red-bodied *Rhinocypha* species listed in Table 1; their known distribution is shown in Figure 13. Members of the *R. drusilla* group share the following combination of characteristics, which distinguishes them from all other *Rhinocypha* species: male abdomen has reddish orange markings including a unique spade-shaped marking on dorsum of S2. The females of the *R. drusilla* group are without a reddish abdomen except in *R. uenoi* and *R. ogasawarensis* (Hamada & Inoue, 1985; Ozono et al., 2012). There are at least two forms (black and red forms) of *R. ogasawarensis* female in the Ogasawara islands (Ozono et al., 2012).

Distinguishing characters

The male of *R. taiwana* sp. nov. can be separated from males of the other species of the *R. drusilla* group by morphological characters. It differs from *R. huai* by having hind wings with the distal third brown and a sub-hyaline tip, pterostigma bicoloured, no lateral yellow basal stripe on abdomen S2 (Figure 8e, h) and dorsal abdomen S5–S6 with distal black markings not connected to the intersegmental black ring. It differs from *R. drusilla* by S3 having a pair of broad distal black markings connected to the intersegmental black ring (Figure 9a–c, e) and having a lateral yellow distal spot on S3 (Figure 8h). In both these species the hind wing distal third is brown with a whitish tip, a character found within the *R. drusilla* group only in these two species. *R. ogasawarensis* also has distal brown patches in the hind wings but they lack a whitish tip. *R. arguta* can be separated from *R. taiwana* by having broader bands (Figure 6a, g–h) on the metepisternum

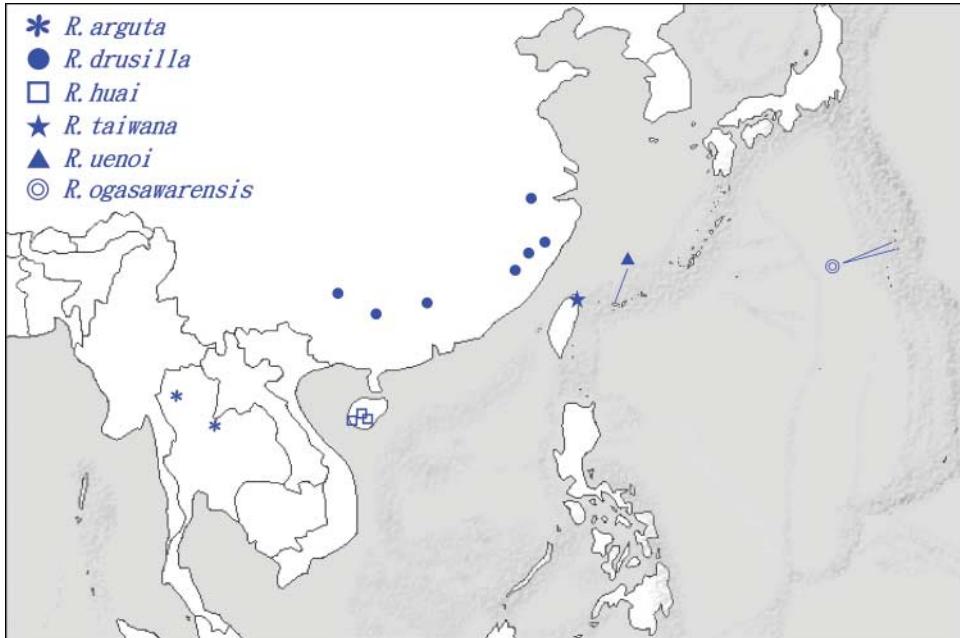


Figure 13. Geographical distribution of species in the *Rhinocypha drusilla* group.

and metepimeron, abdomen S9–10 lacking reddish orange markings, the hind wing hyaline and the pterostigma not bicoloured. *R. taiwana* differs from *R. uenoi* by S3–S4 having a pair of broad distal black markings connected to the intersegmental black ring (Figure 9a–c, d), abdomen S2 having a yellow distal spot laterally on S3 (Figure 8g–h) and the hind wing with the distal third brown with a whitish tip, pterostigma bicoloured (Figure 7a). *R. ogasawarensis* has the following characters in which it differs from all other species in the *R. drusilla* group: colour pattern with only two vague stripes on metepisternum and mesepimeron respectively (Figure 6i) and abdomen laterally without any spot on S1 and S3, only with a reddish apical spot on S2 (Figure 8f).

