A new species in the genus *Anthocoris* (Heteroptera: Anthocoridae) from China based on morphological and molecular data

Zechen TANG, Ying WANG, Xujin HE, Siying FU①, Wenjun BU①

College of Life Sciences, Nankai University, Tianjin 300071, China

Abstract: Based on morphological and molecular evidence, a new species in the genus *Anthocoris*, *Anthocoris zhangi* **sp. nov.**, in the *A. chibi* group, is described from Zhejiang, China. Illustrations of the adults and key diagnostic characteristics including the paramere are provided.

Key words: taxonomy; morphology; pirate bugs

基于形态及分子证据记述中国原花蝽属一新种（半翅目：花蝽科）

汤泽辰，王莹，贺煦锦，傅思颖①，卜文俊①

南开大学生命科学学院，天津 300071

摘要：基于形态及分子证据记述中国浙江原花蝽属小原花蝽群 1 新种：张氏原花蝽 *Anthocoris zhangi* **sp. nov.**，提供了成虫、重要鉴别特征及抱器图片。

关键词：分类；形态学；花蝽

Introduction

The genus *Anthocoris* Fallén, 1814 (Heteroptera: Anthocoridae) represents the second largest genus within the family Anthocoridae, with most species being medium to large in body size. This genus exhibits high diversification across the Qinghai-Tibet Plateau and its surrounding mountainous regions. Comprising approximately 80 described species, 37 species of *Anthocoris* have been recorded in China and are distributed among nine species groups (Bu & Zheng 2001; Yamada & Yasunaga 2021).

Among them, the *A. chibi* group is characterized by its smaller body size and includes two previously-described species distributed in eastern China, Japan, Korea, and the Far East of Russia. In this study, we describe a new species belonging to this group based on morphological and molecular data.

Material and methods

All specimens examined in this study are housed in the collection of the Institute of

Accepted 10 July 2025. Published online 4 December 2025.

① Corresponding authors, E-mails: nkufsy@163.com; wenjunbu@nankai.edu.cn

Entomology, Nankai University Museum (NKUM), Tianjin, China. Images of the dorsal view of the insect body and the abdominal apex were captured using a Canon EOS 90D digital camera in conjunction with associated imaging software. The paramere was meticulously extracted from the terminal abdominal segments, cleared by boiling in a potassium hydroxide (KOH) solution, and subsequently mounted on microscope slides for detailed observation. Photographic documentation of the parameres was carried out using an Olympus BX53 microscope equipped with a Canon Olympus DP72 digital camera and processed with CellSens Standard Software.

Genomic DNA was isolated from body tissues, excluding head and abdomen, using the Universal Genomic DNA Kit (CWBIO, China). Subsequent library preparation and high-throughput sequencing was conducted on the Illumina NovaSeq 6000 platform. The sequencing process utilized a paired-end strategy with a read length of 150 bp and an insert size of 350 bp, yielding 150 bp paired-end reads for downstream analysis. The *COI*, *COII*, and *Cytb* (with evolutionary rates relatively slow) were analyzed using Geneious v9.1.4 software (Kearse *et al*. 2012).

Genetic distance estimates based on the *COI* and (*COI* + *COII* + *Cytb*) datasets were calculated using MEGA X (Kumar *et al*. 2018) with the Kimura 2-Parameter (K2P) substitution model, 1,000 bootstrap replicates, and the "pairwise deletion" option for handling missing data. With the exception of the newly-described species *A. zhangi* **sp. nov.**, all remaining taxa are classified into four species groups: *A. pilosus* (Jakovlev, 1876) and *A. sibiricus* Reuter, 1875 belonging to the *sibiricus* group; *A. chibi* Hiura, 1959 belonging to the *chibi* group; *A. montanus* Zheng, 1984 and *A. kerzhneri* Bu & Zheng, 2001 belonging to the *nemorum* group; and *A. thibetanus* Poppius, 1909 and *A. hsiaoi* Bu & Zheng, 1991 belonging to the *thibetanus* group. Both Maximum Likelihood (ML) and Bayesian Inference (BI) methods were utilized for the analysis.

Under the guidance of the Bayesian Information Criterion (BIC), ModelFinder (Kalyaanamoorthy *et al*. 2017) was used in this study to optimize the partitioning schemes and substitution models for both ML and BI analyses. The ML analysis was conducted using IQ-TREE v2.2.0 (Minh *et al*. 2020), with 1,000 ultrafast bootstrap approximation approach (UFBoot2) replicates (Hoang *et al*. 2018) for support estimation. For the BI analysis, we employed MrBayes 3.2.7a (Ronquist *et al*. 2012), as implemented in PhyloSuite 1.2.3 (Zhang *et al*. 2020). Two independent Markov Chain Monte Carlo (MCMC) runs were performed, each spanning 10 million generations, with tree sampling every 1,000 generations. The first 25% of the sampled trees were discarded as burn-in. Convergence of the chains was assessed using TRACER v1.7 (Rambaut *et al*. 2018), ensuring the robustness of the phylogenetic inferences.

