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Syscia chinensis sp. nov., a tiny novel ant species of *Syscia* (Hymenoptera, Formicidae, Dorylinae) from Southwest China

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ABSTRACT. The ants of genus *Syscia*, are cryptic with an unequal distribution in Asia and the Americas; Currently, there are 34 species known in the New World, but only a mere 10 species are recognized in Asia. The New World species have been systematized, whereas Old World species are currently still at the stage of isolated species descriptions. Herewith a new species, namely *Syscia chinensis* **sp. nov.**, is described and illustrated based on the worker caste. *S. chinensis* is the first species reported with 10-segmented antennae in this genus, and it is also one of the smallest minority species in this genus. These two characteristics readily distinguish the new species, and these morphological differences are supported by a phylogenetic analysis. A key based on the worker caste is provided for the known Asian species.

Keywords	Dorylinae, 10-segmented antennae, Yunnan province, China, taxonomy, Phylogenetic
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INTRODUCTION

The ant genus *Syscia*, initially defined by Roger in 1861 with the Sri Lankan species *S. typhla* as the type species, now comprises 42 valid species (Aswaj et al. 2021; Bolton 2024). These species are recorded in Asia, North America, and South America, exhibiting a pattern of disjunct distribution (Borowiec 2016) in 16 countries or regions (Borowiec 2016; Jaitrong et al. 2020; Aswaj et al. 2021; Longino and Branstetter 2021; Bolton 2024). These ants are often found in soil or leaf litter and are considered part of the cryptobiotic fauna (Jaitrong et al. 2020; Longino & Branstetter 2021).

In more than 160 years since the establishment of the genus *Syscia*, the taxonomic status of the genus has undergone many changes. Because of its similarity to the genus *Cerapachys* Smith, 1857, myrmecologists have different views in the process of taxonomic research. Dalla Torre (1893), Forel (1900) and Bingham (1903) regarded *Syscia* as a valid genus, while Wheeler (1902, 1910, 1922), Emery (1902, 1911), Forel (1917) and Donisthorpe (1943) regarded it as a subgenus of *Cerapachys*. Kempf (1972) and Brown (1975) treated *Syscia* as a junior synonym of *Cerapachys*. It was not until the past decade that myrmecologists reconfirmed the taxonomic status of *Syscia* as a valid genus through phylogenetic inference from molecular data (Brady 2014; Borowiec 2016).

Borowiec (2016) defined the diagnostic features of *Syscia* as: Antennae with nine or 11 segments; eyes small or absent; body with densely sculptured and abundant pilosity; body color relatively uniform, with yellow, red or dark brown but never black; posterior tarsus basal segment widened distally, with a light-colored patch of cuticle medially (flexor); abdominal tergite iv anteriorly folding over sternite.

Yamane & Mizuno (2024) described two species of *Syscia* from Sabah, Borneo. Currently, there are 34 species known in the New World, with ten species recognized in Asia (Bolton 2024). Here we report on a new species with 10-segmented antennae from China. Before this study, three *Syscia* species had already been recorded in China. Du et al. (2024) removed *S. typhla* Roger 1861 from the ant fauna of China, moved *Ooceraea guizhouensis* (Zhou 2006) into *Syscia*, and added two new species: *S. arcodorsa* Du et al., 2024 and *S. zhoui* Du et al., 2024. Including the new species described herein, there are four species known from China. A key to all known Asia species and a map of the distribution data of the Chinese species is provided.

MATERIALS AND METHODS

The specimens were collected in the field by sample-plot and search-collecting methods (e.g., Xu 2002) in Huanglianshan National Nature Reserve, Lvchun County, Honghe Prefecture, Yunnan Province, China, between 102. 03930 ~ 102. 61638E, 22. 50525 ~ 22. 92658N (Fig. 1). Thirteen workers were collected from the same soil nest. All the samples were preserved in 75% ethanol for transport back to the insect herbarium of the Kunming Natural History Museum of Zoology. The specimens were cleaned and organized in the laboratory. Subsequently, they were prepared as dry specimens and point-mounted. The specimens were identified using a SDPTOP-SZM stereomicroscope, photographs were taken of the multilayered superimpositions using a Keyence VHX-6000 digital microscope, and the images were combined into graphics using Adobe Photoshop 2020. Maps were constructed using the software package ArcGIS v. 10.8.2. Comparisons were made with species from China (Zhou 2006; Du et al. 2024). Morphological terminology follows Borowiec (2016), Jaitrong et al. (2020) and Aswaj et al. (2021). The key was prepared using the examined specimens, images available on AntWeb (2024) and AntWiki (2024), and original descriptions of the species. All measurements are in millimeters.

