

Additions to the knowledge of the genus *Allorhynchium* van der Vecht, 1963 from China (Hymenoptera, Vespidae, Eumeninae)

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Academic editor: Michael Ohl | Received 23 March 2020 | Accepted 12 June 2020 | Published 29 June 2020

<http://zoobank.org/111BE0A9-E64B-4C58-92D2-65C532B33AB8>

Citation: Luo L, Zhang Q-H, Chen B, Li T-J (2020) Additions to the knowledge of the genus *Allorhynchium* van der Vecht, 1963 from China (Hymenoptera, Vespidae, Eumeninae). Journal of Hymenoptera Research 77: 119–137. <https://doi.org/10.3897/jhr.77.52309>

Abstract

In this study, *Halysituberosus* Dong & Wang, 2017 is treated as a synonym of *Allorhynchium* van der Vecht, 1963 (**syn. nov.**). *Halysituberosus yingjiangensis* Dong & Wang, 2017 is a new synonym of *Allorhynchium lugubrinum* (Cameron, 1900) (**syn. nov.**) and *Halysituberosus menglianensis* Dong & Wang, 2017 is transferred to *Allorhynchium* as a new combination (**comb. nov.**). Based on additional *COI* gene sequencing and morphological characters including genitalia characters, both *Allorhynchium diffinis* (Giordani Soika, 1986) and *Allorhynchium radiatum* Li, Barthélémy & Carpenter, 2019 are confirmed to be valid species, and their males of the two species are described for the first time. *Allorhynchium quadrimaculatum* Gusenleitner, 1997 is newly recorded from China. A key to the Chinese species of *Allorhynchium* are also updated.

Keywords

Allorhynchium, Eumeninae, *Halysituberosus*, new synonym, new record

Introduction

At present, *Allorhynchium* van der Vecht, 1963 contains 20 species and four subspecies worldwide, which are mostly distributed in the Oriental region (Smith 1861; Giordani Soika 1986; Girish Kumar et al. 2016; Tan et al. 2018; Li et al. 2019). Tan et al. (2018)

revised the genus from Northeast Asia and provided a key to the Oriental species. In our study, the type species of *Halysituberosus* Dong & Wang, 2017 is examined and verified that *Halysituberosus* is a synonym of *Allorhynchium* van der Vecht, 1963 (syn. nov.), *H. yingjiangensis* Dong & Wang, 2017 is a synonym of *Allorhynchium lugubrinum* (Cameron, 1900) (syn. nov.), and *H. menglianensis* Dong & Wang, 2017 should be transferred to *Allorhynchium* (comb. nov.). Meanwhile, seeing that the two related species *A. diffinis* (Giordani Soika, 1986) and *A. radiatum* Li, Barthélémy & Carpenter, 2019 were originally described on a single female specimen and confusing to distinguish, we provided some more morphological characters from both female and male and their *COI* (cytochrome oxidase subunit 1) sequence features. Finally, *A. quadrimaculatum* Gusenleitner, 1997 is newly recorded from China. And some diagnosis and figures of these species and an updated key to the Chinese species of *Allorhynchium* are also given.

DNA barcode was first proposed by Hebert (Hebert et al. 2003), and in his study, a model *COI* profile, based upon the analysis of a single individual from each of 200 closely allied species of lepidopterans, was 100% successful in correctly identifying subsequent specimens. Hebert's results provided reliable evidences for DNA barcode systems. After that, many scholars began to use DNA barcode technology for species identification, diversity analysis and phylogenetic analysis (Ball et al. 2005; Hajibabaei et al. 2006; Ceccarelli et al. 2012). Herein, with the development of sequencing technology and the reduction of sequencing costs, more scholars conducted in-depth researches on the genome of species and found the use of *COI* to identify species was a great controversial issue because it's difficult to provide a unified discrimination standard that what's the range of *COI* sequence variation rate between two different species (Moritz et al. 2004; Dasmahapatra et al. 2010). Thereinto, Consortium for the Barcode of Life (CBOL) initiated scientific research activities using *COI* for species identification on a global scale, and the data showed that the *COI* sequences of most species exhibited low intraspecific genetic differences and relatively high interspecific genetic differences (Schindel et al. 2005; Ratnasingham et al. 2007; CBOL Plant Working Group 2009). Research data in recent years have also reflected that the similarity of the same species is above 98%, and the sequence difference between species is greater than 2% (Hebert et al. 2010; Zhang et al. 2011; Schmid-Egger et al. 2017; Abd-El-Samie et al. 2018; Halim et al. 2018; Fernandez-Triana et al. 2019). So, in our work, the intraspecific and interspecific differences of *COI* between *A. diffinis* and *A. radiatum* are analyzed.

Materials and methods

Specimens examined are deposited in Chongqing Normal University (China) and Kunming Institute of Zoology, Chinese Academy of Sciences (China). Descriptions were made under a stereomicroscope (Olympus SZ61). All figures were taken and measured with Keyence VHX-5000 digital microscope. Body length was measured from the anterior margin of head to the posterior margin of metasomal tergum II by

KEYENCE-VHX-5000. Photoshop CS6 was used to make the figure plates. For the description of punctures, “sparsely” means that interspaces are larger than one puncture diameter, “moderately” means equal to the diameter, and “densely” means less than one diameter.

A total of 19 dried and pinned specimens belonging to *A. diffinis* and *A. radiatum* were examined, among which some were difficult to separate from *A. diffinis* and *A. radiatum*. In order to exactly identify these specimens, we selected seven specimens of *A. diffinis*, *A. radiatum* and three other species (*Allorhynchium argentatum*, *Allorhynchium chinense*, and *Anterhynchium flavomarginatum*) for molecular identification (Table 1). According to the manufacturer’s instructions (<https://www.qiagen.com>), genomic DNAs were extracted from muscle tissues using QIAamp DNA Mini Kit (QIAGEN, Germany). The *COI* genes were amplified by using standard primers LCO1490 and HCO2198 (Folmer et al. 1994). PCRs were performed with the manufacturer’s instructions (<https://www.cwbiotech.com>). Products of PCRs were sequenced in Sangon Biotech (Shanghai) Co., Ltd. Seven *COI* sequences newly obtained and the *COI* sequence of *Vespa mandarinia* (Sample ID: AAW6949) downloaded from Centre for Biodiversity Genomics (<http://v4.boldsystems.org/index.php>) were aligned with Clustal W version 1.8 (Altschul et al. 1997) in this study (Table 1). These sequences were checked for stop codons and frame shifts using the invertebrate mitochondrial code and the standard code respectively as implemented in MEGA 6.0 (Molecular Evolutionary Genetics Analysis version 6.0) (Tamura et al. 2013). The maximum likelihood (ML) tree (Felsenstein 1981; Kishino et al. 1990) of the *COI* sequences was analyzed in PhyML 3.0 (Guindon et al. 2010).

Abbreviations:

- CQNU** Chongqing Normal University, Chongqing, China;
KIZ Kunming Institute of Zoology, Kunming, China;
A1 for antennal segment 1;
A2 for antennal segment 2;
T1 for metasomal tergum 1;
T2 for metasomal tergum 2;
S1 for metasomal sternum 1;
S2 for metasomal sternum 2, and so on.

Table 1. The information of *COI* genes used in this study.

Species	Collecting site	Subfamily	Accession number
<i>Al. diffinis</i>	Sichuan (China)	Eumeninae	MT196405
<i>Al. radiatum</i>	Guizhou (China)	Eumeninae	MT188371
<i>Al. A</i>	Guangxi (China)	Eumeninae	MT188373
<i>Al. B</i>	Guangdong (China)	Eumeninae	MT188372
<i>Al. argentatum</i>	Guangxi (China)	Eumeninae	MT178403
<i>Al. chinense</i>	Yunan (China)	Eumeninae	MT178402
<i>An. flavomarginatum</i>	Hubei (China)	Eumeninae	MT178404
<i>Vespa mandarinia</i>	Primorskiy (Russia)	Vespinae	AAW6949

Taxonomy

Allorhynchium van der Vecht, 1963

Allorhynchium van der Vecht, 1963: 57–58. Type species: *Vespa argentata* Fabricius, 1804, by original designation.

Archancistrocerus Giordani Soika, 1986: 143–146. Type species: *Archancistrocerus diffinis* Giordani Soika, 1986, by original designation.

Halysituberosus Dong & Wang, 2017: 184. Type species: *Halysituberosus menglianensis* Dong & Wang, 2017, by original designation (syn. nov.).

