

A review of *Vietanna* (Hemiptera: Cicadidae) with descriptions of two new species from China

Jiali WANG¹, Lei FENG², Jinyuan JIANG³, Cong WEI^{1①}

1. Key Laboratory of Plant Protection Resources and Pest Management of Ministry of Education, Entomological Museum, College of Plant Protection, Northwest A&F University, Yangling, Shaanxi 712100, China

2. Feng Lei Private Cicada Collection, Weifang, Shandong 261000, China

3. Jiang Jinyuan Private Cicada Collection, Wuxi, Jiangsu 214031, China

Abstract: The cicada genus *Vietanna* is reviewed based on the descriptions of two new species, *V. perparva* sp. nov. and *V. longiloba* sp. nov., from China. The relationship of this genus to related taxa is discussed based on the phylogeny of *Vietanna* and representative species from subtribes Puranina, Leptopsaltriina, Euterpnosiina and Leptosemiina based on the mitochondrial gene *COI* and nuclear genes *EF-1 α* and *ARD1*.

Key words: Cicadoidea; Cicadinae; Leptopsaltriini; revision; phylogeny

越蟪蝉属 *Vietanna* 修订并记二新种（半翅目：蝉科）

王佳丽¹, 冯磊², 江津渊³, 魏琮^{1①}

1. 植保资源与病虫害治理教育部重点实验室, 西北农林科技大学昆虫博物馆, 陕西 杨凌 712100; 2. 冯磊蝉科标本收藏室, 山东 潍坊 261000; 3. 江津渊蝉科标本收藏室, 江苏 无锡 214031

摘要: 对小蝉族 Leptopsaltriini 的越蟪蝉属 *Vietanna* Lee & Pham, 2021 进行了修订, 并记述 2 新种: 小叶越蟪蝉 *Vietanna perparva* sp. nov. 和长突越蟪蝉 *Vietanna longilorba* sp. nov.。基于线粒体基因 *COI* 和核基因 *EF-1 α* 、*ARD1* 对越蟪蝉属及小蝉族的洁蝉亚族 Puranina、小蝉亚族 Leptopsaltriina、真宁蝉亚族 Euterpnosiina 及细蝉亚族 Leptosemiina 进行了系统发育分析, 并讨论了越蟪蝉属与相关单元的关系。

关键词: 蝉总科; 蝉亚科; 小蝉族; 修订; 系统发育

Introduction

The subtribe Leptopsaltriina was established by Moulton (1923) in the tribe Dundubiini Distant, 1905 of the subfamily Cicadinae Batsch, 1789. Leptopsaltriina had been redefined as one of the subtribes within the tribe Cicadini Batsch, 1789 of Cicadinae, and 14 genera were placed in this subtribe (Lee & Hill 2010). Later, Leptopsaltriina was elevated to the tribal level, i.e., Leptopsaltriini, by Lee & Emery (2013), who placed six subtribes within Leptopsaltriini, i.e., Puranina Lee, 2013, Leptopsaltriina, Gudabina Lee, 2013, Euterpnosiina Lee, 2013, Leptosemiina Lee, 2013 and Mosaicina Lee, 2013. However, there is clearly confusion at the subtribe level of the presumed Leptopsaltriini in the phylogenetic trees of

Accepted 30 May 2024. Published online 26 August 2024.

① Corresponding author, E-mail: congwei@nwsuaf.edu.cn

Hill *et al.* (2021), in which species from Leptopsaltriina, Leptosemiina and Euterposiina were strongly conflicting, and where only the monophyly of Puranina and Gudabina was supported (species of Mosaicina were not included in the analysis of Hill *et al.* (2021)).

Pham & Lee (2021) erected *Vietanna* for the subtribe Leptopsaltriina based on a single species, *Vietanna hanoiensis* Pham & Lee, 2021. Wang *et al.* (2023) described *Duffelsa* Wang *et al.*, 2023 without subtribe assignment based on *Tettigia orientalis* Distant, 1912 as its type species, which together with other three species, *D. parvula* Wang, Jiang & Wei, 2023, *D. grandia* Wang, Jiang & Wei, 2023, and *D. rubida* Wang, Jiang & Wei, 2023, were described from China. However, *Duffelsa* was synonymized with *Vietanna*, and the species formerly placed in *Duffelsa* were transferred to *Vietanna* (Lee 2023). In this paper, two new species of *Vietanna* from China are described. *Vietanna* is reviewed based on the descriptions of the two new species, and the relationship of *Vietanna* to related taxa is discussed.

Material and methods

Morphology. Photos of habitus were taken with a Canon macro-lens EF 100 mm on a Canon 550D (Canon INC, Japan). Images of the same object at different focal planes were combined using Helicon Focus 8.2.2 stacking software. The pygofers were carefully extracted from the terminal abdominal segment of relaxed specimens. Genitalia together with sternite VIII were prepared with a 10% NaOH at room temperature for 12 hours. After rinsing the NaOH with distilled water, genitalia together with sternite VIII were transferred to glycerin for further examination. The photos of male genitalia were taken with a Scientific Digital micrography system equipped with an Auto-montage imaging system and a QIMAGING Retiga 4000R digital camera (CCD) (QImaging, Surrey, BC, Canada). Photographs were adjusted with Adobe Photoshop CS3.0. Morphological terminology follows Moulds (2005, 2012) and Marshall *et al.* (2018).

The holotypes of *V. perparva* **sp. nov.** and *V. longiloba* **sp. nov.** and four paratypes of *V. perparva* **sp. nov.** are deposited in the Entomological Museum, Northwest A&F University (NWAUFU), Yangling, China. One paratype of *V. longiloba* **sp. nov.** is deposited in Jiang Jinyuan Private Cicada Collection (JJPC), Wuxi, China. One paratype of *V. longiloba* **sp. nov.** is deposited in Feng Lei Private Cicada Collection (FLPC), Weifang, China.