TL	Total length: total length of head, mesosoma, petiole and gaster in lateral view
HL	Head length: length from the anterior of clypeus to the posterior of head in full-face view
HW	Head width: width of head in full-face view
SL	Scape length: straight-line length of the antennal scape, excluding the basal constriction or neck
PrW	Pronotal width: width of pronotum in dorsal view
WL	Weber's length: diagonal length of mesosoma in lateral view
PL	Petiolar length: length of petiole in lateral view (excluding helcium)
PH	Petiolar height: height of petiole in lateral view (including subpetiolar process)
PW	Petiolar width: width of petiole in dorsal view
PpL	Postpetiolar length: length of postpetiole in lateral view (excluding helcium)
PpH	Postpetiolar height: height of postpetiole in lateral view
PpW	Postpetiolar width: width of postpetiole in dorsal view

AIVL abdominal tergite IV length: length of abdominal tergite IV in lateral view
AIVH abdominal tergite IV height: height of abdominal tergite IV in lateral view
AIVW abdominal tergite IV width: width of abdominal tergite IV in dorsal view
CI Cephalic index: HW/HL × 100
SI Scape index: SL/HW × 100
PI1 Petiolar index one: PL/PH × 100
PI2 Petiolar index two: PW/PL × 100
PPI1 Postpetiolar index one: PPL/PPH × 100
PPI2 Postpetiolar index two: PPW/PPL × 100
AIVI1 abdominal tergite index one: AIVL/AIVH × 100
AIVI2 abdominal tergite index two: AIVW/AIVL × 100
WI Waist index: PPW/PW × 100

To confirm the taxonomic status of *Syscia chinensis* **sp. nov.** and evaluate its phylogenetic placement within the genus, we generated mitochondrial COI sequences for comparative analysis with published data from other *Syscia* species. DNA extraction of tissue fragments from ants was performed using the TSINGKE TSP202-50 Trelief® Hi-Pure Animal Genomic DNA Kit following manufacturer instructions. The standard cytochrome oxidase subunit I (COI) barcoding fragment (Hebert et al. 2003) was amplified using the primers LCO1490 (GGTCAACAAATCATAAAGATATTGG) and HCO2198 (TAAACTTCAGGGTGACCAAAAAATCA) (Folmer et al. 1994). Amplification was performed using TSINGKE Gold Mastermix (green), PCR reactions contained. PCR was performed using an initial denaturation step of two min at 98 ℃, followed by 30 cycles of 10 s at 98 ℃, 10 s at 50 ℃ and 10 s at 72 ℃, and finishing with an extension of five min at 72 ℃. The amplified PCR products were subjected to agarose gel electrophoresis (two ul sample + six ul bromophenol blue) at 300V for 12 min to obtain the identification gel graphs. The products were purified and sequenced by Tsingke Biotechnology (Beijing) Co., Ltd., using the same primers as in PCR. Sequences were edited using SeqMan in Lasergene 7.1 (DNASTAR Inc., Madison, WI, USA) and MEGA 11 (Tamura et al. 2021).

The COI sequences were compared to 35 COI sequences of subfamily Dorylinae species (33 *Syscia* and two outgroup specimens from the genus *Ooceraea* Roger, 1862 and *Chrysapace* Crawley, 1924) downloaded from the National Center for Biotechnology Information (NCBI) GenBank database using PhyloSuite v1.2.2 (Zhang 2020), for which data were extracted from Borowiec (2019), Branstetter et al. (2017), Longino & Branstetter (2021) and Yamada & Eguchi (2019), with their accession numbers listed in Suppl Table S3.

