

A new species in the genus *Malcus* Stål (Hemiptera: Heteroptera: Malcidae) from China based on morphological and molecular data

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Abstract: Morphological and molecular data confirm a new species in genus *Malcus* from Xizang, China. *Malcus zhengi* **sp. nov.** is described and illustrated. Photos and illustrations of the adult, critical morphological characteristics and pygophore are provided.

Key words: Lygaeoidea; morphology; molecular data; taxonomy

基于形态及分子证据记述中国西藏束长蝽属一新种（半翅目：异翅亚目：束长蝽科）

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摘要：基于形态及分子证据记述中国西藏束长蝽属 1 新种——郑氏束长蝽 *Malcus zhengi* **sp. nov.**，提供了成虫、重要鉴别特征及生殖囊图片。

关键词：长蝽总科；形态学；分子数据；分类

Introduction

The genus *Malcus* was established by Stål (1859) based on one species, *Malcus flavidipes* Stål, 1859. Until the 1960s only 4 species were known (Horváth 1914; Ishihara & Hasegawa 1941; Stål 1859; Distant 1901). Štys (1967) described 19 species in his monograph. Zheng *et al.* (1979) added 7 species from China. Kondorosy (2000) described 3 species from Vietnam. Wang & Bu (2020) added 4 species from China. Until now, 33 known species have been described in this genus.

Material and methods

Morphological terminology follows Štys (1967) and Zheng & Zou (1981). The male pygophore was prepared using the techniques described by Štys (1967). Male specimens were dissected using an insect pin under an OLYMPUS SZ11 stereoscope. The dissected parts were placed in micro-tubes with glycerin and attached below the specimens to which they belong. Drawings were made by using an OLYMPUS SZ11 stereoscope. Photographs and dimensions were taken with a Canon EOS 5D Mark II camera, and synthesized with Helicon software.

Accepted 22 September 2020. Published 25 December 2020. Published online 30 November 2020.

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Material examined is deposited in the insect collection of Institute of Entomology, College of Life Sciences, Nankai University, Tianjin, China (NKU).

Genomic DNA was extracted from a mid-leg using a DNeasy Blood & Tissue Kit (QIAGEN). Sequencing was performed by Novogene (Tianjin, China) with an insert size of 350 bp and a pair-end 150 bp sequencing strategy on the Illumina platform. *COI*, *COII* and *Cytb* (with evolutionary rates relatively slow) were acquired by Genious v9.1.4 (Kearse *et al.* 2012).

The genetic distance estimations based on *COI* and (*COI* + *COII* + *Cytb*) data-sets were calculated in MEGA X (Kumar *et al.* 2018) using the Kimura 2-Parameter (K2P) substitution model, 1000 bootstrap replicates and the “pairwise deletion” option for missing data. Phylogenetic analyses based on a concatenated data-set (*COI* + *COII* + *Cytb*) of seven species (*M. zhengi* **sp. nov.**, *M. externus* Wang & Bu, 2020, *M. furcatus* Štys, 1967, *M. gibbus* Zheng, Zou & Hsiao, 1979, *M. inconspicuous* Štys, 1967, *M. noduliferus* Zheng, Zou & Hsiao, 1979, and *M. sinicus* Štys, 1967) were carried out by using both maximum likelihood (ML) and Bayesian inference (BI) methods. The ML tree was constructed in IQ-TREE (Nguyen, *et al.* 2015; Guindon *et al.* 2010; Minh *et al.* 2013) under the models selected for each identified partition with 10,000 ultrafast bootstraps. The BI tree was constructed in MrBayes v3.2 (Ronquist *et al.* 2012), the most appropriate model of sequence evolution (*GTR* + *I* + *G*) was selected using PartitionFinder 2 (Lanfear *et al.* 2016) and four chains were run for 5 million generations and sampling every 200th generation.

