

Research article

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***Biema* Huo & Zhao gen. nov., a new flower fly genus
(Diptera, Syrphidae) from China**Ke-Ke HUO ^{1,*,#}, Le ZHAO ^{2,#}, Ximo MENGUAL ^{3,#}, Gang LI ⁴,
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Abstract. A new flower fly genus (Diptera, Syrphidae), *Biema* Huo & Zhao gen. nov. from China is described based on two new species: *Biema wanglangensis* Huo & Zhao gen. et sp. nov. (designated as type-species) and *Biema qilianensis* Huo & Liu gen. et sp. nov. The new genus can easily be distinguished by the following morphological features: head, mesonotum and scutellum black; postpronotum without pile; metasternum not reduced, posterior margin shallowly concave; katepisternum only with ventral pile patches; alula narrow, as wide as basal width of cell c; male postabdomen conspicuously more swollen than other segments, surstylus and postgonite complex, phallus unsegmented. The results of our Bayesian inference and Maximum Likelihood analysis based on sequences of the Cytochrome *c*

oxidase subunit I (COI) gene, as well as the species delimitation tests, support the separation of *Biema* Huo & Zhao gen. nov. from its related taxa. Additionally, an identification key to the genera of the tribes Bacchini and Melanostomini occurring in China is provided.

Keywords. Syrphinae, Melanostomini, Bacchini, new genus, new species.

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Introduction

Among the most species-rich dipteran families, Syrphidae Latreille, 1802 (Insecta, Diptera) is well-known by nature enthusiasts and researchers because they provide several crucial ecosystem services (Dunn *et al.* 2020). Commonly known as flower or hover flies, syrphids are important pollinators, biological control agents of pests and recyclers of organic matter (Morales & Wolff 2010; Inouye *et al.* 2015; Arcaya *et al.* 2017; Moerkens *et al.* 2021). The family is currently divided into four subfamilies and 15 tribes (Mengual *et al.* 2015; Young *et al.* 2016).

The first scientific reference on the Chinese hover fly fauna was given by Sack (1922). To date, about 900 species of Syrphidae in 120 genera have been recorded in China (Huo 2020), but a better understanding of the Chinese syrphid fauna is needed.

The old concept of the tribe Bacchini Bigot, 1883 has recently been extensively discussed (Huo 2014; Thompson & Skevington 2014). The tribe as defined by Vockeroth (1992) for those syrphines with an unsegmented phallus is now divided into two tribes, i.e., Bacchini and Melanostomini Williston, 1885 (Mengual 2020). So far, two genera of Melanostomini have been recorded in China, i.e., *Melanostoma* Schiner, 1860 with eight species, and *Xanthandrus* Verrall, 1901 with three species (Cheng *et al.* 1998; Thompson & Rotheray 1998; Huo *et al.* 2007; Huo 2014). In the present work, the current knowledge on Chinese hover flies is expanded with the addition of a new genus and two new species belonging to Melanostomini. Moreover, an identification key to genera of Bacchini and Melanostomini recorded from China is also provided.

Material and methods

Collecting sites

Field work was carried out between 2016 and 2018 in the Wanglang National Nature Reserve, Sichuan Province, China. The reserve, located between 103°55'–104°10' E and 32°49'–33°02' N, belongs to the Palaearctic Region (Procheş & Ramdhani 2012) and was established in 1963 for giant panda protection. It has a total area of about 322.97 km², an elevation between 2300–4980 m and the average elevation is 3200 m. Collected specimens possess a distinctive and apomorphic combination of characters that identify them as a member of the bacchines *sensu lato*, but not concordant with any of the known genera (Vockeroth 1992). In 2021, we did another expedition to the Qilian Mountain National Park (2600–3248 m above sea level), Qinghai Province, China. The Qilian Mountain National Park also belongs to the Palaearctic Region and has a total area of 50 200 km² with a complex ecosystem of mountain forests, temperate desert grasslands, alpine meadows, and glacial snow-capped mountains. More unknown specimens, similar to the previous specimens collected from Sichuan Province in appearance, were collected. Figure 1 shows the location of the sampling site and it was created with the help of SimpleMapp (Shorthouse 2010).

Morphological examination

All specimens were generally pinned directly or stored in ethanol after collecting by hand net, then stored at Shaanxi University of Technology, Hanzhong, China (SNUT) and at the Zoologisches Forschungsmuseum Alexander Koenig, Bonn, Germany (ZFMK). The male genitalia were extracted using an insect pin with a hooked tip. Genitalia were cleared by boiling in tubes of water-diluted KOH pellets for 5 min and brief immersion in glacial acetic acid to neutralize the alkaline, then rinsed twice in ethanol to remove the acid before storage in microvials containing glycerol. Morphological terminology follows Thompson (1999). Body length is measured from the frontal prominence excluding antenna to the apex of the abdomen, wing length from the base to its apex, all presented in millimeters.

DNA extraction, sequencing and assembly

The mitochondrial cytochrome *c* oxidase subunit I (COI) gene has frequently been employed as a molecular marker for phylogenetic studies on Syrphidae, and it has been shown to be informative for both generic and species level studies (Radenković *et al.* 2020; Young *et al.* 2020). Thus, we generated the complete COI sequences of these two unknown taxa and compared the obtained sequences with all available sequences of other species from Bacchini and Melanostomini to test their systematic status. The genomic DNA extraction of *Biema wanglangensis* Huo & Zhao gen. et sp. nov. and *Biema qilianensis* Huo & Liu gen. et sp. nov. was done using the DNEasy kit (Qiagen, Hilden, Germany). One paired-end sequencing library (2×150 base pairs, bp) with insert sizes of 350 bp was constructed with VAHTS Universal DNA Library Prep Kit for Illumina V2 kit (Vazyme, Nanning, China) and sequenced on the Illumina HiSeq 4000 platform. The generated reads were filtered by the software fastp ver. 0.20.1 (Chen *et al.* 2018). After removing unpaired reads, adapter sequences, low-quality reads, and duplicated reads, the complete mitochondrial COI gene sequences of *B. wanglangensis* and *B. qilianensis* were assembled and annotated using the software Geneious R11 (Biomatters, New Zealand) (Kearse *et al.* 2012). The new generated mitogenomic data are submitted to GenBank (<https://www.ncbi.nlm.nih.gov/>) with the accession number starting with ON067497 and ON067496, respectively.