DNA sequencing and molecular phylogenetic analysis. In this study, four species of *Vietanna* (i.e., two samples of *V. grandia*, four samples of *V. parvula*, one sample of *V. longiloba* **sp. nov.**, and two samples of *V. perparva* **sp. nov.**) were sequenced. Genomic DNA of cicadas were extracted from the hind legs using a Biospin Genomic DNA Extraction Kit (Bioer Technology Co., Ltd, Hangzhou, China) following the manufacturer's instructions. Standard PCR methods were used to amplify partial sequences of two nuclear genes of cicadas (the elongation factor-1 alpha (*EF-1a*) and acetyltransferase (*ARD1*)), and one mitochondrial gene of cicadas (cytochrome c oxidase subunit I (*COI*)). PCR primers for *EF-1a* are EF1-PA-f650 (5'-TGC TGC GGG TAC TGG TGA AT-3') and EF1-N-1419 (5'-ACA CCA GTT TCA ACT CTG CC-3') (Arensburger *et al.* 2004). PCR primers for *ARD1* are ARD1-1041F (5'-TGG AAA GTG TTT CTG TCA CAT TTT CG-3') and ARD1-1733R (5'-ATC TCT TTT CAT AGC GTA TGC GTC-3') (Owen *et al.* 2015). PCR primers for *COI* are LCO1490 (5'-GGT CAA CAA ATC ATA AAG ATA TTG G-3') and HCO2198 (5'-TAA ACT TCA GGG TGA CCA AAA AAT

CA-3') (Folmer *et al.* 1994). The following thermal profile was used for 25 µL amplification reactions: initial denaturation for 3 min at 94°C, followed by 34 cycles of 30 s at 94°C, 0.5 min at 51.4°C, 55°C and 56°C for *COI*, *ARD1* and *EF-1α*, 1 min at 72°C and a subsequent final extension at 72°C for 10 min. After the PCR products were checked with 1% agarose gel staining with ethidium bromide to ensure the products were the target fragments we needed, sequencing was performed at Sunny Biotechnology Co., Ltd. (Shanghai, China) using the same primers as in PCR. The sequences of the above mentioned three species have been submitted to GenBank (for accession numbers see Table 1).

Sequences of the three *Vietanna* species and that of other 21 species of Leptopsaltriini downloaded from GenBank (Table 1) were assembled, adjusted, aligned, and the gappy columns at the beginning and end of the alignment were manually deleted using MEGA X v.10.1.8 (Kumar *et al.* 2018). Among the 21 species whose sequences were downloaded from the GenBank, six species belong to Puranina, four species belong to Euterpnosiina, eight species belong to Leptopsaltriina, and three species belong to Leptosemiina; and two other species of Ayuthiini were included as outgroups (Table 1).

Partitioning schemes and substitution models were estimated by the best-fit partition model (Edge-unlinked) using the AICc criterion by ModelFinder (Kalyaanamoorthy *et al.* 2017) included in PhyloSuite v.1.2.2 (Zhang *et al.* 2020). According to the AICc, the best-fit model was GTR for the concatenated dataset of the three genes (*COI* + *EF-1α* + *ARD1*). Phylogenetic trees were reconstructed using maximum-likelihood (ML) inference by IQ-TREE v.1.6.8 (Nguyen *et al.* 2015) and Bayesian inference (BI) by MrBayes v.3.2.6 (Ronquist *et al.* 2012) in PhyloSuite v.1.2.2 (Zhang *et al.* 2020). The ML tree was inferred under an edge-linked partition model for 1,000,000 ultrafast bootstraps (Minh *et al.* 2013). For the BI analysis, Markov chain Monte Carlo (MCMC) settings were as follows: two independent runs, four Markov chains, run for 10⁶ generations with sampling every 100 generations and the initial 25% of sampled data discarded as burn-in. When the standard deviation of clade frequencies fell below 0.01, the analyses terminated. The obtained trees were visualized in Figtree v.1.4.4 (Rambaut 2018).

Abbreviations used are as follows: as — anal styles; bl — basal lobe; db — dorsal beak; ds — distal shoulder; mdl — median lobe of uncus; psp — primary spine; sasp — subapical spine; ssp — secondary spine; lbu — lateral branches of uncus.

Taxonomy

Family Cicadidae Batsch, 1789

Remarks. The International Commission of Zoological Nomenclature recently published a correction to Opinion 2475 (ICZN, 2023). The Commission determined that Batsch (1789) has priority over the previously used Latreille (1802) as the authority of Cicadidae.

Subfamily Cicadinae Batsch, 1789

Tribe Leptopsaltriini Moulton, 1923

Subtribe Leptopsaltriina Moulton, 1923

Genus *Vietanna* Lee & Pham, 2021

Vietanna Pham & Lee, 2021: 1203; Lee, 2023: 292. Type species: *Vietanna hanoiensis* Pham & Lee, 2021.

Duffelsa Wang, Jiang & Wei, 2023: 397. Type species: *Tettigia orientalis* Distant, 1912.

