WESTERDIJK FUNGALBIO DIVERSITY INSTITUTE

Phylogeny and taxonomy of *Acer* powdery mildews, including genera *Sawadaea* and *Takamatsuella* (*Erysiphaceae*, *Ascomycota*)

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Abstract: *Acer* (*Sapindaceae*) is a major genus of broadleaf trees dominating deciduous forests in the Northern Hemisphere, with Asia exhibiting the highest species diversity. Many economically important *Acer* species are cultivated for ornamental or timber purposes. *Acer* powdery mildew, caused by fungi in the tribe *Cystotheceae*, poses significant global economic and ecological threats. The pathogenicity spectrum remains unclear due to taxonomic uncertainties in its primary causal genera, *Sawadaea* and *Takamatsuella*. This study presents a comprehensive phylogenetic-taxonomic analysis of the two genera across East Asia, Europe, and North America. Using 75 ITS and 58 28S rDNA newly obtained sequences, we resolved 12 *Sawadaea* species and one *Takamatsuella* species into nine monophyletic clades, revealing marked cryptic diversity (three new species: *S. acerina*, *S. aceris-arguti*, *S. taii*) and two paraphyletic groups (*S. bifida*/*S. negundinis*). Taxonomic revisions include: *S. bicornis* split into two *formae* (*f. bicornis* and *f. polyphaga f. nov.*) with distinct host preferences; *S. tulasnei* (sensu stricto) restricted to Europe/North America, invalidating previous Asian records; *S. nankinensis* and *S. koelreuteriae* form two basal lineages. Phylogenetic positioning confirmed *Takamatsuella* as a distinct genus sister to *Sawadaea*, supported by an ITS1 26 bp deletion. Host specificity analysis revealed narrow host ranges (primarily *Acer*) with two evolutionary host expansions to *Koelreuteria*, *Aesculus*, and *Liquidambar*. This study also newly describes the asexual morphs of four species (*S. aesculi*, *S. bifida*, *S. bomiensis* and *S. kovaliana*) and establishes a molecular framework for disease management through clarified phylogeny and taxonomy. Our findings provide critical insights into fungal evolution, host-pathogen interactions, and strategies for mitigating powdery mildew impacts in forest ecosystems.

Key words: Diversity, *Erysiphaceae*, *formae*, *Helotiales*, new species.

Taxonomic novelties: New *forma*: *Sawadaea bicornis f. polyphaga* M. Bradshaw & U. Braun. **New species:** *Sawadaea acerina* G.X. Guan & S.Y. Liu, *Sawadaea aceris-arguti* S. Takam. & U. Braun, *Sawadaea taii* G.X. Guan & S.Y. Liu.

Citation: Feng J, Guan GX, Wu XL, Liu SY, Song JG, Bradshaw M, Götz M, Braun U, Takamatsu S, Heluta V, Jin DN, Wang SB, He YH, Zhang ZY, Liu L, Liu TZ, Ilyukhin EV, Lu XX, Li Y (2025). Phylogeny and taxonomy of *Acer* powdery mildews, including genera *Sawadaea* and *Takamatsuella* (*Erysiphaceae*, *Ascomycota*). *Studies in Mycology* **112**: 1–38. doi: 10.3114/sim.2025.112.01
Received: 23 November 2024; **Accepted:** 15 February 2025; **Effectively published online:** 25 April 2025
Corresponding editor: R.A. Samson

INTRODUCTION

Acer (*Sapindaceae*, incl. *Aceraceae*) is an important broad leaves genus that prominent deciduous forests of the Northern Hemisphere, and comprises about 125 to 156 species based on the applied species concepts. Asia harbours the highest species diversity, where multiple species are important economically in that they are planted as ornamental trees or for timber (Gao *et al.* 2020). East Asia, especially China is considered the present centre of diversification for *Acer* (Suh *et al.* 2000). The taxonomy of *Acer* species is well documented (Li *et al.* 2006, Grimm *et al.* 2007), whereas Li *et al.* (2019) provided a modern classification of *Acer* into sections, substantiated by phylogenetic data, which largely coincides with previous subgeneric concepts (de Jong 2002). Microfungi associated with *Acer* species have diverse host-plant interactions. Among these phytopathogenic ascomycetes, including powdery mildews is one of the important diseases on acer plants (Johnston *et al.* 2019, Haelewaters *et al.* 2021).

Powdery mildews are obligate biotrophic fungi forming characteristic, conspicuous symptoms caused by whitish superficial mycelial patches or films of the sexual morph (Braun & Cook 2012). They are cosmopolitan in distribution and occur on more than 10,000 plant species, including numerous important crops (Amano 1986, Braun & Cook 2012; Bradshaw *et al.* 2022). The currently accepted generic system of powdery mildews in the world containing five tribes, including 17 sexual morph genera and two asexual morph

Studies in Mycology

Sawadaea and *Takamatsuella*
Cystotheceae
Acer
Sawadaia
Uncinula aceris (= *Sawadaea aceris*)
Sawadaia's
Sawadaea
Sawadaea
S. negundinis
U. tulasnei *Sawadaea*
Sawadaea
Sawadaea
Otani 1988, Heluta 1989). Scanning electron microscopy revealed
Sawadaea
embossed strips, which significantly differs from outer conidial
Erysiphe *Uncinula*,
Sawadaea
Erysiphaceae
Sawadaea
Braun & Cook 2012). And five of these eight species were proposed
S. aesculi and *S. bomiensis*
et al.
Sawadaea *nankinensis* [≡ *Uncinula nankinensis*] *Acer buergerianum*
Sawadaea
S. bicornis [≡ *Uncinula aceris*]
Acer barbinerve *S. tulasnei*
[≡ *Uncinula aceris* *tulasnei*] *Acer*
S. koelreuteriae [≡ *Erysiphe koelreuteriae*]
Koelreuteria paniculata *S. polyfida* [≡ *Uncinula polyfida*] *Acer amplum* *latalpifolium*
et al. *S. negundinis* [≡ *Uncinula negundinis*] *Acer negundo*
S. aesculi *Aesculus chinensis* *wilsonii* *S. bomiensis*
Acer caudatum
S. bicornis *S. tulasnei*
Sawadaea
S. bicornis
S. tulasnei *Sawadaea*
Sawadaea
Sapindaceae
Oceania, and South America [Argentina] (Braun & Cook 2012).

Sawadaea
Sawadaea (*et al.*
Sawadaea
S. bicornis *S. tulasnei*
et al. *et al.*
Sawadaea
Takamatsuella
superficial mycelium, composed of hyaline thin-walled, septate,
likely not formed at all. Chasmothecium is somewhat flattened,
aseptate, hyaline, subcylindrical-filiform, uncinuloid, apices circinate;
Takamatsuella
a monospecific genus containing only *T. circinata*
Uncinula circinata *Acer spicatum*
U. bicornis
Erysiphe circinata.
Sawadaea
T. circinata *S. bicornis*
Sawadaea
T. circinata
Cook (2012) confirmed that the appendages in this species remain
Takamatsuella *T. circinata* (≡ *Uncinula circinata*)
Sawadaea
A Chinese collection identified as *Uncinula circinata* on
T. circinata
Acer wilsonii
(HMAS 37698), identified as *U. circinata*
n. wilsonii
Acer griseum
U. circinata,
Uncinula *Erysiphe*
griseum *Erysiphe*
circinata
ljubarskii.

Uncinula circinata *Dodonaea viscosa*
et al. (2000). Other records on *Sapindus drummondii* *S. marginatus* *Sapindus* deposited at BPI, have been examined by U. Braun and confirmed to be *E. flexuosa* (
Takamatsuella *Sawadaea* and its affiliation to tribe *Cystotheceae* have been insufficiently examined so far, and require further research. Therefore, the clarifications of these problems have been
Sawadaea
Takamatsuella *Sawadaea*
Takamatsuella
Sawadaea *Takamatsuella*

MATERIALS AND METHODS

Fungal materials

countries. In total, 123 specimens from five countries (China,
Of these, 62 specimens of *Sawadaea* *Takamatsuella*

Morphological examination

DNA extraction, PCR amplification and sequencing

et al.

spacer (ITS) regions, including the 5.8S rDNA, were amplified *et al.*
amplified with primers pairs LSU1/LSU2 (Scholin *et al.* *et al.*
components were 2 µL of total genomic DNA, 2.5 µL 10× PCR buffer plus) (TaKaRa, Japan), 2 µL dNTP mixture (10 mM total, 2.5 mM each), 1 µL each primer (20 ng/µL), 0.1 µL *Taq* (TaKaRa, Japan) (5 U/µL) and sterile ddH_2O up to a final volume of 25 µL. The amplification reactions were conducted under the
52–56 °C for annealing, and 30 s at 72 °C for extension, and a final
gel in 0.5× TBE buffer. The amplicons were sent to Sangon Biotech

Phylogenetic analyses

et al.
et al.
additions to find the global optimum tree. All gaps were treated as
et al.
both analyses. For BI analysis, the best-fit substitution models
and trees were sampled every 100 generations. The first 25 %

RESULTS

The phylogeny of *Sawadaea* and *Takamatsuella*

Seventy-five ITS sequences including the ITS1-5.8S rDNA-ITS2 and 58 28S rDNA sequences including D1/D2 domains were generated in this study and were aligned with sequences retrieved from the NCBI GenBank nucleotide database. The ITS+28S rDNA sequence alignment matrix consisted of 203 sequences including 950 characters, of which 168 (17.7 %) were parsimony informative and 18 (1.2 %) were parsimony-uninformative. *Cystotheca castanopsidis* and *C. wrightii* were selected as outgroups. The maximum parsimony (MP) and maximum likelihood (ML) tree with the highest likelihood value of more than 70 % and posterior probabilities value greater than 0.90 for Bayesian Inference (BI) are shown in Fig. 1. Phylogenetic trees generated from ML and BI analyses are almost identical to the MP tree, which is, therefore, not shown.

