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A new felt scale genus *Macroporicoccus* gen. n. (Hemiptera: Coccoidea: Eriococcidae) from China, with a redescription of *Macroporicoccus ulmi* (Tang & Hao) comb. n.

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Abstract

The Chinese species *Cryptococcus ulmi* Tang & Hao is found to be distantly related to other sampled *Cryptococcus* species based on both molecular and morphological study. A new felt scale genus, *Macroporicoccus* Nan & Wu gen. n., is erected therefore for *C. ulmi*. The new genus differs from other eriococcid genera due to the presence of large simple pores, here referred to as macrodisc pores. The adult female of *Macroporicoccus ulmi* (Tang & Hao) comb. n. is redescribed and illustrated. Some important taxonomic characters are illustrated with SEM photographs.

Key words: *Cryptococcus ulmi*, phylogeny, 18S, 28S, new genus, new combination, SEM

Introduction

Cryptococcus ulmi was originally described and illustrated by Tang and Hao (1995) based on adult female specimens collected from Shanxi Province and Beijing City under the bark of *Ulmus pumila* (Ulmaceae). Wu (2000) described and illustrated the adult male and all immature stages of both sexes and provided a key to all stages. He also briefly reported its biology based on field studies at Taigu County, Shanxi Province, between 1996 and 1998 and added a new host plant, *Syringa oblata* (Oleaceae). Gwiazdowski *et al*. (2006) used 18S ribosomal DNA sequences to investigate the phylogenetic relationships of *C. fagisuga* Lindinger to other species of *Cryptococcus* and related species in Eriococcidae. They found that *C. ulmi* is only distantly related to the other species of *Cryptococcus* they included (namely *C. nudatus* Brittin, *C. williamsi* Kosztarab & Hale and the type species, *C. fagisuga*, all of which fell within the "Gondwanan" clade of Cook and Gullan (2004)), but they found that *C. ulmi* had close relationships with representatives of Beesoniidae and Stictococcidae, and the eriococcid taxa *Cylindrococcus* spp., *Eriococcus buxi* (Boyer de Fonscolombe) and *E. williamsi* Danzig, all of which formed part of Cook and Gullan's (2004) "BSE" clade. Our study on the phylogeny of Eriococcidae, using both 18S and 28S rDNA sequences, gave similar results (see below). *C. ulmi* has a unique type of large simple pore present on the dorsum and ventral margin. This pore was noted by Tang and Hao (1995) and was referred to as a macrodisc pore by Wu (2000). This pore has now been studied under SEM and found to be a weakly convex closed pore. Considering the differences between the morphology of the adult females of the other *Cryptococcus* species and *C. ulmi* and, bearing in mind the results of the above-mentioned molecular studies, we consider that *C. ulmi* should be removed from *Cryptococcus*, and a new genus erected. Therefore, here we introduce the new genus *Macroporicoccus* Nan & Wu, with *C. ulmi* as the type species. The adult female of *C. ulmi* is redescribed and illustrated, and SEM pictures are presented of some of the more significant characters.

Materials and methods

Morphological work. The specimens examined were either from Beijing Forestry University or were newly

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collected and taken to the laboratory for examination. Slide-mounted specimens were prepared using the method of Borchsenius (1950), stained in acid fuchsin and mounted in Canada balsam. Morphological terms generally follow those of Williams (1985) and Kozár *et al*. (2009), except that the large simple pore on the dorsum and ventral margin is referred to as the macrodisc pore. Measurements are in micrometres (μm) except that the length and width of the body are in millimetres (mm). The drawings are as usual for illustrating Coccoidea, with the central drawing showing the outline of body, dorsum on the left and venter on the right, and showing the distribution of such characteristics as pores, setae, etc. Enlarged drawings (not to scale) are provided around the main figure showing the structure of important features.

All specimens (dry and mounted) are deposited in the Insect Collection, the Department of Forestry Protection, Beijing Forestry University, Beijing, China (BFUC).

Scanning Electron Microscopy (SEM). Specimens of *C. ulmi* used in this study were collected from the campus of Tsinghua University, Beijing, China, on *Ulmus pumila* 'Tenue' by San-an Wu between July and September, 2010. Fresh specimens were fixed in 2.5% glutaraldehyde, prepared in 0.1M phosphate buffer at pH 7.4 and preserved at 4°C. For the SEM study, the prepared materials were washed 3 times in 0.1M phosphate buffer and then 3 times in distilled water, and some specimens were cut into dorsal and ventral parts to investigate the structure beneath the derm. Then all specimens were treated in KOH (10%) either to remove wax from body surfaces or to clear tissues within the derm. After being washed in distilled water, specimens were dehydrated in a graded series of ethanol (10%, 30%, 50%, 75%, 90%, 95%, 100%), mounted onto copper stubs, air dried and coated with gold in a sputter coater for 5 minutes. The SEM illustrations were made using Hitachi Stereoscan S-3400N SEM in the Electron Microscope Laboratory of Beijing Forestry University.

Molecular work. Two ribosomal genes (28S and 18S) were used to reconstruct phylogenetic trees, respectively. Most of the sequences analyzed were obtained from GenBank except *C. ulmi*, *Kuwanina betula* Wu & Liu and *K. parva* (Maskell). Specimens of *C. ulmi* used in this study has the same collection information as used in SEM work; specimens of *K. betula* were collected from Baiyun Mountain, Henan, China, on *Betula ablo-sinensis* by San-an Wu and Yuan Lu on August 19, 2010; and specimens of *K. parva* were collected from the campus of Beijing Forestry University, Beijing, China, on *Prunus armemiaca* by San-an Wu in April, 2010. *Dysmicoccus neobrevipes* Beardsley and *Ferrisia virgata* (Cockerell) were chosen as outgroups. The species used, their current taxonomic classification and GenBank Accession No. are given in Appendix 1.