Taxonomy

Malcus zhengi Wang & Bu **sp. nov.** (Fig. 1)

Description. Large and robust species. General ground color dark brown. Head, 1st antennal segment reddish brown, 4th antennal segment black. Collar of pronotum and posterior pronotal lobe dark brown. Pronotal callar region, median line, scutellum and corial tubercle black. Posteromedial tubercle and posterolateral angle of pronotum dark brown. Clavus and corium brown, apical and basal portions of corium are light in color. Membrane yellowish brown with a few dark brown patches.

Head with erect hairs, shorter than eye's width. Labium reaching between the middle coxae.

Pronotum considerably declivent, without erect hairs, with a distinct black median line, the posterior end of the median line strongly emergent, formed as an oblate tubercle. Posterolateral angle significantly raised, formed as oblong tubercle (Fig. 1C). Lateral margin of pronotum with 9–10 small teeth.

Abdominal laterotergite V only slightly outwardly expanding, triangular, lateral margin with 3–4 small teeth; laterotergite VI expanding outwardly into a hook shape, lateral margin with regular small teeth; laterotergite VII significantly outwardly expanding, trapezoidal. The front part of lateral margin of laterotergite VII is provided with 6–7 small teeth, with an obvious notch in the middle, and 3–4 small teeth after the notch (Fig. 1D).

Membrane slightly surpassing the tip of abdomen.

The 7th ventrite of male without any processes.