Table 1. Specimens sampled and included in the molecular phylogenetic analyses

Species	Location	Date (D/M/Y)	COI	EF-1 α	ARD1
<i>Euterpnosia cucphuongensis</i> *	Vietnam: Cuc Phuong National Park	24/5/2012	MT639286	MT599233	MT599078
<i>Euterpnosia viridifrons</i> *	China: Taiwan, Taipei	4/6/2003	MT639302	MT599249	MT599094
<i>Formosemia apicalis</i> *	China: Taiwan, Kaohsiung	20/10/2003	GQ527098	MT599165	–
<i>Galgoria herzbergi</i> *	Laos: Mount, Pan	–/4–5/2003	MT639229	MT599160	MT599012
<i>Leptosemia takanonis</i> *	Korea	–/7/2005	GQ527090	MT599177	–
<i>Maua philippinensis</i> *	Philippines: Mindanao	25/4/2012	MT639279	MT599226	MT599071
<i>Miniterpnosia chorus</i> *	Laos: Mount, Pan	–/4–5/2003	MT639226	MT599157	MT599009
<i>Neocicada chisos</i> *	USA: Texas, Jeff Davis	29/6/2007	GQ527101	MT599195	MT599041
<i>Neocicada hieroglyphica</i> *	USA: Oklahoma, Latimer	17/6/2011	GQ527093	MT599219	MT599064
<i>Purana capricornis</i> *	Malaysia: Sarawak	–/1/2009	MT639338	MT599292	MT599128
<i>Purana capricornis</i> *	Philippines: Camiguin, Sagay	29/6/2010	MT639261	MT599206	MT599051
<i>Purana pryeri</i> *	Malaysia: Sarawak	–/1/2009	MT639337	MT599291	MT599127
<i>Purana trui</i> *	Vietnam: Bach Ma National Park	17/5/2012	MT639291	MT599238	MT599083
<i>Tanna infuscata</i> *	China: Taiwan, Taitung	5/6/2018	MT639306	MT599255	MT599100
<i>Tanna sozanensis</i> *	China: Taiwan, Taipei	3/6/2004	GQ527094	MT599166	–
<i>Tanna japonensis</i> *	Japan: Miunami, Ashikara	–/8/2003	MT639225	MT599155	MT599007
<i>Tanna kimtaewooi</i> *	Vietnam: Tam Dao National Park	27/5/2012	MT639299	MT599246	MT599091
<i>Yezoterpnosia vacua</i> *	Japan: Hiroshima, Miyoshi	21/5/2005	MT639305	MT599254	MT599099
<i>Vietanna rubida</i> *	China: Yunnan, Hekou	27/4/2013	OR769047	OR801368	–
<i>Vietanna grandia</i> [1]*	China: Yunnan, Hekou	27/4/2013	OR769048	OR801369	–
<i>Vietanna grandia</i> [2]*	China: Yunnan, Hekou	27/4/2013	OR769049	–	–
<i>Vietanna grandia</i> [3]	China: Yunnan, Hekou	27/4/2013	PP473459	–	–
<i>Vietanna grandia</i> [4]	China: Yunnan, Hekou	27/4/2013	PP473460	–	–
<i>Vietanna parvula</i> [1]*	China: Yunnan, Mengla	10/5/2021	OR769050	OR801370	OR786184
<i>Vietanna parvula</i> [2]*	China: Yunnan, Mengla	10/5/2021	OR769051	OR801371	–
<i>Vietanna parvula</i> [3]	China: Yunnan, Mengla	10/5/2021	PP473461	–	–
<i>Vietanna parvula</i> [4]	China: Yunnan, Mengla	10/5/2021	PP473462	–	–
<i>Vietanna parvula</i> [5]	China: Yunnan, Mengla	10/5/2021	PP473463	–	–
<i>Vietanna parvula</i> [6]	China: Yunnan, Mengla	10/5/2021	PP473464	–	–
<i>Vietanna perparva</i> sp. nov. [1]	China: Yunnan, Pu'er, Ximeng	14/6/2022	PP473465	PP488513	–
<i>Vietanna perparva</i> sp. nov. [2]	China: Yunnan, Pu'er, Ximeng	10/6/2022	PP473466	PP488514	PP488515
<i>Vietanna longiloba</i> sp. nov.	China: Yunnan, Xishuangbanna Tropical Botanical Garden	12/5/2023	PP848317	–	–
<i>Distantalna splendida</i> *	Vietnam: Cuc Phuong National Park	24/5/2012	MT639287	MT599234	MT599079
<i>Ayuthia spectabile</i> *	Malaysia: Perak, Tapah Hills	–/4/2021	MT639267	MT599213	MT599058

*Sequences of *COI*, *EF-1 α* and *ARD1* were downloaded from the GenBank.

Included species. *Vietanna hanoiensis* Pham & Lee, 2021 (Hanoi, Vietnam); *Vietanna orientalis* (Distant, 1912) (southern Vietnam; Thailand); *Vietanna parvula* (Wang, Jiang & Wei, 2023) (Yunnan, China); *Vietanna grandia* (Wang, Jiang & Wei, 2023) (Yunnan, China); *Vietanna rubida* (Wang, Jiang & Wei, 2023) (Yunnan, China); *Vietanna perparva* **sp. nov.** (Yunnan, China); *Vietanna longiloba* **sp. nov.** (Yunnan, China).

Diagnosis. Medium to large cicadas. Head including eyes about as wide as or slightly wider than the base of mesonotum. Postclypeus moderately prominent with symmetrical series of fuscous fasciae along transverse grooves. Pronotum much longer than head and distinctly shorter than mesonotum excluding cruciform elevation. Lateral pronotal collar obtusely angled. Mesonotum with the following blackish fuscous markings: medial longitudinal fascia from anterior margin of mesonotum to anterior margin of cruciform elevation, sometimes disconnected in the middle; pair of inwardly curved fasciae along parapsidal suture; pair of fasciae or spots along lateral margins of mesonotum; pair of small spots on scutal depression. Wings hyaline, with eight and six apical cells on forewing and hindwing, respectively. Forewing with comparatively short apical cells, and usually with infuscations on radial, radiomedial, medial, and mediocubital crossveins. Male abdomen cylindrical, distinctly longer than distance from head and thorax together. Male abdominal tergite 3 distinctly wider than mesonotum; male abdominal sternite III with small bump on each lateral surface. Timbal mostly concealed by timbal cover. Male opercula nearly triangular and as long as wide, widely separated from each other, slightly extending beyond posterior margin of abdominal sternite II. Male pygofer elliptical in ventral view, with dorsal beak and distal shoulder; upper lobe of pygofer absent; basal lobe of pygofer present; uncus slightly curved inwardly in lateral view, and bifurcated in ventral view. Aedeagus protruding out of uncus.

Remarks. *Vietanna* was erected in the subtribe Leptopsaltriina (Pham & Lee 2021). Wang *et al.* (2023) described *Duffelsa* in Leptopsaltriini but without subtribe assignment, which was recently recognized to be junior a synonym of *Vietanna* by Lee (2023). *Vietanna* and other sampled taxa of Leptopsaltriina did not nest in the same lineage in a previous study (Wang & Wei 2024). Further studies are needed to elucidate the phylogenetic placement of *Vietanna* within Leptopsaltriini (see Discussion).

1. *Vietanna perparva* **sp. nov.** (Figs 1, 2)

Measurements (in mm; 5♂). Body length: 37.5–39.8; forewing length: 44.3–48.2; forewing width: 14.6–15.7; width of head including eyes: 9.2–9.9; pronotum width (including pronotal collar): 12.1–13.3; mesonotum width: 9.1–10.3.

Description of male. Head (Figs 1A, 1B, 1D). Mostly ochraceous. Eyes blackish brown, with dense golden hair along posterior margin. Median black spot enclosing ocelli. Lorum with pair of black markings. Anteclypeus with black patches laterally. Postclypeus prominent with symmetrical series of fuscous fasciae along transverse grooves, transverse cross-section rounded. Rostrum with apex fuscous, extending to hind trochanters.