DNA extraction, amplification and sequencing. Total DNA was extracted from each individual preserved in 95% ethanol using DNeasy Blood & Tissue Kit (Qiagen). The 5' region of 18S rDNA was amplified using the primers 2880 (5'-CTGGTTGATCCTGCCAGTAG-3') (Tautz *et al*., 1988) and B- (5'-CCGCGGCTGCTGGCACC AGA-3') (von Dohlen & Moran, 1995). The primers D2-3549F (5'-TGCAGCTCTAAGTTGGTGGT-3') (Campbell *et al*., 1993) and D2-4068 (5' -TTGGTCCGTGTTTCAAGACGGG-3') (Campbell *et al.*, 1993) were used to amplify 28S rDNA. All PCR amplifications were carried out in Eppendorf Mastercycler Thermal Cyclers. Each 50 μL reaction comprised with 4μL DNA template, 5μL 10X Buffer (Takara), 25mM $MgCl_2$, 2.5mM dNTP mixture, 10 pmol of each primer and 1 unit of ExTaq DNA polymerase (Takara). PCR conditions were as follows: an initial step of 3 min at 95°C followed by 35 cycles of 30 s at 94°C, annealing at 58°C for 50 s, extension at 72°C for 1 min, and final extension of 5 min at 72°C. Products were visualized on 1% agarose, and the most intense products were sequenced bidirectionally using BigDye v3.1 on an ABI3730xl DNA Analyzer (Applied Biosystems).

Phylogenetic analyses. Sequences were edited using BIOEDIT version 5.0.9 (Hall, 1999) and aligned using the CLUSTAL W algorithm (Thompson *et al*., 1994) with default parameters. Bayesian analyses were performed using MrBayes version 3.2 (Ronquist & Huelsenbeck, 2003). jModelTest 2.1.3 (Darriba *et al*., 2012) was used to assess the evolution models that best fits the data, based on the Akaike information criterion (AIC). The GTR+I+G model and GTR+G was selected for 18S and 28S sequences, respectively. The Markov chain Monte Carlo (MCMC) analysis was run for 10,000,000 generations and sampled every 100 generations, and twenty-five percent of the samples were discarded as burnin. Posterior probability values (PP) were calculated from the remaining trees.

Results

Phylogenetic analysis. Both the phylogenetic trees based on 18S (Fig. 1) and 28S (Fig. 2) sequences indicate the non-monophyly of the family Eriococcidae and three main clades of eriococcids, as suggested by the earlier phylogenetic studies (Cook *et al*., 2002; Cook & Gullan, 2004; Gwiazdowski *et al*., 2006; Gullan & Cook, 2007). The analyses strongly support a clade consisting of *Cryptococcus* species (namely *C. fagisuga*, *C. williamsi* and *C. nudatus* on 18S data and *C. fagisuga* on 28S data), *K. betula*, *Pseudochermes fraxini* (Kaltenbach), *E. arcanus* Hoy, *E. phyllocladi* Maskell, *E. tholothrix* Miller & González, *E. brittini* Hoy and *Madarococcus totarae* (Maskell) or *M*. nr. *totarae*, which fall within the "Gondwanan" clade of Cook and Gullan (2004). *C. ulmi*, however, belongs to Cook and Gullan's (2004) "BSE" clade, having close affinities with representatives of Beesoniidae and Stictococcidae, and the eriococcid taxa *Cylindrococcus* spp., *E. buxi*, *E. williamsi* and *K. parva* in 18S tree, and showing extremely sister relationships with *K. parva* in 28S tree.

The above results indicate the distant relationship between *C. ulmi* and the other *Cryptococcus* species, so *C. ulmi* should be removed from *Cryptococcus*, and a new genus should be erected for it. Below we name and describe this new genus based on morphological study.

Macroporicoccus Nan & Wu gen. n.

Type species: *Cryptococcus ulmi* Tang & Hao, 1995.

Description. *Adult female*: Body in life subglobular, orange-red, covered by a white ovisac. On slide, body circular or ovate. Antennae reduced, 6-segmented. Mouthparts developed, labium 3-segmented. Thoracic spiracles each with a group of disc pores, each with 3 or 5 loculi, near opening. Legs much reduced, only distal part of tarsus and complete claw visible; each claw with a denticle, hind legs each located on a pore plate. Anal ring circular or oval, with 6 short setae and no pores. Anal lobes indistinct. Macrotubular ducts with a cup-shaped invagination, present on both sides of body except ventral middle area. Microtubular ducts present on dorsum and margin of venter. Quinquelocular pores mainly present ventrally. Macrodisc pores present on dorsum and margin of venter. Setae small, sparsely distributed on venter.

First-instar nymph: In life, body bright yellow. Body on slide oval. Antennae 6-segmented. Eyes present. Mouthparts and legs well developed. Anal ring circular, with 6 setae and without pores. Anal lobes each with one long and one short flagellate seta. Macrotubular and microtubular ducts absent. Quinquelocular disc pores present on ventral abdominal segments and near spiracles. Macrodisc pores distributed on dorsal surface. Setae present, forming transverse or longitudinal rows on body surface.

Remarks. Adult females of *Macroporicoccus* Nan & Wu gen. n. can be easily distinguished from other eriococcid genera due to the presence of macrodisc pores, which occur throughout the dorsum and ventral margin of *C. ulmi*. Tang and Hao (1995) described this type of pore as a macroduct, but they noticed also that it was a rather large disc pore; Wu (2000) referred to it as a macrodisc pore and described it as a kind of large invaginated pore. As this pore is markedly larger than the simple pores in other Coccoidea (usually 2–3 μm in diameter), we consider the term macrodisc pore to be most appropriate. However, after SEM study, we can confirm that it is a simple closed pore (Foldi, 1997), about 10 μm in diameter, with a narrow rim and a weakly convex surface (Fig. 20, 21); it secretes long solid wax filaments, which make up the outline of the ovisac (Fig. 3) (Wu, unpublished data).