Diagnosis. Anterior face of pronotum without foveae; tegula longer than wide, emarginated apically and not reaching posterior end of parategula; epicnemial carina present; dorsolateral margin of propodeum somewhat rounded and without teeth-like projections; T1 either evenly rounded or rather rectangular in lateral view, in some species T1 with somewhat transverse carina basally; in some species, S2 of male convex, or protruding medially into a transverse crest in lateral view; S7 of male with flat uplifted area or 1–3 teeth; metasoma sessile (Tan et al. 2018).

Notes. Dong and Wang (2017) established the genus *Halysituberosus* by the three following characters: apical margin of clypeus widely emarginated (Figs 2, 12), vertex without cephalic foveae, and both S2 and S7 with tubercles in male (Figs 6, 7, 16, 17). After our examination of its type species, it is verified that *Halysituberosus* Dong & Wang, 2017 belongs to *Allorhynchium* van der Vecht, and *Halysituberosus yingjiangensis* Dong & Wang, 2017 is a new synonym of *Allorhynchium lugubrinum* (Cameron, 1900) and *Halysituberosus menglianensis* Dong & Wang, 2017 should be transferred to *Allorhynchium*.

Distribution. Oriental, Australian and Palearctic regions.

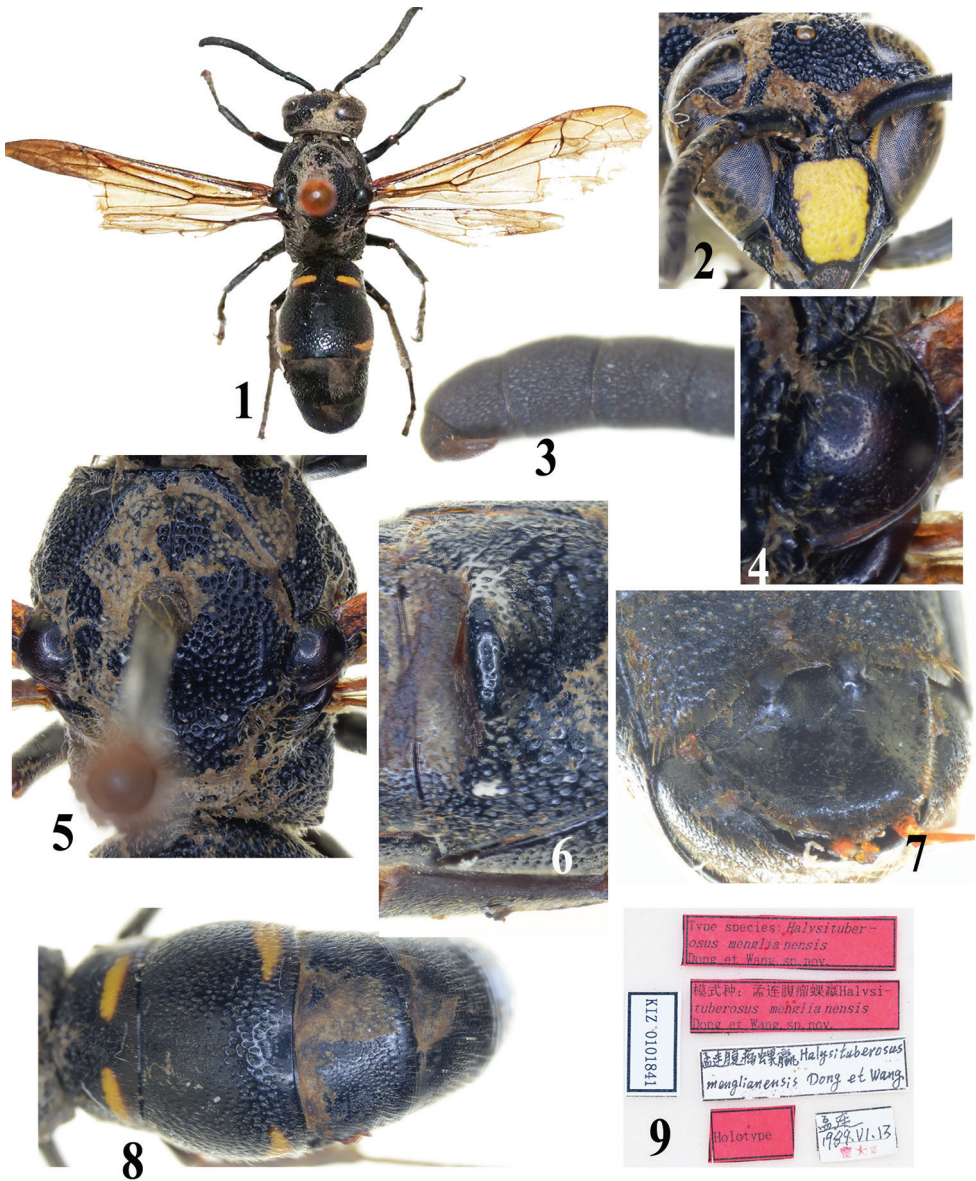
Allorhynchium menglianensis (Dong & Wang, 2017) comb. nov.

Figs 1–9

Halysituberosus menglianensis Dong & Wang, 2017: 184.

Material examined. Holotype, ♂, CHINA, Yunnan Prov., Puer City, Menglian County, 22°19.746'N, 99°35.049'E, 962 m, 13.VI.1989, Dazhi Dong (KIZ 0101842).

Diagnosis. Dong and Wang (2017) reported *Halysituberosus menglianensis* from China (one male). After our examination of the type specimen (Fig. 1), we verify that *Halysituberosus menglianensis* Dong & Wang, 2017 should be transferred to *Allorhynchium*, which is a new combination. It differs from *A. lugubrinum* and other congeners by the combination of the following characters: a yellow square central spot on clypeus (Fig. 2); A13 (Fig. 3) elongate, slightly curved and bent backward beyond the middle of A11; tegula dark black (Figs 4, 5); wings pale brown, without purple



Figures 1–9. *Allorhynchium menglianensis* (Dong & Wang, 2017) comb. nov. **1** habitus (dorsal view) ♂ **2** clypeus, ♂ **3** apex of antenna, ♂ **4** tegula, ♂ **5** mesosoma (dorsal view), ♂ **6** S2, ♂ **7** S7, ♂ **8** metasoma (dorsal view), ♂ **9** information of type specimen.

luster; T1 rather rectangular from lateral view (Fig. 8); apical bands of both T1 and T2 medially interrupted (Figs 1, 8); S2 of male with a large ridge in the middle (Fig. 6); S7 of male with a pair of triangular teeth (Fig. 7).

Distribution. China (Yunnan).