Thorax (Figs 1A, 1B). Pronotum almost ochraceous with the following blackish markings: pair of tiny spots just below paramedian fissures, pair of discontinuous fasciae along lateral fissures, narrow fascia along posterior margin of inner area; pronotal collar symmetrically with three paired blackish spots on posterolateral area, and lateral part of

pronotal collar obtusely angled. Mesonotum fundamentally ochraceous with following blackish markings: medial longitudinal arrow-shaped marking from anterior margin of mesonotum reaching anterior margin of cruciform elevation, paired inwardly curved markings along each parapsidal sutures, paired markings along lateral margins of mesonotum reaching to anterior angles of cruciform elevation, pair of small spots on scutal depressions.

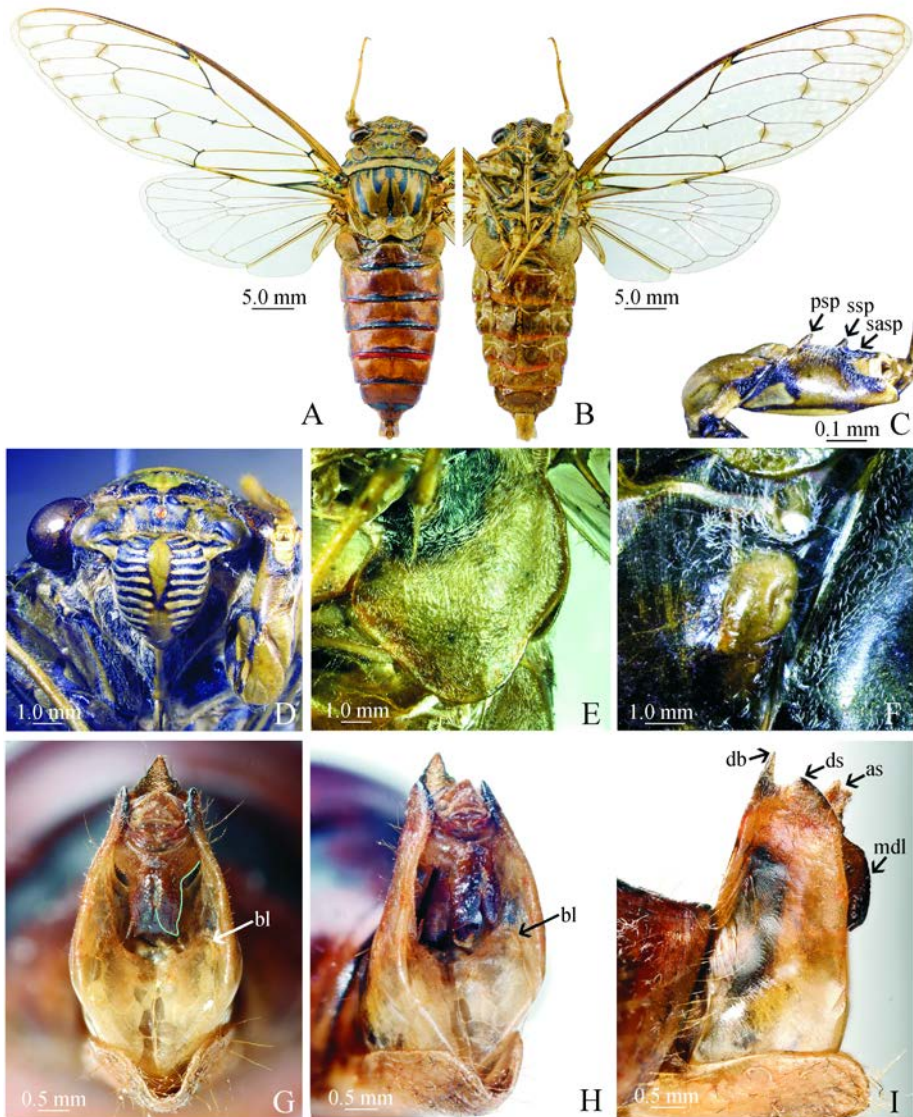


Figure 1. *Vietanna perparva* sp. nov., holotype, ♂. A, B. Habitus, dorsal and ventral views; C. Left fore leg, showing the spines on femur; D. Head, frontal view; E. Opercula, ventral view; F. Small bump on each lateral surface of sternite III; G–I. Pygofer, ventral, posterolateral and lateral views.

Legs (Fig. 1C). Ochraceous with fuscous patches. Fore femora swollen and equipped with three spines beneath: primary spine ochraceous, pointed and oblique to femur; secondary spine ochraceous, broader with obtuse tip; subapical spine fuscous, very short and small.

Wings (Figs 1A, 1B). Hyaline. Forewing with comparatively short eight apical cells, with infuscations on radial, radiomedial, medial, and mediocubital crossveins, with longitudinal fuscous markings on apical cells, and marginal series of minute fuscous spots present on apex of longitudinal veins, basal membrane with a little brownish gray. Hindwing without marking.