Sequences were aligned using ClustalW (Thompson et al. 2002) in MEGA 11 (Tamura et al. 2021) with default parameters. Genetic divergence (uncorrected p-distance) between species was calculated in MEGA 11. The best substitution model HKY+G+I was selected using the Akaike Information Criterion (AIC) in ModelFinder (Nei and Kumar 2000). The evolutionary history was inferred by using the Maximum Likelihood method based on the Hasegawa-Kishino-Yano model, and nodal support was estimated by 1,000 rapid bootstrap replicates in MEGA 11. Bayesian Inference phylogenies were inferred using MrBayes v3.2.7a (Ronquist et al., 2012) under GTR+I+G+F model (2 parallel runs, 2000000 generations, average standard deviation of split frequencies: 0.008), in which the initial 25% of sampled data were discarded as burn-in. Phylogenetic trees were edited with iTOL v5 (Letunic and Bork 2021).

Institutional abbreviations

KIZ Kunming Natural History Museum of Zoology, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, Yunnan Province, China

SWFU Insect Collection, Southwest Forestry University, Kunming, Yunnan Province, China

GXNU Insect Collection, Guangxi Normal University, Guilin, Guangxi, China

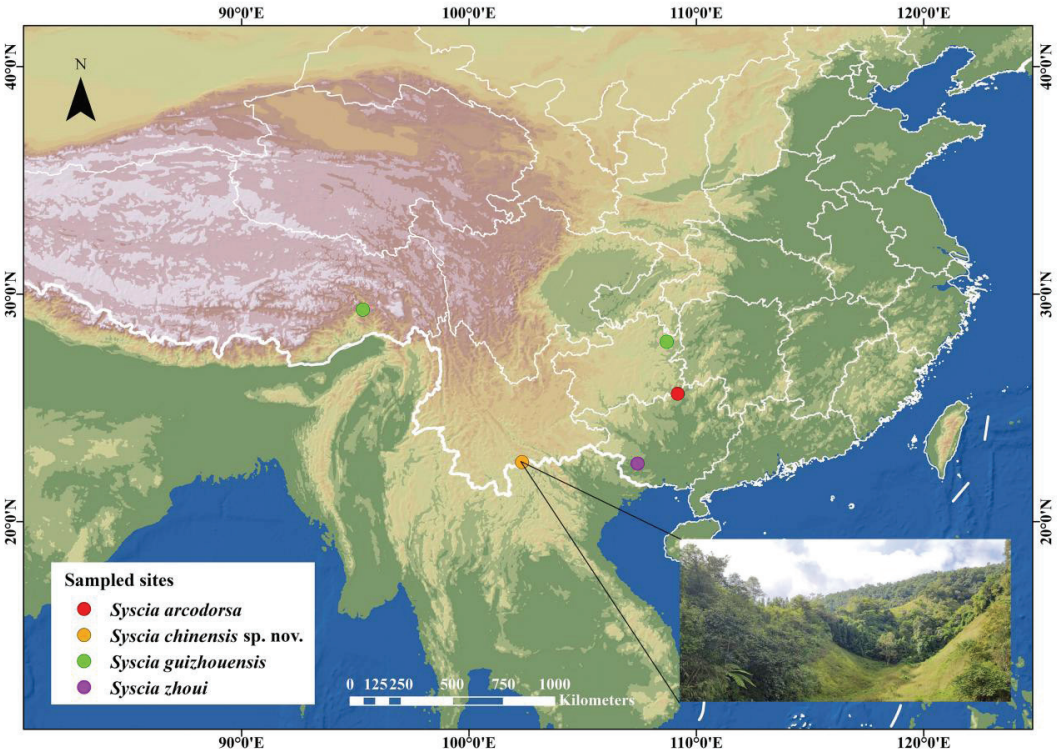

Fig. 1. The sampled sites of four species of genus *Syscia* distributed in China (Source: Drawing approval number: GS (2019) 1823. ArcGIS v. 10.8.2.) and habitat at the type locality of *S. chinensis* **sp. nov.** (This map image can be reproduced).

TAXONOMIC RESULTS

***Syscia chinensis* sp. nov. Chen, 2025**
https://zoobank.org/DA141DA3-6EEC-4EA9-A592-2DA513DD416E
Figs. 2 (A-D)

Etymology: The name refers to the terra typica China.