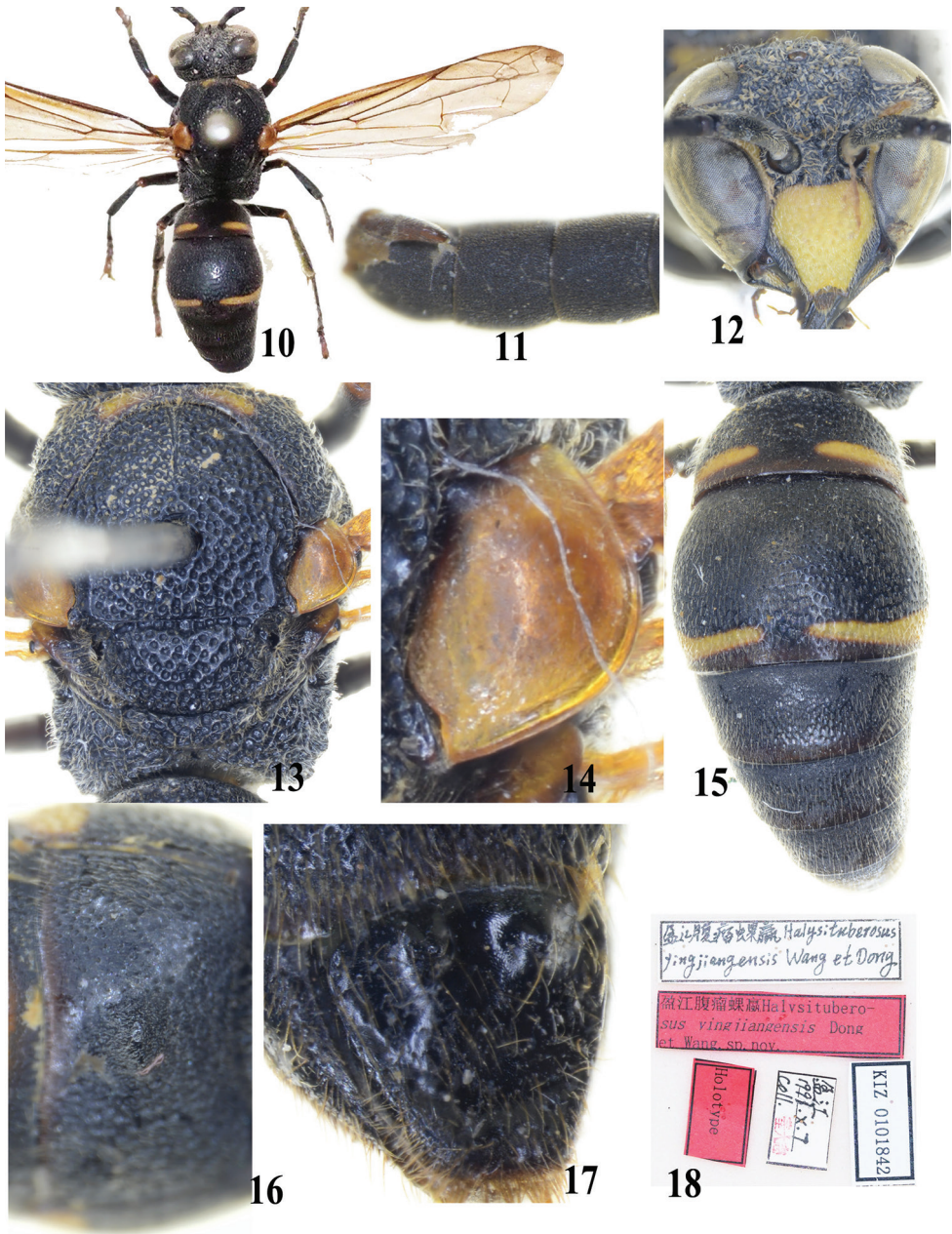
***Allorhynchium lugubrinum* (Cameron, 1900)**

Figs 10–18

Rhynchium lugubrinum Cameron, 1900: 532.*Allorhynchium lugubrinum*: van der Vecht, 1963: 60; Giordani Soika 1996: 37; Girish Kumar and Sharma 2015: 21; Girish Kumar et al. 2016: 30.*Halysituberosus yingjiangensis* Dong & Wang, 2017: 184–186. (syn. nov.)**Material examined.** 1♂, CHINA, Yunnan Prov., Dehong City, Yingjiang County, 24°41.722'N, 97°56.772'E, 844 m, 7.X.1997, Dazhi Dong (KIZ 0101842).**Diagnosis.** Dong and Wang (2017) reported *Halysituberosus yingjiangensis* from China (one male). After our examination of the type specimen (Fig. 10), *Halysituberosus yingjiangensis* Dong & Wang, 2017 is identified to be new synonym of *Allorhynchium lugubrinum* (Cameron, 1900). It differs from *A. quadrimaculatum* and other congeners by the combination of the following characters: clypeus rugose-punctate medially, almost yellow (Fig. 12); apex of pronotum with yellow band (Figs 10, 13); tegula reddish brown (Fig. 14); wings pale brown, without purple luster; T1 rather rectangular from lateral view, yellow apical bands of both T1 and T2 medially interrupted (Fig. 15); S2 slightly convex, not protruding medially into a crest in lateral view (Fig. 16); S7 of male with a pair of flat lobe-shaped protuberances (Fig. 17).**Distribution.** China (Yunnan); India.***Allorhynchium diffinis* (Giordani Soika, 1986)**

Figs 20–28

Archancistrocerus diffinis Giordani Soika, 1986: 143–146.*Allorhynchium diffinis* (Giordani Soika, 1986): Tan et al. 2018: 49–64.**Material examined.** 6♀♀1♂, CHINA, Sichuan Prov., Leshan City, Emeishan County, Shaxi Town, 29°25.083'N, 103°26.913'E, 926 m, 11.VIII.2011, Tingjing Li (CQNU); 2♀♀, CHINA, Sichuan Prov., Yaan City, Lushan County, Taiping Town, Chunguang village, 30°18.794'N, 102°59.351'E, 964 m, 12.VIII.2018, Xue Zhang (CQNU); 1♀, CHINA, Sichuan Prov., Yaan City, Lushan County, Shuangshi Town, Xichuan village, 30°16.129'N, 102°53.403'E, 982 m, 11.VIII.2018, Huachuan Wang and Qian Han (CQNU).**Notes.** The species *A. diffinis* in the original description was identified on a single female from Sichuan, China (Giordani Soika 1986) and *A. radiatum* Li et al., 2019 was related to it. In this study, some more specimens of *A. diffinis*, including one male were also collected from Sichuan. Meanwhile, some specimens (*Allorhynchium* A, Figs 37–46) from Guangxi, China are similar to both *A. diffinis* and *A. radiatum*, and some other female specimens (*Allorhynchium* B, Figs 47–52) from Guangdong, China are similar to *A. radiatum* by black body (Fig. 47). To precisely classify these specimens, *COI* genes of *A. diffinis*, *A. radiatum*, *Allorhynchium* A and *Allorhynchium* B



Figures 10–18. *Allorhynchium lugubrinum* (Cameron, 1900) **10** habitus in dorsal view, ♂ **11** apex of antenna, ♂ **12** clypeus, ♂ **13** mesosoma (dorsal view), ♂ **14** tegula, ♂ **15** metasoma (dorsal view), ♂ **16** S2, ♂ **17** S7, ♂ **18** information of type specimen.

are sequenced and analyzed. Four other *COI* sequences of *A. argentatum*, *A. chinense*, *Anterhynchium flavomarginatum* and *Vespa mandarinia* of the same family Vespidae are selected for comparison.