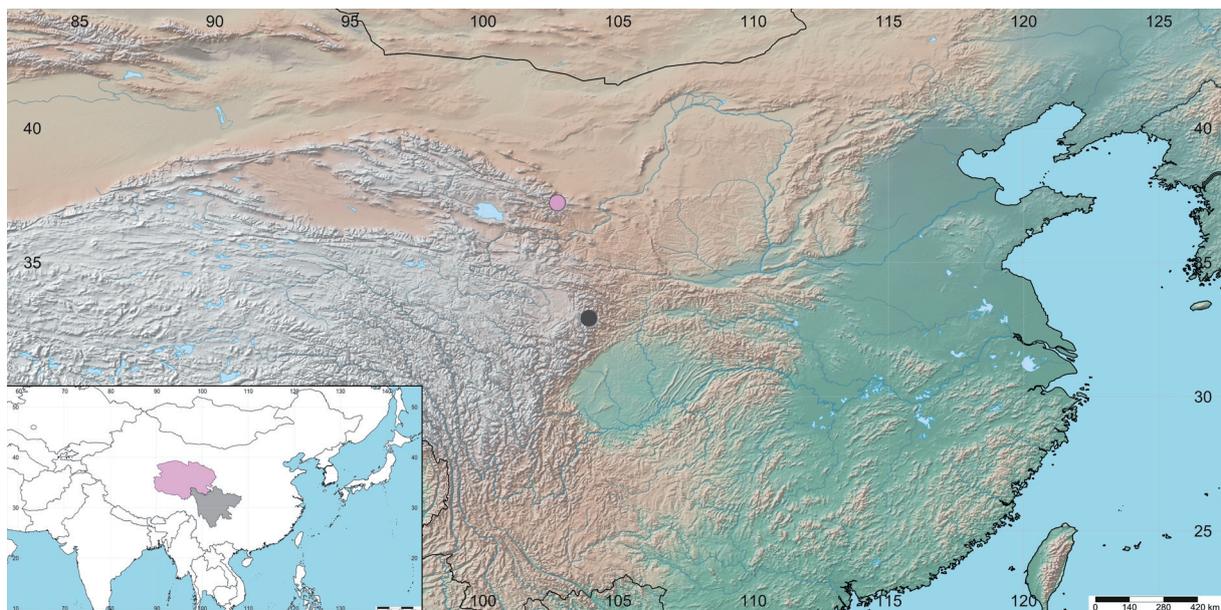


Fig. 1. Known distribution of genus *Biema* Huo & Zhao gen. nov. in China. Pink dot represents *Biema qilianensis* Huo & Liu gen. et sp. nov.; black dot represents *Biema wanglangensis* Huo & Zhao gen. et sp. nov.; pink area represents Sichuan Province, China; grey area represents Qinghai Province, China.

Molecular analysis

The genetic distances between species of Bacchini and Melanostomini were calculated with the software MEGA ver. 7 under a K2P model based on the COI dataset (Kimura 1980). For the General Mixed Yule-Coalescent Model (GMYC) analysis (Fujisawa & Barraclough 2013), an ultrametric tree was reconstructed by Beast ver. 2.6.2 (Bouckaert *et al.* 2014) using the GTR+ Γ +I model, a relaxed clock lognormal and Birth-death process, the resulting ultrametric tree was used for GMYC analyses on the web interface (<http://species.h-its.org/gmyc>) under the single-threshold method to generate the putative species. For the java Molecular Operational Taxonomic Units (jMOTU) analysis, the low BLAST identity filter was set to 97 and percentage of minimum sequence length to 95 in jMOTU ver. 4.1 (Jones *et al.* 2011). The automatic barcode gap discovery (ABGD) analysis (Puillandre *et al.* 2012) was performed on the web interface (<https://bioinfo.mnhn.fr/abi/public/abgd/abgdweb.html>) under Kimura (K80) TS/TV ver. 2.0 model with default parameters except the values of steps = 50, relative gap width (X) = 0.5. To infer the phylogenetic status of *Biema* Huo & Zhao gen. nov., we reconstructed the phylogenetic tree using the concatenated sequences data of COI sequences from 68 species of Bacchini and Melanostomini, and two species of genus *Episyrphus* Matsumura & Adachi, 1917 were used as outgroups. MAFFT ver. 7.429 was applied for sequences alignment with the E-INS-I strategy (Katoh & Standley 2013), and the aligned data matrix were trimmed by the software TrimAI ver. 1.2 (Capella-Gutiérrez *et al.* 2009). Phylogeny estimation was performed using Maximum Likelihood (ML) and Bayesian inference (BI) methods. PartitionFinder2 ver. 2.1.1 (Lanfear *et al.* 2017) was used to estimate the best substitution model and partitioning scheme selection for tree building. MrBayes ver. 3.2.7 (Ronquist *et al.* 2012) were used for Bayesian inference (BI) tree building, four simultaneous Markov chains were run for 10 million generations, with tree sampling occurring every 1000 generations and a burn-in of 25% of trees. Maximum Likelihood tree were reconstructed using IQ-tree ver. 2.0.3 (Nguyen *et al.* 2015) with 1000 bootstrap replicates.

Results

Taxonomy

Phylum Arthropoda Latreille, 1829
 Class Insecta Linnaeus, 1758
 Order Diptera Linnaeus, 1758
 Family Syrphidae Latreille, 1802
 Subfamily Syrphinae Newman, 1834

Genus *Biema* Huo & Zhao gen. nov.
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Type species

Biema wanglangensis Huo & Zhao gen. et sp. nov.

Diagnosis

Biema gen. nov. can be distinguished by the following morphological features: head deeply concave posteriorly with a concealed postpronotum; postpronotum without pile; head, mesonotum and scutellum black; metasternum not reduced, with posterior margin shallowly concave similar to that in *Platycheirus* Le Peletier & Serville, 1828; alula narrow, as wide as basal width of cell c; male postabdomen conspicuous more swollen than other segments, surstylus and postgonite complex, phallus unsegmented. In the identification key to bacchine and melanostomine groups by Thompson & Skevington (2014), the new genus keys out to couplet 2. Further, males of *Biema* key out to *Baccha* Fabricius, 1805 based on its short pilose antennal arista, unmodified hind tibia, distinct facial tubercle and bare metathoracic pleuron. Our

new genus can be easily distinguished from *Baccha* by the incomplete postmetacoxal bridge (complete postmetacoxal bridge in *Baccha*) and by the sparse but present scutellar fringe (absent in *Baccha*). Females of *Biema*, with a parallel-sided abdomen, key out to couplet 11 and are morphologically related to *Platycheirus*, *Argentinomyia* Lynch-Arribálzaga, 1891 and *Melanostoma*.

Etymology

The new genus is named after the Biema Zang people, who live where the type specimens were collected.

Description

Small sized flies. Head hemispherical. Eye bare. Vertex, frons and face black, densely white pollinose obscures ground colour. Facial tubercle rounded and produced, bare and shinning. Arista extremely short pilose. Antennal sockets confluent. Scutellum black, row of short bristles on posterior margin and one pair of bristles elongated in the middle. Katepisternum only with ventral patches. Metasternum not reduced, posterior margin shallowly concave similar to that in *Platycheirus*. Legs slender, not modified, hide-coxa without tuft of pile on anteromedial corner. Wing membrane entirely microtrichose. Vein R_{4+5} straight; spurious vein rudimentary; crossvein *r-m* slightly inclined, located before basal $\frac{1}{3}$ of cell *dm*; alula narrow, as wide as width of cell *c*. Male abdomen nearly parallel-sided, slightly constricted at tergite 2 posterior margin, broadened from tergite 3 and widest part at end of tergite 4, postabdomen conspicuous more swollen than other segments. Tergite 2 slightly longer than tergite 3, and tergite 3 slightly longer than tergite 4. Abdomen blackish brown with yellow maculae or fasciae. Male surstylus and postgonite complex, phallus unsegmented.

Biology and distribution

Biema gen. nov. occurs in forest areas, at or above 2300 m altitude in China (Sichuan, Qinghai) (Fig. 1).

Biema wanglangensis Huo & Zhao gen. et sp. nov.

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Figs 2–23

Diagnosis

Mesonotum sparsely light yellow pollinose, only thickened on lateral sides before transverse suture; pleuron and scutellum sparsely pollinose; male tergite 4 with dark brown or yellow broad median fascia; female tergites 3 and 4 with yellow fasciae, not extended to the anterior margin; female tergites 5 to 7 with yellow maculae basolaterally.

Etymology

The specific name is derived from the locality where type specimens were collected.

Material examined

Holotype

CHINA • ♂; Sichuan Province, Pingwu County, Wanglang Natural Reserve; 4 Aug. 2016; Ke-Ke Huo leg.; sub-alpine forest; specimen identifier: SYR-2016080001; SNUT.