The tree topology revealed the molecular phylogeny among species in *Sawadaea* and a much higher species diversity than

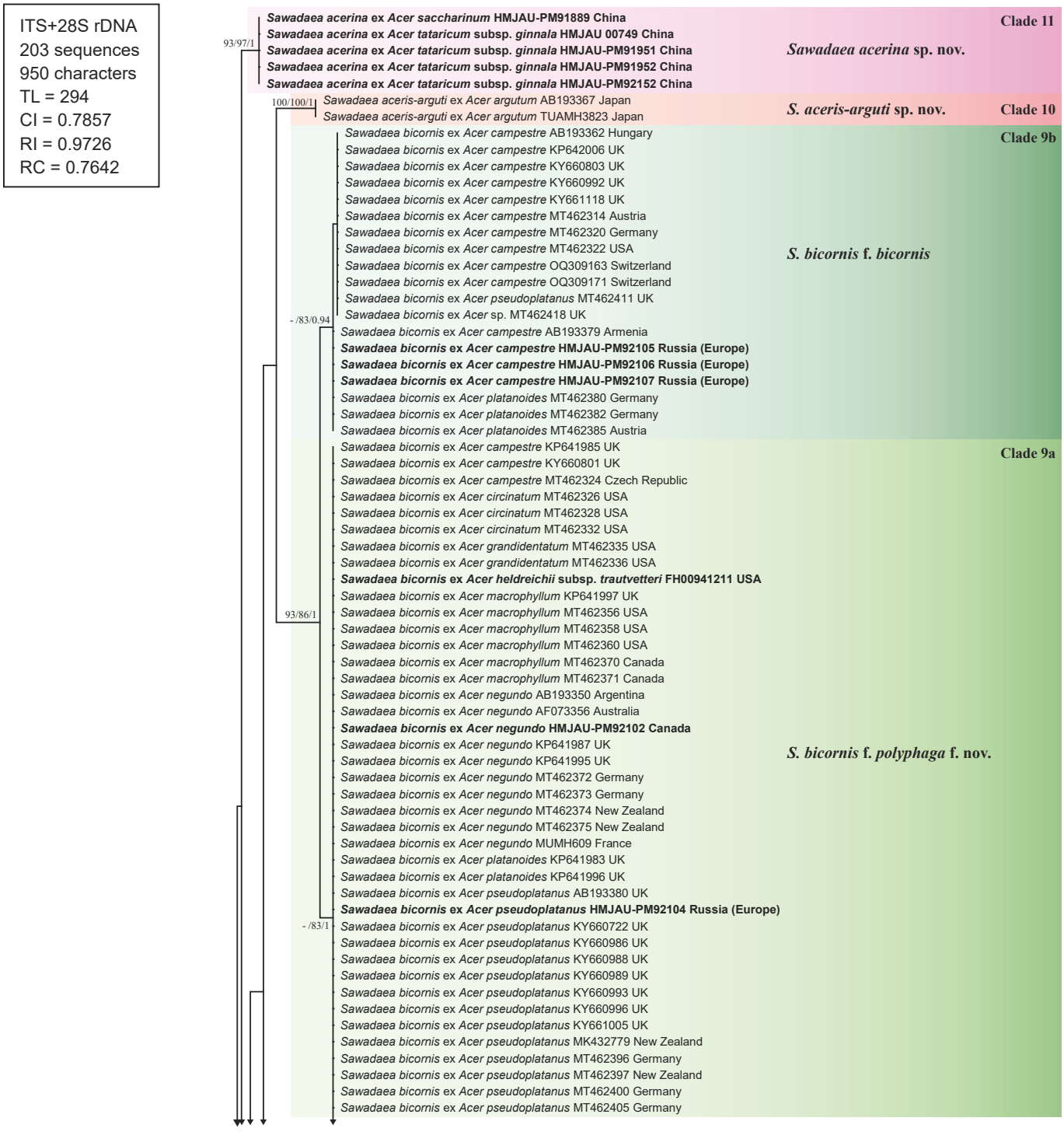

Fig. 1. Phylogenetic analysis of the ITS+28S rDNA regions. Nodes are labelled with bootstrap values from Parsimony bootstrap/Maximum likelihood/Bayesian posterior probabilities values. Posterior probabilities greater than bootstrap support values (> 70 %) by maximum parsimony (MP), maximum likelihood (ML) and 0.90 for Bayesian Inference (BI) methods are shown on the respective branches. The newly generated sequences in this study are in bold. *Cystotheca castanopsidis* and *C. wrightii* are used as outgroup taxa.

previously assumed, especially in Eastern Asia. Twelve species of *Sawadaea* and one species of *Takamatsuella* formed nine monophyletic clades (clades 1–5, 7, 9–11) and two non-monophyletic clades (clade 6 and clade 8). The insertion/deletion differences between sites 60 and 107 of the ITS1 region were summarized among these clades (Fig. 2). *Takamatsuella circinata* (Clade 1; MP = 100 %, ML = 100 %, BI = 1.00) formed a sister clade to genus *Sawadaea* with high support which is mainly caused by a 26 bp deletion between sites 64 and 89 of the ITS1 region. This result supports the treatment of *Takamatsuella* as an independent genus. The differences among *Sawadaea* species were caused mainly by a 6–14 bp insertion/deletion (indel) between sites 65 and 101 of the ITS1 region. *Sawadaea nankinensis* (Clade 2), *S. koelreuteriae* (Clade 3), *S. aesculi* (Clade 4), *S. negundinis* (Clade 6), *S. bifida* (Clade 6), *S. tulasnei* (Clade 7), *S. taii* (Clade 8) and *S. kovaliana* (Clade 8) had 10 bp deletions. *Sawadaea nankinensis* formed a separate clade (Clade 2; MP = 100 %, ML = 100 %, BI = 1.00) with the other species of *Sawadaea*, which was mainly caused by the two bases insertion at sites 65 and 66 and one base deletion at site 89 (Fig. 2), and its distinguished unbranched uncinate-circinate appendages (Fig. 3). *Sawadaea koelreuteriae* formed a separate clade with high support (MP = 100 %, ML = 100 %, BI = 1.00). *Sawadaea aceris-arguti* has a 6 bp deletion between sites 93 and 98, and *S. acerina* has a 7 bp deletion between sites 94 and 100.

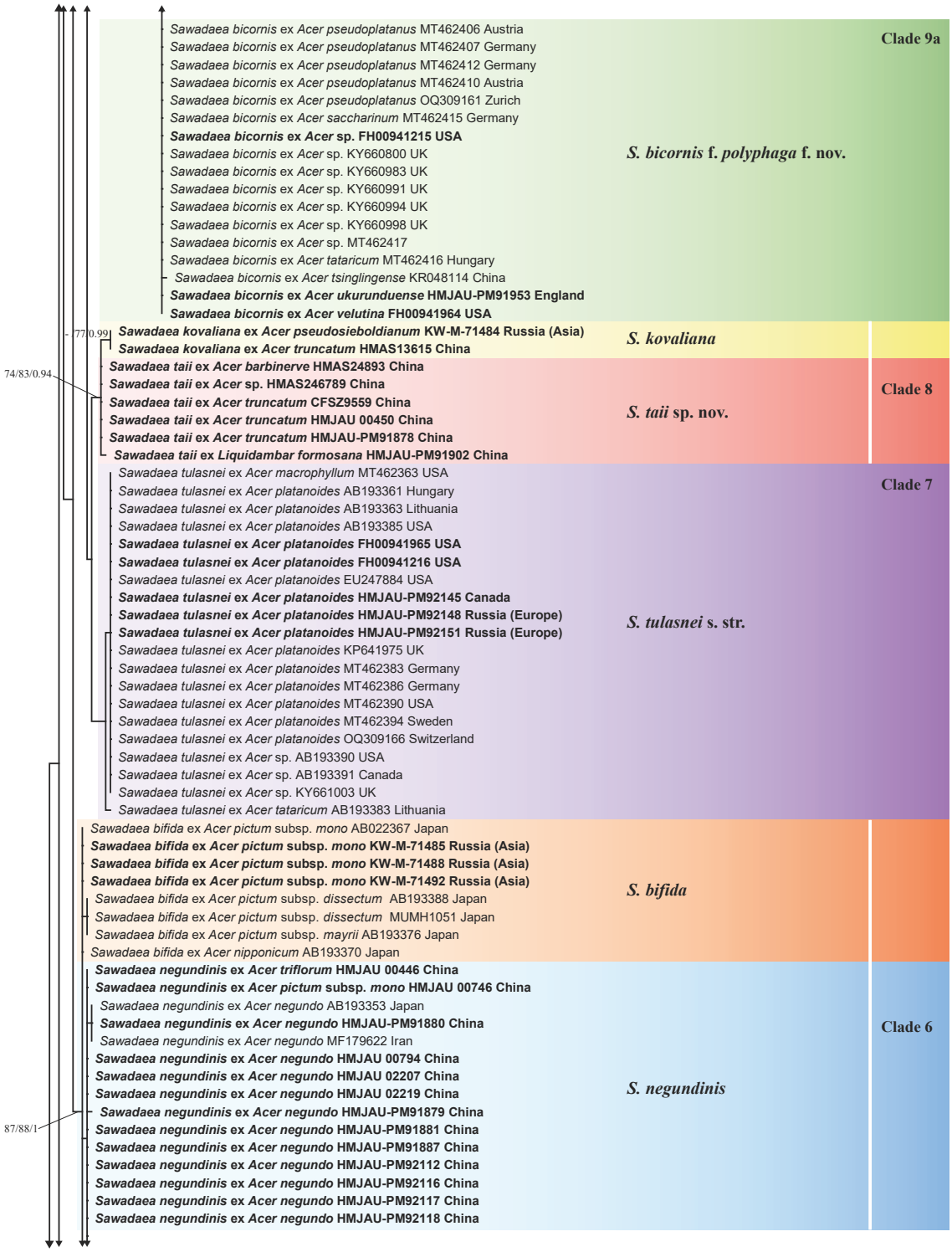

Fig. 1. (Continued)

They form two separate clades with high support in the phylogenetic tree, viz., *S. aceris-arguti* (Clade 10, MP = 100 %, ML = 100 %, BI = 1.00), and *S. acerina* (Clade 11; MP = 93 %, ML = 97 %, BI = 1.00). *Sawadaea bicornis* and *S. polyfida* had no deletion between sites 92 and 101.

Furthermore, specimens of *S. polyfida* (Clade 5) from six countries (China, Japan, Korea, Australia, USA, and Switzerland) exhibit a high degree of genetic diversity. *Sawadaea bifida* and *S. negundinis* form a non-monophyletic clade (Clade 6) including a sequence of a collection on *Acer ginnala* from Japan identified as *S. tulasnei*. Sequences of collections on *Alectryon excelsus* from New Zealand, previously identified as *S. negundinis*, and isolates on *Acer* spp. (*A. crataegifolium*, *A. ginnala*, *A. platanoides* and *A. rufinervis*) from Japan, previously assigned to *S. tulasnei*, are nested in the *S. negundinis* clade (Clade 6), but cluster distant from the true *S. negundinis* clade as well as the *S. tulasnei* clade. *Sawadaea kovaliana* and *S. taii* form sister groups in Clade 8, which are clustered with *S. tulasnei* s. str. (Clade 7). *Sawadaea bicornis* (clade 9) is divided into two highly supported subclades that are taxonomically considered genetically established biological races, treated as *formae*, viz., *S. bicornis f. bicornis* (Clade 9b) and *S. bicornis f. polyphaga* (Clade 9a).