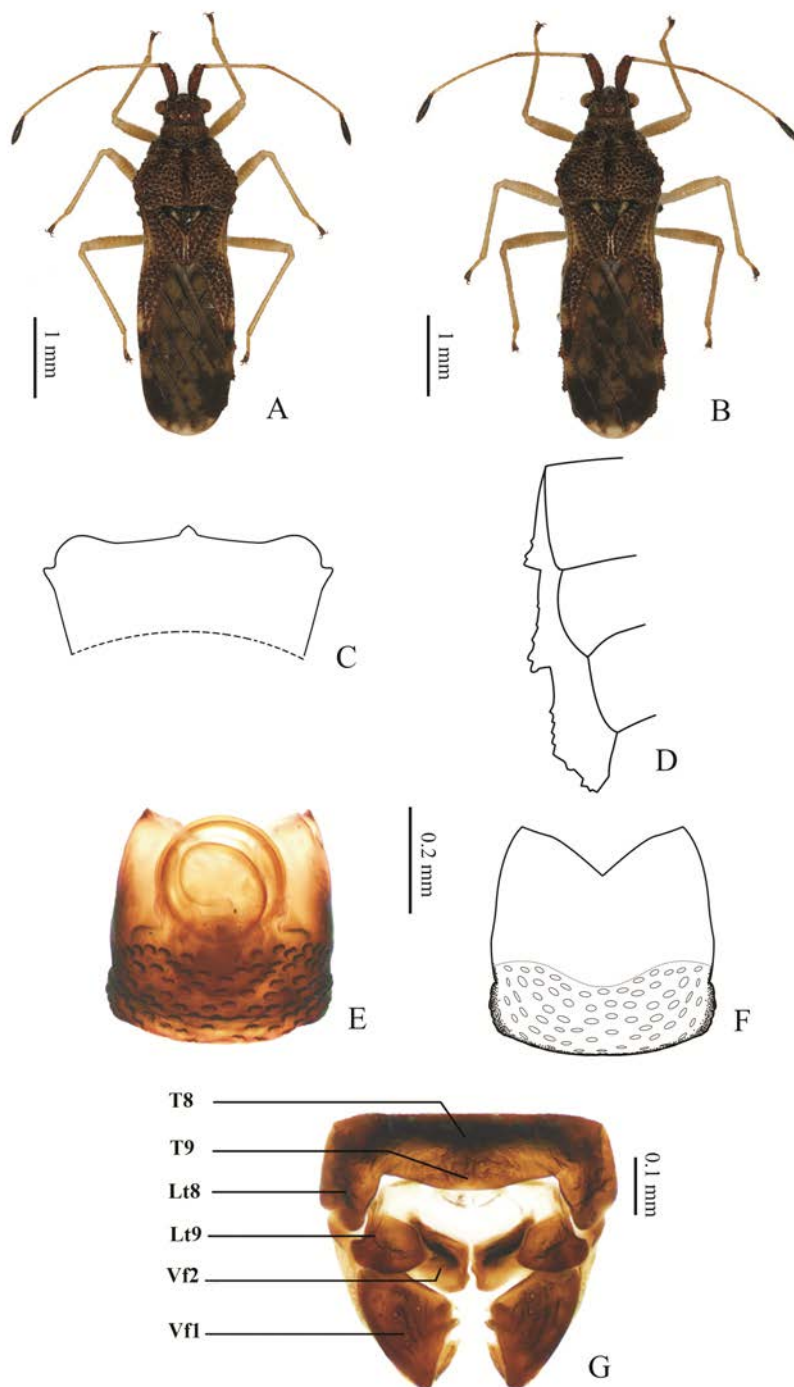


Figure 1. *M. zhengi* sp. nov. A. Holotype, male, habitus, dorsal view; B. Paratype, female, habitus, dorsal view; C. Pronotum, frontal view; D. Abdominal laterotergites V, VI & VII, ventral view; E, F. Male, pygophore, ventral views; G. Female, external genitalia, posterior view. Abbreviations: T8 – 8th tergum; T9 – 9th tergum; Lt8 – 8th ventral laterotergite; Lt9 – 9th ventral laterotergite; Vf1 – 1st valvifers; Vf2 – 2nd valvifers.

Pygophore broad, slightly convex of distal margin and slightly extending to both sides of distal lateral margin (Figs 1E, 1F).

Female. The 1st valvifers large and triangular. The 2nd valvifers wide and the medial half of each valvifer internally thickened. The 9th ventral laterotergites irregularly oblong. The 8th ventral laterotergites fused with each side of 8th tergum. The 9th tergum immovably fused with the hind margin of 8th tergum (Fig. 1G).

Measurements (includes both males and females). Length of body: 4.35–4.43 mm. Length of first segment of antenna: 0.4–0.45 mm; second 0.83–0.85 mm; third 1.06–1.12 mm and fourth 0.4–0.45 mm; total length of antenna 2.80–2.96 mm; length of pronotum 0.90–0.95 mm; length of clavus 0.52–0.55 mm; length of membrane 2.24–2.28 mm. Width of head (include width of eyes) 0.74–0.75 mm; maximum width of pronotum 1.30–1.38 mm; minimum width of hemelytra 1.05–1.1 mm.

Holotype. ♂, **China**, Xizang, Nyingchi City, Zayu County, next to the highway of Ping'an Hotel, alt. 1254 m, 97.017E 28.5014N, 06-VIII-2019, Jingyu LIANG & Kun JIANG leg. **Paratypes.** 1♂5♀, same data as the holotype. Type specimens are deposited in the insect collection of Institute of Entomology, College of Life Sciences, Nankai University, Tianjin, China.

Etymology. This species is dedicated to Prof. Leyi ZHENG to thank him for providing an outstanding work on *Malcus* in China.

Remarks. The developed posteromedial pronotal tubercle closely resembles *M. tuberculatus* Štys, *M. subauriculatus* Zheng, Zou & Hsiao and *M. noduliferus* Zheng, Zou & Hsiao, but these three species are without any erect hairs on head and the shape of abdominal laterotergite VII triangular which differs from the trapezoidal shape of *M. zhengi*. *M. externus* Wang & Bu is also distributed in Xizang, but *M. externus* is of a flat pronotum, abdominal laterotergite VI significantly large and pygophore without any extension of distal lateral margin.

The evidence based on molecular data

The minimum interspecific genetic distance of *M. zhengi* **sp. nov.** based on *COI* is 11.12% from *M. externus* (Table 1). The minimum interspecific genetic distance of *M. zhengi* **sp. nov.** based on (*COI* + *COII* + *Cytb*) data-sets is 13.33% to *M. externus* (Table 2).