Paratypes

CHINA • 6 ♂♂, 1 ♀; same collection data as for holotype; specimen identifiers: SYR-2016080002 to 2016080008; SNUT • 4 ♂♂, 3 ♀♀; same collection data as for holotype; Fei Lan Leg.; specimen identifiers: SYR-2016080009 to 2016080015; SNUT • 1 ♂, 1 ♀; same collection data as for holotype; 5 Aug. 2016; specimen identifiers: SYR-2016080016 to 2016080017; SNUT • 1 ♂; same collection data as for holotype; 5 Aug. 2016; Fei Lan Leg.; specimen identifier: SYR-2016080018; Genbank:

ON067497; SNUT • 11 ♂♂; same collection data as for holotype; 6 Aug. 2016; specimen identifiers: SYR-2016080019 to 2016080029; SNUT • 1 ♂; same collection data as for holotype; 5 Aug. 2017; specimen identifier: SYR-2016080030; SNUT • 1 ♂, 2 ♀♀; same collection data as for holotype; 6 Aug. 2017; Yan Bai leg.; specimen identifiers: SYR-2016080031 to 2016080033; ZFMK • 1 ♀; same collection data as for holotype; 6 Aug. 2017; Yan Bai leg.; specimen identifier: ZFMK-DIP-00097116; photographed in Figs 5–7; SNUT • 17 ♂♂; same collection data as for holotype; 9 Aug. 2017; specimen identifiers: SYR-2016080034 to 2016080050; ZFMK • 1 ♂; same collection data as for holotype; 9 Aug. 2017; specimen identifier: ZFMK-DIP-00097117; photographed in Figs 2–4; SNUT • 7 ♂♂; same collection data as for holotype; 9 Aug. 2017; Yan Bai leg.; specimen identifiers: SYR-2016080051 to 2016080057; SNUT • 3 ♂♂, 2 ♀♀; same collection data as for holotype; 10 Aug. 2017; specimen identifiers: SYR-2016080058 to 2016080062; ZFMK • 1 ♂, 1 ♀; same collection data as for holotype; 10 Aug. 2017; specimen identifiers: ZFMK-DIP-00097118 and ZFMK-DIP-00097119; SNUT • 1 ♀; same collection data as for holotype; 10 Aug. 2017; Yan Bai leg.; specimen identifiers: SYR-2016080065; SNUT.

Description

Male (Figs 2–4, 8–9, 11–12, 14–23)

MEASUREMENTS. Body length: 5 mm. Wing length: 5 mm.

HEAD (Figs 2–4, 8–9, 11). Hemispherical, deeply concave posteriorly with a concealed postpronotum. Eye bare, with eye contiguity longer than frons. Vertex slightly convex, black, yellow pilose and pollinose. Ocellar triangle equilateral, located at the anterior half of vertex. Occiput densely yellow pilose and pollinose on dorsal and upper half of lateral portions, yellowish white pilose and pollinose on lower half, obscures ground colour. Frons densely white pollinose obscures ground colour, short light



Figs 2–4. *Biema wanglangensis* Huo & Zhao gen. et sp. nov., paratype, ♂ (ZFMK-DIP-00097118). 2. Habitus, dorsal view. 3. Habitus, left lateral view. 4. Head, frontal view. Scale bars: 2–3 = 1 mm; 4 = 0.5 mm.

pile along the margins. Lunule narrow, light yellowish brown. Face almost vertical in lateral view, facial tubercle rounded and produced, anterior margin of oral open not pointed. Face black and densely white to light yellow pollinose obscures ground colour, facial tubercle and lateral oral margins shiny black and bare. Face short light pilose laterally. Gena densely light yellowish white pilose and pollinose. Antennal sockets confluent. Antenna light yellow; basoflagellomere dark brown dorsally; arista dark brown with extremely short pile, thickened basally.

THORAX (Figs 2–3). Black. Mesonotum metallic golden green, with subappressed short yellow pile; sparsely light yellow pollinose, thickened on lateral sides before transverse suture. Postpronotum light yellow pollinose. Scutellum shining black, metallic green, with subappressed short yellow pile, row of light yellow bristle-like pile on posterior margin and two pile elongated in middle. Subscutellar fringe short and sparse, absent medially. Pleuron shining black, light yellow pollinose. Posterior convex part of anepisternum and anterior anepimeron sparsely short yellow pilose. Katepisternum sparsely short yellow pilose, only with ventral pile patches. Metasternum not reduced, posterior margin shallowly concave similar to that in *Platycheirus*, yellow, bare.

LEGS (Figs 2–4). Light yellow to yellowish white; two apical tarsomeres of mid-tarsi light brown; hind-tibiae, hind-tarsi and apical ½ of hind-femora black to blackish brown, hind-knees and apical of hind-tibiae light yellow. Legs yellow pilose, apical three tarsomeres of tarsi dorsally black pilose.

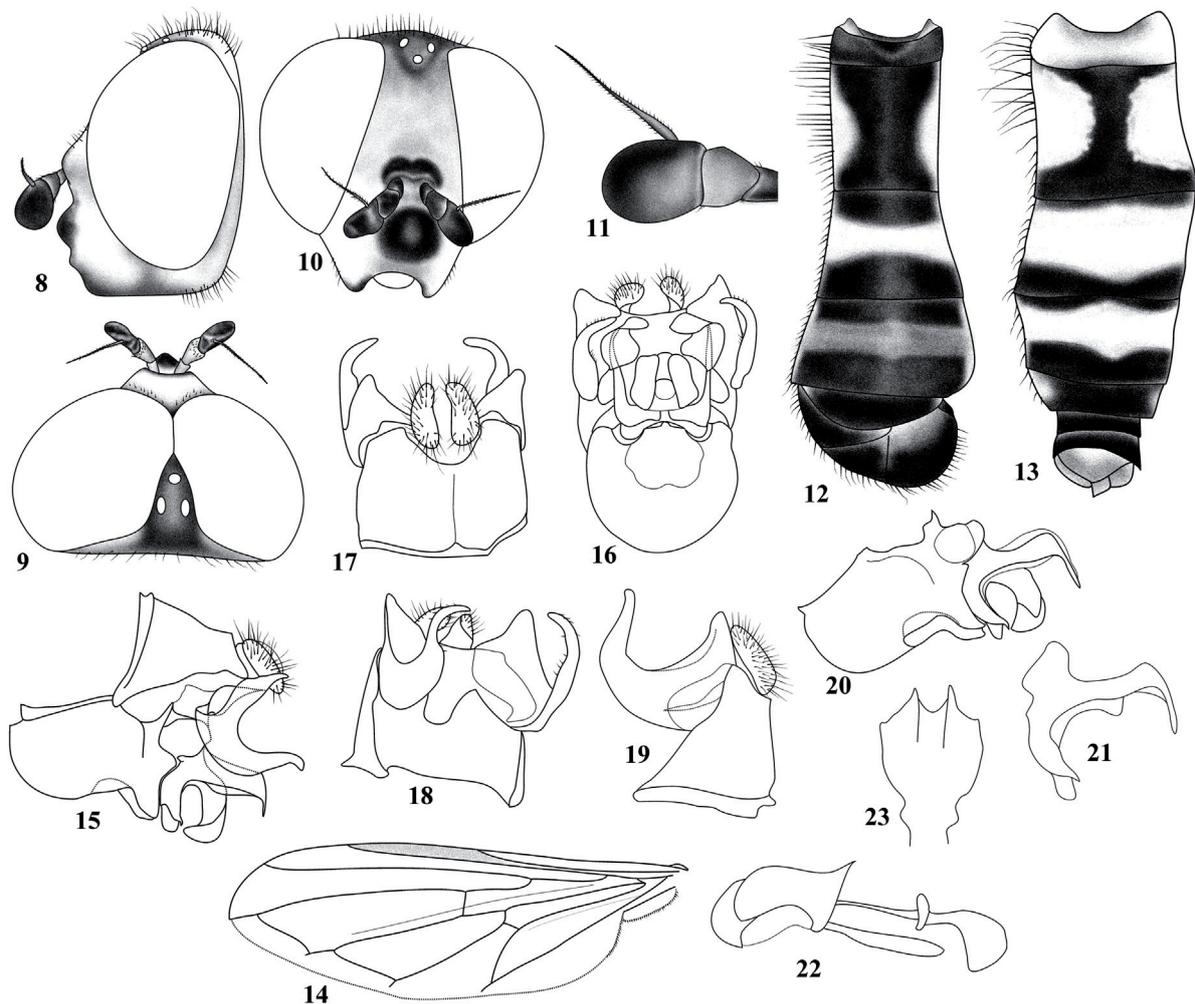
WING (Figs 2–3, 14). Transparent, stigma light yellow, membrane entirely microtrichose. Vein R_{4+5} straight, spurious vein rudimentary, corssvein $r-m$ slightly inclined, located before the basal ⅓ of cell dm . Vein M_1 bent basally and formed s-shaped slightly. Vein M_1 and vein $dm-cu$ parallel with wing margin.