Taxonomy

***Anthocoris zhangi* Tang, Fu & Bu sp. nov.** (Fig. 1)

Description. Coloration. Head blackish brown; eyes reddish black; margin of ocellus light white to red. Male antenna blackish brown. Female antenna segment I blackish brown, 4/5 of segment II yellowish brown, basal half of segment III yellowish brown, segment IV blackish brown. Pronotum, scutellum, claval suture, corium, clavus, endocorium and callus

overall blackish brown; female basal half of exocorium brown. Cuneus wholly black, male inner apex of cuneal suture with a pale spot. Membrane evenly grayish, apical half greyish brown. Legs reddish brown to blackish brown. Female 8th abdominal segment medially yellowish-brown.

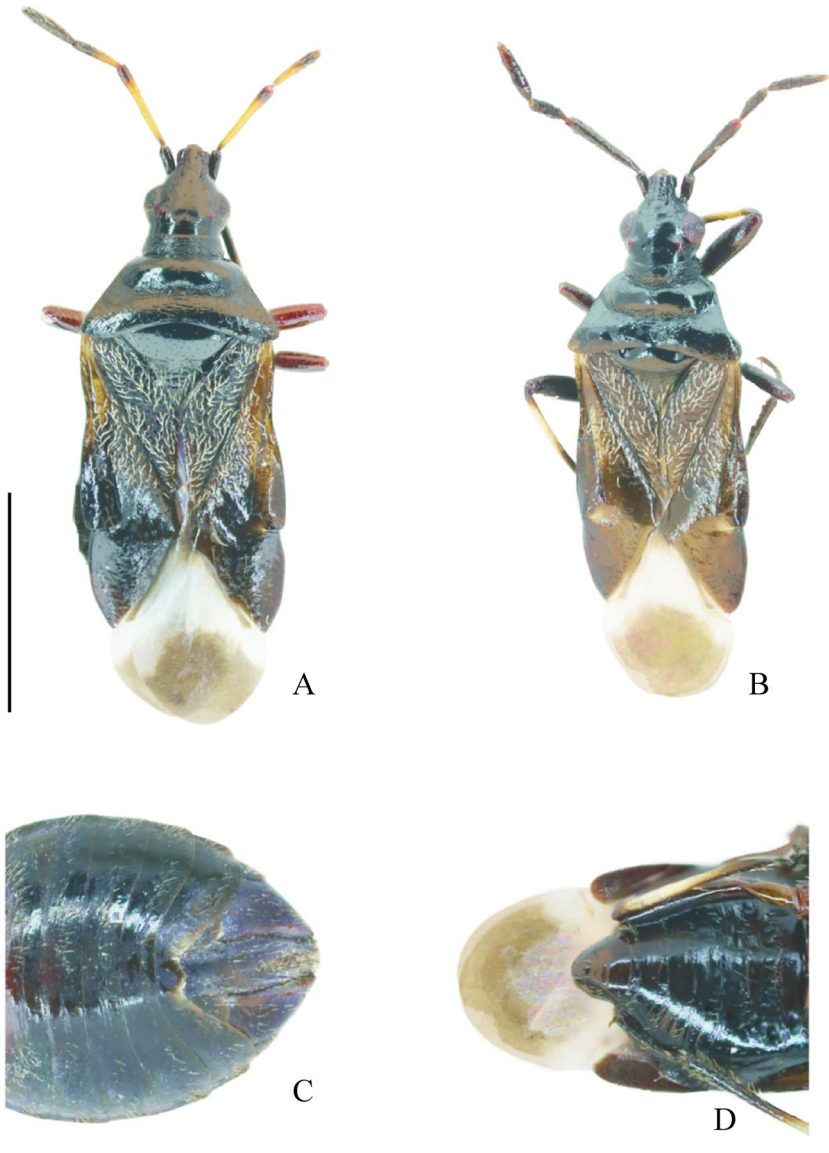

Figure 1. *Anthocoris zhangi* Tang, Fu & Bu **sp. nov**. A, B. Habitus of female and male, dorsal views; C, D. Abdomen of female and male, ventral views. Scale bars = 1.0 mm.