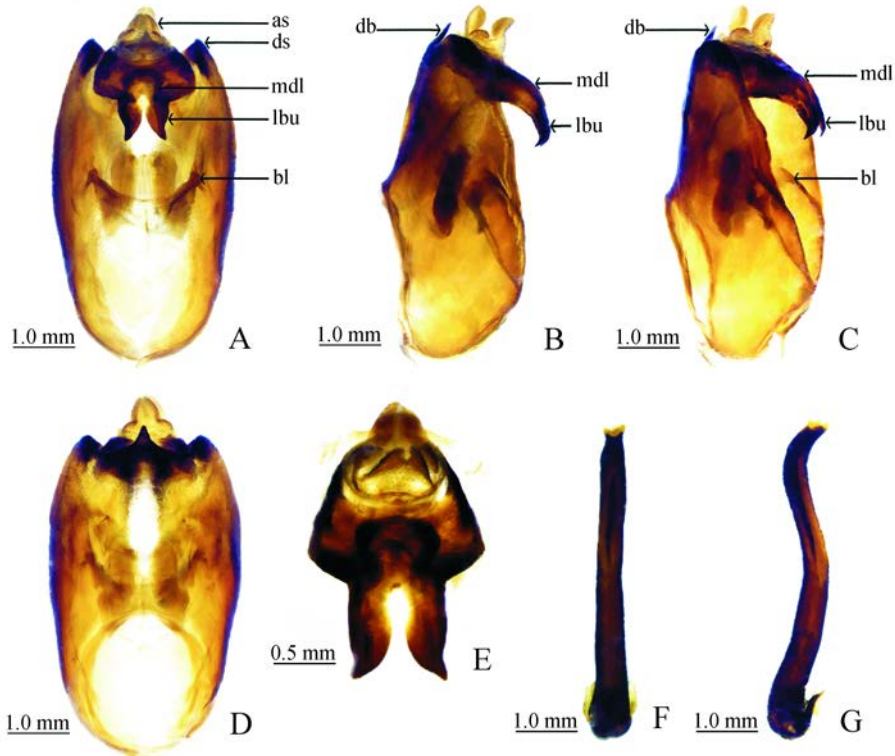


Figure 2. *Vietanna perparva* sp. nov., holotype, ♂. A–D. Pygofer, ventral, lateral, posterolateral and rear views; E. Uncus, apical view; F–G. Aedeagus, ventral and lateral views.

Abdomen (Figs 1A, 1B, 1E, 1F). Cylindrical balloon, ochraceous, noticeably longer than head and thorax together. Male abdominal tergite 3 distinctly wider than mesonotum, abdominal tergites 2–6 brown with blackish markings on posterior margins of tergites. Male abdominal sternite III with small bump on each lateral surface. Timbal cover scale-like, timbal mostly concealed by timbal cover. Opercula triangular, widely separated and slightly longer than wide, slightly extending beyond posterior margin of abdominal sternite II.

Genitalia (Figs 1G–I, 2). Pygofer elliptical in ventral view, ochraceous with apex blackish brown. Dorsal beak pointed, higher than the height of anal styles. Distal shoulders broadly triangular, as high as anal styles, distally extended into pointed lobe. Basal lobes relatively short and very small, substantially confluent with pygofer margin. Median lobe of uncus thick and wide, bifurcated at apex with pair of lateral branches of uncus in ventral view, slightly curved inwardly in lateral view. Aedeagus straight and thick, slightly broader at base and gradually narrowed apically in ventral view, somewhat S-shaped in lateral view, with apex extending the apex of uncus and nearly truncate in lateral view.

Holotype. ♂ (NWAUFU), **China**, Ximeng Wazu Autonomous Co., Pu'er, Yunnan Prov., 14-VI-2021, Zhihong LI coll. **Paratypes.** 1♂ (NWAUFU), same location as holotype, 10-VI-2021, Zhihong LI coll.; 1♂ (NWAUFU), same location as holotype, V-2022, Zhihong LI coll.; 2♂ (NWAUFU), same location as holotype, VI-2023, Zhihong LI coll.

Etymology. The specific epithet is derived from Latin adjective “parvus” meaning very small, signifying the pygofer with a pair of very small basal lobes.

Remarks. This new species can be easily distinguished from other species of *Vietanna* by the following characteristics: median lobe of uncus thick and wide, bifurcated at apex with two short lateral branches of uncus (median lobe of uncus shorter, slightly bifurcated at apex in *V. hanoiensis*; median lobe of uncus narrower, slightly bifurcated at apex in *V. rubida* and *V. parvula*, further bifurcated at apex in *V. orientalis* and *V. grandia*; median lobe of uncus narrower, bifurcated at middle with two very long lateral branches of uncus in *V. longiloba* **sp. nov.**); basal lobes of pygofer short and small, substantially confluent with pygofer margin (basal lobes bigger, partly confluent with pygofer margin in *V. hanoiensis*, *V. rubida* and *V. grandia*; basal lobes slightly bigger, substantially confluent with pygofer margin in *V. parvula*; basal lobes very small, almost confluent with pygofer margin in *V. longiloba* **sp. nov.**); aedeagus thick, somewhat S-shaped in lateral view (aedeagus slender, more curly S-shaped in lateral view in *V. grandia*, *V. parvula* and *V. longiloba* **sp. nov.**).

2. *Vietanna longiloba* **sp. nov.** (Figs 3, 4)

Measurements (in mm; 2♂). Body length: 39.8–40.2; forewing length: 44.9–45.7; forewing width: 14.7–15.4; width of head including eyes: 9.8–10.2; pronotum width (including pronotal collar): 13.1–13.4; mesonotum width: 11.5–12.3.

Description of male. Head (Figs 3A, 3B, 3D). Mostly blackish brown. Eyes yellowish, with dense golden hair along posterior margin. Median spot enclosing ocelli black. Lorum and anteclypeus almost blackish. Postclypeus not very prominent with symmetrical series of blackish fasciae along transverse grooves, transverse cross-section rounded. Rostrum with apex blackish, extending to hind trochanters.

Thorax (Figs 3A, 3B). Pronotum almost blackish brown with the following blackish markings: pair of tiny spots just below paramedian fissures, pair of discontinuous fasciae along lateral fissures, narrow fascia along posterior margin of inner area; pronotal collar symmetrically with three paired blackish spots on posterolateral area, and lateral part of pronotal collar obtusely angled. Mesonotum fundamentally blackish brown with following blackish markings: medial longitudinal arrow-shaped marking from anterior margin of mesonotum reaching anterior margin of cruciform elevation, paired inwardly curved markings along each parapsidal sutures, paired discontinuous markings along lateral margins of mesonotum reaching to anterior angles of cruciform elevation, pair of small spots on scutal depressions.

Legs (Fig. 3C). Brown with fuscous patches. Fore femora swollen and equipped with three spines beneath: primary spine ochraceous, pointed and oblique to femur; secondary spine blackish, broader with obtuse tip; subapical spine blackish, very short and small.

Wings (Figs 3A, 3B). Hyaline. Forewing with comparatively short eight apical cells, with infuscations on radial, radiomedial, medial, and mediocubital crossveins, with longitudinal fuscous markings on apical cells, and marginal series of minute fuscous spots

present on apex of longitudinal veins, basal membrane a little brownish gray. Hindwing without markings.