Figs 5–7. *Biema wanglangensis* Huo & Zhao gen. et sp. nov., paratype, ♀ (ZFMK-DIP-00097119). 5. Habitus, dorsal view. 6. Habitus, left lateral view. 7. Head, frontal view. Scale bars: 5–6 = 1 mm; 7 = 0.5 mm.

Alula narrow, as wide as basal width of cell c. Calypters narrow, yellowish white. Halteres yellowish white, except yellowish green apically.

ABDOMEN (Figs 2–3, 12). Male abdomen parallel-sided, slightly constricted at tergite 2 posterior margin, broadened from tergite 3 and widest part at end of tergite 4, postabdomen conspicuous more swollen than other segments. Tergite 2 slightly longer than tergite 3, and tergite 3 slightly longer than tergite 4. Abdomen blackish brown, yellowish white to yellow laterally; tergite 2 with two triangular yellow markings merged into yellow lateral margin and broadly separated on inner end; tergite 3 with broad median yellow fascia, sometime interrupted medially; tergite 4 with dark broad median brown fascia, sometimes absent. Terminalia yellowish brown. Tergites with light yellow pile on lateral margin, appressed black pile medially. Sternites light pilose; sternites 1 and 2 yellowish white, 3 and 4 brownish yellow.



Figs 8–23. *Biema wanglangensis* Huo & Zhao gen. et sp. nov. **8.** Male, head in lateral view. **9.** Male, head in dorsal view. **10.** Female, head in frontal view. **11.** Antenna, inside view. **12.** Male, abdomen in dorsal view. **13.** Female, abdomen in dorsal view. **14.** Wing. **15.** Male, terminalia in lateral view. **16.** Male, terminalia in ventral view. **17.** Male, epandrium and appendages in dorsal view. **18.** Male, epandrium and appendages in ventral view. **19.** Male, epandrium and appendages in lateral view. **20.** Male, hypandrium and appendages in lateral view. **21.** Superior lobe in lateral view. **22.** Phallus. **23.** Distal end of phallus in dorsal view.

MALE TERMINALIA (Figs 15–23). Dark brown. Cercus small, weakly sclerotized, with yellow pile. Epandrium nearly quadrilateral in lateral view, broad slightly longer than high, basal margin broader than apical margin. Surstylus triangular in dorsal view, broadened basally, then gradually narrowed ventrad, with apex acute, and bent posterodorsally; in posterior view expanded into broad triangle towards middle line along posterior margin of epandrium, with pile on inner margin. Hypandrium circular and expanded basally, with transparent circular membrane area on postmedial portion ventrally, without lingula. Postgonite divided into dorsal and ventral branches, dorsal branch broadly striped, transparent on margins, with circular apex, bent posteroventrally in middle right angled. Ventral branch narrowly striped, expanded posteroventrally. Phallus unsegmented, with 2 ridges dorsally, apical end of ridges pointed.

Female (Figs 5–7, 10, 13)

MEASUREMENTS. Body length: 5 mm. Wing length: 5 mm.

HEAD (Figs 5–7, 10). Vertex and frons densely gray yellow pollinose and yellow pilose, with blackish brown spot in front of lunule. Antenna dark brown.

LEGS. Tarsi with black pile dorsally.

ABDOMEN (Figs 5–6, 13). Abdomen parallel-sided, blackish brown, yellow laterally. Tergite 1 yellow or dark brown. Tergite 2 with lateral yellow markings medially, separated at inner ends and merged into lateral yellow. Tergites 3 and 4 with broad anterior yellow fasciae, with its anterior and posterior margins projecting medially. Tergites 5 to 7 yellow laterally. Sternites yellowish white, with light pile. Female terminalia brownish yellow. Remainder similar to male.

Immature stages

Unknown.

Distribution

This species was collected from sub-alpine forest at Wanglang National Nature Reserve, Pingwu County, Sichuan Province, China (103°55′–104°10′ E, 32°49′–33°02′ N, 2300–4980 m a.s.l.) during 2016–2018 (Fig. 24).

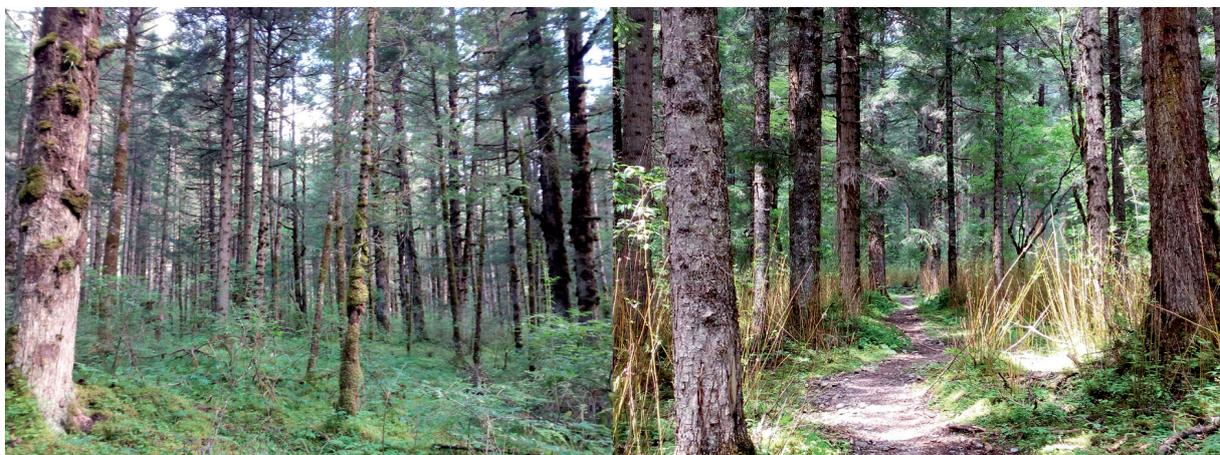


Fig. 24. The ecological environment of *Biema wanglangensis* Huo & Zhao gen. et sp. nov. collection area in China.

Biema qilianensis Huo & Liu gen. et sp. nov.

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Figs 25–41

Diagnosis

Mesonotum densely pollinose, anterior area with one pair of inconspicuous submedial pollinose vittae extended posteriad of transverse suture; scutellum densely pollinose; male tergite 4 without macula or with a small yellow macula/fascia anteromedially; female tergites 2 to 7 with broad yellow fasciae, extended to the anterior margin of tergites.

Etymology

The specific name is derived from the locality where the type specimens were collected.

Material examined

Holotype

CHINA • ♂; Qinghai Province, Menyuan County, Zhugu village, Sigou township; 24 Jul. 2021; Ke-Ke Huo leg.; sub-alpine forest; specimen identifier: SYR-2021070001; SNUT.

Paratypes

CHINA • 1 ♂; same collection data as for holotype; Xin Liu leg.; Genbank: ON067496; specimen identifier: SYR-2021070002; SNUT • 6 ♂♂; same collection data as for holotype; 28 Jul. 2021; Xin Liu leg.; specimen identifiers: SYR-2021070003 to 2021070008; SNUT • 1 ♂; Qinghai Province, Menyuan County, Xianmi village, Qihankai Nature reserve; 30 Jul. 2021; Xin Liu leg.; specimen identifiers SYR-2021070009; SNUT • 1 ♀; Qinghai Province, Menyuan County, Xianmi village, Meihua township; 30 Jul. 2021; Xin Liu leg.; specimen identifiers: SYR-2021070010.