Cryptococcus, *Kuwanina* Cockerell and the new genus *Macroporicoccus* live in crevices in the trunks and branches, and have many similar morphological characters. The shared features of the adult female are: (1) body subglobular covered by a white ovisac; (2) antennae reduced; (3) legs absent or reduced to tubercles, hind legs always replaced by pore-plates or vestigial flaps; and (4) anal lobes absent (Williams, 1985; Tang & Hao, 1995; Wu, 2000; Henderson, 2007; Wu & Liu, 2009). However, adult female *Kuwanina* apparently differ from those of other two genera in the absence of macrotubular ducts (*C. nudata* Brittin is an exception) and in the presence of unique invaginated 5-locular disc pores (Williams, 1985; Henderson, 2007). As indicated above, adult female *Macroporicoccus* differ from *Cryptococcus* in the presence of macrodisc pores. In addition, *Macroporicoccus* has 6-segmented antennae whereas *Cryptococcus* has 1–4-segmented antennae (Kosztarab & Hale, 1968; Tang & Hao, 1995).

Etymology. The new genus name means those scale insects with macrodisc pores.

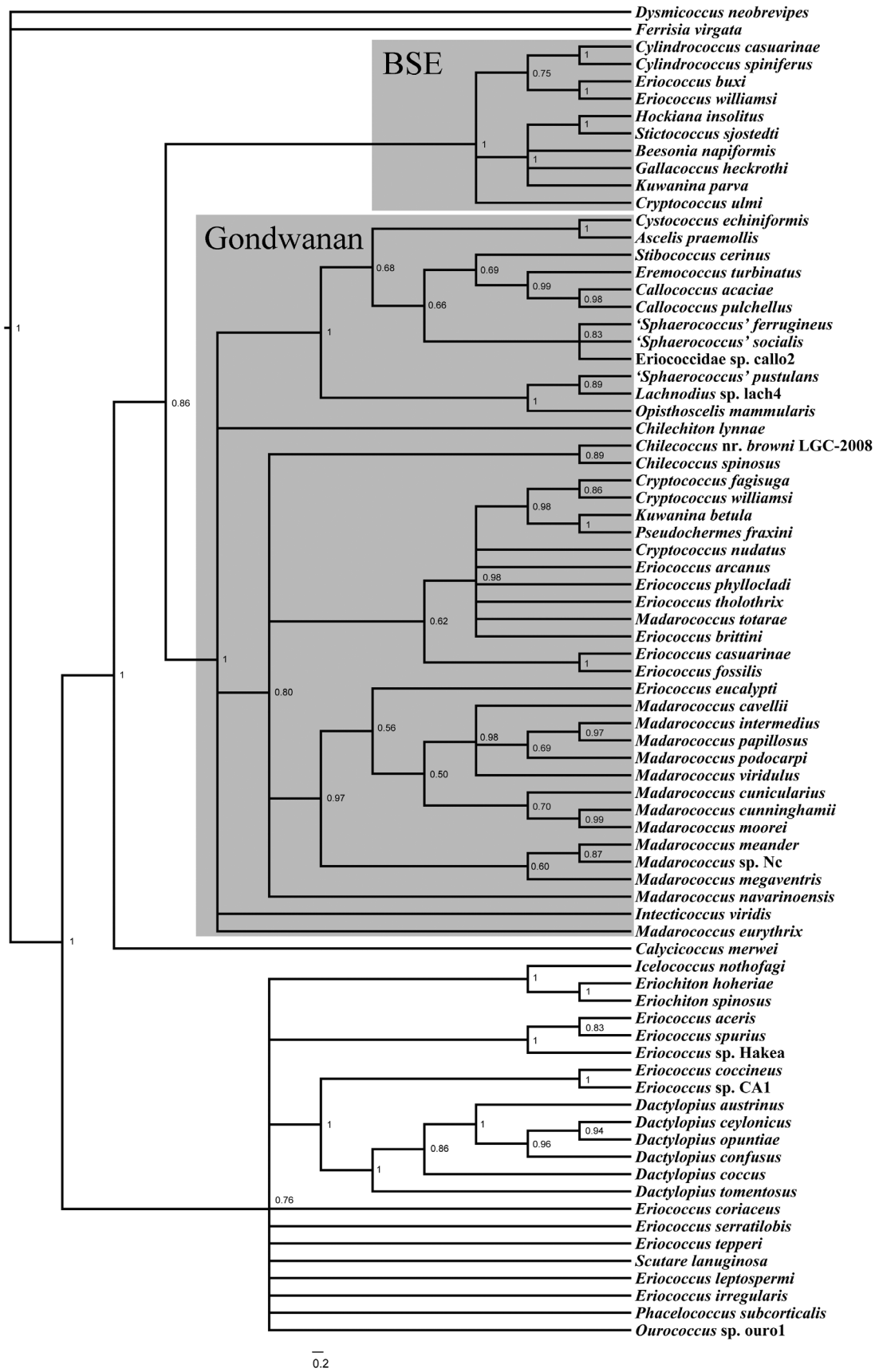


FIGURE 1. Phylogenetic tree from Bayesian analyses of sequences from the nuclear small subunit ribosomal DNA gene (SSU rDNA or 18S) obtained from 75 species of eriococcids and related scale insects and rooted using 2 outgroup taxa from the family Pseudococcidae. Bayesian posterior probabilities (BPP) are shown at the nodes.