Type material. ***Holotype*:** worker, **CHINA**: Yunnan Province, Honghe Hani and Yi Autonomous Prefecture, Lvchun County, Banpo Township, Mohelongtang, 22.61721 N, 102.33585 E (Fig. 1), 1263 m above sea level, from soil in mixed coniferous and broad-leaved forest, 13.iv.2023, leg. Chao Chen, No. KIZ20230160 (KIZ). ***Paratypes***: five workers, same data as holotype. KIZ20230160A and KIZ20230160B (SWFU); KIZ20230160C and KIZ20230160D (GXNU); KIZ20230160E (KIZ)

Description. Holotype worker: TL 2.52 HL 0.53 HW 0.43 SL 0.21 PrW 0.31 WL 0.68 PL 0.26 PH 0.36 PW 0.26 PpL 0.31 PpH 0.37 PpW 0.38 AIVL 0.48 AIVH 0.39 AIVW 0.47 CI 81 SI 49 PI1 72 PI2 100 PPI1 73 PPI2 123 AIVI1 123 AIVI2 98 WI 146. **Paratype workers:** (n = 5) (Supp 2. Table S1): TL 2.40-2.69 HL 0.49-0.54 HW 0.41-0.43 SL 0.21-0.25 PrW 0.27-0.31 WL 0.62-0.67 PL 0.22-0.25 PH 0.31-0.36 PW 0.26 PpL 0.30-0.37 PpH 0.38-0.39 PpW 0.37-0.39 AIVL 0.48-0.61 AIVH 0.37-0.42 AIVW 0.47-0.50 CI 78-84 SI 51-59 PI1 61-79 PI2 102-120 PPI1 81-96 PPI2 99-130 AIVI1 124-146 AIVI2 78-103 WI 142-151.

In full-face view (Fig. 2A): Head rectangular, longer than broad, lateral margin moderately convex, posterior margin straight and posterior corners narrowly rounded. Frontal carinae extend posteriorly to less than ⅓ head length. Clypeus short, anterior margin weakly convex. Mandibles triangular, masticatory margin denticulate. Eyes absent. Antennae 10-segmented, scape short,