Description

Male (Figs 25, 27–29, 31–41)

MEASUREMENTS. Body length: 5 mm. Wing length: 5 mm.

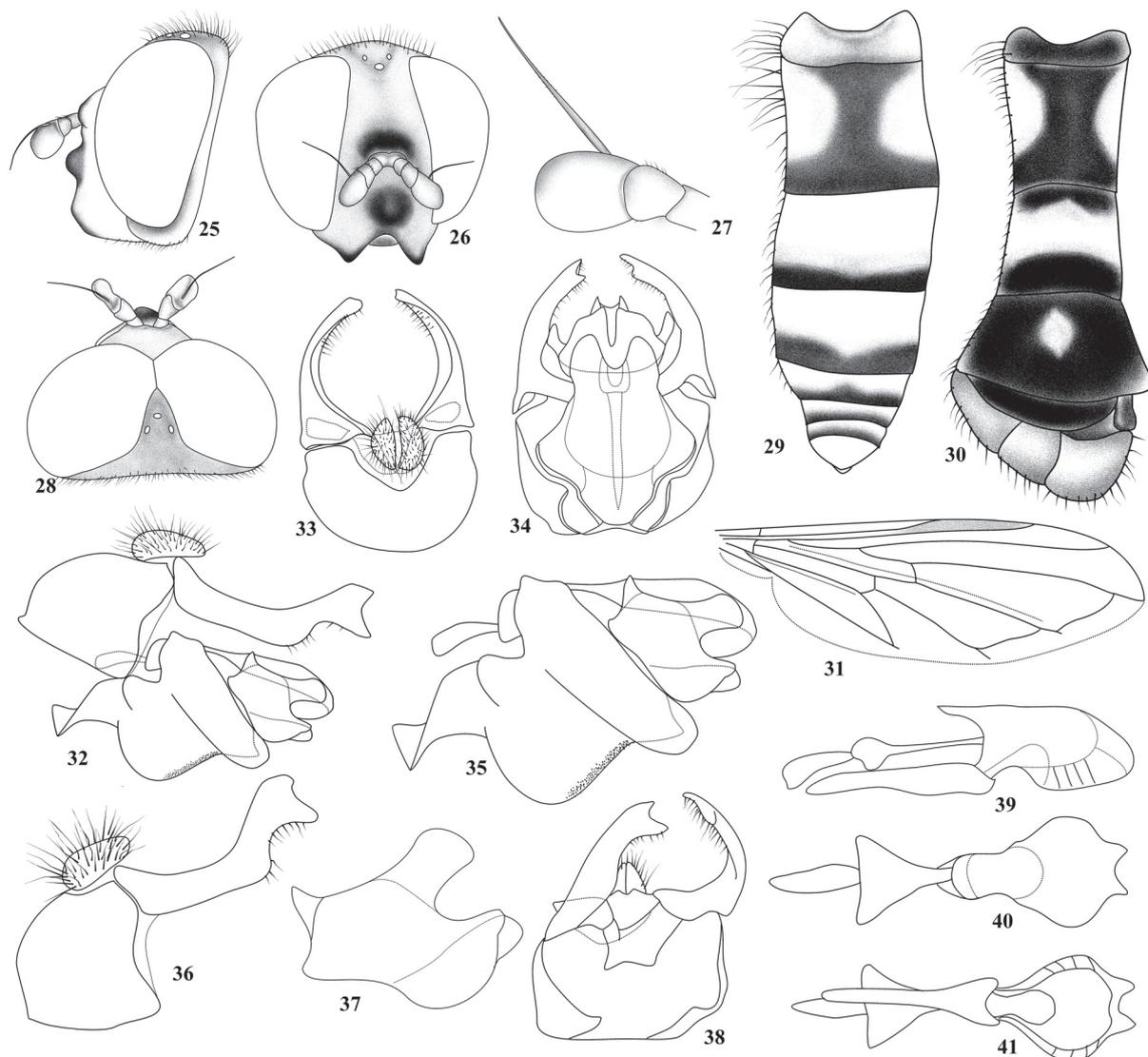
HEAD (Figs 25, 27–28). Hemispherical, deeply concave posteriorly with concealed postpronotum. Eye bare, with eye contiguity longer than frons. Vertex slightly convex, black, yellow pilose and pollinose. Ocellar triangle equilateral, located at anterior half of vertex. Occiput densely yellow pilose and pollinose on dorsal and upper half of lateral portions, yellowish white pilose and pollinose on lower half of lateral portions, obscures ground colour. Frons densely white pollinose obscures ground colour, short light pile along eye margins. Lunule narrow, light yellowish brown. Face almost vertical in lateral view, facial tubercle rounded and produced, anterior margin of oral open not pointed. Face black, densely white to light yellow pollinose obscures ground colour, facial tubercle and lateral oral margins shining black and bare. Face short light pilose laterally. Gena densely light yellowish white pilose and pollinose. Antennal sockets confluent. Antenna light yellow; basoflagellomere dark brown dorsally; arista dark brown with extremely short pile, thickened basally.

THORAX. Black. Mesonotum metallic golden green, subappressed short yellow pilose, light yellow pollinose and thickened laterally, anterior area with one pair of inconspicuous submedial pollinose vittae extended posteriad of transverse suture. Postpronotum light yellow pollinose. Scutellum shining black, metallic golden green, subappressed short yellow pilose, row of light yellow bristle-like pile on posterior margin and two pile elongated in middle. Subscutellar fringe short and sparse, central area of posterior margin bare. Pleuron shining black, light yellow pollinose. Posterior convex part of anepisternum and anterior anepimeron sparsely short yellow pilose. Katepisternum sparsely short yellow pilose, only with

ventral pile patches. Metasternum not reduced, with posterior margin shallowly concave similar to that in *Platycheirus*, yellow, bare.

LEGS. Light yellow to yellowish white; two apical tarsomeres of mid-tarsi light brown; hind-tibiae, hind-tarsi and apical $\frac{1}{2}$ to $\frac{2}{3}$ of hind-femora black to blackish brown, hind-knees and apical of hind-tibiae light yellow. Yellow pilose.

WING (Fig. 31). Transparent, stigma light yellow, membrane entirely microtrichose. Vein R_{4+5} straight, spurious vein rudimentary, corssvein $r-m$ slightly inclined, located before basal $\frac{1}{3}$ of cell dm . Vein M_1



Figs 25–41. *Biema qilianensis* Huo & Liu gen. et sp. nov. **25.** Male, head in lateral view. **26.** Female, head in frontal view. **27.** Antenna, inside view. **28.** Male, head in dorsal view. **29.** Female, abdomen in dorsal view. **30.** Male, abdomen in dorsal view. **31.** Wing. **32.** Male, terminalia in lateral view. **33.** Male, epandrium and appendages in dorsal view. **34.** Male, terminalia in ventral view. **35.** Male, hypandrium and appendages in lateral view. **36.** Male, epandrium and appendages in lateral view. **37.** Male, superior lobe in lateral view. **38.** Male, epandrium and appendages in ventral view. **39.** Phallus in lateral view. **40.** Phallus in dorsal view. **41.** Phallus in ventral view.

bent basally and formed s-shaped slightly, Vein M_1 and vein *dm-cu* parallel with wing margin. Alula narrow, as wide as basal width of cell c. Calypters narrow, yellowish white. Halteres yellowish white, except yellowish green apically.