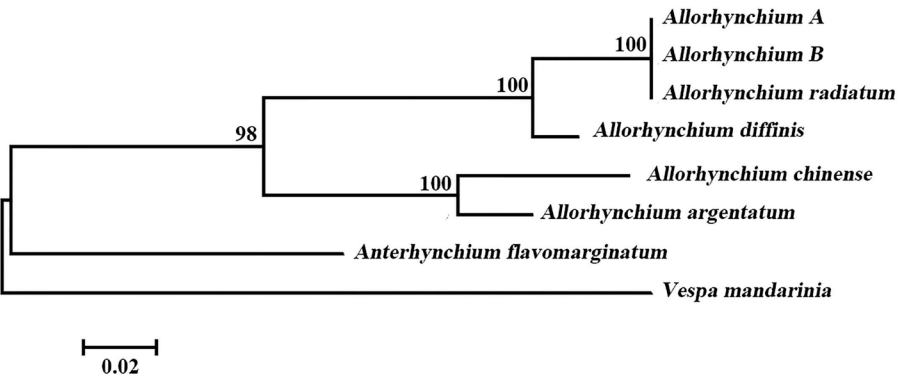


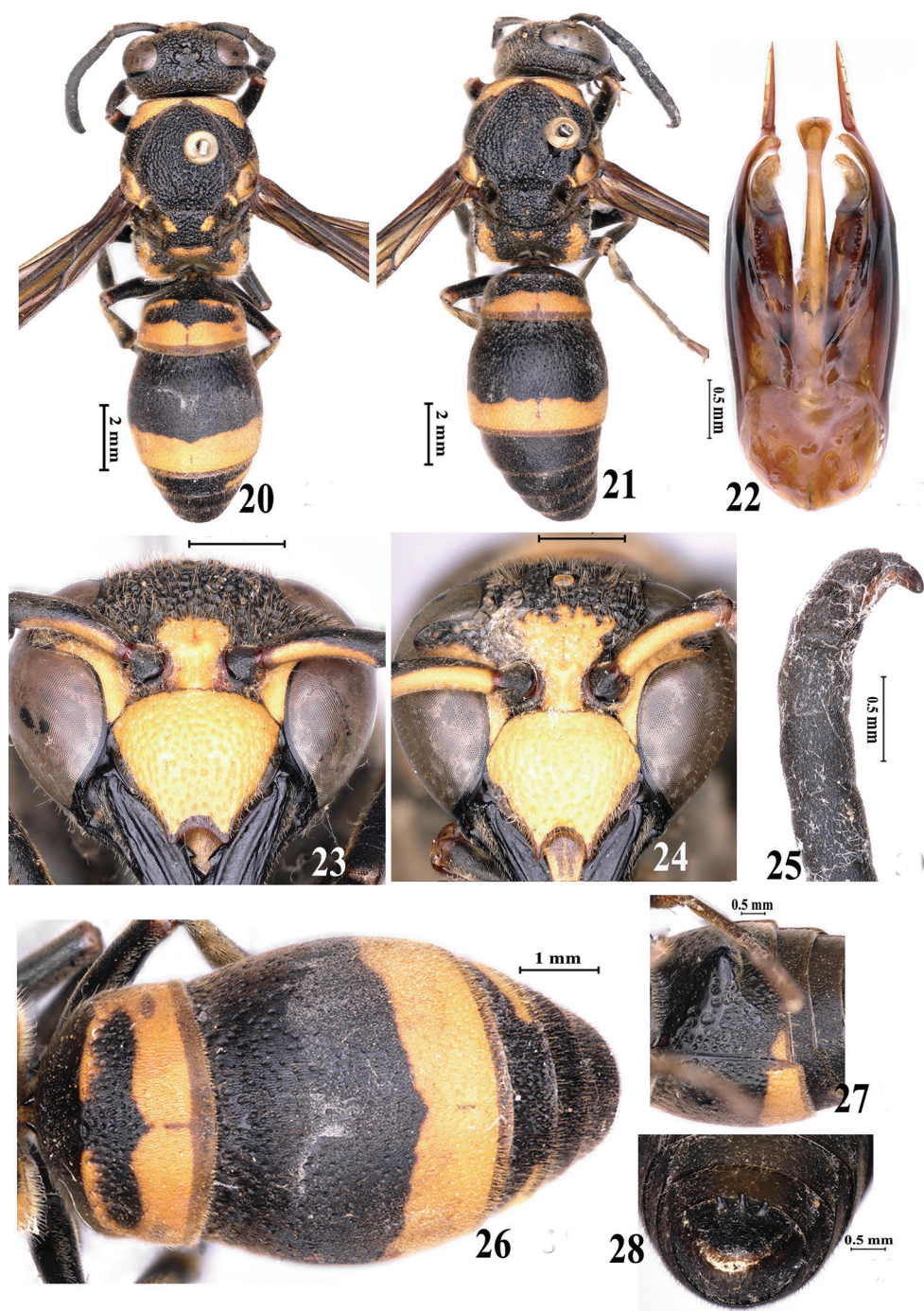
Figure 19. Maximum likelihood tree of eight *COI* sequences (The nodes are shown with their bootstrap values; *Vespa mandarinia* was used as the out-group)

Sequence alignment results display that the same *COI* sequence occurs in *Allorhynchium* A, *Allorhynchium* B and *A. radiatum*, and 29 different nucleic acids are present in *A. radiatum*, *Allorhynchium* A, *Allorhynchium* B and *A. diffinis* (Suppl. material 1: Figure S1). ML tree topology reflects that *A. diffinis* is sister of *A. radiatum*, *Allorhynchium* A and *Allorhynchium* B, with 100% bootstrap value of support for the branch(Fig. 19); the genetic pairwise distance based on K2P (Kimura-2-parameter substitution model) (Kimura 1980) among *Allorhynchium* A, *Allorhynchium* B and *A. radiatum* is 0 and the distance between *A. diffinis* and *A. radiatum*, *Allorhynchium* A, and *Allorhynchium* B is 4.3% (Table 2). According to Hebert’s view that the average difference of *COI* sequences within the same species is usually less than 2% (Hebert et al. 2003), our results suggest that both *Allorhynchium* A and *Allorhynchium* B belong to *A. radiatum*, and *A. diffinis* and *A. radiatum* be valid species, respectively.

First description of male (Fig. 21): sculpture, punctuation, setae, and coloration similar to female (Figs 20, 23, 26); body length 13.5 mm, with large yellow spots and bands (Fig. 21): clypeus (Fig. 24) wholly, wide band along lower inner eye orbit, large inter-antennal spot, scape ventrally, wide anterior band of pronotum, large spot

Table 2. Genetic distance among eight specimens based on K2P and *COI* sequences.

	(1)	(2)	(3)	(4)	(5)	(6)	(7)
(1) <i>Allorhynchium diffinis</i>							
(2) <i>Allorhynchium radiatum</i>	0.043						
(3) <i>Allorhynchium</i> A	0.043	0.000					
(4) <i>Allorhynchium</i> B	0.043	0.000	0.000				
(5) <i>Allorhynchium chinense</i>	0.152	0.166	0.166	0.166			
(6) <i>Allorhynchium argentatum</i>	0.130	0.146	0.146	0.146	0.064		
(7) <i>Anterhynchium flavomarginatum</i>	0.182	0.176	0.176	0.176	0.192	0.186	
(8) <i>Vespa mandarinia</i>	0.248	0.248	0.248	0.248	0.230	0.229	0.214



Figures 20–28. *Allorhynchium diffinis* (Giordani Soika, 1986) **20** habitus (dorsal view) ♀ **21** habitus (dorsal view) ♂ **22** genitalia (front view), ♂ **23** clypeus, ♀ **24** clypeus, ♂ **25** apex of antenna, ♂ **26** metasoma (dorsal view), ♀ **27** S2, ♂ **28** S7, ♂.

on mesepisternum, tegula except a central translucent spot, parategula, two spots of metanotum, dorsal and posterior faces of propodeum largely, wide apical band on each of both terga I and II; head and mesosoma coarsely punctate, punctures of metasoma sparser than those of head and mesosoma; A13 (Fig. 25) blunt, short and bent backward not beyond the middle of A11; S2 (Fig. 27) protruding medially into a big and strong crest in lateral view and rounded apically; S7 (Fig. 28) with three distinct teeth at basal area; genitalia as in Fig. 22: apex of penis valve not round in frontal view, apex of volsella slightly narrow in frontal view.

Diagnosis. Body with large yellow markings: clypeus wholly, anterior half of pronotum, propodeum largely, tegula except brown spot, parategula, and wide apical bands on T1–T2; clypeal apex deeply emarginated and forming acute tooth on each lateral side; body with coarse punctures, punctures on both head and mesosoma denser than those on metasoma; A13 short, bent backward, and not beyond the middle of A11; S2 protruding medially into a big and strong crest and rounded apically; S7 with three distinct teeth at basal area.

Distribution. China (Sichuan).