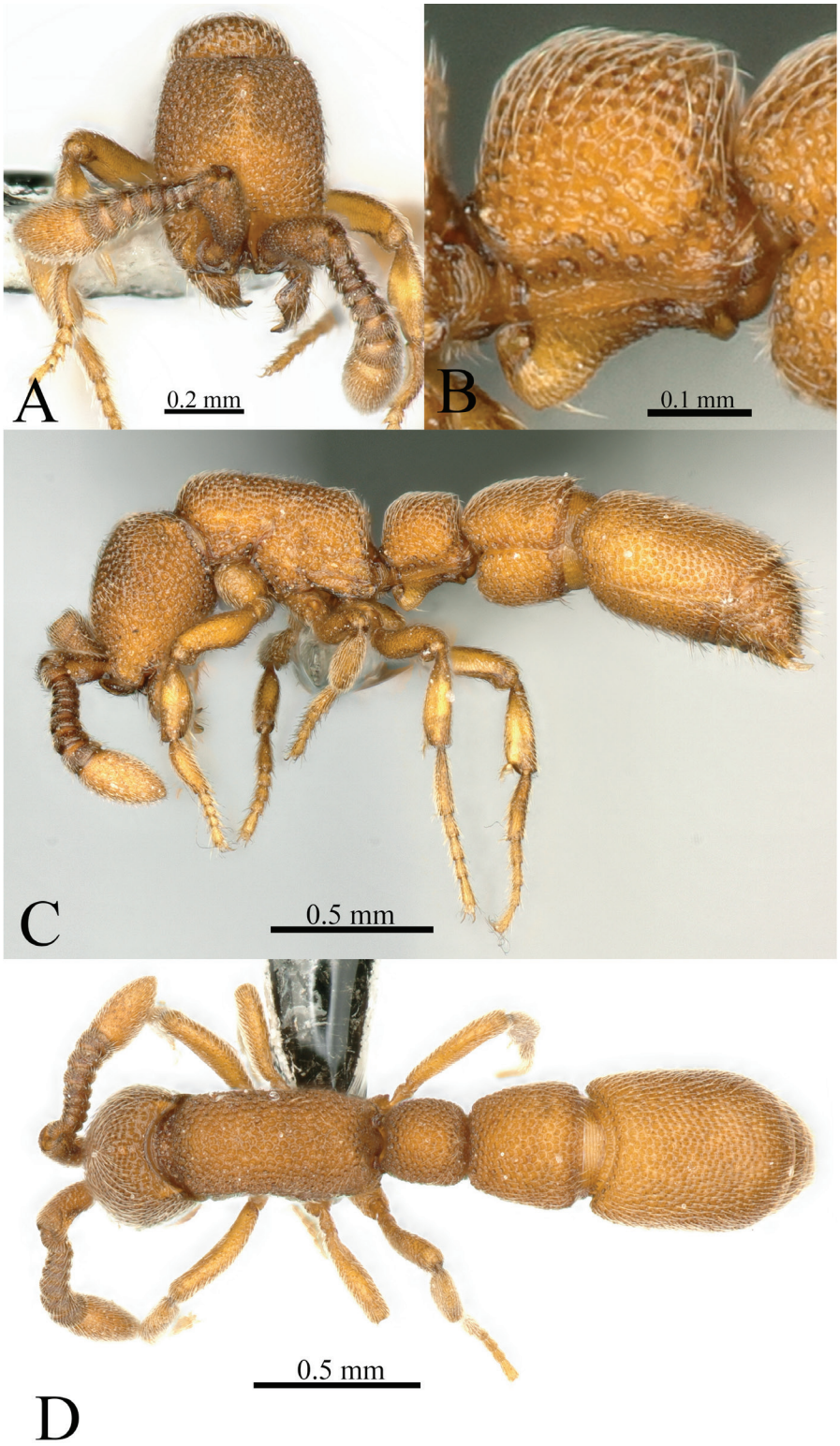

Fig. 2. *Syscia chinensis* **sp. nov.** worker (Holotype, imaged by Chao Chen) (A) head in full-face view (B) Petiolar node in lateral view (C) body in lateral view (D) body in dorsal view.

widened distally, not reaching mid-length of head, antennal segment (x) significantly larger than the rest of the antennal segments (ii-ix).

In lateral view (Fig. 2B, C): Mesosoma in profile view with slightly straight dorsal outline, lateral face of pro-mesonotum suture only reaches half the height of the side of mesosoma, unfused up to notal surface. Mesometapleural groove weakly impressed, transverse groove absent. Pleural endophragmal pit concavity present. Propodeal declivity moderately concave, with a distinct thin rim. Propodeal lobes present, well developed. Petiolar node (excluding sternite) square, roughly equal in length and height; dorsal outline weakly convex; anterior and posterior margins slightly straight. Subpetiolar process subtriangular, with ventral outline concave. Ventrolateral surface of petiole above the subpetiolar process with carinae. Postpetiole slightly higher than long, dorsal outline slightly convex; postpetiolar sternite shallow, ventral margin moderately convex, anteroventrally produced into a blunt angle.

In dorsal view (Fig. 2D): Mesosoma elongate with almost parallel lateral sides, anterior margin convex, cervical shield present, posterior margin weakly concave. Promesonotal suture and metanotal groove absent. Petiole subrectangular, slightly broader than long, lateral margins slightly convex, anterior and posterior margins slightly straight. Postpetiole larger than petiole, trapezoidal, anterior margin straight, posterior margin slightly concave, posterior margin longer than anterior margin, lateral margins slightly convex. Abdominal tergite iv (second gastral tergite) elongate, subrectangular, anterior margin obviously concave, lateral margins weakly convex.

Body entirely yellowish brown (Fig. 2). Entire body with numerous closely-spaced foveolae, entirely reticulate, with deep bottoms. Antennal scape, outer surface of mandibles and legs with fine dense micropunctures. Body entirely covered with sub-erect hairs. Antennae and legs with dense short decumbent hairs.

Comparative notes: *Syscia chinensis* **sp. nov.** is clearly distinguished from all other species in the genus by Antennae having 10 segments (Fig. 2C).

This new species is most similar to *S. arcodorsa*. In full-face view of the new species, posterior margin of head nearly straight; frontal carinae short, less than one-third of head length; anterior margin of clypeus weakly convex (Fig. 2A); in lateral view, mesosoma dorsal outline slightly straight (Fig. 2C); petiolar node (excluding sternite) square, slightly equal in length and height (Fig. 2B). Conversely, in full-face view of *S. arcodorsa*, middle part of posterior margin of head slightly concave; frontal carinae slightly long, less than half of the head length; anterior margin of clypeus almost straight (Supp 1. Fig. S6A); in lateral view, mesosoma dorsal outline strongly convex; petiolar node (excluding sternite) trapezoidal, slightly longer than high (Suppl 1. Fig. S6C).