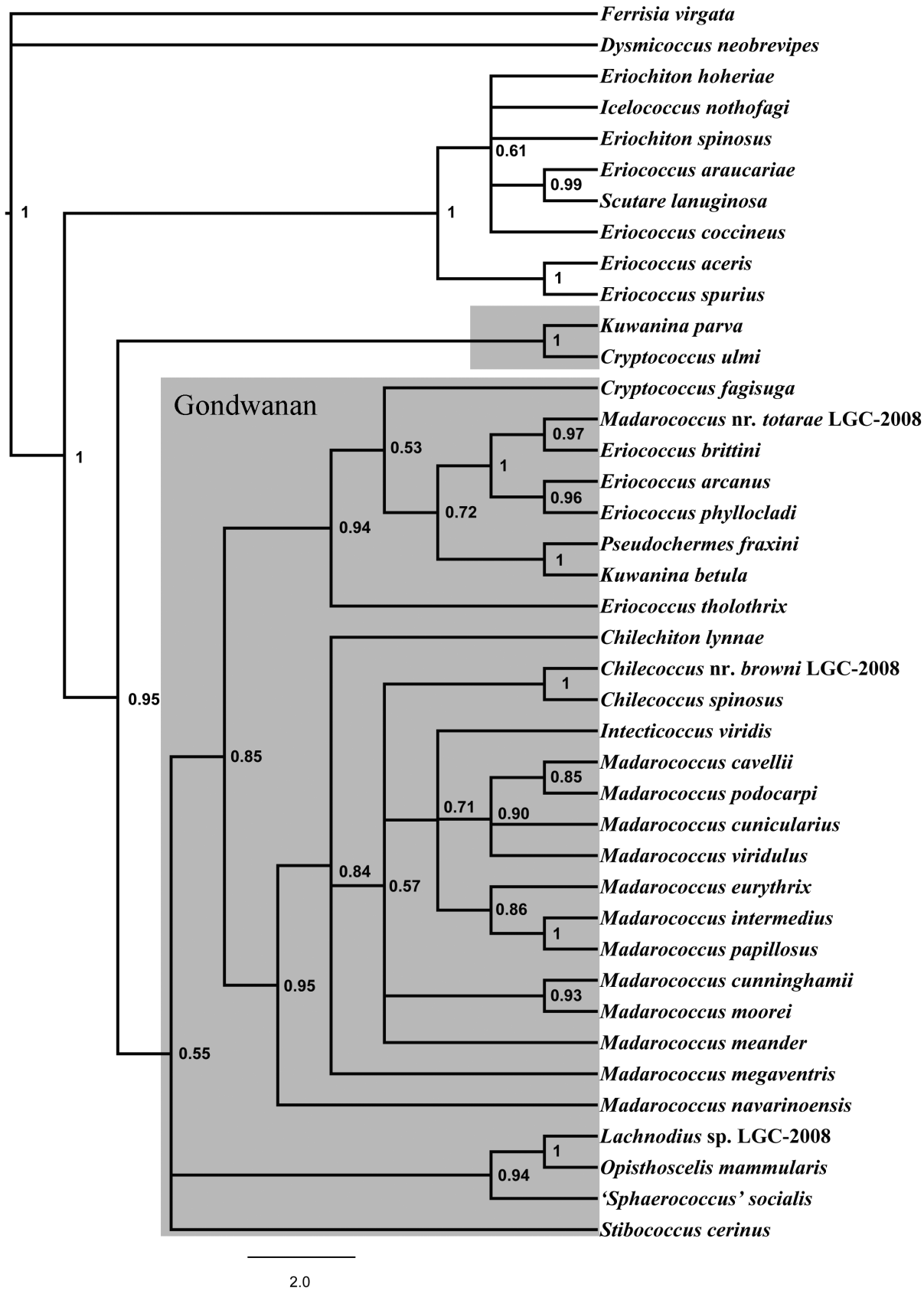


FIGURE 2. Phylogenetic tree from Bayesian analyses of sequences from the nuclear large subunit ribosomal DNA gene (LSU rDNA or 28S) obtained from 38 species of eriococcids and related scale insects and rooted using 2 outgroup taxa from the family Pseudococcidae. Bayesian posterior probabilities are shown at the nodes.

***Macroporicoccus ulmi* (Tang & Hao) comb. n.**
(Figs 3–22)

Cryptococcus ulmi Tang & Hao, 1995: 429; Xie, 1998: 101; Tao, 1999: 31; Miller & Gimpel, 2000: 90; Wu, 2000: 251, 256; Kozár, 2009: 96.

Material examined. 12 ad ♀♀, China, Shanxi Province, Taigu County, campus of Shanxi Agricultural University in crevices in the trunks of *Ulmus pumila*, 10 December 1997, Coll. San-an Wu (the measurements and illustration are based on this slide); 4 ad♀♀, China, Tianjin City on *U. pumila*, 15 June 1999, Coll. San-an Wu; 7 ad♀♀, China, Beijing City, Songshan Mountain in the crevices of trunks of *U. japonica*, 29 May 2012, Coll. Nan Nan.

Redescription of adult female. Body in life sub-globular, orange-red, covered by white waxy ovisac. Body on slide circular or ovate, 0.90–1.45 mm long and 0.70–1.33 mm wide. Antennae (Fig. 7) reduced, 6-segmented, length of each segment (μm): I 14–18, II 8–11, III 6–7, IV 4–6, V 5–6, VI 12–16; segment II with one campaniform sensillum, segment IV and V each bearing a fleshy seta, segment VI with 3 fleshy and 4 long flagellate setae and a pair of coeloconic sensilla at apex. Mouthparts developed, clypeolabral shield (Fig. 8) with 2 small setae in middle of surface; labium (Fig. 9) 3-segmented, 56–62 μm long, with 5 pairs of short setae on apical segment. Thoracic spiracles each 34–40 μm long and atrium 19–21 μm wide, each with a group of quinquelocular (rarely trilocular) (Fig. 12) pores near opening, with 6–21 near each anterior spiracle (Fig. 10) and 6–23 near each posterior spiracle (Fig. 11). Legs (Figs 13–15) much reduced, only distal part of tarsus and complete claw visible; each claw with a denticle near apex; fore and middle claw 9–10 μm long, hind claw stouter, 6–8 μm long; each leg with one pair of tarsal digitules and one pair of claw digitules, all slightly knobbed, tarsal digitule longer than claw, claw digitule nearly equal to length of claw; each leg with several setae around base; hind legs each located on a 51–70 μm long and 42–50 μm wide pore plate (Fig. 16). Anal ring (Fig. 17) circular to oval, 26–28 μm long and 18–26 μm wide, with 6 short setae, each 17–20 μm long, and without pores. Anal lobes absent, each represented by a long flagellate seta, 48–70 μm long at posterior end of body. Vulva (Fig. 18) distinct, located on ventromedial area between abdominal segments VI and VII.