Key to the males

1. Metepisternum and metepimeron with broad bands (Figure 6a–h), abdomen S1 with one lateral yellow spot (Figure 8a–e, g–h).....2
- 1'. Metepisternum with a vague stripe (Figure 6i), metepimeron without any band or stripe, abdomen S1 without lateral yellow spot (Figure 8f).....*R. ogasawarensis*
2. Hind wing with pale brown tint, distal third darker brown with whitish tip, pterostigma bicoloured with basal half brown and distal half pale brown or whitish.....3
- 2'. Hind wing hyaline, pterostigma uniform brown.....4
3. Abdomen S3 laterally with a small apical yellow spot (Figure 8h), and dorsally with a pair of broad distal black markings connected to the intersegmental black ring (Figure 9a–c)....
.....*R. taiwana* sp. nov.
- 3'. Abdomen S3 laterally without a small apical yellow spot (Figure 8b–d), and dorsally with two thin black apical stripes (Figure 9e).....*R. drusilla*
4. Abdomen S9–10 dorsally with reddish orange markings.....5
- 4'. Abdomen S9–10 dorsally black without reddish orange markings.....*R. arguta*

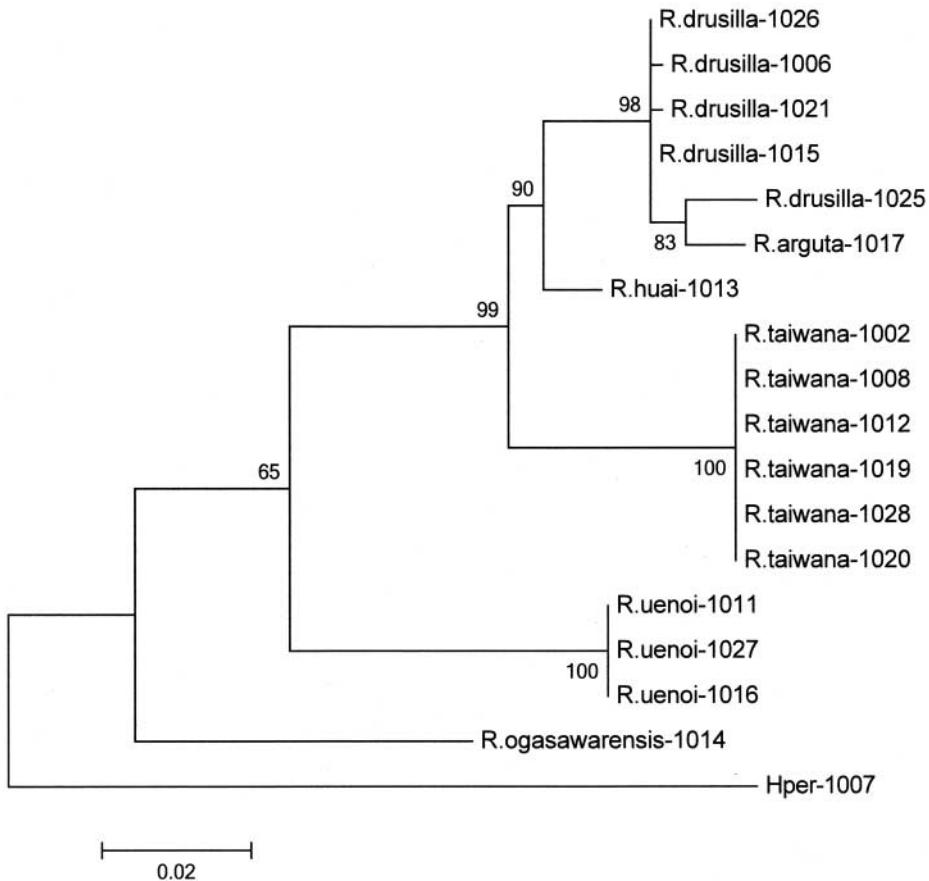


Figure 14. Phylogenetic tree of the *Rhinocypha drusilla* group derived from the maximum likelihood analyses of COI data based on a GTR+G+I model. Nodes are labelled with support from 1000 bootstrap replicates. The outgroup is *Heliocypha perforata*.

- 5. Mesepisternum with a lower yellow patch connected to the broad patch on metepimeron (Figure 6e); abdomen S2 laterally with a yellow basal middle stripe not connected to the apical yellow spot (Figure 8e); abdomen S3–8 reddish orange with distinct apical black bands.....*R. huai*
- 5'. Mesepisternum with a lower yellow stripe not connected to the broad stripe on metepimeron (Figure 6f); abdomen S2 laterally with a yellow basal middle stripe connected to the apical yellow spot (Figure 8g); abdomen S3–8 reddish orange only with black intersegmental ring (Figure 9d).....*R. uenoi*

Results and discussion of molecular studies

Sequences

The DNA barcode region of 646 bp of COI gene was sequenced from 20 individuals belonging to six *Rhinocypha* species and one outgroup species of Chlorocyphidae (Table 2). The alignment was unambiguous and without gaps for the present COI data. There are 108 (148) variable sites in the ingroup (including outgroup), 72 (85) of which are parsimony informative. Total number

Table 2. List of specimens included in the molecular analysis and their provenance.