Distribution: China (Yunnan).

Habitat: It is a forest ecosystem dominated by tropical monsoon forests, mountain rain forests, wet monsoon evergreen broad-leaved forests, and mountain moss evergreen broad-leaved forests; it is an important component and biological corridor of the "Green Triangle" at the junction of China, Vietnam and Laos. The understory herbs are *Ageratina adenophora* (Spreng.) R. M. King & H. Rob. 1826 and Poaceae plants (Fig. 1). This new species nests in wet soil in an open area of a coniferous and broad-leaved mixed forest at an altitude of 1263m and forages on the ground. Temperature at midday sampling was 25℃ and the relative humidity was 40%.

Molecular Phylogenetic Analyses

The phylogenetic trees generated by Bayesian inference and maximum likelihood methods exhibit similar topological structures (Suppl 1. Fig. S11-12). Two specimens of *Syscia chinensis* **sp**. **nov**. (KIZ20230160F and KIZ20230160G), form a separate clade with high support (Bayesian posterior probabilities 1.00; Bootstrap support 100%). The clade nodes of the new species showed weak support when compared with other species in the genus in both tree-building methods, so we cannot determine the exact position of this clade (Fig. 3). Genetic distance to the most closely related species (*S. volucris* and *S. setosa*) was 16.90-16.93% (see Suppl 2. Table S4). These patterns support morphological analyses indicating that *S. chinensis* is a distinct species.