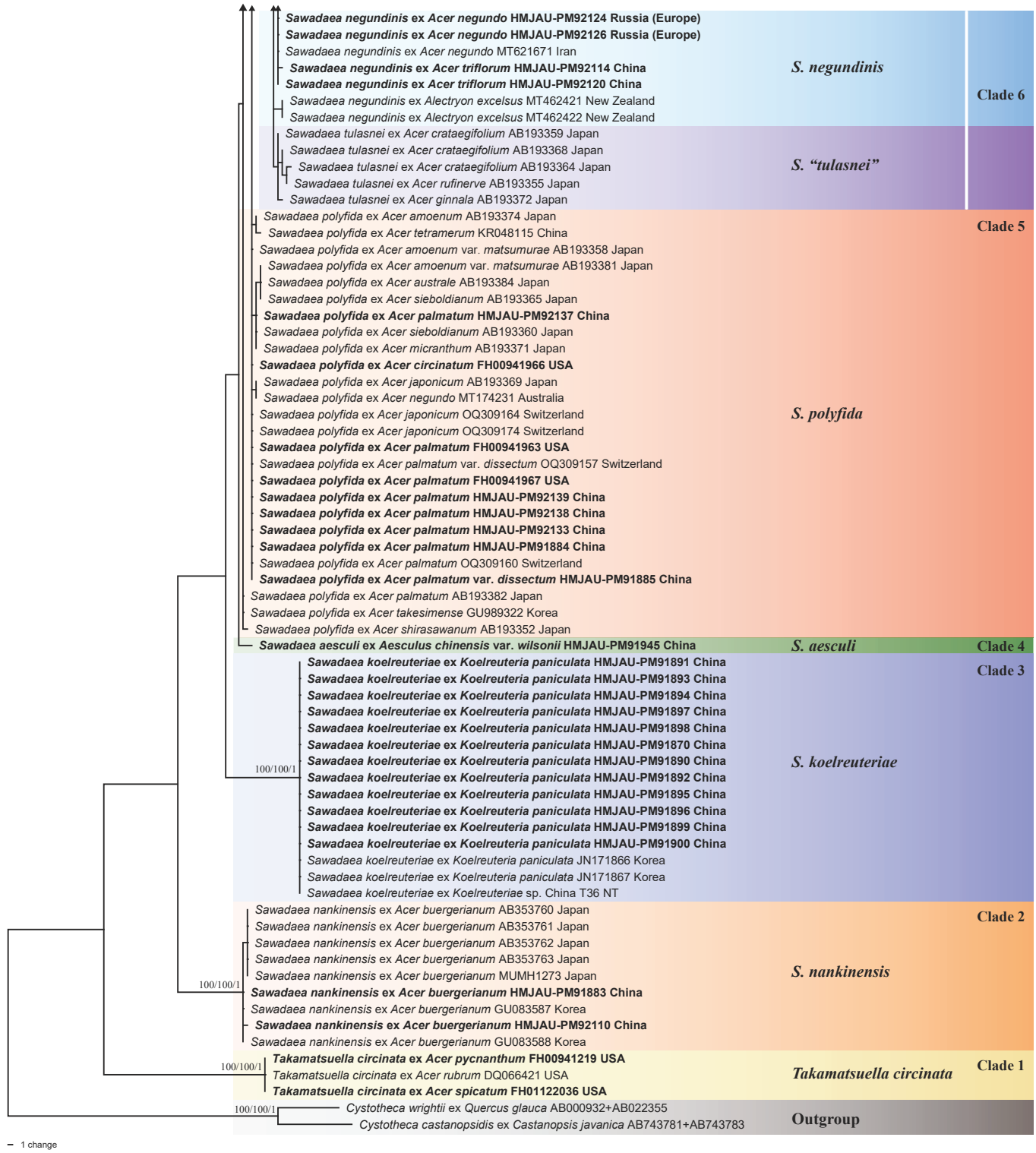

Fig. 1. (Continued)

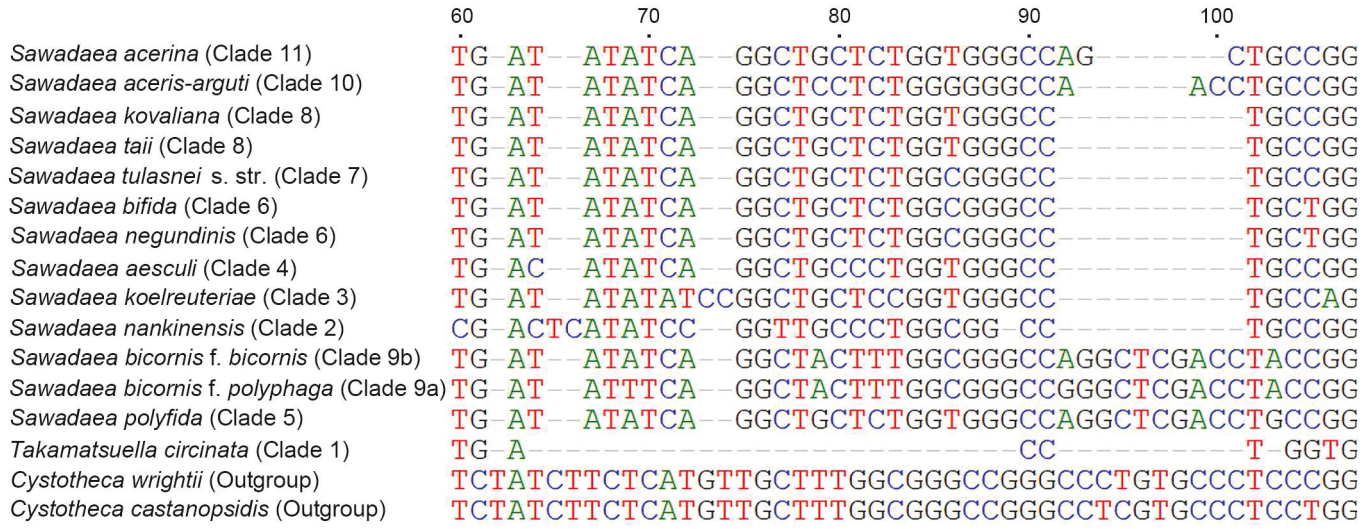

Fig. 2. Insertion/deletion (indel) found between sites 60 and 107 of ITS1 regions of *Sawadaea*, *Takamatsuella* and *Cystotheca*. The insertion or deletion is related to the formation of clades in the phylogenetic tree and the presentation of phylogenetic relationships.

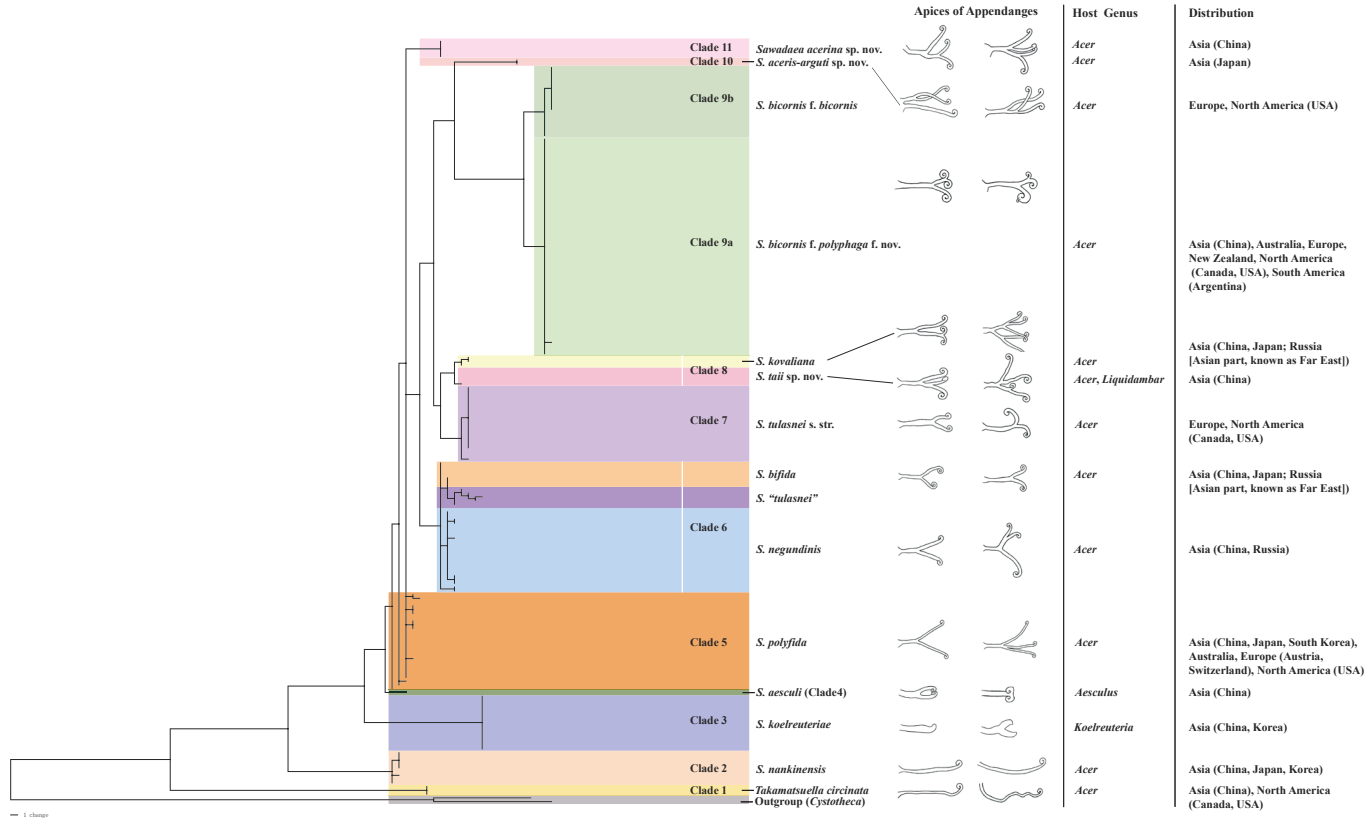

Fig. 3. Phylogenetic outline of the ITS+28S rDNA regions combining typical characteristics of appendages on chasmothecia.

Taxonomy

Twelve species of *Sawadaea* and one species of *Takamatsuella* were recognized, including three new species, namely *Sawadaea acerina sp. nov.*, *Sawadaea aceris-arguti sp. nov.*, and *Sawadaea taii sp. nov.* described from Asia. *Sawadaea bicornis* comprises two biological *formae*, *Sawadaea bicornis f. bicornis* and *f. polyphaga f. nov.*, with different host preferences. Asexual morphs of *S. aesculi*, *S. bifida*, *S. kovaliana* and *T. circinata* have also been detected and described for the first time.

Sawadaea Miyake, *Special Bull Agric. Exp. Stat. Formosa* **9**: 49. 1914.

Synonyms: *Uncinula* sect. *Sawadaea* (Miyake) U. Braun, *Feddes Repert.* **88**: 663. 1978.

Oidium subgen. *Octagoidium* R.T.A. Cook *et al.*, *Mycol. Res.* **101**: 998. 1997 [type species: *Oidium aceris* Rabenh.].

Octagoidium (R.T.A. Cook *et al.*) R.T.A. Cook & U. Braun, in Braun & Cook, *Taxonomic manual of the Erysiphales (powdery mildews)*: 172. 2012.

Table 1.