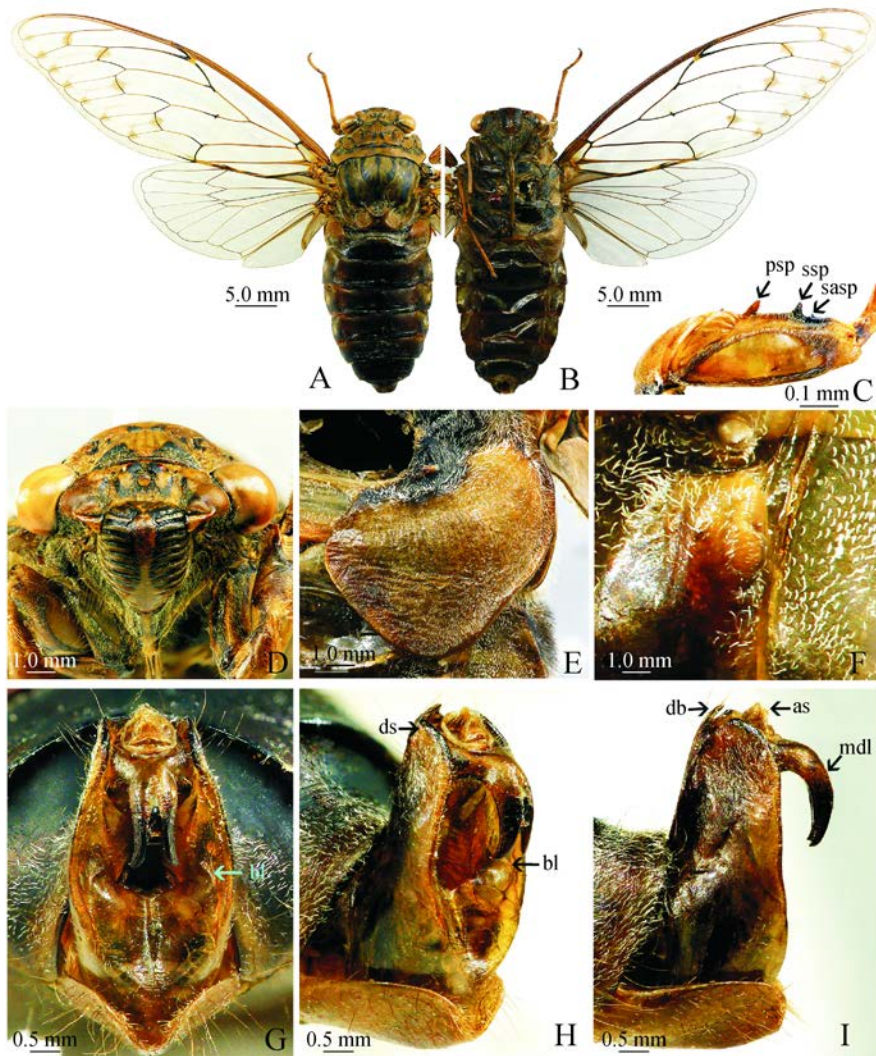


Figure 3. *Vietanna longiloba* sp. nov., holotype, ♂. A, B. Habitus, dorsal and ventral views; C. Left fore leg, showing the spines on femur; D. Head, frontal view; E. Opercula, ventral view; F. Small bump on each lateral surface of sternite III; G–I. Pygofer, ventral, posterolateral and lateral views.

Abdomen (Figs 3A, 3B, 3E, 3F). Cylindrical balloon, blackish brown, noticeably longer than head and thorax together. Male abdominal tergites 3 and 4 distinctly wider than mesonotum, abdominal tergites 2–6 with blackish markings on posterior margins. Male abdominal sternite III with small bump on each lateral surface. Timbal cover scale-like, timbal mostly concealed by timbal cover. Opercula triangular, widely separated and slightly longer than wide, slightly extending beyond posterior margin of abdominal sternite II.

Genitalia (Figs 3G–I, 4). Pygofer elliptical in ventral view, brown with apex blackish brown. Dorsal beak pointed, as high as anal styles. Distal shoulders broadly triangular, lower

than anal styles, distally extended into obtuse lobe. Basal lobes very small, almost confluent with pygofer margin. Median lobe of uncus thick and wide, bifurcated at middle, with pair lateral branches of uncus in ventral view, slightly curved inwardly in lateral view. Aedeagus straight and thick, slightly broader at base and gradually narrowed apically in ventral view, somewhat S-shaped in lateral view, mostly concealed by uncus and nearly truncate in lateral view.

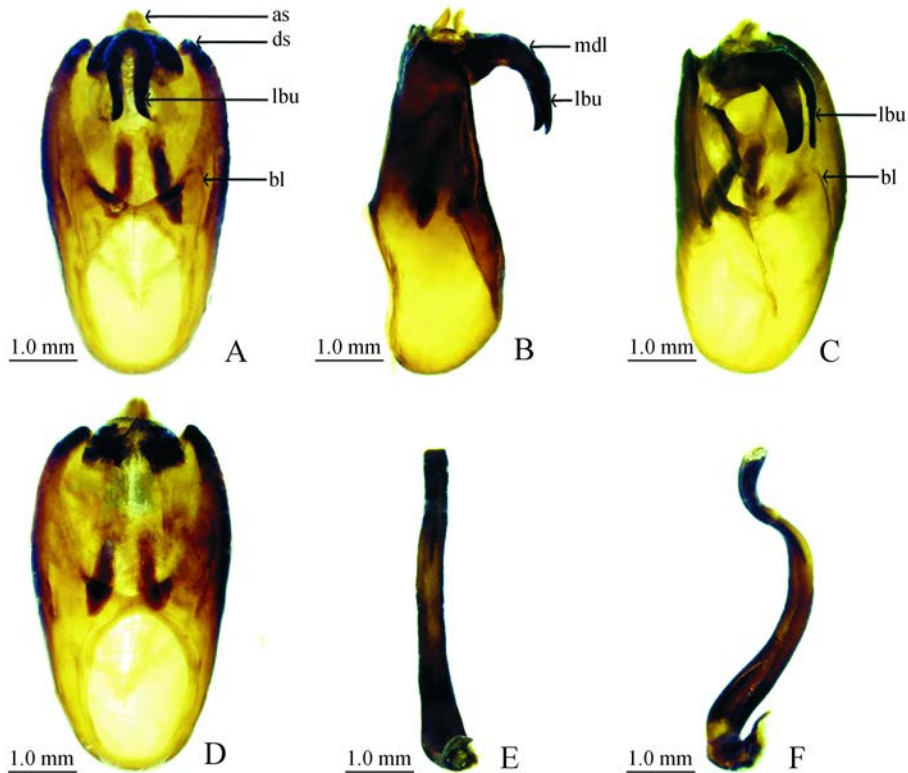


Figure 4. *Vietanna longiloba* sp. nov., holotype, ♂. A–D. Pygofer, ventral, lateral, posterolateral and rear views; E, F. Aedeagus, ventral and lateral views.