FIGURE 3. Adult female *Macroporicoccus ulmi* (Tang & Hao) in crevices of *Ulmus pumila*, Beijing of China (San-An Wu).

Dorsum (Fig. 5). Setae absent. Macrotubular ducts (Fig. 19) with a cup-shaped invagination, each 20–26 μm long and about 3 μm wide, with an inner ductule 17–19 μm long; numerous, distributed over all surface. Microtubular ducts each with an outer ductule about 2 μm long and a dermal orifice about 2 μm wide; sparse on dorsum. Macrodisc pores (Figs 20, 21) with rim slightly protruding, each about 10 μm in diameter, forming transverse rows across dorsum. Quinquelocular disc pores, each about 5 μm in diameter; few on margin.

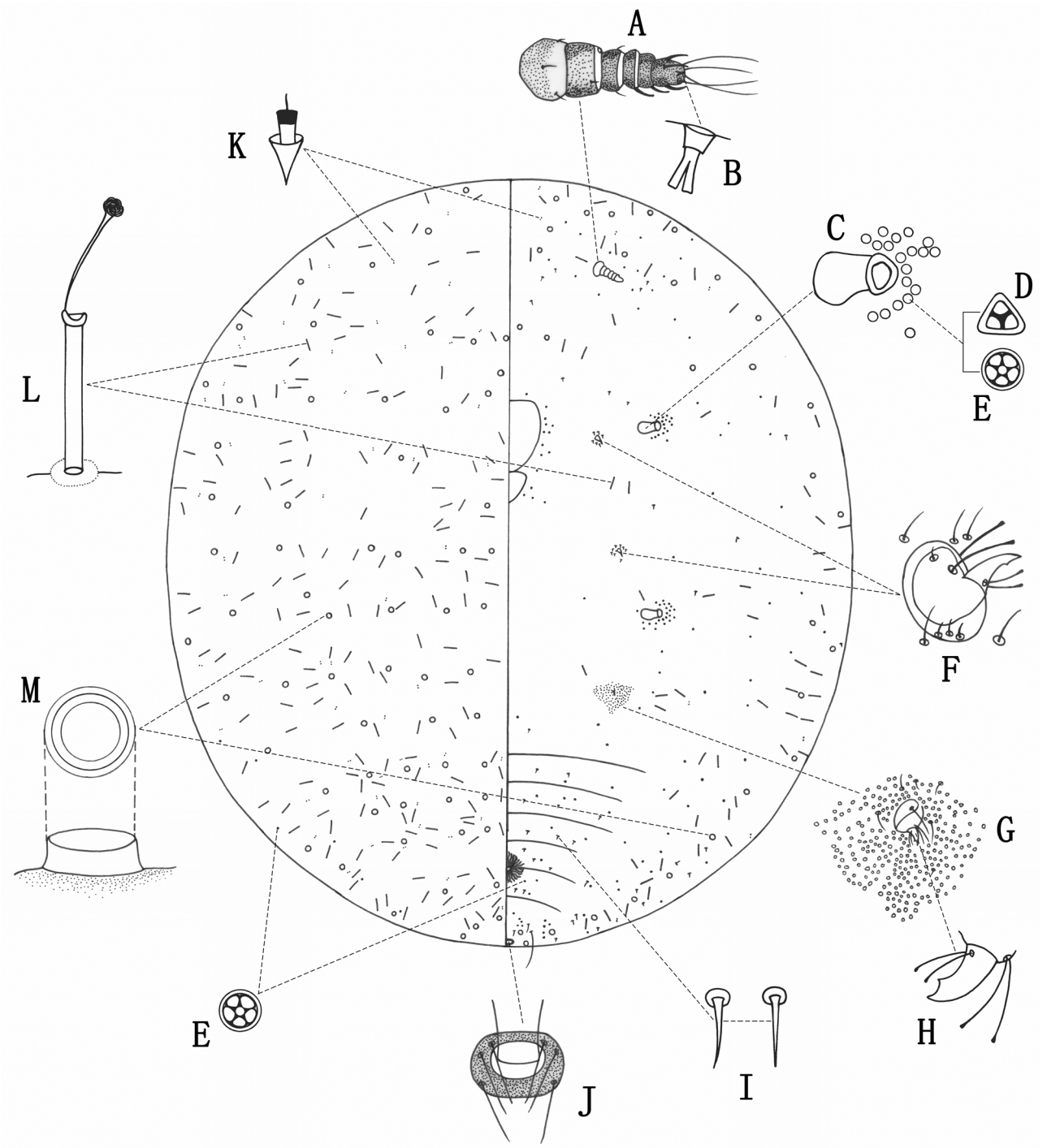
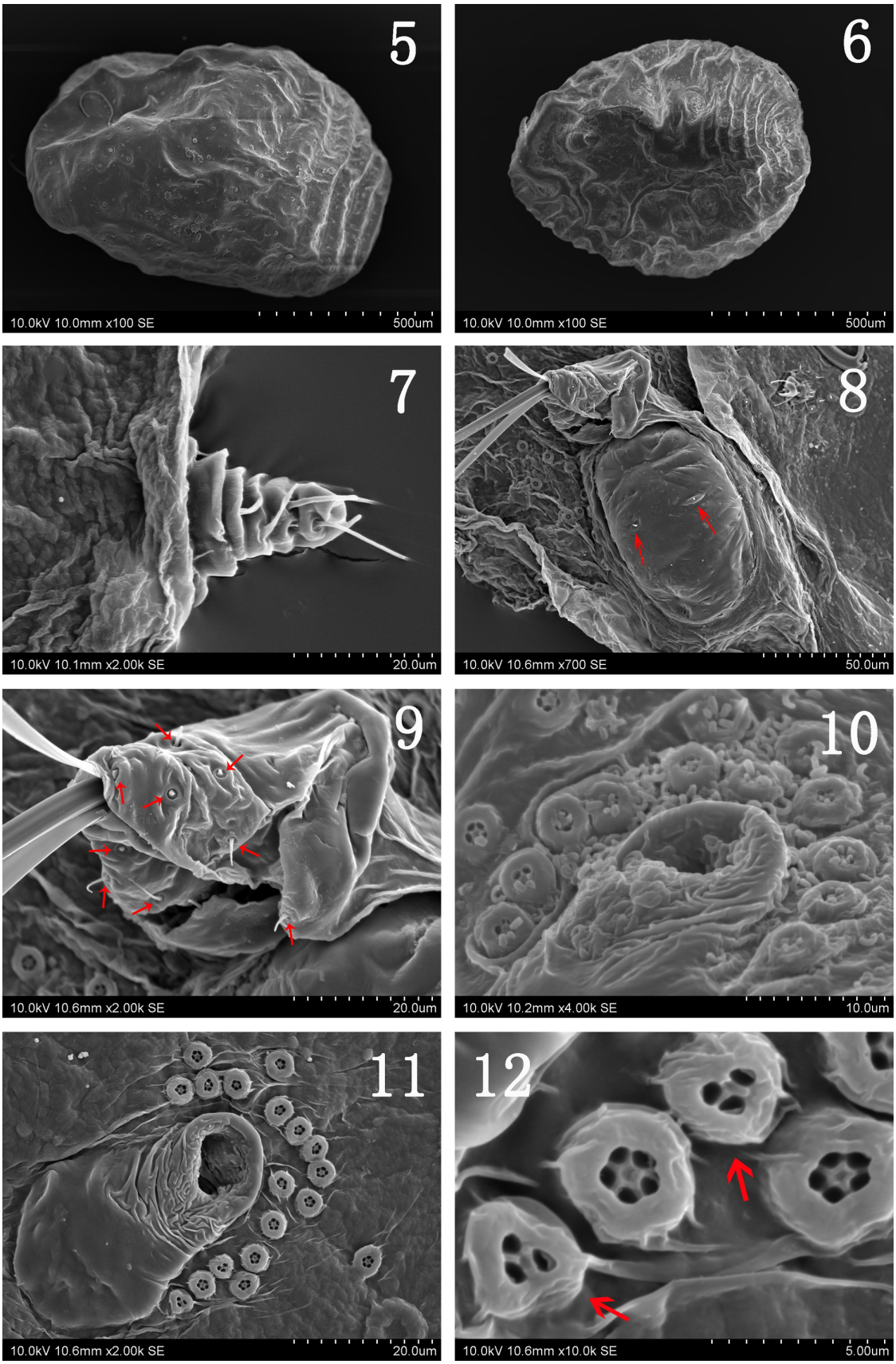