Allorhynchium radiatum Li, Barthélémy & Carpenter, 2019

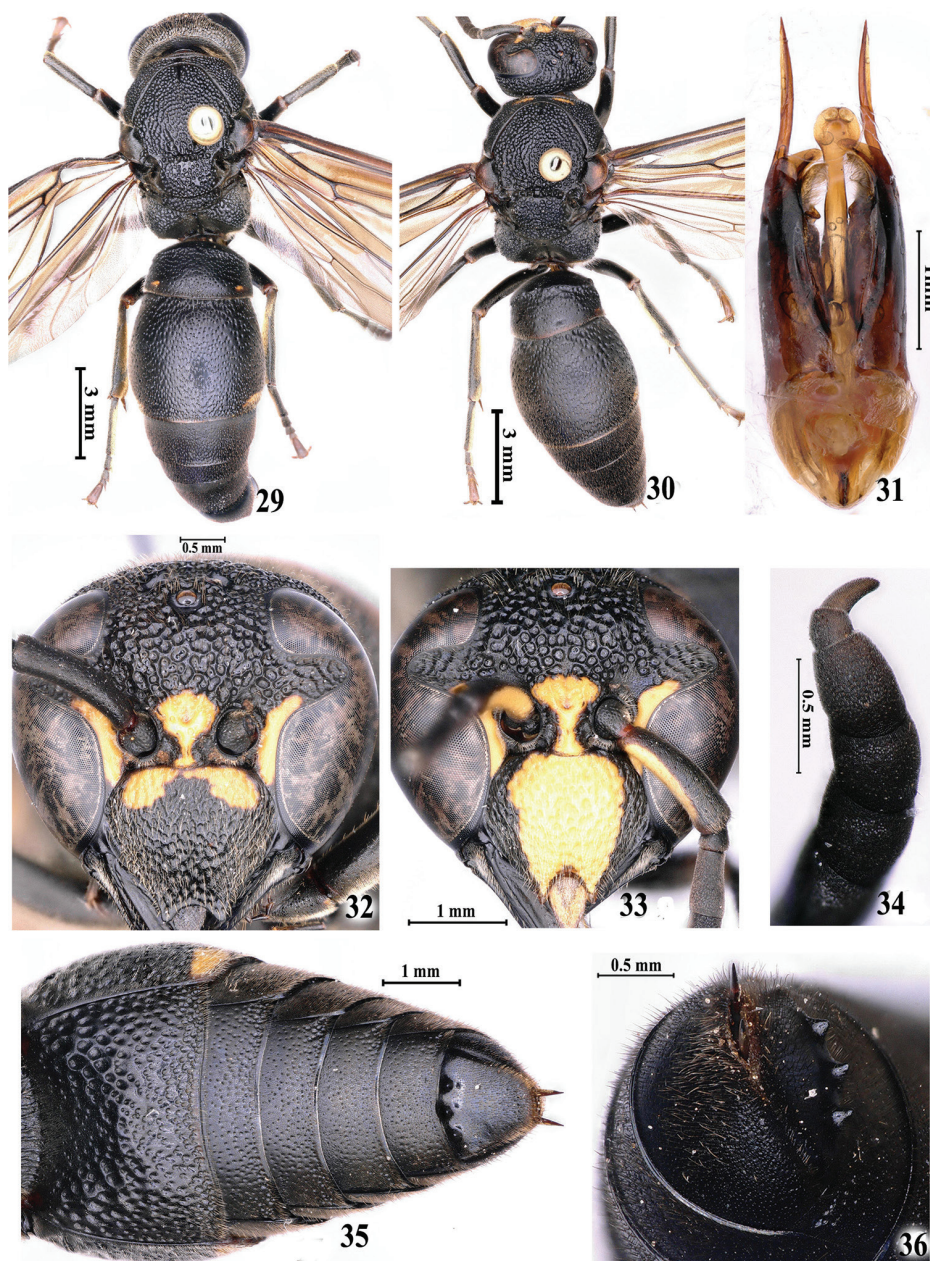
Figs 29–52

Allorhynchium radiatum Li, Barthélémy & Carpenter, 2019: 139–140.

Material examined. 1♀1♂, CHINA, Guizhou Prov., Qiannan City, Libo County, Maolan National Nature Reserve, Dongdai Village, 25°23.408'N, 108°04.374'E, 576 m, 21.VI.2015, Tingjing Li and Yan Peng (CQNU); 2♀♀3♂♂, CHINA, Guangxi Prov., Guilin City, Longsheng County, Sanmen Town, Huaping National Nature Reserve, 25°37.454'N, 109°54.957'E, 740 m, 16.VII.2018, YanPeng and Xue Zhang (CQNU); 2♀♀, CHINA, Guangdong Prov., Shaoguan City, Shixing County, Chebal-ing National Nature Reserve, 24°43.503'N, 114°15.658'E, 357 m, VI.2018, Feiyue Du (CQNU).

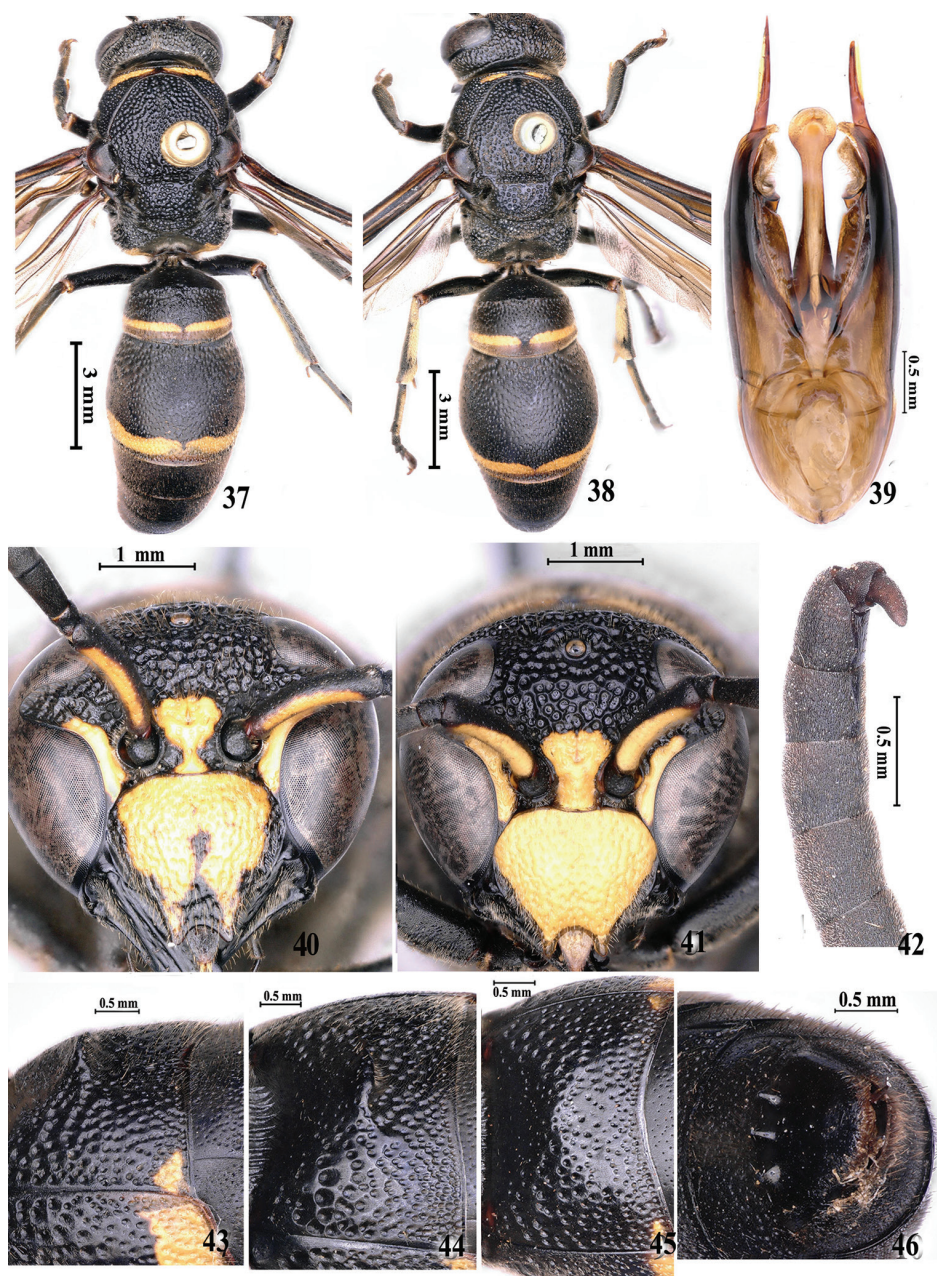
Notes. The species *A. radiatum* was described on a single female from Hong Kong, China (Li et al. 2019). The type specimen is almost wholly black except yellow spots on head. According to the results of *COI* genes in this study (Fig. 19), there are some variations of morphological characters within the species. Among the specimens which are collected from other areas of China, those from Guizhou (Figs 29–36) and Guangxi (Figs 37–46, *Allorhynchium* A) are with more yellow markings than the type specimen (figs 33, 34 of Li et al. 2019) and those from Guangzhou (Figs 47–52, *Allorhynchium* B), and S2 of male protruding medially into a transverse crest or indistinctly convex (Figs 35, 43–45).