Fungal species[a]	Host	Specimen No.[b]	Collection locality	GenBank accession number	
				ITS	28S rDNA
Sawadaea acerina sp. nov.	*Acer tataricum* subsp. *ginnala*				
	A. tataricum subsp. *ginnala*			—	OQ866185
	A. tataricum subsp. *ginnala*				
	A. tataricum subsp. *ginnala*			—	OQ866186
	A. tataricum subsp. *ginnala*			OQ875005	—
	A. tataricum subsp. *ginnala*			OQ866170	—
-	*A. tataricum* subsp. *ginnala*			—	—
	A. tataricum subsp. *ginnala*				
	A. saccharinum				
S. aceris-arguti sp. nov.	*A. argutum*				—
	A. argutum			—	—
	A. argutum				
	A. argutum			—	—
	A. argutum			—	—
S. aesculi	*Aesculus chinensis* var. *wilsonii*			—	—
	Aesculus chinensis				
	Aesculus chinensis var. *wilsonii*			—	—
S. bicornis f. bicornis	*Acer campestre*			OQ866160	OQ866160
	A. campestre			OQ866171	—
	A. campestre			OQ866172	—
S. bicornis f. polyphaga f. nov.	*A. heldreichii* subsp. *trautvetteri*			OR166375	—
	A. negundo			OQ866159	OQ866159
	A. pseudoplatanus		—		—
	A. ukurunduense				
	A. velutina			OR166383	OR166383
	Acer sp.			OR166382	OR166382
	Acer sp.			—	OQ866189
S. bifida	*A. pictum* subsp. *mono*			OR166385	OR166385

Table 1. [illegible]

Fungal species[a]	Host	Specimen No.[b]	Collection locality	GenBank accession number	
				ITS	28S rDNA
	A. pictum subsp. *mono*	[illegible]	[illegible]	OR166373	—
	A. pictum subsp. *mono*	[illegible]	[illegible]	OR166374	—
	A. pictum subsp. *mono*	[illegible]	[illegible]	—	—
	A. pictum subsp. *mono*	[illegible]	[illegible]	—	—
	A. pictum subsp. *mono*	[illegible]	[illegible]	—	—
	A. pictum subsp. *mono*	[illegible]	[illegible]	—	—
S. bomiensis	*A. caudatum*	[illegible]	[illegible]	—	—
	Acer sp.	[illegible]	[illegible]	—	—
S. koelreuteriae	*Koelreuteria paniculata*	[illegible]	[illegible]	[illegible]	[illegible]
	K. paniculata	[illegible]	[illegible]	[illegible]	[illegible]
	K. paniculata	[illegible]	[illegible]	[illegible]	[illegible]
	K. paniculata	[illegible]	[illegible]	[illegible]	[illegible]
	K. paniculata	[illegible]	[illegible]	[illegible]	[illegible]
	K. paniculata	[illegible]	[illegible]	[illegible]	[illegible]
	K. paniculata	[illegible]	[illegible]	[illegible]	[illegible]
	K. paniculata	[illegible]	[illegible]	—	OQ866184
	K. paniculata	[illegible]	[illegible]	OQ866179	—
	K. paniculata	[illegible]	[illegible]	OQ866180	—
	K. paniculata	[illegible]	[illegible]	OQ866181	—
	K. paniculata	[illegible]	[illegible]	OQ866182	OQ866187
	K. paniculata	[illegible]	[illegible]	OQ866183	OQ866188
	K. paniculata	[illegible]	[illegible]	—	—
	K. paniculata	[illegible]	[illegible]	—	—
	K. paniculata	[illegible]	[illegible]	—	—
S. kovaliana	*A. pseudosieboldianum*	[illegible]	[illegible]	OQ866167	OQ866167
	A. truncatum	[illegible]	[illegible]	OQ866168	—
S. nankinensis	*A. buergerianum*	[illegible]	[illegible]	[illegible]	[illegible]
	A. buergerianum	[illegible]	[illegible]	OQ866173	—

Table 1.

Fungal species[a]	Host	Specimen No.[b]	Collection locality	GenBank accession number	
				ITS	28S rDNA
	A. buergerianum			—	—
	A. buergerianum			—	—
	A. buergerianum			—	—
S. negundinis	*A. negundo*				
	A. negundo				
	A. negundo				
	A. negundo			—	—
	A. negundo				
	A. negundo			OQ866163	OQ866163
	A. negundo			OQ866174	—
	A. negundo			OQ866162	OQ866162
	A. negundo			OQ866175	—
	A. negundo			OQ866176	—
	A. triflorum			OQ866161	OQ866161
	A. triflorum			OQ866177	—
	A. negundo				
	A. negundo				
	A. negundo			OR711904	
	A. triflorum			OR708548	
	A. pictum subsp. *mono*			OR711903	
	A. negundo			OR708549	
	A. negundo			—	—
S. polyfida	*A. amplum* subsp. *catalpifolium*			—	—
	A. amplum subsp. *catalpifolium*			—	OQ874975
	A. circinatum			OR166376	—
	A. palmatum			OR166379	—
	A. palmatum			OR166384	OR166384
	A. palmatum				

Table 1. [illegible]

Fungal species[a]	Host	Specimen No.[b]	Collection locality	GenBank accession number	
				ITS	28S rDNA
	A. palmatum ‘dissectum’	[illegible]	[illegible]	[illegible]	
	A. palmatum	[illegible]	[illegible]	—	—
	A. palmatum	[illegible]	[illegible]	—	—
	A. palmatum	[illegible]	[illegible]	—	—
	A. palmatum	[illegible]	[illegible]	—	—
	A. palmatum	[illegible]	[illegible]	OR863613	OR863613
	A. palmatum	[illegible]	[illegible]	—	—
	A. palmatum	[illegible]	[illegible]	—	—
	A. palmatum	[illegible]	[illegible]	—	—
	A. palmatum	[illegible]	[illegible]	OR701408	OR701408
	A. palmatum	[illegible]	[illegible]	OR701409	OR701409
	A. palmatum	[illegible]	[illegible]	OR701411	OR701411
	Acer sp.	[illegible]	[illegible]	—	—
S. taii sp. nov.	*Acer truncatum*	[illegible]	[illegible]	[illegible]	
	A. truncatum	[illegible]	[illegible]	[illegible]	
	A. truncatum	[illegible]	[illegible]	—	—
	A. truncatum	[illegible]	[illegible]	—	—
	A. truncatum	[illegible]	[illegible]	OQ866158	OQ866158
	A. barbinerve	[illegible]	[illegible]	OQ866169	—
	Liquidambar formosana	[illegible]	[illegible]	[illegible]	
	Acer sp.	[illegible]	[illegible]	OR841072	OR841072
S. tulasnei s.	*A. platanoides*	[illegible]	[illegible]	OR166380	OR166380
	A. platanoides	[illegible]	[illegible]	OR166381	OR166381
	A. platanoides	[illegible]	[illegible]	OQ866165	OQ866165
	A. platanoides	[illegible]	[illegible]	—	—
	A. platanoides	[illegible]	[illegible]	—	OQ866193
	A. platanoides	[illegible]	[illegible]	OQ866178	—
	A. platanoides	[illegible]	[illegible] —		—

Table 1.

Fungal species[a]	Host	Specimen No.[b]	Collection locality	GenBank accession number	
				ITS	28S rDNA
	A. platanoides			OQ866166	OQ866166
	A. platanoides				
Takamatsuella circinata	*A. pycnanthum*			OR166378	
	A. rubrum				
	A. spicatum			OR166377	
	A. wilsonii				
	Acer				
	Acer				
	A. platanoides				
	A. tataricum				
	A. tataricum				

Type species: *Sawadaea aceris* (DC.) Miyake (≡ *S. bicornis*

Sawadaea we

Sawadaea acerina ***sp. nov.***

Etymology cer,
+ Latin adjectival suffix -ina (belonging to).

Typus: **China**,
cer tataricum innala, *X. Guan & J. Feng* **holotype** otype

Diagnosis: *Sawadaea polyfida*,

Mycelium

hyphae
thin-walled, 27.0–69.5(–83.0) × 2.5–6.5 µm; *hyphal appressoria*
micro-conidiophores
59.5 × 4.0–6.5 µm, arising from the mother cell centrally or towards one septum, foot-cells cylindrical, straight, 12.5–29.0 × 4.0–6.0 µm, basal septum sometimes elevated, 7.0–16.5 µm distant from
micro-conidia
ovoid, 5.5–9.5(–13.5) × 5.0–7.5(–11.0) µm, length/width ratio 1.0–1.5(–2.5) (av. 1.3), with fibrosin bodies; *macro-conidiophores* 25.5–79.0 × 5.5–10.5 µm, arising from the upper surface of the mother cells, foot-cells cylindrical, straight, 13.5–36.0 × 5.5–10.5 µm, basal septum sometimes elevated, 3.5–18.5 µm distant from
macro-conidia
doliiform, fresh conidia 20.5–38.5(–54.5) × 12.5–23.0 µm, length/width ratio 1.0–4.0 (av. 1.8), with fibrosin bodies; *germ tubes*
rthotubus
Fibroidium *Chasmothecia*
(126.5–)141.5–211.5 µm diam.; *peridium cells*
4.0–19.5 µm diam., arranged ± radially; *appendages*
branched, (31.5–)63.0–195.5 × 4.5–14.0 µm, 0.2–1.3 (av. 0.8) times
asci
56.0–98.0 × 35.0–53.0 µm, length/width ratio 1.2–2.5 (av. 1.8), wall up to 4.7 µm, short-stalked or almost sessile, (6–)8-spored; *ascospores* ellipsoid-ovoid, 12.5–26.5 × 11.0–15.0 µm, length/width

Additional materials examined: **China**, [illegible] *Acer tataricum* subsp. *ginnala* [illegible] *S. Takamatsu, V.N. Nguyen, J. Feng & W.W. Yan* [illegible] PM91886, 28S rDNA GenBank No.: OQ866185; HMJAU-PM92100); [illegible] *Acer tataricum* subsp. *ginnala*, [illegible] *G.X. Guan & J. Feng* [illegible] GenBank No.: OQ875005; HMJAU-PM92099, ITS rDNA GenBank No.: OQ866170); Jilin Province, Changchun City, on *Acer tataricum* subsp. *ginnala* [illegible] *S.R. Tang, G.X. Guan & J. Feng* [illegible] *Acer tataricum* subsp. *ginnala*, 2 Oct. 2010, *W.T. Jiang* [illegible] *Acer saccharinum* [illegible], 24 Oct. 2018, *S.R. Tang & L. Liu* [illegible] [illegible] *Acer tataricum* subsp. *ginnala*, 24 Oct. 2018,