Table 1. Kimura 2-parameter pairwise *COI* genetic distances of species in *Malcus*

	1	2	3	4	5	6	7
<i>M. zhengi</i> sp. nov.							
<i>M. externus</i> Wang & Bu, 2020	0.1112						
<i>M. subauriculatus</i> Zheng, Zou & Hsiao, 1979	0.1314	0.1266					
<i>M. furcatus</i> Štys, 1967	0.1295	0.1281	0.0357				
<i>M. sinicus</i> Štys, 1967	0.1343	0.1450	0.1428	0.1331			
<i>M. noduliferus</i> Zheng, Zou & Hsiao, 1979	0.1201	0.1232	0.1212	0.1141	0.1262		
<i>M. inconspicuous</i> Štys, 1967	0.1527	0.1562	0.1563	0.1521	0.1518	0.1402	

Table 2. Kimura 2-parameter pairwise (*COI* + *COII* + *Cytb*) genetic distances of species in *Malcus*

	1	2	3	4	5	6	7
<i>M. zhengi</i> sp. nov.							
<i>M. externus</i> Wang & Bu, 2020	0.1333						
<i>M. subauriculatus</i> Zheng, Zou & Hsiao, 1979	0.1503	0.1473					
<i>M. furcatus</i> Štys, 1967	0.1495	0.1489	0.0452				
<i>M. sinicus</i> Štys, 1967	0.1479	0.1541	0.1529	0.1509			
<i>M. noduliferus</i> Zheng, Zou & Hsiao, 1979	0.1364	0.1419	0.1394	0.1390	0.1326		
<i>M. inconspicuous</i> Štys, 1967	0.1666	0.1620	0.1701	0.1705	0.1621	0.1511	

The ML tree and BI tree based on (*COI* + *COII* + *Cytb*) data-sets of seven morphospecies within the genus *Malcus* reveals four similar distinct genetic clusters (Fig. 2). All trees show that *M. zhengi* sp. nov. is closely related to *M. externus*. However, the significant morphological differences (different shapes of pronotum and abdominal laterotergites) and the sufficient genetic distance between these two close species suggest that *M. zhengi* is a distinct species new to science.

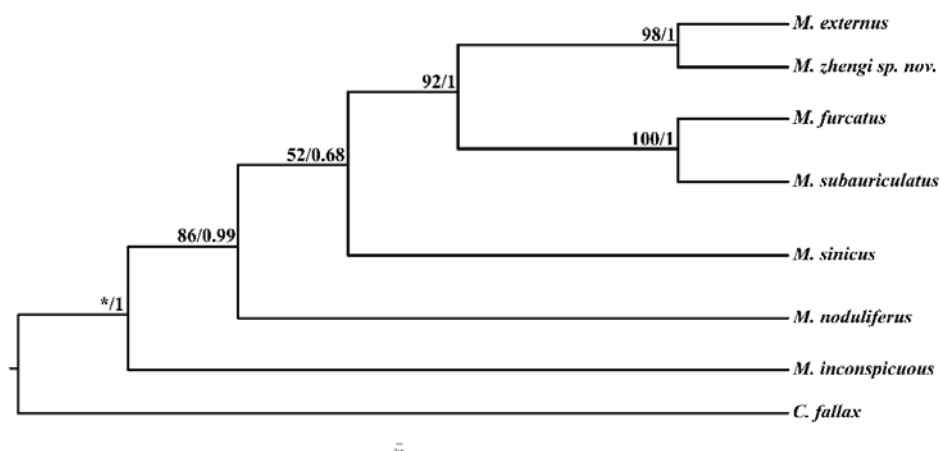


Figure 2. ML and BI tree inferred from (*COI* + *COII* + *Cytb*) data-sets. Bootstrap support and posterior probabilities are indicated at nodes.

Acknowledgements

This study received financial support from the National Natural Science Foundation of China (31820103013, 31430079) and the Project of Ministry of Science and Technology of the People's Republic of China (2015FY210300).

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