First description of male (Figs 30, 38): body length 12.8–13.3 mm, forewing length 12.5–12.9 mm. Sculpture, punctuation, setae, and coloration as in female (Figs 29, 37, 47); the following parts yellow: clypeus wholly or except lateral side (Figs 33, 41), scape ventrally, anterior small separated spots of pronotum, and dorso-



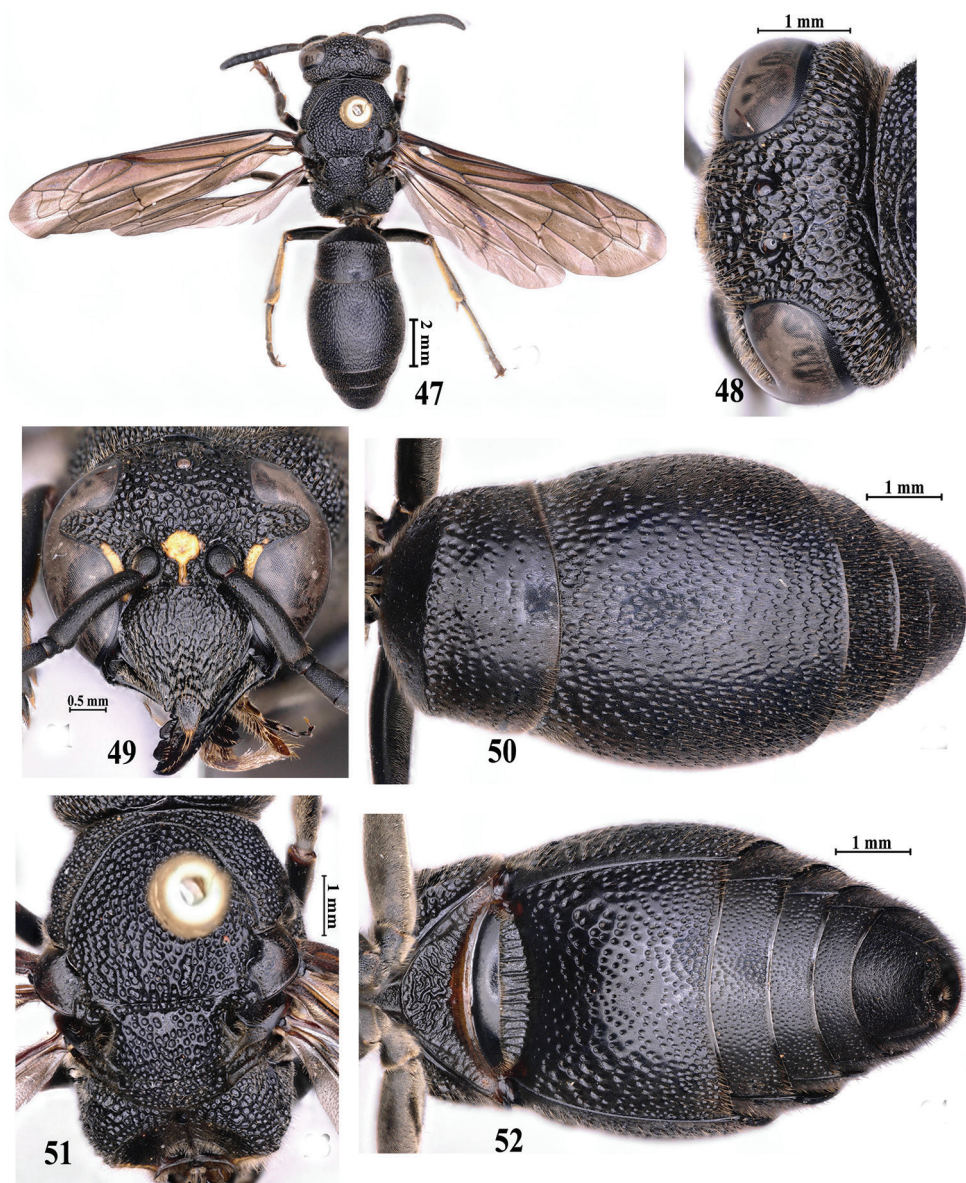
Figures 29–36. *Allorhynchium radiatum* Li et al., 2019 (from Guizhou) **29** habitus (dorsal view), ♀ **30** habitus (dorsal view), ♂ **31** genitalia (front view), ♂ **32** clypeus, ♀ **33** clypeus, ♂ **34** apex of antenna, ♂ **35** metasoma (ventral view), ♂ **36** S7, ♂.

lateral spots of propodeum; A3–A12 ventrally dark brown; T1 and T2 almost black or with thin and interrupted apical bands (Figs 30, 38); clypeus almost as wide as long, moderately punctate, apical margin strongly emarginated medially, apical width: emar-



Figures 37–46. *Allorhynchium radiatum* (*Allorhynchium* A, from Guangxi) **37** habitus (dorsal view), ♀ **38** habitus (dorsal view), ♂ **39** genitalia (front view), ♂ **40** clypeus, ♀ **41** clypeus, ♂ **42** apex of antenna, ♂ **43–45** variations of S2, ♂ **46** S7, ♂.

gination depth = 0.58: 0.21, total width: apical width = 1.8: 0.58; A13 (Figs 34, 42) slightly curved and longer than that of *A. diffinis*; S2 protruding medially into a transverse crest or indistinctly convex (Figs 35, 43–45); S7 with three distinct tubercles at



Figures 47–52. *Allorhynchium radiatum* (*Allorhynchium* B, from Guangzhou) **47** habitus (dorsal view) ♀ **48** head, (dorsal view) ♀ **49** clypeus, ♀ **50** metasoma (dorsal view), ♀ **51** mesosoma (dorsal view), ♀ **52** metasoma (ventral view), ♀.

basal area (Figs 36, 46); genitalia as in Figs 31, 39, apical tip of penis valve somewhat inflated and round.

Diagnosis. Compared with the related *A. diffinis*, body of *A. radiatum* almost black or just with a few thin yellow markings, A13 elongated and longer than that of *A. diffinis*, punctures on both T2 and S2 distinctly coarser, S2 protruding medially into

a transverse crest or indistinctly convex (in *A. diffinis*, S2 protruding medially into a big and strong crest in lateral view and rounded apically), apex of penis valve round in frontal view (in *A. diffinis*, apex of penis valve not round).

Distribution. China (Hong Kong, Guangdong, Guangxi, Guizhou).

In addition, there was an error that needs to be corrected in the reference (Li et al. 2019): figure 38 of *A. radiatum* in p.138 was misplaced and should be exchanged with figure 89 in page 152.

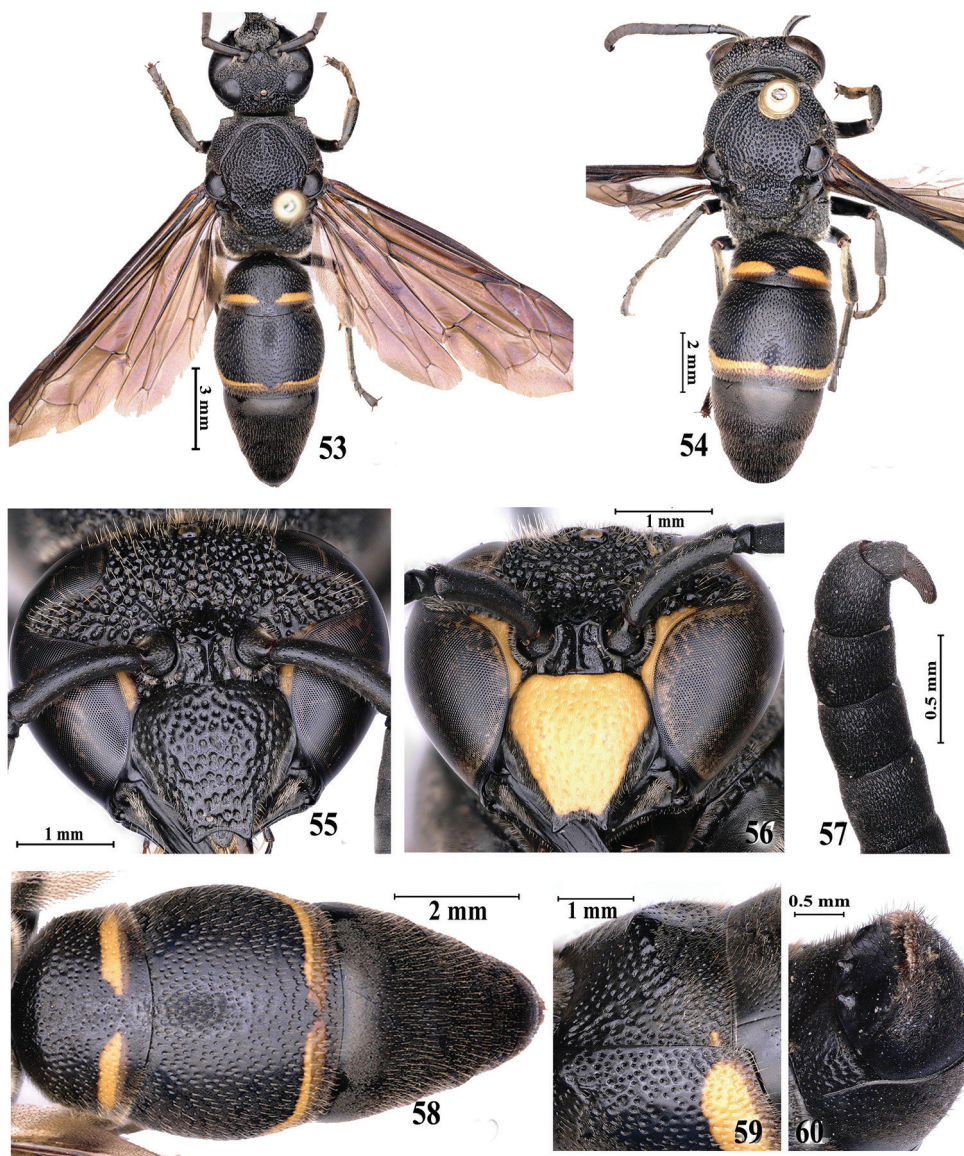
Allorhynchium quadrimaculatum Gusenleitner, 1997 new record

Figs 53–60

Allorhynchium quadrimaculatum Gusenleitner, 1997: 759; 2011: 1362; Tan et al. 2018: 49–64.