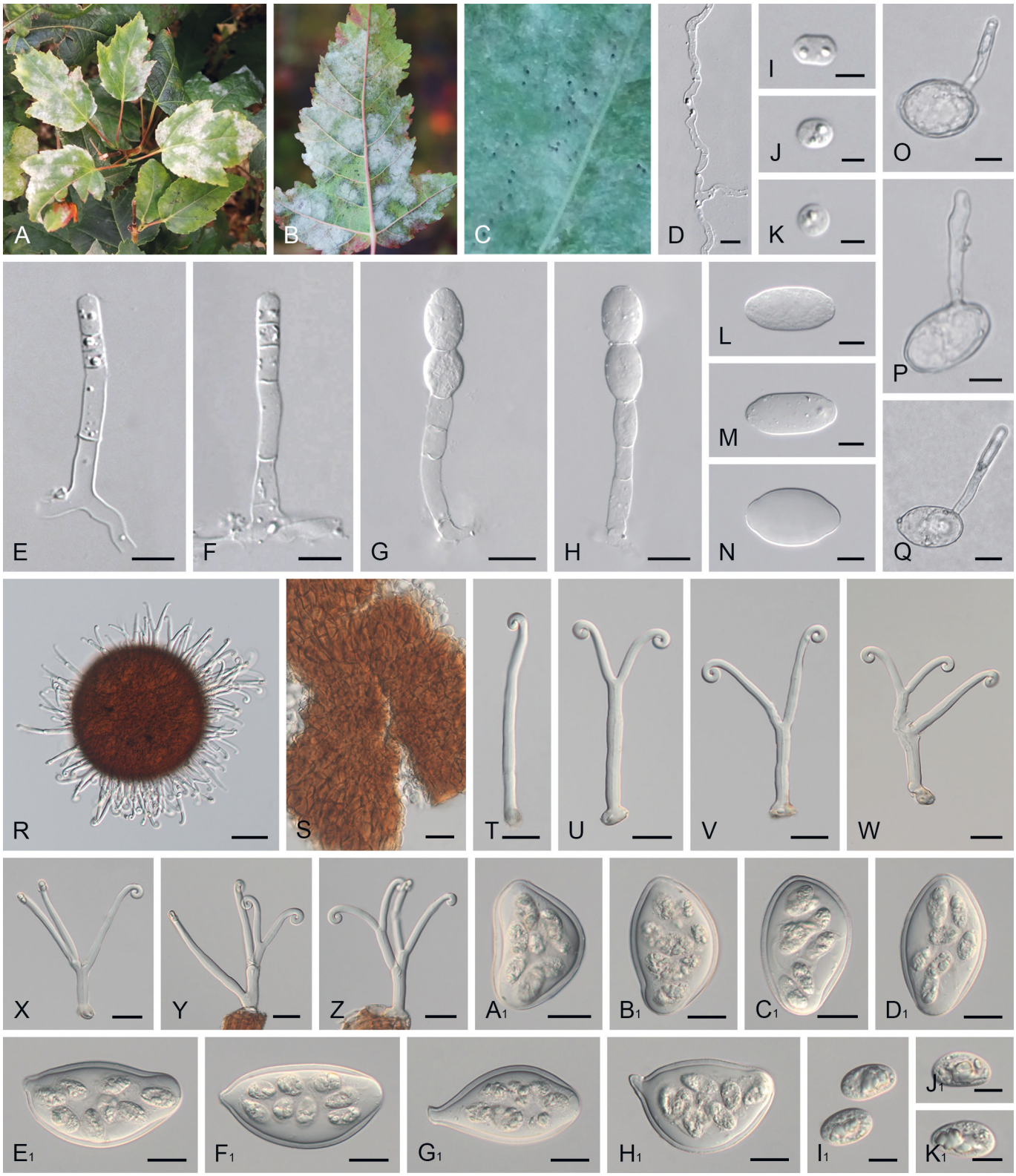

Fig. 4. *Sawadaea acerina sp. nov.* [illegible] *Acer tataricum* subsp. *ginnala* [illegible] C. [illegible] D. [illegible] E, F. [illegible] G, H. [illegible] I–K. [illegible] L–N. [illegible] O–Q. [illegible] R–Z. [illegible] A1–H1. [illegible] I1–K1. [illegible]
R = 50 µm; G,H, S–H1 = 20 µm; D–F, L–Q, I1–K1 = 10 µm; I–K = 5 µm.

S.R. Tang & L. Liu (HMJAU-PM91888, 28S rDNA GenBank No.: OQ866186).

Host range and distribution: On *Acer* (*saccharinum*, *tataricum* subsp. *ginnala*), *Sapindaceae*, Asia (China).

Notes: The new species can be morphologically readily distinguished from other species of *Sawadaea*: (1) from *S. koelreuteriae* and *S. nankinensis* by having branched appendages; (2) from *S. aesculi* and *S. bomiensis* by having a much larger number of chasmothecial appendages (58–142 vs < 50); (3) by having chasmothecial appendages branched in the middle or lower part (vs appendages branched in the middle or upper part of the appendages in *S. bicornis*); (4) by having larger chasmothecia (141–212 µm diam., vs 115–185 µm in *S. bifida*); (5) by having shorter macro-conidiophores (up to 79 µm vs 150 µm) and shorter foot-cells (21–31 µm vs 25–50 µm) compared with *S. negundinis*, but larger macro-conidia and micro-conidia compared with *S. negundinis* and *S. tulasnei* (macro-conidia 25–55 × 13–21 µm vs 24–30 × 15–19 µm and vs 16–28 × 10–18 µm, micro-conidia 21–31 × 13–23 µm vs 6–8 × 5–7 µm and vs 2–11 × 6–9 µm). The new species is morphologically similar to *S. polyfida*, but it differs in having mainly unbranched or 1–2 times branched chasmothecial appendages and it forms a separate well-supported species clade in the molecular phylogenetic tree. In addition, we need a special explanation that there were only a few fully mature chasmothecia on the holotype specimen, due to the early collection season.

Sawadaea aceris-arguti S. Takam. & U. Braun, ***sp. nov.*** MycoBank MB 849117. Fig. 5.

Etymology: Epithet derived from the name of the host plant, *Acer argutum*.

Typus: **Japan**, Nagano Pref., Ueda-shi, Sugadaira, Tsukuba University, Sugadaira Research Station, on *Acer argutum*, 30 Sep. 2000, *S. Takamatsu* [**holotype** TNS-F-87577, ex-holotype sequence: GenBank No. AB193367 (ITS rDNA)].

Diagnosis: Morphologically close to *Sawadaea polyfida*, but chasmothecia only with 50–100 appendages, fewer asci, 7–13, and shorter and, above all, narrower ascospores, 17–22 × 9–11 µm (vs 100–250 appendages, 8–38 asci, 12.5–33 × 9.5–19 µm in *S. polyfida*). Genetically different from all other species within *Sawadaea* by forming a well-supported separate species clade.

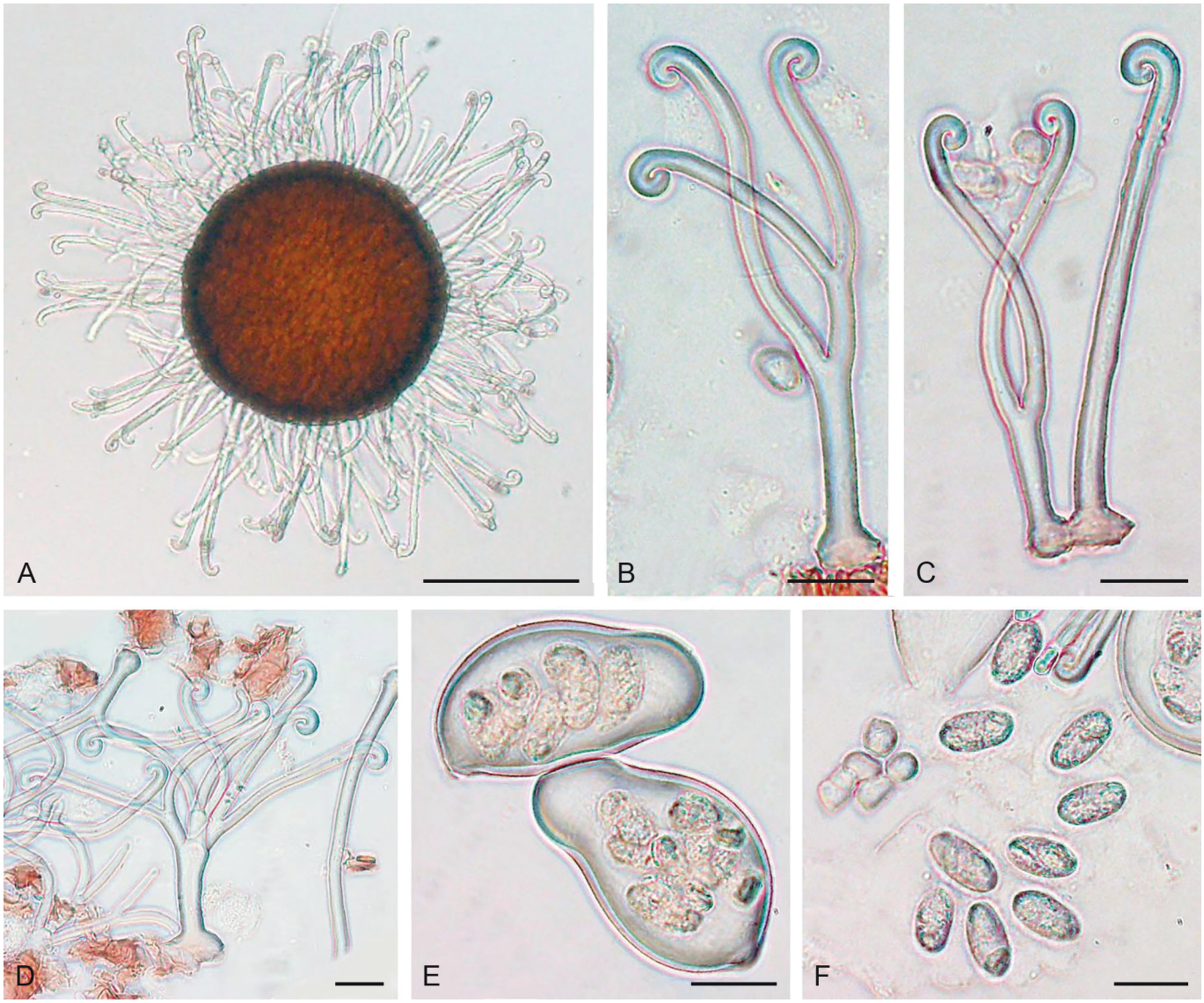

Fig. 5. *Sawadaea aceris-arguti sp. nov.* (TNS-F-87577, holotype). **A.** Chasmothecium. **B–D.** Appendages. **E.** Asci. **F.** Ascospores. Scale bars: A = 100 µm; B–D = 50 µm; E, F = 20 µm.

Mycelium [illegible]
hyphae [illegible]
µm wide, hyaline, septate, thin-walled, smooth. *Chasmothecia* scattered, depressed globose, (130.0–)140.0–180.0 µm diam.; *peridium cells* [illegible] *appendages* [illegible]
[illegible]
apices uncinate to circinate, 60.0–120.0 µm in length (0.3–0.7 times [illegible]
smooth to rough-walled, main axis 5.0–8.0 µm wide throughout; *asci* 7–13, saccate, 55.0–77.0 × 32.0–47.0 µm, short-stalked or almost [illegible] *ascospores* [illegible]
ovoid, 17.0–22.0 × 9.0–11.0 µm, colourless.