FIGURE 4. Adult female *Macroporicoccus ulmi* (Tang & Hao). Where: A. antenna; B. a pair of coeloconic sensilla; C. thoracic spiracle; D. trilocular pore; E. quinquelocular pore; F. fore or middle leg; G. pore plate; H. hind claw; I. ventral setae; J. anal ring; K. microtubular duct; L. macrotubular duct; M. macrodisc pore.

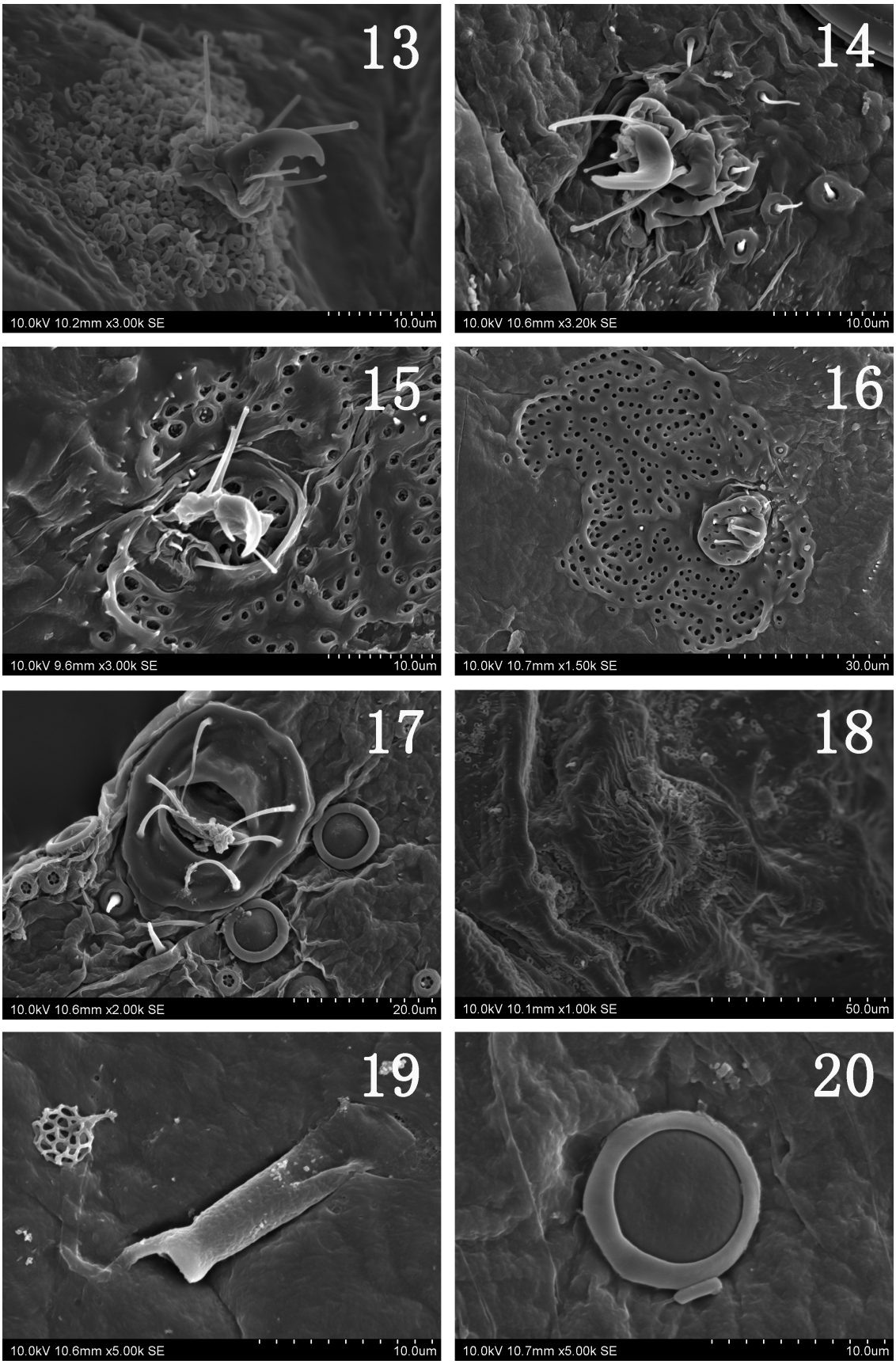
Venter (Fig. 6). Setae (Fig. 22) spine- or hair-like, 4–16 μm long, sparsely distributed on venter but with a small group around each leg. Macroducts, microducts and macrodisc pores similar to those on dorsum, present on marginal and submarginal areas. Quinquelocular pores also similar to those on dorsum, but with a group near each spiracle and mouthparts; also distributed on abdominal venter and in marginal and submarginal areas, sometimes with a few near spiracles replaced by trilocular pores.