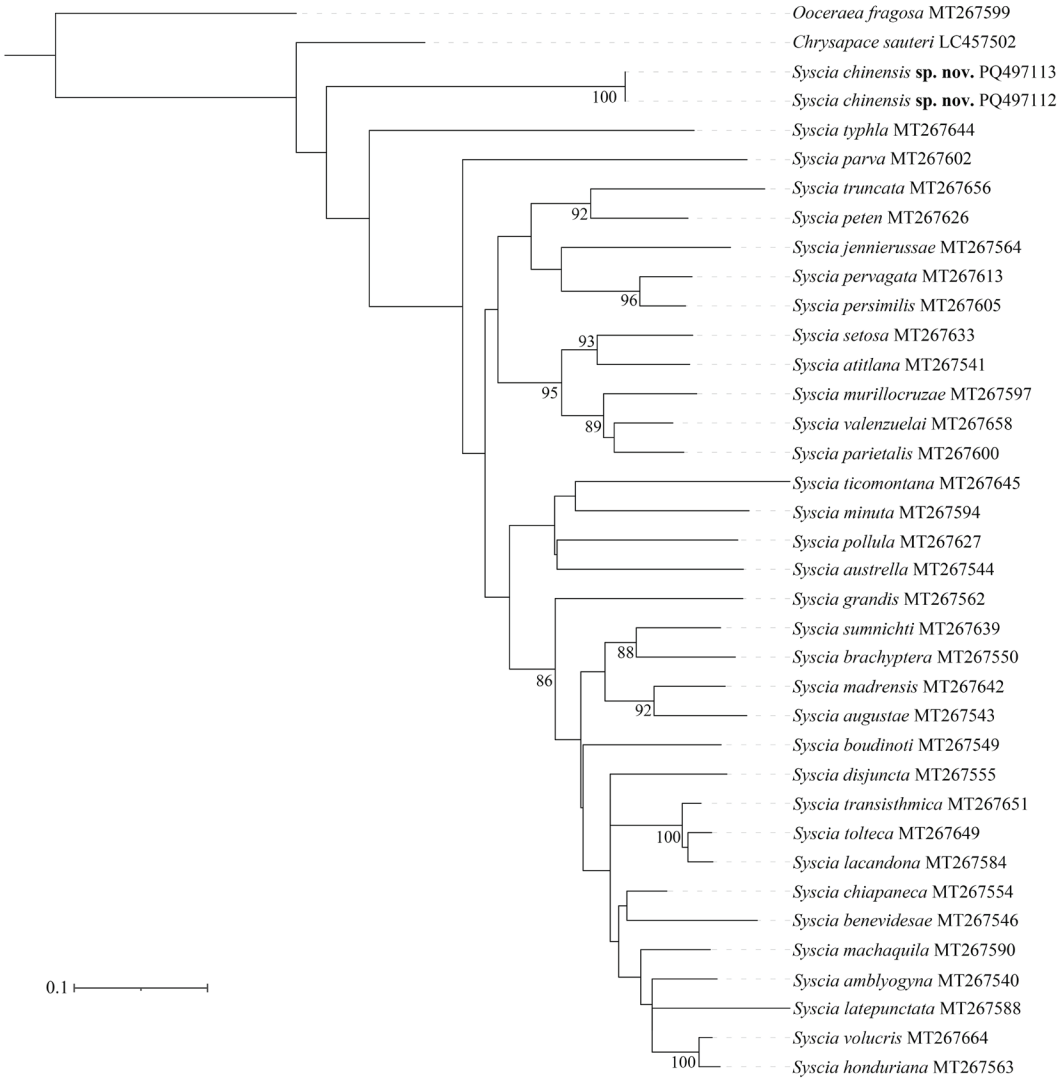

Fig. 3. Maximum likelihood methods phylogenetic tree of *Syscia* species based on COI fragments. Node numbers indicate bootstrap support in maximum-likelihood analyses (values below 70% not shown) (Felsenstein 1985). Note: The scale bar represents the number of nucleotide substitutions per site. A scale bar of 0.1 indicates that a branch length of 0.1 corresponds to an average of 10% nucleotide changes between the sequences compared.

Key to species of *Syscia* found in Asia based on the worker caste

The key is based on the update of Du et al. (2024) for Asian species, with the addition of three species (*Syscia sabahna*, *S. yekzoeae* and *S. chinensis* **sp. nov.**). Most of the species images in this key are in Suppl Figures.

1. Small species, body length less than 3 mm (Fig. 2, S1, S2, S3)..... 2
- Large species, with a body length greater than 3 mm (Fig. S4, S5)..... 5

2. Antennae with 9 or 10 segments (Fig. 4A, B).. 3
- Antennae with 11 segments (Fig. 4C, D)..... 4

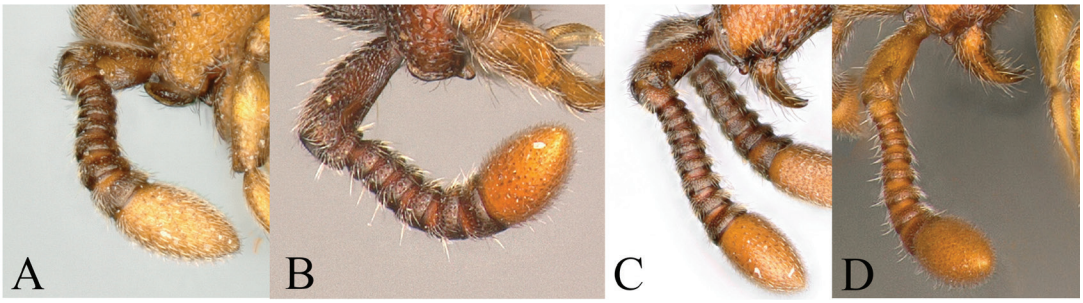

Fig. 4. Antennae segments. (A) *S. chinensis* **sp. nov.** (B) *S. zhoui* Du et al. (C) *S. arcodorsa* Du et al. (D) *S. guizhouensis* (Zhou)

3. Antennae with 9 segments (Fig. S1A); In lateral view, dorsal outline of mesosoma distinctly convex; propodeal declivity sloped (Fig. S1D); Petiole, in dorsal view, lateral margins slightly straight (Fig. S1C); body reddish brown (Sri Lanka, India)..... ..... *Syscia typhla* Roger, 1861
- Antennae with 10 segments (Fig. 2A); In lateral view, dorsal outline of mesosoma straight; propodeal declivity steep (Fig. 2C); Petiole, in dorsal view, lateral margins slightly convex (Fig. 2D); body entirely yellowish brown (China)..... .....*Syscia chinensis* **sp. nov.** Chen, 2025