ABDOMEN (Fig. 29). Male abdomen parallel-sided, slightly constricted at tergite 2 posterior margin, broadened from tergite 3 and the widest part at the end of tergite 4, postabdomen conspicuous more swollen than other segments. Tergite 2 slightly longer than tergite 3, and tergite 3 slightly longer than tergite 4. Abdomen blackish brown, yellowish white to yellow laterally; tergite 2 with two triangular yellow markings merged into yellow lateral margin and broadly separated on inner end; tergite 3 with yellow broad median fascia, sometime interrupted medially; tergite 4 without macula, sometime with median small yellow macula or fascia anteriorly. Terminalia yellowish brown. Tergites with light yellow pile on lateral margin and appressed black pile medially. Sternites light pilose; sternites 1 and 2 yellowish white, 3 and 4 brownish yellow.

MALE TERMINALIA (Figs 32–41). Yellowish brown. Cercus small, weakly sclerotized, yellowish brown with yellow pile. Epandrium nearly quadrilateral in lateral view, slightly longer than high, with the dorsal margin slightly convex. Surstylus elongated, slightly expanded inwards basodorsally, narrowly stripe-like in lateral view, dorsal and ventral margins at basal $\frac{2}{3}$ nearly parallel, apical $\frac{1}{3}$ bent posterodorsally, ventral margin with circularly concave, apical with two triangular dentate-shaped point, inner surface with short brown setae. Hypandrium rounded and enlarged, with short brown setae posteroventrally and concave posteromedial margin. Postgonite bluntly basodorsally with a prominent tooth in lateral view, posterior part divided into dorsal and ventral branches, dorsal branch blunt and broad apically, ventral branch slightly sharp apically with dentate-shaped towards midline. Phallus unsegmented, in lateral view bluntly rounded apically, in dorsal view enlarged medially, arc-shaped laterally, two dentate-shaped apically, arc-shaped between dentate-shape.

Female (Figs 26, 30)

MEASUREMENTS. Body length: 5 mm. Wing length: 5 mm.

HEAD (Fig. 26). Vertex and frons densely gray yellow pollinose and yellow pilose, with a blackish brown spot in the front of lunule. Antenna dark brown.

LEGS. Tarsi with black pile dorsally.



Fig. 42. The ecological environment of *Biema qilianensis* Huo & Liu gen. et sp. nov. collection area in China.

ABDOMEN (Fig. 30). Abdomen parallel-sided, blackish brown, yellowish laterally. Tergite 1 yellow or dark brown. Tergite 2 with lateral yellow spots medially, separated at the inner ends and merged into lateral yellow. Tergites 3 to 7 with broad yellow fasciae, anterior border of fasciae contacts anterior margin of tergites, covering about $\frac{2}{3}$ of tergites 3 and 4, about $\frac{1}{2}$ of tergites 5 to 7. Sternites yellow with light pile. Remainder similar to male.

Immature stages

Unknown.

Distribution

This species was obtained from sub-alpine forest at Qilian Mountain National Park, Qinghai Province, China (102°24' E, 37°7' N, 2600–3248 m above sea level) (Fig. 42).

Molecular analyses

The mtDNA COI dataset comprised 1539 nucleotides with 552 variable and 426 parsimony informative sites for 68 Bacchini and Melanostomini taxa and two outgroups. *Biema wanglangensis* gen. et sp. nov. was found to have a 2.93% sequence divergence from *Biema qilianensis* gen. et sp. nov., and averaged 11.54% divergent from other species of Bacchini and Melanostomini (Supp. file 1: Table S1). Based on the COI gene, all three species delimitation methods consistently supported our morphological results and the newly described species *Biema wanglangensis* and *Biema qilianensis* were well supported as two distinct and separate taxa (Fig. 43). Both the consensus trees inferred using BI and ML analyses produced an identical topological structure, where the placement of *Biema* gen. nov. was clearly distinct from other taxa and recovered as a highly supported monophyletic clade within tribe Melanostomini (PP = 100, BS = 100), but the phylogenetic relationships amongst genera *Biema*, *Melanostoma* and *Argentinomyia* are unclear.

Identification key to genera of the tribes Bacchini and Melanostomini in China

1. Abdomen slender, usually petiolate, with the second abdominal segment 2 narrower than the tergite 3 2
– Abdomen usually parallel-sided or oval 3
2. Abdomen elongate, strongly petiolate, with abdominal segments 2 and 3 obviously narrower than scutellum *Baccha* Fabricius, 1805 (There are three species distributed in China)
– Abdomen short, with abdominal segment 2 as wide as scutellum, segment 3 wider than scutellum. Arista plumose. Face black *Spazigaster* Rondani, 1843 (Only one species distributed in China)
3. Metepisternum with subappressed fine pile. Katepisternum with upper and lower pile patches joined anteriorly, broadly separated posteriorly; hind coxa with a tuft of pile at posteromedial apical angle *Xanthandrus* Verrall, 1901 (There are three species distributed in China)
– Metepisternum bare. Katepisternum with pile patches broadly separated thoroughly. Hind coxa without a tuft of pile at posteromedial angle 4
4. The widest part of abdomen at the end of abdominal segment 4, postabdomen conspicuous more swollen to a large volume than other segments in male. Alula narrow, as wide as basal width of cell c *Biema* Huo & Zhao gen. nov. (There are two species distributed in China)
– Postabdomen not swollen in male. Alular lobe broader than width of cell c 5
5. Metasternum greatly reduced, with deep posterior incision laterally so that sclerotized portion consists of median diamond-shaped area with narrow anterior and lateral strips. Face not produced

- below, with small facial tubercle. Male legs slender, without bristles, pile tufts or modified pile
 *Melanostoma* Schiner, 1860 (There are eight species distributed in China)
- Metasternum not reduced, posterior margin shallowly concave, without distinct incision. Face straight or with undeveloped facial tubercle, moderately or strongly produced forwards and/or ventrally below. Legs in male sometimes broadened and flattened, or with specialized bristles, pile tufts or modified pile 6
6. Frons, mesonotum and scutellum irregularly wrinkled by coarse punctations. Face widened downwards in male. Abdomen with patterns of light colour
 *Rohdendorfia* Smirnov, 1924 (Only one species distributed in China)
- Body smooth, or with fine punctuations, but not wrinkled 7
7. Wing shorter than abdomen. Abdomen broadened, red in most part, or black with two enlarged yellow spots on tergite 3 ... *Pyrophaena* Schiner, 1860 (There are two species distributed in China)
- Wing longer than abdomen. Abdomen narrow, without spots as above. Legs sometimes with modified pile, pile tuft or bristles in male and flattened and broadened anterior tibiae and tarsi
 *Platycheirus* Le Peletier & Serville, 1828 (There are 25 species distributed in China)

Discussion

The discovery of a new flower fly genus, *Biema* gen. nov., with two new species presented in this study increases the knowledge not only of the Chinese syrphids, but also gives valuable data on Bacchini and Melanostomini species in the Palaearctic Region.

Based on the key of Vockeroth (1992), *Biema* gen. nov. belongs to the old concept of the tribe Bacchini with the following synapomorphies: head, mesonotum and scutellum black; deeply concave posteriorly with a concealed postpronotum; postpronotum bare; and phallus unsegmented. Further, in the Palaearctic key of genera by Thompson & Rotheray (1998), *Biema* keys out to couplet 52 and runs close to *Melanostoma*, *Platycheirus* and *Xanthandrus*, but *Biema* has an entire metasternum (greatly reduced in the species of *Melanostoma* found in China), only ventral pile patches on katapisternum (pile patches broadly separated posteriorly on katapisternum in *Xanthandrus*), narrow alula as broad as costal cell (broader in *Platycheirus*). In addition, as mentioned in the diagnosis, males of *Biema* can key out to the group of genera with petiolate abdomens (Thompson & Skevington 2014), and it is easy to distinguish from *Baccha*, *Spazigaster* Rondani, 1843 and *Leucopodella* Hull, 1949 by its short pilose antennal arista, unmodified hind tibia, distinct facial tubercle, bare metathoracic pleuron, and complete postmetacoxal bridge.