Host plants. *Ulmus japonica*, *U. pumila*, *U. pumila* 'Tenue' (Ulmaceae), *Syringa oblata* (Oleaceae).

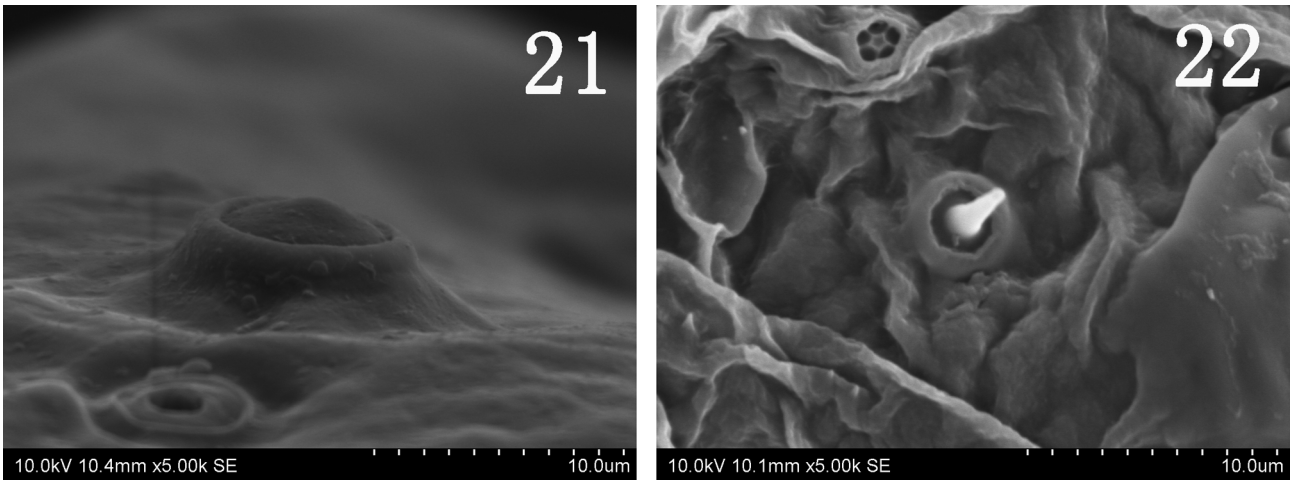
Distribution. China (Beijing, Shanxi, Tianjin).



FIGURES 5–12. Scanning electron micrographs of some features of adult female *Macroporicoccus ulmi* (Tang & Hao). 5. dorsum (×100); 6. venter (×100); 7. antenna (×2,000); 8. mouthparts, arrows showing two setae on clypeolabral shield (×700); 9. labium, arrows showing setae on surface (×2,000); 10. anterior spiracle (×4,000); 11. posterior spiracle (×2,000); 12. trilocular or quinquelocular disc pores around spiracle, arrows showing trilocular ones (×10,000).



FIGURES 13–20. Scanning electron micrographs of some features of adult female *Macroporicoccus ulmi* (Tang & Hao). 13. fore leg (×3,000); 14. middle leg (×3,200); 15. hind leg (×3,000); 16. pore plate (×1,500); 17. anal ring (×2,000); 18. vulva (×1,000); 19. macrotubular duct (×5,000); 20. macrodisc pore (×5,000).



FIGURES 21–22. Scanning electron micrographs of some features of adult female *Macroporicoccus ulmi* (Tang & Hao). 21. macrodisc pore (×5,000); 22. ventral seta (×5,000).

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APPENDIX 1. Family classification and GenBank accession numbers for Coccoidea species used in this study.