4. Body entire reticulate, with deep bottoms (Fig. S2); In lateral view, propodeal declivity slightly straight (Fig. S2D) (Thailand, Malaysia ....*Syscia reticularis* Jaitrong et al., 2020
- Body covered with punctures or shallow fovea (Fig. S3); In lateral view, propodeal declivity slightly concave (Fig. S3B) (Malaysia) ....*Syscia sabahna* Yamane & Mizuno, 2024

5. Antennae with 9 segments (Fig. 4B) (China)... ..... *Syscia zhoui* Du et al., 2024
- Antennae with 11 segments (Fig. 4C, D).....6

6. Mesosoma in lateral view, dorsal outline distinctly convex (Fig. S5B, S6C) 7
- Mesosoma in lateral view, dorsal outline slightly straight (Fig. S7D, S8D, S9C, S10D) 8

7. In dorsal view, petiole as broad as or slightly broader than long; postpetiole broader than long (Fig. S5A); Body dark reddish brown (Fig. S5) (Malaysia) ....*Syscia yekzoeae* Yamane & Mizuno, 2024
- In dorsal view, petiole and postpetiole slightly longer than broad (Fig. S6B); Body yellowish brown (Fig. S6) (China)..... .....*Syscia arcodorsa* Du et al., 2024

8. Petiole in dorsal view broader than long (Fig. S7C); in lateral view the front and the back margins of the petiole vertical (Fig. S7D) (Thailand, Malaysia)..... ..... *Syscia chaladthanyakiji* Jaitrong et al., 2020
- Petiole in dorsal view longer than broad or as long as broad (Fig. S8C, S9B, S10C); in lateral view the front and the back margins of petiole steep or sloped (Fig. S8D, S9C, S10D) 9

9. Subpetiolar process in lateral view subtriangular; anterior margin of petiole slightly convex (Fig. S8D) (Japan, South Korea) ....*Syscia humicola* (Ogata, 1983)
- Subpetiolar process in lateral view subrectangular; anterior margin of petiole slightly concave (Fig. S9C, S10D) 10

10. Propodeal declivity straight or slightly convex in lateral view (Fig. S9C) (China)..... .....*Syscia guizhouensis* (Zhou, 2006)
- Propodeal declivity slightly concave in lateral view (Fig. S10D) (India)..... .....*Syscia indica* Aswaj et al., 2021

DISCUSSION

The ant genus *Syscia* Roger, 1861 is a cryptobiotic group of the subfamily Dorylinae Leach, 1815. Up to now, it is the only doryline genus with a disjunct distribution between the Old and New World. The molecular phylogenetic tree of the subfamily Dorylinae made by Borowiec (2019) showed that *Syscia* is in the middle group of the subfamily's evolutionary development. The number of antennal segments is often not fixed among genera of the subfamily Dorylinae, and there is some variation in the number of antennal segments among different species of the same genus (e.g., *Cerapachys* Smith, 1857 9, 11 or 12; *Dorylus* Fabricius, 1793 8, 9, 11 or 12; *Yunodorylus* Xu, 2000 11-12; *Ooceraea* Roger, 1862 8-11). *Syscia chinensis,* a new species with 10 antennal segments found in the Old World, is in line with expectations and adds to our knowledge of the species diversity of this genus.

Our phylogenetic analysis, based on COI sequences, supports the distinctiveness of *Syscia chinensis* from other *Syscia* species. While COI-based phylogenies may be limited by potential homoplasy or incomplete lineage sorting (Hebert et al. 2003; Pons et al. 2006), the observed genetic distance between *S. chinensis* and known species (e.g., 16.9%, see Suppl 2. Table S4) exceeds typical intraspecific variation in ants (Jansen and Savolainen 2020), aligning with clear morphological differences. Specifically, *S. chinensis* is diagnosable by antennae having 10 segments, which is absent in all other *Syscia* species. These congruent molecular and morphological divergences strongly support the recognition of *S. chinensis* as a new species.

During our survey, only a small number of workers were found (no queen and male). So we need to conduct more extensive surveys to determine the distribution range of the new species. Due to the incomplete survey of China, given the complexity and heterogeneity of China's geography and climate, there are more hidden and undescribed *Syscia* species waiting to be discovered.

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