Additional materials examined: **Japan**, [illegible]
on *Acer argutum*, 12 Oct. 1986, *S. Tanda* [illegible]
[illegible] *Acer argutum*, [illegible] *S. Takamatsu* [illegible]
[illegible]
on *Acer argutum*, [illegible] *C. Nakashima* [illegible]
[illegible] *Acer argutum*, [illegible] *S. Tanda* [illegible]
[illegible]

Host range and distribution: On *Acer argutum*, *Sapindaceae* [illegible]

Notes: *Sawadaea aceris-arguti* [illegible]
S. polyfida [illegible]
[illegible]
[illegible] *S. aceris-arguti* [illegible] *polyfida* [illegible] *Sawadaea* [illegible]
it was not possible to find any trace of asexual morphs, which [illegible] *S. aceris-arguti* [illegible]
[illegible]

Sawadaea aesculi [illegible] *Acta Microbiol. Sin.* **20**: [illegible]

Typus: **China**, [illegible]
[illegible] *Aesculus chinensis* [illegible] *wilsonii*, [illegible] *X.N. Yu & Y.S. Xing* (**holotype**) [illegible]

Mycelium [illegible]
[illegible] *hyphae* [illegible]
sinuous, septate, branched, thin-walled, 24.5–65.5 × 3.0–8.0(–8.5) µm; *hyphal appressoria* [illegible]
micro-conidiophores 20.0–43.0 × 5.0–7.0 µm, arising from the [illegible]
cells cylindrical, straight, 7.0–21.5 × 4.5–7.5 µm, basal septum sometimes elevated, 2.5–11.5 µm from the junction with the mother [illegible] *micro-conidia* variable in shape, ellipsoid-ovoid, 4.5–15.5 × 4.5–11.0 µm, [illegible] *macro-conidiophores* [illegible]
85.5) × 4.5–8.5 µm, arising from mother cells, foot-cells cylindrical, straight, (12.0–)23.5–36.0(–56.0) × 4.5–9.0 µm, basal septum sometimes elevated, 1.5–12.5 µm from the junction with the mother [illegible] *macro-conidia* [illegible]
32.0(–48.5) × 10.0–18.0 µm, length/width ratio 1.3–3.1(–3.8), with fibrosin bodies; *germ tubes* [illegible]
[illegible] *orthotubus*, *fibroidium* [illegible] *Chasmothecia* [illegible]

Additional materials examined: **China**, [illegible]
[illegible] *Aesculus chinensis* [illegible] *wilsonii*, [illegible] *G.Q. Chen* [illegible]
[illegible] *Aesculus chinensis*, [illegible] *S.R. Tang & J. Feng* [illegible]
[illegible]

Host range and distribution: On *Aesculus chinensis*, *Sapindaceae*, [illegible]

Notes: [illegible] *awadaea aesculi* [illegible]
[illegible] *Aesculus chinensis* [illegible]
wilsonii [illegible] *S. aesculi* [illegible] *Aesculus chinensis* [illegible] *et al.* [illegible]
[illegible]
[illegible] *S. aesculi* [illegible] *et al.* [illegible]
[illegible]

Sawadaea bicornis [illegible] *Fac. Agric. Hokkaido Univ.* **3**: [illegible]
Basionym: *Alphitomorpha bicornis* [illegible] *Verh. Ges. Naturf. Freunde Berlin* **1**: [illegible]
Synonyms: *Erysiphe bicornis* [illegible] *Erysibe*] *Sp. pl. 4*, [illegible] *nom. sanct.* [illegible] *Syst. Mycol.* **3**: [illegible]
Uncinula bicornis [illegible] *Ann. Sci. Nat., Bot., Sér. 3*, **15**: [illegible]
Erysiphe aceris [illegible] *Syn. pl. Fl. gall.* [illegible]
Uncinula aceris [illegible] *Syll. Fung.* **1**: [illegible]
Oidium aceris [illegible] *Flora* **12**: [illegible]
Oidium dodonaeae [illegible] *Palestine J. Bot., Rehovot Ser.*, **5**: [illegible]

Typus: On *Acer campestre* [illegible] *Erysiphe aceris* fl. Fr. 732" [**lectotype** [illegible]
epitype [illegible] **Austria**, [illegible] *Acer campestre*, [illegible] *U. Kruse*, [illegible]
[illegible]

Mycelium [illegible]
[illegible] *hyphae* [illegible]
sinuous, septate, branched, thin-walled, 26.5–55.0 × 3.0–8.0 µm; *hyphal appressoria* [illegible] *micro-conidiophores* (23.5–)37.5–71.5(–123.5) × 5.0–9.0 µm, arising from [illegible]
straight, 16.5–42.0(–61.0) × 5.0–8.5 µm, basal septum sometimes elevated, up to 13.5 µm from the junction with the mother cell,

micro-conidia variable in shape, ellipsoid-ovoid, 18.0–28.0 × 13.5–19.0 µm, length/width ratio 1.0–1.7 (av. 1.5), with fibrosin bodies; *macro-conidiophores* 52.5–88.5(–112.5) × 5.5–8.0 µm, arising from mother cells, foot-cells cylindrical, straight, 18.5–54.5 × 5.5–8.5 µm, basal septum sometimes elevated, to 17.5 µm from the junction with the

macro-conidia

4.0(–65.0) × 10.5–20.0 µm, length/width ratio 1.7–4.1(–5.1) (av. 2.4), with fibrosin bodies; germ tubes terminal, short to moderately

rthotubus *ibroidium* *Chasmothecia* scattered to ± gregarious, 102.0–170.0 µm diam.; *peridium cells* irregularly polygonal, 3.0–14.0 µm diam., arranged ± radially;

appendages

31.5–137.5 × 4.5–8.5 µm, 0.2–1.2 times (av. 0.8) as long as the

asci

8–20, ellipsoid-obovoid, saccate-clavate, 57.0–98.0(–108.0) × 40.0–65.0 µm, length/width ratio 1.0–2.0 (av. 1.4), wall up to 4.6 µm thick, short-stalked or almost sessile, (6–)8-spored; *ascospores* ellipsoid-ovoid, 19.5–28.0 × 11.0–21.0 µm, length/width ratio 1.1–

Subspecific classification:

Sawadaea bicornis

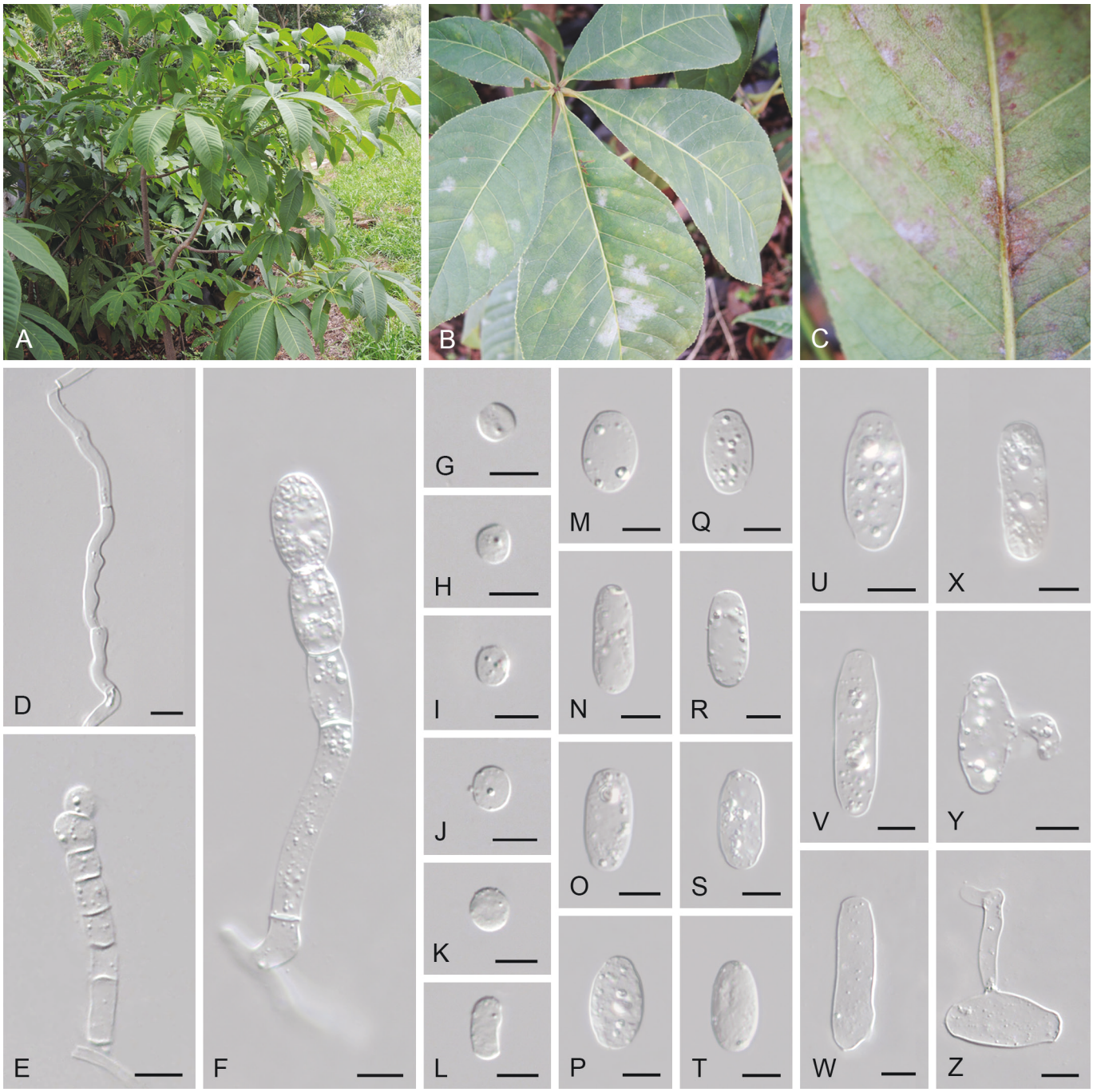

Fig. 6. *Sawadaea aesculi* A. B. C. D. F–L. M–X. Z. tubes. Scale bars = 10 µm.

subclades that reflect two biological races with different host
genetically established and verifiable, they deserve a formal naming
ormae speciales
ormae'.
ormae' is that it is an official taxonomic
S. bicornis , *bicornis* *polyphaga*
S. bicornis
subclades with specific host preferences (Fig. 1).

Sawadaea bicornis f. bicornis, *Acer campestre* *Acer platanoides* (*Acer* Platanoidea)

Additional materials examined: **Russia**
Acer campestre,
T.S. Bulgakov
OQ866171); Rostov region, Shakhty, Alexandrovsky Park, on *Acer campestre*, *T.S. Bulgakov*
rDNA GenBank No.: OQ866172); Rostov region, Shakhty, Hospital
Acer campestre, 24 Oct. 2018, *T.S. Bulgakov*
PM92107, ITS+28S rDNA GenBank No.: OQ866160).

***Sawadaea bicornis f. polyphaga* nov.**

Etymology

Typus: **Germany**
Acer pseudoplatanus, *J. Kruse*
holotype

Diagnosis *bicornis*
Acer *Acer*
Acer Sinalla, Negundo, Palmata, Platanoidea,
polyphaga

Additional materials examined: **Canada**, Ontario, Niagara Region,
Acer negundo *S.V. Ilyukhin*

Fig. 7. *Sawadaea bicornis* **A, B.** **C.** **D.** **E, F.** **G–I.** **J–L.** **M–O.** **P, Q.** Germ tubes. Scale bars = 10 µm.

(HMJAU-PM92102, ITS+28S rDNA GenBank No.: OQ866159). **Russia** (
Ro *Acer pseudoplatanus*, 4
UK (*Acer ukurunduense*
Liu
o *Acer* (
GenBank No.: OQ866189). **USA**, Bo *Acer heldreichii* (
trautvetteri, 2
ITS rDNA GenBank No.: OR166375); Boston, on *Acer velutina*, 3
(
No.: OR166383); Boston, on *Acer* (
(FH00941215, ITS+28S rDNA GenBank No.: OR166382).