Structure. Male body elongate, smaller than female; female body elongately oval, with slightly broader abdomen. Head cylindrical. Vertex smooth, anteocular region slightly longer than length of eye in dorsal view. Eyes oblong. Antennal hairs mostly decumbent, not longer than segment diameter. Pronotum smooth, lateral margin slightly sinuate. Collar distinctly

rugulose. Callus area comparatively large, moderately swollen, smooth. Hemelytra covered with short golden brown denser pubescence, mostly decumbent. Abdominal dorsal plate covered with decumbent long sparse pubescence, sometimes exhibiting a slight expansion (Figs 1C, 1D, 2A). Female 9th gonocoxite covered with multiple short, stout setae (Fig. 1C).

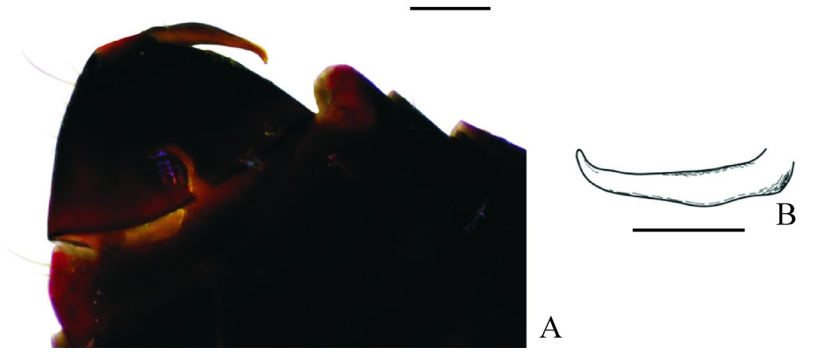

Figure 2. *Anthocoris zhangi* Tang, Fu & Bu **sp. nov**. A. Male genitalia; B. Paramere. Scale bars = 0.1 mm.

Measurements. Body length 2.36–3.07 mm; width 0.79–1.06 mm; head width 0.40–0.44 mm; head length 0.42–0.51 mm; pronotum length 0.39–0.45 mm; pronotum width 0.79–0.93 mm; segments length: I 0.12–0.17 mm, II 0.38–0.43 mm, III 0.19–0.23 mm, IV 0.27–0.36 mm; scutellum length 0.31–0.38 mm; scutellum width 0.42–0.56 mm; collar width 0.36–0.41 mm. (male 2/female 2)

Holotype. ♂, **China**, Zhejiang, Hangzhou City, Lin'an District, Qingliangfeng National Nature Reserve, 1,100–1,787 m, 23-V-2012, Haiguang ZHANG. **Paratype.** 1♀, **China**, Zhejiang, Hangzhou City, Lin'an District, Qingliangfeng National Nature Reserve, 1,100–1,787 m, 23-V-2012, Haiguang ZHANG.

Diagnosis. Recognized by the following combination of characters: Body dark brown to black, with the head and callus of pronotum black (Figs 1A, 1B). Male smaller than female, parallel-sided and slightly broader abdomen in female. Pronotal pubescence short, dense, golden brown. Male antenna blackish brown; in female, 4/5 of segment II and basal portion of segment III yellow to yellow-brown, with the remainder dark brown. Clavus and endocorium dark brown; male exocorium blackish brown, female basal half of exocorium brown. Cuneus blackish brown. Membrane evenly pale greyish, apical half greyish brown. Paramere slender, basal half of portion slight expanded, inner margin curved, gradually pointed apex (Fig. 2).

Remarks. The new species is similar to *A. chibi* in body form, color pattern and size; but differ in paramere with different curvature and contour.

The etymology is derived from the collector of the holotype, Dr. Haiguang ZHANG, who now works at Linyi University, Shandong, China.

Evidence based on molecular data. The minimum interspecific genetic distance for *A. zhangi* **sp. nov.** is 13.68% based on the *COI* dataset, with *A. chibi* being the closest species (Table 1). Similarly, using the combined dataset (*COI* + *COII* + *Cytb*), the minimum genetic distance is 13.69%, also with *A. chibi* as the closest relative (Table 2). In both the *COI* and combined datasets, these interspecific genetic distances are significantly higher than the average interspecific level.

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

	1	2	3	4	5	6	7
A. montanus Zheng, 1984							
A. thibetanus Poppius, 1909	0.1213						
A. hsiaoi Bu et Zheng, 1991	0.1221	0.0603					
A. chibi Hiura, 1959	0.1377	0.1393	0.1322				
A. kerzhneri Bu, 2001	0.0504	0.1292	0.1285	0.1386			
A. sibiricus Reuter, 1875	0.1474	0.1369	0.1386	0.1426	0.1457		
A. pilosus (Jakovlev, 1876)	0.1500	0.1332	0.1404	0.1487	0.1483	0.1015	
A. zhangi **sp.nov.**	0.1518	0.1592	0.1693	0.1368	0.1634	0.1534	0.1479