Material examined. 2♀♀, CHINA, Guangxi Prov., Baise City, Lingyun County, Yuhong Town, Hexiang Village, 24°29.355'N, 106°29.664'E, 791 m, 31.VII.2018, Yan Peng and Zhang Xue (CQNU); 1♀, CHINA, Guangxi Prov., Baise City, Lingyun County, Yuhong Town, Panxian Village, 24°28.157'N, 106°33.762'E, 964 m, 30.VII.2018, Zhang Xue and Han Qian (CQNU); 1♀, CHINA, Guangxi Prov., Guilin City, Longsheng County, Sanmen Town, 25°43.789'N, 109°51.905'E, 236 m, 17.VII.2018, Yan Peng and Xue Zhang (CQNU); 1♀, CHINA, Guangxi Prov., Guilin City, Xingan County, Huajiang Town, Gaozhai Village, 25°50.901'N, 110°28.976'E, 430 m, 19.VII.2015, Tingjing Li (CQNU); 1♀, CHINA, Guangxi Prov., Fangchenggang City, Shangsi County, Jaoanzhen Town, Shiwandashan National forest park, 22°06.404'N, 107°58.381'E, 280 m, 16.VIII.2017, Xudong Li (CQNU); 1♂, CHINA, Guangxi Prov., Hechi City, Huanjiang County, Chuanshan Town, Leyi Village, 25°07.015'N, 107°58.820'E, 533 m, 23.VII.2018, Yan Peng (CQNU); 1♀, CHINA, Sichuan Prov., Pengzhou City, Xiaoyudong Town, Luoyangba Village, 31°11.607'N, 103°45.290'E, 1013 m, 19.VII.2015, Zhang Xue and Han Qian (CQNU); 2♀♀1♂, CHINA, Guizhou Prov., Qiannan City, Libo County, Maolan National Nature Reserve, Dongdai Village, 25°23.408'N, 108°04.374'E, 576 m, 21.VI.2015, Tingjing Li and Yan Peng (CQNU); 1♀, CHINA, Yunnan Prov., Hekou County, Nanxi Town, 22°37.546'N, 103°56.892'E, 220 m, 19.VII.2015, Liang Wang (CQNU); 1♂, CHINA, Yunnan Prov., Hekou County, Nanxi Town, 22°37.546'N, 103°56.892'E, 220 m, 18.VII.2018, Chunfa Chen and Liping Zhao (CQNU).

Diagnosis. Body length 12.2–13.0 mm in female (Fig. 53), 11.9–12.3 mm in male (Fig. 54). Clypeus in female length and width equal, moderately punctate, entirely black, with apical margin strongly emarginate medially, apical width: emargination depth = 0.57: 0.10, total width: apical width = 1.7: 0.57 (Fig. 55); clypeus in male yellow, total width: apical width = 1.5: 0.55, apical margin moderately emarginate medially, apical width: emargination depth = 0.55: 0.12 (Fig. 56); A13 elongate, slightly curved and backward about reaching the middle of A11 (Fig. 57); anterior vertical face of pronotum with smooth; tegula not exceeding parategula; wings dark



Figures 53–60. *Allorhynchium quadrimaculatum* Gusenleitner, 1997 **53** habitus (dorsal view) ♀ **54** habitus (dorsal view) ♂ **55** clypeus, ♀ **56** clypeus, ♂ **57** apex of antenna, ♂ **58** metasoma (dorsal view), ♀ **59** S2, ♂ **60** S7, ♂.

brown, with purple luster; (apical yellow bands of T1 and T2 medially interrupted (Figs 53, 58); anterior surface of T1 rectangular in lateral view; S2 in male protruding medially into a transverse crest in lateral view (Fig. 59); S7 of male with pair of triangular teeth (Fig. 60).

Distribution. China (new record: Guangxi, Sichuan, Guizhou, Yunnan); Vietnam; Laos.

Key to the Chinese species of *Allorhynchium* van der Vecht*

- 1 T1 evenly rounded in lateral view and without transverse rim at junction of anterior and dorsal faces.....2
- T1 rather rectangular in lateral view and with transverse rim at junction of anterior and dorsal faces.....4
- 2 Occipital carina relatively wide laterally; clypeus of male entirely black.....*A. chinense* (de Saussure, 1862)
- Occipital carina narrower laterally than the above species; clypeus of male with yellow spots3
- 3 T1 and T2 with very small, sparse and thin punctures except lateral and apical portions.....*A. argentatum* (Fabricius, 1804)
- T1 and T2 with relatively bigger and denser punctures except lateral and apical portions.....*A. metallicum* (de Saussure, 1852)
- 4 Emargination of clypeal apex relatively wider and shallower (Figs 2, 12, 55, 56); S7 of male with two small teeth basally (Figs 7, 17, 60).....5
- Emargination of clypeal apex narrower and deeper, almost semicircular (Figs 23, 24, 32, 33, 40, 41, 49); S7 of male with three small teeth basally (Figs 28, 36, 46)7
- 5 Tegula reddish brown (Fig. 14); S7 of male with pair of flat lobe-shaped protuberances (Fig. 17)*A. lugubrinum* (Cameron, 1900)
- Tegula dark black (Figs 4, 5, 53, 54); S7 of male with pair of triangular teeth (Figs 7, 60)6
- 6 Wings dark brown, with purple luster (Fig. 53); S2 of male protruding medially into a short and high tuber (Fig. 59).....*A. quadrimaculatum* Gusenleitner, 1997
- Wings pale brown, without purple luster (Fig. 1); S2 of male protruding medially into a transverse high and strong crest (Fig. 6).....*A. menglianensis* (Dong & Wang, 2017) comb. nov.
- 7 Body almost black or with few yellow markings, T1 and T2 without apical bands or just with interrupted yellow apical bands or small spots (Figs 29, 30, 37, 38, 47); A13 in male elongate (Figs 34, 42); S2 protruding medially into a transverse crest or indistinctly convex (Figs 35, 43–45); apex of volsella round in frontal view (Figs 31, 39)*A. radiatum* Li, Barthélémy & Carpenter, 2019
- Body largely with yellow markings, both T1 and T2 with great wide yellow apical bands (Figs 20, 21, 31); A13 in male relatively shorter (Fig. 25); S2 protruding medially into a big, round and strong crest (Fig. 27); apex of volsella not round in frontal view (Fig. 22)*A. diffinis* (Giordani Soika, 1986)

* The characters are applicable to both sexes unless the sex is specified; the female of *A. menglianensis* (Dong & Wang, 2017) is unknown.

Acknowledgements

We are very grateful to Kunming Natural History Museum of Zoology (Kunming Institute of Zoology, Kunming, China) for helping us to take pictures of the type specimens deposited in KIZ. We thank Prof. James M. Carpenter (American Museum of Natural History, New York, USA) and Dr. P. Girish Kumar (Western Ghat Regional Centre, Zoological Survey of India, Kozhikode, India) for their important comments and providing copies of many references. This study was funded by the National Natural Science Foundation of China (Nos: 31772490, 31372247, 31000976), Young Talent Incubation Programme of Chongqing Normal University (14CSDG07).