Species	Code	Locality	Gender
<i>R. arguta</i>	1017	Mae Ton Luang, Chiang Mai, Thailand	M
<i>R. drusilla</i>	1006	Linan, Hangzhou, Zhejiang, China	M
	1015	Taishun, Wenzhou, Zhejiang, China	F
	1021	Taishun, Wenzhou, Zhejiang, China	M
	1026	Taishun, Wenzhou, Zhejiang, China	M
	1025	Shaoguan, Guangtong, China	M
<i>R. huai</i>	1011	Diaoluoshan, Hainan, China	M
<i>R. ogasawarensis</i>	1014	Ani jima, Ogasawara Islands, Japan	M
<i>R. taiwana</i>	1002	Site 1, Pinling, New Taipei, Taiwan	M
	1008	Site 2, Pinling, New Taipei, Taiwan	F
	1012	Site 2, Pinling, New Taipei, Taiwan	M
	1019	Site 3, Pinling, New Taipei, Taiwan	M
	1020	Site 3, Pinling, New Taipei, Taiwan	M
	1028	Site 2, Pinling, New Taipei, Taiwan	F
<i>R. uenoi</i>	1011	Aira river, Iriomote island, Japan	M
	1016	Aira river, Iriomote island, Japan	F
	1027	Aira river, Iriomote island, Japan	M
<i>Heliocypha perforata</i>	1007	Laomei, New Taipei, Taiwan	M

of mutations are 113 (167) in the ingroup (including outgroup). The base composition was AT biased (62.4%) as in other insect mitochondrial genomes (60–80%; Simon et al., 1994).

Intraspecific and interspecific sequence divergence

The intraspecific COI sequence divergence in *Rhinocypha taiwana* ($n = 6$), *R. uenoi* ($n = 3$) and *R. drusilla* ($n = 5$) are 0%, 0% and 0–1.5% respectively. The interspecific p-distances of *R. taiwana* among the other related species are: *R. huai* (4.2%), *R. arguta* (4.8%), *R. drusilla* (4.8–5.6%), *R. uenoi* (8.7%) and *R. ogasawarensis* (10.4%). The above data reveal that *R. taiwana* is a genetically distinct species among its congeners in the *R. drusilla* group. The other two insular species *R. uenoi* and *R. ogasawarensis* have higher interspecific sequence divergences: 7.4–9.3% and 9.3–10.4%, respectively. The fourth insular species, *R. huai*, has lower divergence with two continental species: *R. arguta* (3.1%) and *R. drusilla* (2.2–3.6%). Two morphologically distinct continental species, *R. arguta* and *R. drusilla*, have the lowest interspecific p-distances: 1.2–1.7% which are under 2%.

Phylogenetic analysis

Based on the lowest value of BIC, The best GTR+G+I model was chosen for the maximum likelihood analysis. The tree with the highest log likelihood (–1803.9710) is shown in Figure 14. Six individuals (from three sites) of *R. taiwana* sharing the identical COI sequence form a good phylogenetic lineage which is close to the group including *R. huai* (*R. arguta* and *R. drusilla*). The continental species, *R. arguta* and *R. drusilla*, form a strongly supported clade (bootstrap value 98%). The paraphyly of *R. drusilla* reveals the incongruence of morphological data and COI data.

Obvious morphological differences between *R. arguta* and the Fujian specimens of *R. drusilla* were discussed by Hämäläinen and Divasiri (1997). Our present material of *R. drusilla* (from Zhejiang and Guangdong) also indicates morphological differences between *R. arguta* and *R. drusilla*, although a similar character (lateral yellow basal stripe connected to the dorsal spade marking on abdomen S2) appear in *R. arguta* and *R. drusilla* from Guangdong (Figure 8a–b, d). It is necessary to study more material of continental “populations” by morphological and molecular

characters in order to clarify the phylogenetic relationships and to stabilize the taxonomic system of these taxa. To challenge the monophyly of the *R. drusilla* group more material is needed of other related *Rhinocypha* species or the entire *Rhinocypha* genus for further molecular analyses.

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