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

	1	2	3	4	5	6	7
A. montanus Zheng, 1984							
A. thibetanus Poppius, 1909	0.1200						
A. hsiaoi Bu et Zheng, 1991	0.1204	0.0498					
A. chibi Hiura, 1959	0.1381	0.1371	0.1353				
A. kerzhneri Bu, 2001	0.0477	0.1232	0.1241	0.1384			
A. sibiricus Reuter, 1875	0.1530	0.1475	0.1516	0.1568	0.1545		
A. pilosus (Jakovlev, 1876)	0.1431	0.1348	0.1430	0.1566	0.1423	0.1163	
A. zhangi **sp.nov.**	0.1441	0.1507	0.1545	0.1369	0.1523	0.1759	0.1610

The ML tree and BI tree based on (*COI* + *COII* + *Cytb*) data-sets of eight morphospecies within the genus *Anthocoris* reveal four distinct genetic clusters, corresponding to the four species groups (Fig. 3). All trees show that *A. zhangi* **sp. nov**. is closely related to *A. chibi*. Combined with their similar morphological characteristics, we conclude that *A. zhangi* **sp. nov**. belongs to the *A. chibi* group.

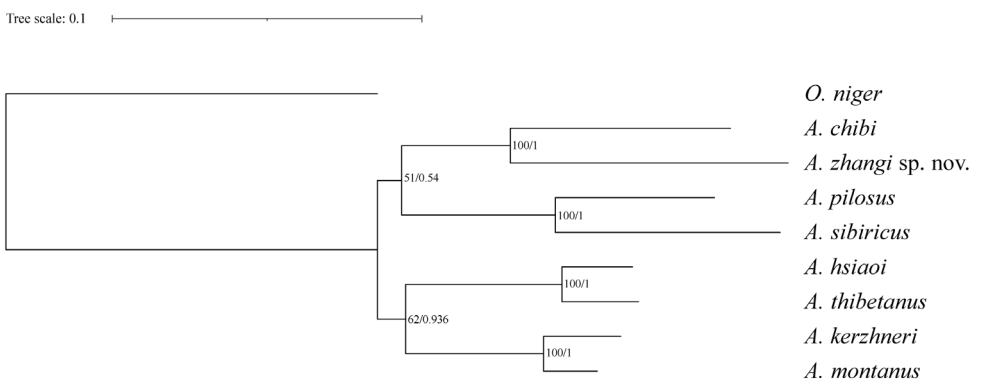

Figure 3. ML and BI tree inferred from (*COI* + *COII* + *Cytb*) data-sets. Bootstrap support and posterior probabilities are indicated at nodes.

Acknowledgements

We thank Prof. Baofa SUN for his support in server computing. This research was supported by the Basic Research Program of National Natural Science Foundation of China (32300377; 32130014; 32400359).

References

Bu WJ & Zheng LY. 2001. Hemiptera: Lasiochilidae Lyctocoridae Anthocoridae. *Fauna Sinica, Insecta*, 24: 1–267.

Hoang DT, Chernomor O, Von Haeseler A, Minh BQ & Vinh LS. 2018. UFBoot2: improving the ultrafast bootstrap approximation. *Molecular Biology and Evolution*, 35: 518–522.

Kalyaanamoorthy S, Minh BQ, Wong TKF, Haeseler A & Jermiin LS. 2017. ModelFinder: fast model selection for accurate phylogenetic estimates. *Nature Methods*, 14: 587–589.

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: 1647–1649.

Kumar S, Stecher G, Li M, Knyaz C & Tamura K. 2018. MEGA X: molecular evolutionary genetics analysis across computing platforms. *Molecular Biology and Evolution*, 35: 1547–1549.

Minh BQ, Schmidt HA, Chernomor O, Schrempf D, Woodhams MD, Von Haeseler A & Lanfear R. 2020. IQ-TREE 2: new models and efficient methods for phylogenetic inference in the genomic era. *Molecular Biology and Evolution*, 37: 1530–1534.

Rambaut A, Drummond AJ, Xie D, Baele G & Suchard MA. 2018. Posterior summarization in Bayesian phylogenetics using Tracer 1.7. *Systematic Biology*, 67: 901–904.

Ronquist F, Teslenko M, Van Der Mark P, Ayres DL, Darling A, Höhna 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: 539–542.

Yamada K & Yasunaga T. 2021. The tribe Anthocorini in Japan (Hemiptera: Anthocoridae): descriptions of new species, review of distribution and bionomics. *Acta Entomologica Musei Nationalis Pragae*, 61(2): 375–426.

Zhang D, Gao FL, Jakovlić J, Zou H, Zhang J, Li WX & Wang GT. 2020. PhyloSuite: An integrated and scalable desktop platform for streamlined molecular sequence data management and evolutionary phylogenetics studies. *Molecular Ecology Resources*, 20: 348–355.