In our inferred topologies based on the COI gene, *Biema* gen. nov. is resolved within the tribe Melanostomini and clearly distinct from other congeners, but the phylogenetic relationships amongst the genera *Biema*, *Melanostoma* and *Argentinomyia* are not fully resolved. Although the accurate taxonomic status of these three genera needs to be revised by further works with extended species sampling and morphological or molecular data, the genus *Biema* can be well distinguished from *Melanostoma* and *Argentinomyia* based on morphological characters. The differences between *Biema* and *Melanostoma* were described above; moreover, *Argentinomyia* is mainly distributed in the Neotropical Region and can be distinguished from *Biema* by the following morphological features: scape elongate, about twice as long as pedicel; antennal pits separated; subscutellar fringe complete; wing membrane broadly bare basally (cells *r* and *bm* bare), microtrichose apically; alula broad; regular-sized terminalia with triangular to rectangular superior lobes, or irregular in shape.

Regarding the two new species, *Biema wanglangensis* gen. et sp. nov. and *Biema qilianensis* gen. et sp. nov., diagnostic characters are found in the male genitalia (especially the hypandrium, surstylus,

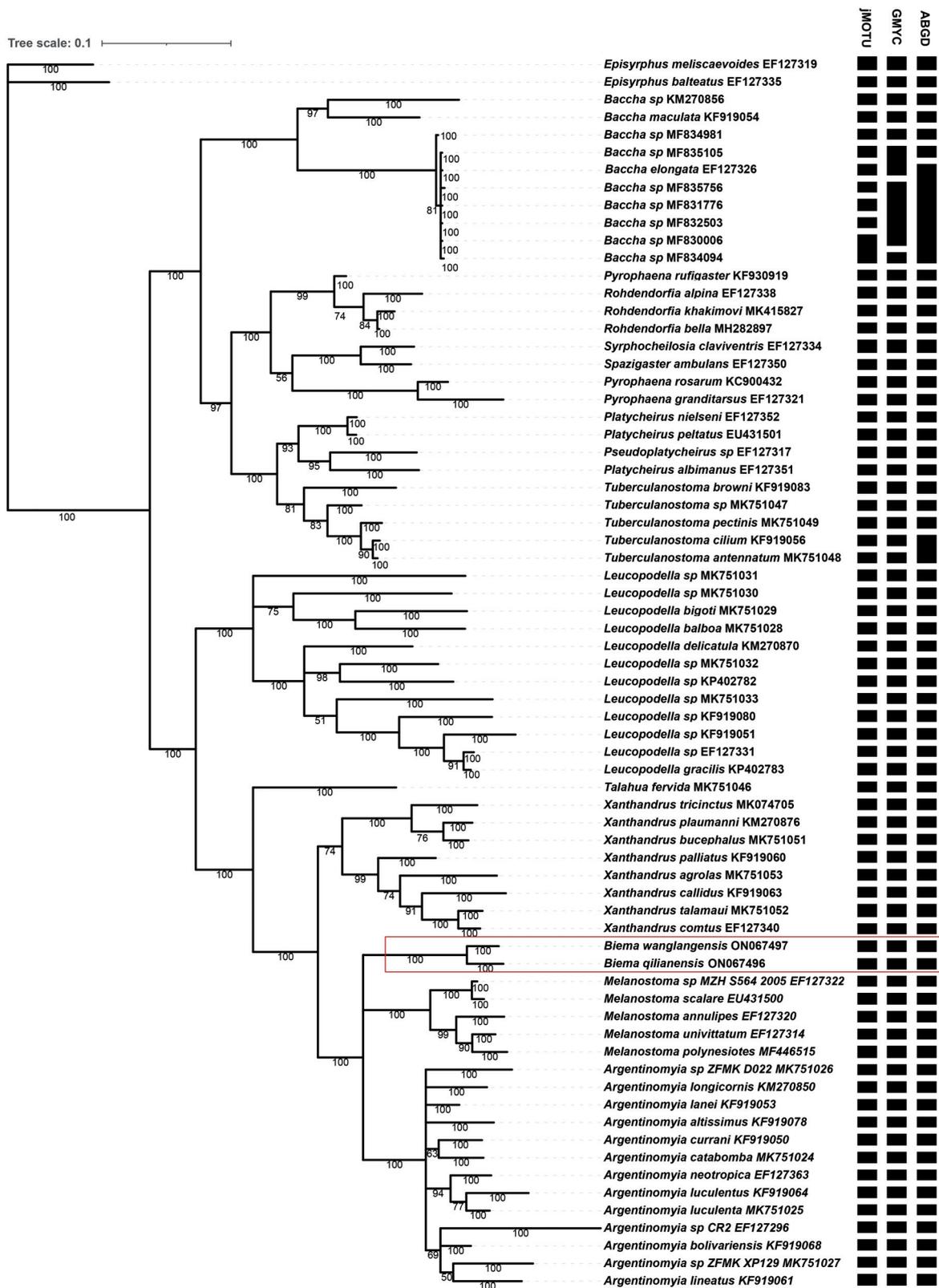


Fig. 43. The phylogenetic tree of the tribes Bacchini Bigot, 1883 and Melanostomini Williston, 1885 based on the COI gene. Statistical support values (posterior probability) of BI methods are shown above each node. Groups resulting from jMOTU, GMYC and ABGD tests are indicated on the right side.

postgonite and apical end of phallus) and the abdominal pattern. In addition to the adult morphological analysis, we used COI sequences to test the delimitation of species of *Biema* gen. nov. within the tribes of Bacchini and Melanostomini, all three species delimitation approaches (ABGD, GMYC and jMOTU) also recognized the newly proposed two species of *Biema* as two separate groups from other studied taxa.

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References

- Arcaya E., Pérez-Bañón C., Mengual X., Zubcoff-Vallejo J.J. & Rojo S. 2017. Life table and predation rates of the syrphid fly *Allograpta exotica*, a control agent of the cowpea aphid *Aphis craccivora*. *Biological Control* 115: 74–84. <https://doi.org/10.1016/j.biocontrol.2017.09.009>
- Bouckaert R., Heled J., Kühnert D., Vaughan T., Wu C.-H., Xie D., Suchard M.A., Rambaut A. & Drummond A.J. 2014. BEAST 2: a software platform for Bayesian evolutionary analysis. *PLoS Computational Biology* 10 (4): e1003537. <https://doi.org/10.1371/journal.pcbi.1003537>
- Capella-Gutiérrez S., Silla-Martínez J.M. & Gabaldón T. 2009. trimAl: a tool for automated alignment trimming in large-scale phylogenetic analyses. *Bioinformatics* 25 (15): 1972–1973. <https://doi.org/10.1093/bioinformatics/btp348>
- Chen S., Zhou Y., Chen Y. & Gu J. 2018. Fastp: an ultra-fast all-in-one FASTQ preprocessor. *Bioinformatics* 34 (17): i884–i890. <https://doi.org/10.1093/bioinformatics/bty560>
- Cheng X.Y., Huang C.M. & Yang J.K. 1998. Syrphidae. In: *Flies of China*: 118–223. Liaoning Science and Technology Press, Shengyang, China.
- Dunn L., Lequerica M., Reid C. & Latty T. 2020. Dual ecosystem services of syrphid flies (Diptera: Syrphidae): pollinators and biological control agents. *Pest Management Science* 76 (6): 1973–1979. <https://doi.org/10.1002/ps.5807>
- Fujisawa T. & Barraclough T.G. 2013. Delimiting species using single-locus data and the generalized mixed Yule coalescent approach: a revised method and evaluation on simulated data sets. *Systematic Biology* 62 (5): 707–724. <https://doi.org/10.1093/sysbio/syt033>
- Huo K.K. 2014. *Spazigasteroides* a new genus from China with a black face and scutellum in the Syrphini (Diptera: Syrphidae). *Zootaxa* 3755 (3): 230. <https://doi.org/10.11646/zootaxa.3755.3.2>
- Huo K.K. 2020. Syrphidae. In: *Species Catalogue of China. Volume 2. Animals. Insecta. Diptera (3). Cyclorrhaphous Brachycera (i)*: 30–181. Science Press.