References

- Abd-El-Samie EM, Elkafrawy I, Osama M, Ageez A (2018) Molecular phylogeny and identification of the Egyptian wasps (Hymenoptera: Vespidae) based on COI mitochondrial gene sequences. *Egyptian Journal of Biological Pest Control* 28(36): 2–7. <https://doi.org/10.1186/s41938-018-0038-z>
- Altschul S, Madden T, Schaffer A, Zhang J, Zhang Z, Miller W, Lipman D (1997) Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. *Nucleic Acids Research* 25: 3389–3402. <https://doi.org/10.1093/nar/25.17.3389>
- Ball SL, Hebert PDN (2005) Biological identification of mayflies (Ephemeroptera) using DNA barcodes. *Journal of the North American Benthological Society* 24(3): 508–524. <https://doi.org/10.1899/04-142.1>
- Cameron P (1900) Descriptions of new genera and species of Hymenoptera. *Annals and Magazine of Natural History* 6: 410–419. [495–506, 530–539] <https://doi.org/10.1080/00222930008678398>
- CBOL Plant Working Group (2009) A DNA barcode for land plants. *PANS* 106(31): 12794–12797. <https://doi.org/10.1073/pnas.0905845106>
- Ceccarelli FS, Sharkey MJ, Zaldívar-Riverón A (2012) Species identification in the taxonomically neglected, highly diverse, Neotropical parasitoid wasp genus *Notiospathius* (Braconidae: Doryctinae) based on an integrative molecular and morphological approach. *Molecular Phylogenetics and Evolution* 62(1): 485–495. <https://doi.org/10.1016/j.ympev.2011.10.018>
- Dasmahapatra KK, Elias M, Hill RI, Hoffman JI, Mallet J (2010) Mitochondrial DNA barcoding detects some species that are real, and some that are not. *Molecular Ecology Resources* 10(2): 264–273. <https://doi.org/10.1111/j.1755-0998.2009.02763.x>
- Dong DZ, Wang YZ (2017) Wasps Fauna of Yunnan. Henan Science and Technology Press, 215 pp.
- Fabricius JC (1804) *Systema Piezatorum, Secundum: Ordines, Genera, Species adiectis Synonymis, locis, observationibus, descriptionibus*. Apud Carolum Reichard Brunsvigae, 439 pp. <https://doi.org/10.5962/bhl.title.10490>

- Felsenstein J (1981) Evolutionary trees from DNA sequences: a maximum likelihood approach. *Journal of Molecular Evolution* 17(6): 368–376. <https://doi.org/10.1007/BF01734359>
- Fernandez-Triana J, Boudreault C, Dapkey T, Smith MA, Hallwachs W, Janzen D (2019) A revision of *Dolichogenidea* (Hymenoptera, Braconidae, Microgasterinae) with the second mediotergite broadly rectangular from Area de Conservación Guanacaste, Costa Rica. *ZooKeys* 835: 83–127. <https://doi.org/10.3897/zookeys.835.33440>
- Folmer O, Black M, Hoeh W, Lutz R, Vrijenhoek R (1994) DNA primers for amplification of mitochondrial cytochrome c oxidase subunit I from diverse metazoan. *Molecular marine biology and biotechnology* 5(3): 294–299.
- Giordani Soika A (1986) Eumenidi paleartic i nuovi o poco noti. *Bollettino del Museo Civico di Storia Naturale di Venezia* 35: 91–162.
- Giordani Soika A (1996) Eumenidi Orientali e Papuani Nuovi o Poco Noti. *Bollettino del Museo civico di storia naturale di Venezia* 45: 35–45.
- Girish Kumar P, Carpenter JM, Sureshan PM (2016) Additions to the knowledge of the genus *Allorhynchium* van der Vecht from the Indian subcontinent with the description of a new species from Kerala (Hymenoptera: Vespidae: Eumeninae). *Halteres* 7: 29–34.
- Girish Kumar P, Sharma G (2015) A review of the genus *Allorhynchium* van der Vecht, 1963 (Hymenoptera: Vespidae: Eumeninae) from the Indian subcontinent. *Prommalia* 3: 20–34.
- Gusenleitner J (1997) *Allorhynchium quadrimaculatum* nov. spec., eine neue Art aus Laos (Hymenoptera, Eumenidae). *Linzer Biologische Beiträge* 29: 759–761.
- Guindon S, Dufayard JF, Lefort V, Anisimova M, Hordijk W, Gascuel O (2010) New Algorithms and Methods to Estimate Maximum-Likelihood Phylogenies: Assessing the Performance of PhyML 3.0. *Systematic Biology* 59: 307–321. <https://doi.org/10.1093/sysbio/syq010>
- Hajibabaei M, Janzen DH, Burna JM (2006) DNA barcodes distinguish species of tropical Lepidoptera. *PNAS* 103(4): 968–971. <https://doi.org/10.1073/pnas.0510466103>
- Halim M, Aman-Zuki A, Syed Ahmad SZ, Mohammad Din AM, Abdul Rahima A (2018) Exploring the abundance and DNA barcode information of eight parasitoid wasps species (Hymenoptera), the natural enemies of the important pest of oil palm, bagworm, *Metisa plana* (Lepidoptera: Psychidae) toward the biocontrol approach and its application in Malaysia. *Journal of Asia-Pacific Entomology* (21): 1359–1365. <https://doi.org/10.1016/j.aspen.2018.10.012>
- Hebert PDN, Cywinska A, Ball SL, deWaard JR (2003) Biological identifications through DNA barcodes. *The Royal Society* 270: 313–321. <https://doi.org/10.1098/rspb.2002.2218>
- Hebert PDN, deWaard JR, Landry JF (2010) DNA barcodes for 1/1000 of the animal kingdom. *Biology letters* 6: 359–362. <https://doi.org/10.1098/rsbl.2009.0848>
- Kimura M (1980) A simple method for estimating evolutionary rate of base substitutions through comparative studies of nucleotide sequences. *Journal of Molecular Evolution* 16: 111–120. <https://doi.org/10.1007/BF01731581>
- Kishino H, Miyata T, Hasegawa M (1990) Maximum likelihood inference of protein phylogeny and the origin of chloroplasts. *Journal of Molecular Evolution* 31(2): 151–160. <https://doi.org/10.1007/BF02109483>
- Li TJ, Barthélémy C, Carpenter JM (2019) The Eumeninae (Hymenoptera, Vespidae) of Hong Kong (China), with description of two new species, two new synonymies and a key to

- the known taxa. *Journal of Hymenoptera Research* 72: 127–176. <https://doi.org/10.3897/jhr.72.37691>
- Moritz C, Cicero C (2004) DNA barcoding: promise and pitfalls. *PLOS Biology* 2: 1529–1531. <https://doi.org/10.1371/journal.pbio.0020354>
- Ratnasingham S, Hebert PND (2007) Bold: The Barcode of Life Data System. *Molecular Ecology Notes*: 1–10.
- Schindel DE, Miller SE (2005) DNA barcoding a useful tool for taxonomists. *Nature* 435(7038): 17–17. <https://doi.org/10.1038/435017b>
- Schmid-Egger C, Achterberg KV, Neumeyer R, Morinière J, Schmidt S (2017) Revision of the West Palearctic *Polistes* Latreille, with the descriptions of two species: an integrative approach using morphology and DNA barcodes (Hymenoptera, Vespidae). *ZooKeys* 713: 53–112. <https://doi.org/10.3897/zookeys.713.11335>
- Smith F (1861) Catalog of hymenopterous insects collected by Mr. A. R. Wallace in the islands of Batschian, Kaisaa, Amboyna, Gilolo and at Dory in New Guinea. *Journal of the Proceedings of the Linnean Society of London, Zoology* 5: 93–143. <https://doi.org/10.1111/j.1096-3642.1860.tb01022.x>
- Tamura K, Stecher G, Peterson D, Filipski A, Kumar S (2013) MEGA6: molecular evolutionary genetics analysis version 6.0. *Molecular Biology and Evolution* 30: 2725–2729. <https://doi.org/10.1093/molbev/mst197>
- Tan JL, van Achterberg C, He YF, Carpenter JM (2018) Northeast Asian *Allorhynchium* van der Vecht (Hymenoptera: Vespidae), with a key to Oriental species. *Zootaxa* 4434 (1): 49–64. <https://doi.org/10.11646/zootaxa.4434.1.3>
- van der Vecht J (1963) Studies on Indo-Australian and East Asiatic Eumenidae (Hymenoptera: Vespoidea). *Zoologische Verhandelingen Leiden* 60: 1–116.
- Zhang YZ, Zheng JT, Li HL, Fang Y, Zhu CD (2011) Vogler DNA barcoding of endoparasitoid wasps in the genus *Anicetus* reveals high levels of host specificity (Hymenoptera: Encyrtidae). *Biological Control* 58: 182–191. <https://doi.org/10.1016/j.biocontrol.2011.05.006>

Supplementary material I

Figure S1

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Data type: multimedia

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