Holotype. ♂ (NWAFU), **China**, Xishuangbanna Tropical Botanical Garden, Yunnan Prov., 12-V-2023, collector unknown. **Paratypes.** 1♂ (JJPC), same location and date as holotype; 1♂ (LFPC), same location and date as holotype.

Etymology. The specific epithet is derived from Latin adjective “long” and noun “lobus”, signifying the uncus with a pair of very long lateral branches.

Remarks. This new species can be easily distinguished from other species of *Vietanna* by the following characteristics: the median lobe of uncus bifurcated at middle with a pair of very long lateral branches of uncus (median lobe of uncus bifurcated or slightly bifurcated at apex with pair of short or very short lateral branches of uncus in other five *Vietanna* species); basal lobes of pygofer very small, almost confluent with pygofer margin (basal lobes large, partly confluent with pygofer margin in *V. hanoiensis*, *V. rubida* and *V. grandia*; basal lobes relatively large, substantially confluent with pygofer margin in *V. parvula* and *V. perparva* sp. nov.).

Results of molecular phylogenetic analysis. Both BI and ML trees were constructed based on the concatenated dataset of three genes (*COI* + *EF-1 α* + *ARD1*) (Fig. 5). The trees recovered the subtribes Puranina, Euterposiina and Leptosemiina as monophyletic groups with robust support. However, the trees do not support the monophyly of the currently defined subtribe Leptopsaltriina. The results show that the relationships are as follows: Puranina + (Leptosemiina + (*Tanna* and *Galgoria* [Leptopsaltriini] + (Euterposiina + *Vietanna* [Leptopsaltriini]))) (Fig. 5). *Vietanna* is sister to the clade comprising the sampled taxa of Euterposiina with good support.

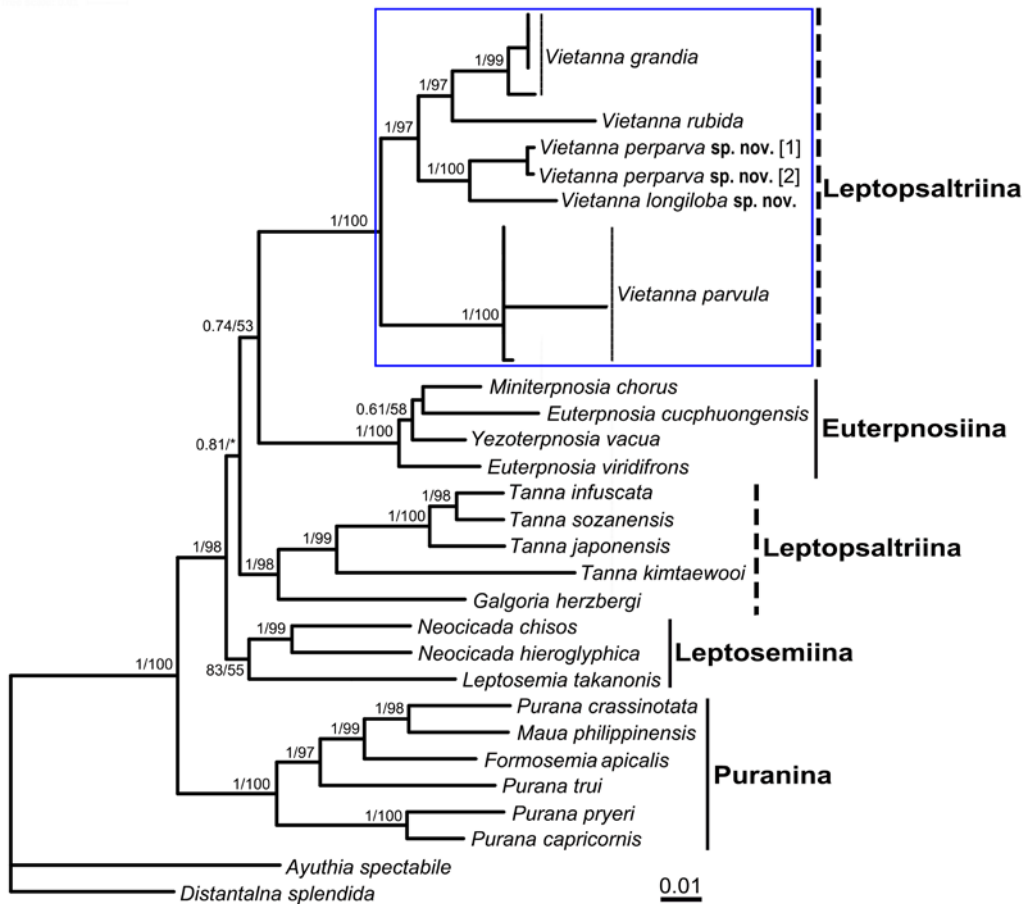


Figure 5. Molecular phylogeny of *Vietanna* and related taxa based on the concatenated dataset of three genes (*COI* + *EF-1 α* + *ARD1*). Numbers above branches represent support values, Bayesian posterior probability and bootstrap pseudoreplicates.

Discussion

The subtribes Puranina, Euterposiina and Leptosemiina are recovered as monophyletic groups in our study (Fig. 5). *Duffelsa* was erected in the tribe Leptopsaltriini without subtribe assignment (Wang *et al.* 2023), but it was recently recognized to be a junior synonym of *Vietanna* by Lee (2023). *Vietanna* is revealed to be sister to the sampled taxa of Euterposiina

(Fig. 5), and this genus and other sampled taxa of Leptopsaltriina (i.e., *Tanna*, *Galgoria*) do not nest in the same lineage in the phylogenetic tree of the present study as well as that of Wang & Wei (2024). Phylogenetic analysis of this study as well as that of Hill *et al.* (2021) indicate that Leptopsaltriini is not a monophyletic group. Further molecular phylogenetic studies are needed to elucidate the phylogenetic placement of *Vietanna* and the relationships within Leptopsaltriini.