- Huo K.K., Ren G.D. & Zheng Z.M. 2007. *Fauna of Syrphidae from Mt. Qinling-Bashan in China (Insecta: Diptera)*. Chinese Agricultural Science and Technology Press, Beijing.
- Inouye D.W., Larson B.M.H., Ssymank A. & Kevan P.G. 2015. Flies and flowers III: ecology of foraging and pollination. *Journal of Pollination Ecology* 16: 115–133.
[https://doi.org/10.26786/1920-7603\(2015\)15](https://doi.org/10.26786/1920-7603(2015)15)
- Jones M., Ghoorah A. & Blaxter M. 2011. jMOTU and Taxonator: turning DNA barcode sequences into annotated Operational Taxonomic Units. *PLoS ONE* 6 (4): e19259.
<https://doi.org/10.1371/journal.pone.0019259>
- Katoh K. & Standley D.M. 2013. MAFFT multiple sequence alignment software version 7: improvements in performance and usability. *Molecular Biology and Evolution* 30 (4): 772–780.
<https://doi.org/10.1093/molbev/mst010>
- Kearse M., Moir R., Wilson A., Stones-Havas S., Cheung M., Sturrock S., Buxton S., Cooper A., Markowitz S., Duran C., Thierer T., Ashton B., Meintjes P. & Drummond A. 2012. Geneious Basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. *Bioinformatics* 28 (12): 1647–1649. <https://doi.org/10.1093/bioinformatics/bts199>
- Kimura M. 1980. A simple method for estimating evolutionary rates of base substitutions through comparative studies of nucleotide sequences. *Journal of Molecular Evolution* 16 (2): 111–120.
<https://doi.org/10.1007/BF01731581>
- Lanfear R., Frandsen P.B., Wright A.M., Senfeld T. & Calcott B. 2017. Partitionfinder 2: new methods for selecting partitioned models of evolution for molecular and morphological phylogenetic analyses. *Molecular Biology and Evolution* 34 (3): 772–773. <https://doi.org/10.1093/molbev/msw260>
- Le Peletier A.L.M. & Serville J.G.A. 1828. Entomologie, ou histoire naturelle des Crustacés, des Arachnides et des Insectes. *Encyclopédie méthodique. Histoire naturelle des animaux* 10: 1–833.
<https://doi.org/10.5962/bhl.title.82248>
- Matsumura S. & Adachi J. 1917. Synopsis of the economic Syrphidae of Japan. *The Entomological Magazine, Kyoto* 2 (4): 133–156.
- Mengual X. 2020. Phylogenetic relationships of the bacchine flower flies (Diptera: Syrphidae) based on molecular characters, with a description of a new species of *Melanostoma* (Schiner, 1860). *Contributions to Zoology* 89 (2): 210–244. <https://doi.org/10.1163/18759866-20191410>
- Mengual X., Ståhls G. & Rojo S. 2015. Phylogenetic relationships and taxonomic ranking of pipizine flower flies (Diptera: Syrphidae) with implications for the evolution of aphidophagy. *Cladistics* 31 (5): 491–508. <https://doi.org/10.1111/cla.12105>
- Moerkens R., Boonen S., Wäckers F.L. & Pekas A. 2021. Aphidophagous hoverflies reduce foxglove aphid infestations and improve seed set and fruit yield in sweet pepper. *Pest Management Science* 77 (6): 2690–2696. <https://doi.org/10.1002/ps.6342>
- Morales G.E. & Wolff M. 2010. Insects associated with the composting process of solid urban waste separated at the source. *Revista Brasileira de Entomologia* 54 (4): 645–653.
<https://doi.org/10.1590/S0085-56262010000400017>
- Nguyen L.T., Schmidt H.A., Von Haeseler A. & Minh B.Q. 2015. IQ-TREE: a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. *Molecular Biology and Evolution* 32 (1): 268–274. <https://doi.org/10.1093/molbev/msu300>
- Procheş S. & Ramdhani S. 2012. The world's zoogeographical regions confirmed by cross-taxon analyses. *BioScience* 62 (3): 260–270. <https://doi.org/10.1525/bio.2012.62.3.7>

- Puillandre N., Lambert A., Brouillet S. & Achaz G. 2012. ABGD, Automatic Barcode Gap Discovery for primary species delimitation. *Molecular Ecology* 21 (8): 1864–1877. <https://doi.org/10.1111/j.1365-294X.2011.05239.x>
- Radenković S., Likov L., Ståhls G., Rojo S., Pérez-Bañón C., Smit J., Petanidou T., Van Steenis W. & Vujić A. 2020. Three new hoverfly species from Greece (Diptera: Syrphidae). *Zootaxa* 4830 (1): 103–124. <https://doi.org/10.11646/zootaxa.4830.1.4>
- Ronquist F., Teslenko M., Van Der Mark P., Ayres D.L., Darling A., Höhna S., Larget B., Liu L., Suchard M.A. & Huelsenbeck J.P. 2012. MrBayes 3.2: Efficient bayesian phylogenetic inference and model choice across a large model space. *Systematic Biology* 61 (3): 539–542. <https://doi.org/10.1093/sysbio/sys029>
- Sack P. 1922. H. Sauter's Formosa-Ausbeute: Syrphiden II (Dipteren). *Archiv für Naturgeschichte* 87: 258–276. Available from <https://www.biodiversitylibrary.org/part/40325> [accessed 25 Nov. 2022].
- Shorthouse D. 2010. SimpleMapp, an online tool to produce publication-quality point maps. Available from <https://www.simplemapp.net/> [accessed 25 Nov. 2022].
- Thompson F.C. 1999. A key to the genera of the flower flies (Diptera: Syrphidae) of the Neotropical Region including descriptions of new genera and species and a glossary of taxonomic terms used. *Contributions on Entomology* 3: 322–373. Available from <https://repository.si.edu/handle/10088/17492> [accessed 25 Nov. 2022].
- Thompson F.C. & Rotheray G. 1998. Family Syrphidae. In: *Contributions to a Manual of Palaearctic Diptera. Vol. 3 Higher Brachycera*: 81–139. Science Herald, Budapest.
- Thompson F.C. & Skevington J.H. 2014. Afrotropical flower flies (Diptera: Syrphidae). A new genus and species from Kenya, with a review of the melanostomine group of genera. *Zootaxa* 3847 (1): 97–114. <https://doi.org/10.11646/zootaxa.3847.1.5>
- Vockeroth J. R. 1992. The flower flies of the subfamily Syrphinae of Canada, Alaska, and Greenland (Diptera: Syrphidae). *The Insects and Arachnids of Canada* 18: 1–456. Available from <https://publications.gc.ca/site/eng/9.811395/publication.html> [accessed 25 Nov. 2022].
- Young A.D., Lemmon A.R., Skevington J.H., Mengual X., Ståhls G., Reemer M., Jordaens K., Kelso S., Lemmon E.M., Hauser M., De Meyer M., Misof B. & Wiegmann B.M. 2016. Anchored enrichment dataset for true flies (order Diptera) reveals insights into the phylogeny of flower flies (family Syrphidae). *BMC Evolutionary Biology* 16 (1): 143. <https://doi.org/10.1186/s12862-016-0714-0>
- Young A.D., Skevington J.H. & Van Steenis W. 2020. Revision of the *Psilota* Meigen, 1822 flower flies (Diptera: Syrphidae) of Australia. *Zootaxa* 4737 (1): 1–126. <https://doi.org/10.11646/zootaxa.4737.1.1>

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Supplementary file

Supp. file 1. Table S1. Kimura 2-parameter pairwise genetic distances based on COI of the taxa of Bacchini Bigot, 1883 and Melanostomini Williston, 1885. <https://doi.org/10.5852/ejt.2022.852.2015.8259>