Host range and distribution (based on collections confirmed by
bicornis o *Acer* (*campestre* , *platanoides*)
(
polyphaga o *Acer* (*circinatum* , *grandidentatum*, *heldreichii* (
trautvetteri, *macrophyllum*, *negundo*, *pseudoplatanus*, *saccharinum*, *tsinglingense*, *tataricum* (
tataricum, *ukurunduense*) A
C
(

Host range and distribution of Sawadaea bicornis (
to Braun & Cook 2012): On *Acer* (*amplum* (
catalpifolium [≡ *catalpifolium*] *barbinerve*, *campestre* , *cappadocicum* (
cappadocicum [= *laetum*] *cappadocicum* (
lobelii [≡ *lobelii*] *caudatum*, *caudatifolium* [= *kawakamii*] *cissifolium* , *heldreichii* (
trautvetteri, *hyrcanum*, *ibericum* , *macrophyllum* , *mandshuricum* , *miyabei*, *mono*, *monspessulanum* (
monspessulanum, *turcomanicum* [*turcomanicum*] *negundo*, *obtusatum*, *oliverianum* , *opalus*, *opulifolium* [= *hispanicum*] *pensylvanicum*, *platanoides* , *pseudoplatanus* , *pseudosieboldianum*, *rubrum*, *rufinerve*, *saccharinum* , *saccharum*, *stevenii* , *tataricum* (
tataricum, *tataricum* (
ginnala [≡ *ginnala*] *tataricum* (
semenovii [≡ *semenovii*] *tegmentosum*, *trautvetteri*, *triflorum*, *trilobum*, *truncatum*, *turkestanicum* [≡ *platanoides* (
turkestanicum] *ukurunduense*, *velutinum*) *Sapindaceae*; A
(
(
(
(
Aesculus hippocastanum, *Alectryon excelsus* D *odonaea viscosa* (
(
(
Acer monspessulanum (
et al. (

Notes: *Sawadaea bicornis* (
(
et al. (
S. bicornis (
(
(
Acer circinatum, *A. macrophyllum* (
A. grandidentatum, (
(
S. bicornis (
subclades. One of them is comprised of sequences obtained from *S. bicornis* o *Acer campestre* (
A. platanoides; (
Acer (
Platanoideae (

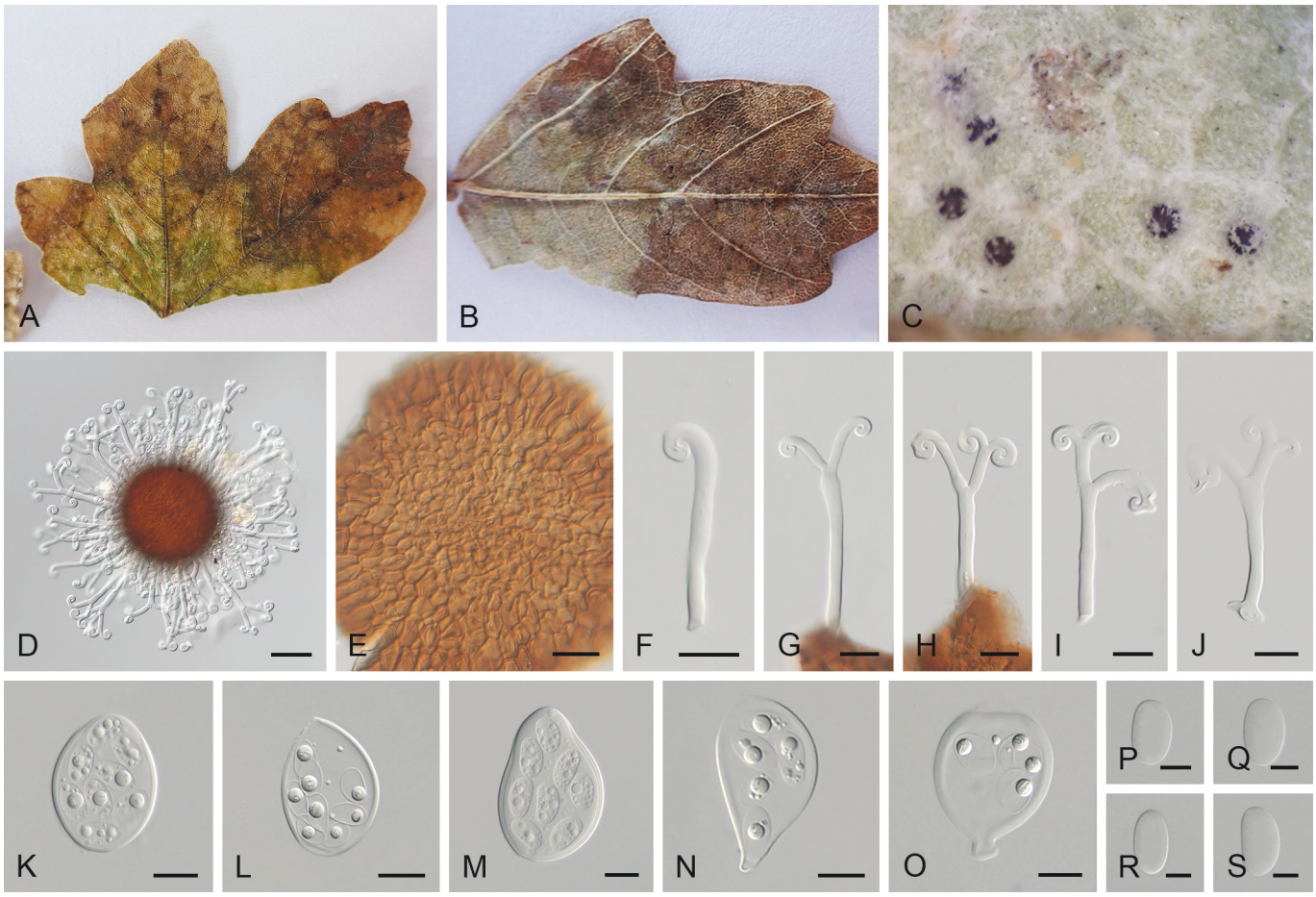

Fig. 8. *Sawadaea bicornis* (
A
D
E
F–J
K–O
P–S. Ascospores. Scale bars: D = 50 µm; E–O = 20 µm; P–S = 10 µm.

Acer pseudoplatanus ;
which might be a misidentification that requires reverification. The
Acer *A. pseudoplatanus* *A. negundo*
Acer *Acer* *Acer* (*A. grandidentata* , *A. heldreichii* *trautvetteri*, *A. monspessulanum*, *A. pseudoplatanus*, *A. velutinum* *Ginnala* (*A. tataricum*) *Lithocarpa* (*A. tsinglingense*) *Macrophylla* (*A. macrophylla*) *Negundo* (*A. negundo*) *Palmata* (*A. circinatum*) *Platanoidea* (*A. cappadocicum*) *Rubra* (*A. saccharinum*)
These results suggest that the first subclade is confined (or largely *Acer* *Platanoidea*
reflects a wide host range within *Acer*
subclades reflect genetically fixed virulence and host preference
formae
Acer
campestre
Sawadaea *A. pseudoplatanus* *A. negundo*

Sawadaea
contamination or host misidentifications. Future research should
Sawadaea *Acer*
et al.
A. campestre *bicornis*
A. pseudoplatanus *f. polyphaga*
Acer campestre *A. pseudoplatanus*

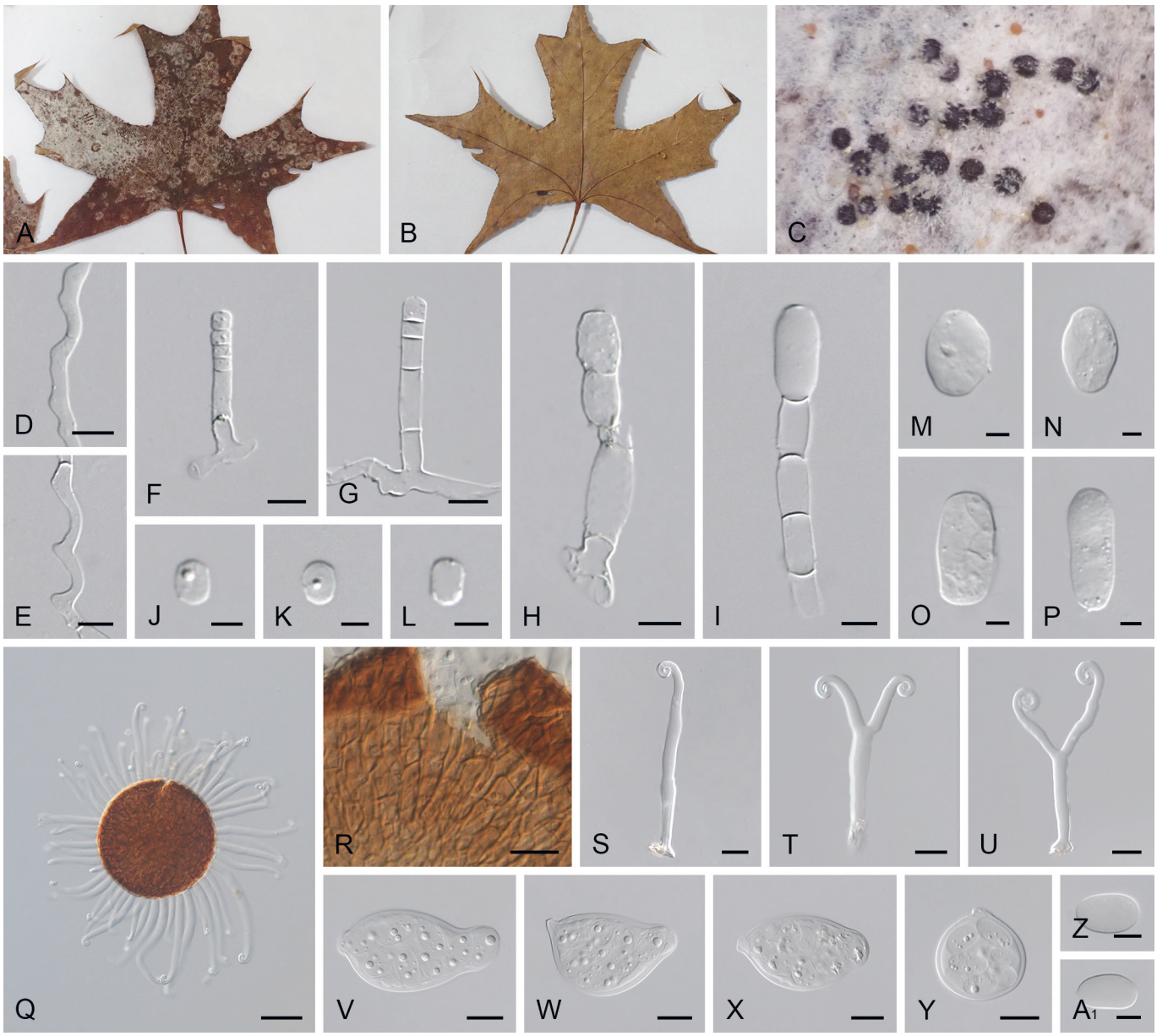

Fig. 9. *Sawadaea bifida* B. C. E. G. H, I, H–L. M–P. R. S–U. V–Y. **Z, A1.** Ascospores. Scale bars: Q = 50 µm; H, I, R–Y = 20 µm; D–G, Z, A1 = 10 µm; J–P = 5 µm.

B. bicornis A cer campestre d A. platanoides, g cer Platanoideag n
forma specialis)
formae b
S. bicornis, S. negundinis, d S. tulasnei
S. bicornis o Acer platanoides d A. negundo
A. platanoides d A. negundo
S. bicornis, and these results have been confirmed by

Sawadaea bifida Wkrayins'k. Bot. Zhurn. 47
Synonyms: *Sawadaea zhengii* Taxonomical study of *Erysiphaceae of Japan*: Acer mono holotype
Sawadaea Trans. Mycol. Soc. Japan 20

Typus: **Russia**
Acer pictum
mono, 1 Oct. 1989, *V.P. Heluta* [**holotype**
sequence: OR166385 (ITS+28S rDNA)].