Current family classification	Species	GenBank Accession No. (18S)	GenBank Accession No. (28S)
Pseudococcidae	*Dysmicoccus neobrevipes* Beardsley	AY426036.1	AY427323.1
	Ferrisia virgata (Cockerell)	AY426022.1	AY179457.1
Beesoniidae	*Beesonia napiformis* (Kuwana)	AY795511.1	–
	Gallacoccus heckrothi Takagi	AY795512.1	–
Dactylopiidae	*Dactylopius austrinus* De Lotto	AY795538.1	–
	Dactylopius ceylonicus (Green)	GQ853357.1	–
	Dactylopius coccus Costa	GQ853359.1	–
	Dactylopius confusus (Cockerell)	U20402.1	–
	Dactylopius opuntiae (Cockerell)	GQ853363.1	–
	Dactylopius tomentosus (Lamarck)	GQ853360.1	–
Eriococcidae	*Ascelis praemollis* Schrader	AY795523.1	–
	Callococcus acaciae (Maskell)	AY795517.1	–
	Callococcus pulchellus (Maskell)	AY795518.1	–
	Calycicoccus merwei Brain	AY795535.1	–
	Chilechiton lynnae Hodgson & Miller	EU746805.1	EU746845.1
	Chilecoccus nr. *browni* LGC-2008	EU746806.1	EU746847.1
	Chilecoccus spinosus Miller & González	EU746807.1	EU746848.1
	Cryptococcus fagisuga Lindinger	DQ125262.1	GU998971.1
	Cryptococcus nudatus Brittin	DQ125263.1	–
	Cryptococcus ulmi Tang & Hao	DQ125265.1	KF548311*
	Cryptococcus williamsi Kosztarab & Hale	DQ125266.1	–
	Cylindrococcus casuarinae Maskell	AY795516.1	–
	Cylindrococcus spiniferus Maskell	AY795515.1	–
	Cystococcus echiniformis Fuller	AY795524.1	–
	Eremococcus turbinatus (Froggatt)	AY795522.1	–
	Eriochiton hoheriae Hodgson	EU746800.1	EU746834.1
	Eriochiton spinosus (Maskell)	EU746799.1	EU746833.1
	Eriococcus aceris (Signoret)	AY795539.1	EU746830.1
	Eriococcus araucariae Maskell	–	EU746832.1
	Eriococcus arcanus Hoy	EU746809.1	EU746850.1
	Eriococcus brittini Hoy	EU746810.1	EU746851.1
	Eriococcus buxi (Boyer de Fonscolombe)	AY795513.1	–
	Eriococcus casuarinae (Maskell)	AY795532.1	–
	Eriococcus coccineus Cockerell	AY795536.1	EU746831.1
	Eriococcus coriaceus Maskell	AY795542.1	–
	Eriococcus eucalypti Maskell	AY795531.1	–
	Eriococcus fossilis Froggatt	AY795533.1	–
	Eriococcus irregularis Froggatt	AY795545.1	–
	Eriococcus leptospermi Maskell	AY795546.1	–
	Eriococcus phyllocladi Maskell	EU746812.1	EU746843.1
	Eriococcus serratilobis Green	AY795544.1	–

	Eriococcus spurius (Modeer)	AY795540.1	GU998969.1
	Eriococcus tepperi Maskell	AY795543.1	–

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APPENDIX 1. (Continued)

Current family classification	Species	GenBank Accession No. (18S)	GenBank Accession No. (28S)
	Eriococcus tholothrix Miller & González	EU746811.1	EU746857.1
	Eriococcus williamsi Danzig	AY795514.1	–
	Eriococcus sp. CA1	AY795537.1	–
	Eriococcus sp. Hakea	AY795541.1	–
	Icelococcus nothofagi Miller & González	EU746801.1	EU746837.1
	Intecticoccus viridis Kondo	EU746808.1	EU746844.1
	Kuwanina betula Wu & Liu	KF548313*	KF548312*
	Kuwanina parva (Maskell)	KF548314*	KF548310*
	Lachnodius sp. lach4	AY795521.1	–
	Lachnodius sp. LGC-2008	–	EU746840.1
	Madarococcus cavellii (Maskell)	EU746818.1	EU746858.1
	Madarococcus cunicularius Hoy	EU746821.1	EU746861.1
	Madarococcus cunninghamii Hardy & Gullan	EU746820.1	EU746860.1
	Madarococcus eurythrix (Miller & González)	EU746816.1	EU746852.1
	Madarococcus intermedius (Maskell)	EU746828.1	EU746869.1
	Madarococcus meander Hardy & Gullan	EU746823.1	EU746862.1
	Madarococcus megaventris Hardy & Gullan	EU746822.1	EU746864.1
	Madarococcus moorei Hardy & Gullan	EU746824.1	EU746866.1
	Madarococcus navarinoensis (Hoy)	EU746817.1	EU746849.1
	Madarococcus nr. *totarae* LGC-2008	–	EU746842.1
	Madarococcus papillosus (Hoy)	EU746829.1	EU746870.1
	Madarococcus podocarpi (Hoy)	EU746825.1	EU746855.1
	Madarococcus totarae (Maskell)	AY795534.1	–
	Madarococcus viridulus Hoy	AY795529.1	EU746871.1
	Madarococcus sp. Nc	AY795528.1	–
	Opisthoscelis mammularis Froggatt	EU746803.1	EU746839.1
	Ourococcus sp. ouro1	AY795550.1	–
	Phacelococcus subcorticalis Gullan & Strong	AY795549.1	–
	Pseudochermes fraxini (Kaltenbach)	DQ125267.1	GU998970.1
	Scutare lanuginosa Hoy	EU746802.1	EU746835.1
	Stibococcus cerinus Miller & González	EU746804.1	EU746841.1
	'Sphaerococcus' ferrugineus Froggatt	AY795526.1	–
	'Sphaerococcus' pustulans Green	AY795519.1	–
	'Sphaerococcus' socialis Maskell	AY795527.1	EU746838.1
	Eriococcidae sp. callo2	AY795525.1	–
Stictococcidae	*Hockiana insolitus* Richard	AY795510	–
	Stictococcus sjostedti Cockerell	AY795509	–

* Sequences we amplified.