Acknowledgements

We would like to express our sincere thanks to Mr. Zhihong LI (Taiyanghe Provincial Nature Reserve Management Administration, Pu'er, China) for collecting specimens of *Vietanna perparva* **sp. nov.**. This work was supported by the National Natural Science Foundation of China (32070476, 32270496).

References

- Arensburger P, Buckley TR, Simon C, Moulds M & Holsinger KE. 2004. Biogeography and phylogeny of the New Zealand cicada genera (Hemiptera: Cicadidae) based on nuclear and mitochondrial DNA data. *Journal of Biogeography*, 31(4): 557–569.
- Folmer O, Black M, Hoeh W, Lutz R & Vrijenhoek R. 1994. DNA primers for amplification of mitochondrial cytochrome oxidase subunit I from diverse metazoan invertebrates. *Molecular Marine Biology and Biotechnology*, 3(5): 294–299.
- Hill KBR, Marshall DC, Marathe K, Moulds MS, Lee YJ, Pham HT, Mohagan AB, Sarkar V, Price BW, Duffels JP, Schouten MA, de Boer AJ, Kunte K & Simon C. 2021. The molecular systematics and diversification of a taxonomically unstable group of Asian cicada tribes related to Cicadini Latreille, 1802 (Hemiptera: Cicadidae). *Invertebrate Systematics*, 35: 570–601.
- ICZN (International Commission on Zoological Nomenclature). 2023. Official Correction 138 (Opinion 2475) – The family-group name CICADIDAE is available from Batsch, 1789. *Bulletin of Zoological Nomenclature*, 80(1): 107–108.
- Kalyaanamoorthy S, Minh BQ, Wong TKF, von Haeseler A & Jermini LS. 2017. ModelFinder: Fast model selection for accurate phylogenetic estimates. *Nature Methods*, 14(6): 587–589.
- Kumar S, Stecher G, Li M, Knyaz C & Tamura K. 2018. MEGA X: Molecular Evolutionary Genetics Analysis across computing platforms. *Molecular Ecology Resources*, 35: 1547–1549.
- Lee YJ. 2023. Circumscription of the genus *Vietanna* Lee & Pham, 2021 (Cicadidae: Leptopsaltriini) resulting in the synonymy of *Duffelsa* Wang et al., 2023. *Zootaxa*, 5361(2): 292–296.
- Lee YJ & Emery D. 2013. New genera and species of Leptopsaltriini (Hemiptera: Cicadidae: Cicadinae) from India and Tibet, with the descriptions of five new subtribes. *Zoosystema*, 35(4): 525–535.
- Lee YJ & Hill KBR. 2010. Systematic revision of the genus *Psithyristria* Stål (Hemiptera: Cicadidae) with seven new species and a molecular phylogeny of the genus and higher taxa. *Systematic Entomology*, 35(2): 277–305.
- Marshall DC, Moulds MS, Hill KBR, Price BW, Wade EJ, Owen CL, Goemans G, Marathe K, Sarkar V, Cooley JR, Sanborn AF, Kunte K, Villet MH & Simon C. 2018. A molecular phylogeny of the cicadas (Hemiptera: Cicadidae) with a review of tribe and subfamily classification. *Zootaxa*, 4424(1): 1–64.
- Minh BQ, Nguyen MA & von Haeseler A. 2013. Ultrafast approximation for phylogenetic bootstrap.

- Molecular Biology and Evolution*, 30(5): 1188–1195.
- Moulds MS. 2005. An appraisal of the higher classification of cicadas (Hemiptera: Cicadoidea) with special reference to the Australian fauna. *Records of the Australian Museum*, 57(3): 375–446.
- Moulds MS. 2012. A review of the genera of Australian cicadas (Hemiptera: Cicadoidea). *Zootaxa*, 3287: 1–262.
- Moulton JC. 1923. Cicadas of Malaysia. *Journal of the Federated Malay States Museum*, 11: 69–182.
- Nguyen LT, Schmidt HA, Von Haeseler A & Minh BQ. 2015. IQ-TREE: a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. *Molecular Biology and Evolution*, 32(1): 268–274.
- Owen CL, Marshall DC, Hill KBR & Simon C. 2015. The phylogenetic utility of acetyltransferase (*ARD1*) and glutamyl tRNA synthetase (*QtRNA*) for reconstructing Cenozoic relationships as exemplified by the large Australian cicada *Pauropsalta* generic complex. *Molecular Phylogenetics and Evolution*, 83: 258–277.
- Pham TH & Lee YJ. 2021. A new genus and species of the subtribe Leptopsaltriina (Hemiptera: Cicadidae: Leptopsaltriini) from Vietnam, with a key to the genera of Leptopsaltriina. *Journal of Asia-Pacific entomology*, 24(4): 1202–1205.
- Rambaut A. 2018. FigTree version 1.4.4. Available from: <http://tree.bio.ed.ac.uk/software/figtree/> (accessed November 25, 2018)
- Ronquist F, Teslenko M, van der Mark P, Ayres DL, Darling A, Hohna S, Larget B, Liu L, Suchard MA & Huelsenbeck JP. 2012. MrBayes 3.2: Efficient Bayesian phylogenetic inference and model choice across a large model space. *Systematic Biology*, 61(3): 539–542.
- Wang J, Jiang J & Wei C. 2023. A new genus, *Duffelsa* gen. n., with descriptions of three new species and one new combination (Hemiptera: Cicadidae). *Zootaxa*, 5323(3): 396–408.
- Wang J & Wei C. 2024. *Angusta* gen. n. of the cicada tribe Leptopsaltriini, with description of a new species from China (Hemiptera: Cicadidae). *Zootaxa*, 5403(5): 571–586.
- Zhang D, Gao FL, Li WX, Jakovlić I, Zou H, Zhang J & Wang GT. 2020. PhyloSuite: an integrated and scalable desktop platform for streamlined molecular sequence data management and evolutionary phylogenetics studies. *Molecular Ecology Resources*, 20(1): 348–355.