Mycelium *hyphae*
branched, thin-walled, 12.0–46.5 × 2.5–6.5 µm; *hyphal appressoria*
micro-conidiophores
43.0 × 3.0–7.0 µm, arising from the upper surface of mother cells,
× 3.5–6.5 µm, basal septum sometimes elevated to 11.0 µm from
micro-conidia

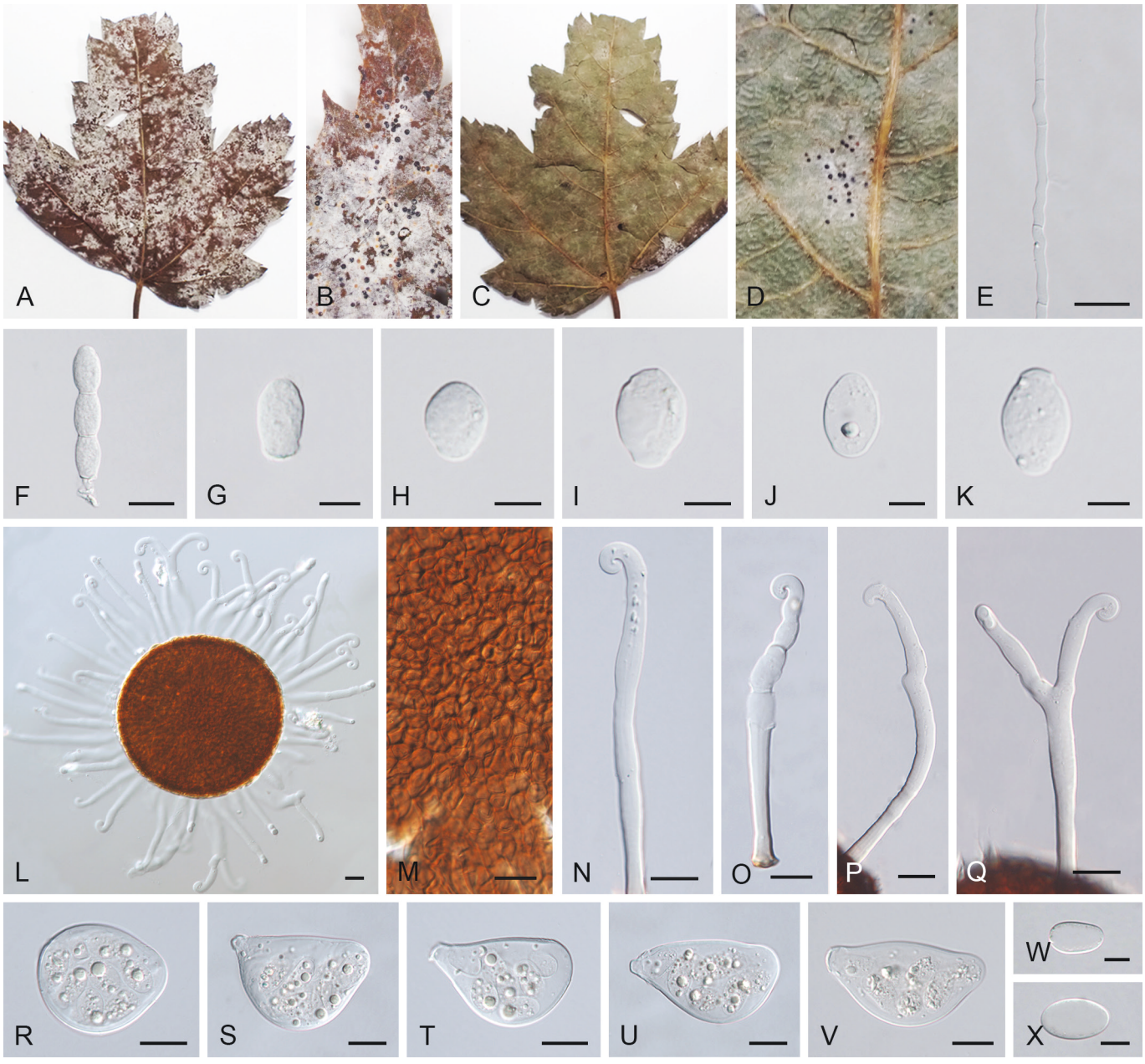

Fig. 10. *Sawadaea bomiensis*
E.
R–V. **W, X.** Ascospores. Scale bars: E, F, L–V = 20 µm; G–K, W, X = 10 µm.

ovoid, 5.0–14.0 × 4.5–12.5 µm, length/width ratio 1.0–1.6; *macro-conidiophores* 27.0–52.5 × 7.5–10.5 µm, arising from the upper surface of mother cells, foot-cells cylindrical, straight, 18.5–34.5 × 4.0–6.5 µm, followed by 1–3 shorter cells and catenescent conidia; *macro-conidia*
17.0–29.0 × 9.5–18.5 µm, length/width ratio 1.2–1.9. *Chasmothecia*
µm diam.; *peridium cells*
oblong, 4.5–23.0 µm diam.; *appendages*
nodulose, deeply cleft, first branching point in the lower half, often
chasmothecial diam., 34.0–187.5 × 7.0–11.5 µm, about 0.2–1.2
47.0–96.5 × 33.5–57.5 µm, length/width ratio 1.0–2.4, wall relatively thick, up to 4.5 µm, almost sessile to short-stalked, (6–)8-spored; *ascospores* ellipsoid, 18.5–30.0 × 10.5–15.0 µm, length/width ratio

Additional materials examined: **China,**
Acer pictum subsp. *mono*, 5 Oct. 1975, *Y.N. Yu & S.J. Han*
Acer pictum subsp. *mono*, *F.Z. Shi*
Acer pictum subsp. *mono*,
Y.J. Lu
Acer pictum subsp. *mono*, 17 Oct. 1979, *H. Huang*; **Russia,**
Acer *pictum* subsp. *mono*, *V.P. Heluta*
ITS rDNA GenBank No.: OR166374); Far East, Primorsky Kray, *Acer pictum* subsp. *mono*, *P. Heluta*
(KW-M-71485, ITS rDNA GenBank No.: OR166373).

Host range and distribution: On *Acer pictum* subsp. *mono*, *pictum* subsp. *dissectum*, *pictum* subsp. *mayrii*) *Sapindaceae*

Notes: *Sawadaea bifida*
Russian Far East, and its host range is confined to *Acer pictum* subsp. *mono* (≡ *A. mono*)
S. negundinis
multilocus approach is needed. The micro-conidiophores (30–82 × 6.5–10 µm, vs 21.5–43 × 3–7 µm) and micro-conidia (16–29 × 13–23.5 µm, vs 5–14 × 4.5–12.5 µm) of *S. negundinis* are significantly *S. bifida*. *Sawadaea bifida* seems to be confined to *Acer pictum*, *Acer* *Platanoidea* in *Acer* *hipponicum* in *et al.*
Sawadaea
from *Acer pictum* subsp. *mono*, *Acer pictum* subsp. *dissectum*, and *Acer pictum* subsp. *mayrii* *A. nipponicum* subsp. *Parviflora* *Acer* (*et al.* 2019). The host identification
misidentification with a species of sect. *Platanoidea* correct identification, to confirm infections of this species on hosts of *Acer*

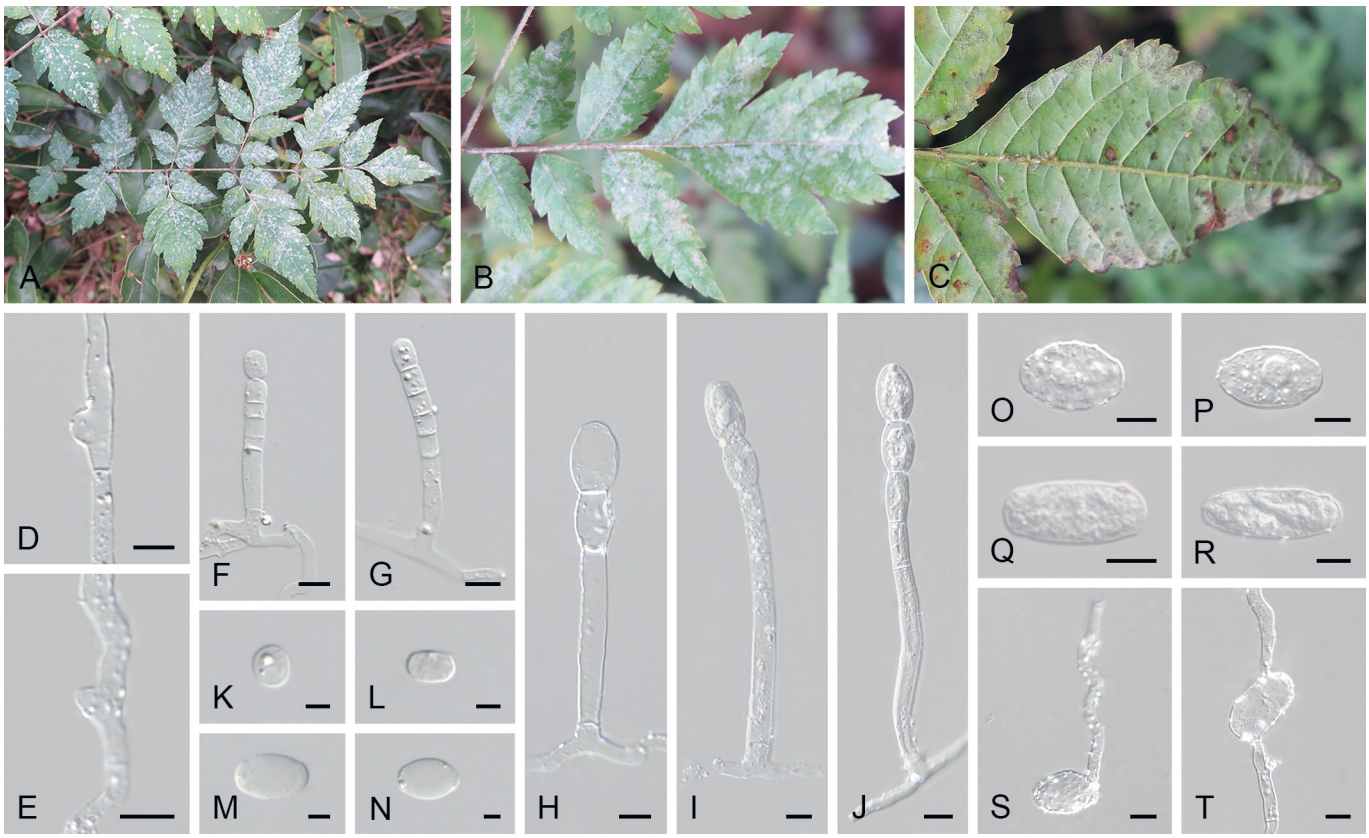

Fig. 11. *Sawadaea koelreuteriae*, **A, B.** **C.** **D, E.** **F, G.** **H–J.** **K–N.** **O–R.** **S, T.** Germ tubes. Scale bars: H–J = 20 µm; D–G, O–T = 10 µm; K–N = 5 µm.

Sawadaea bomiensis *Acta Microbiol. Sin.* **20**

Typus: **China**, *Acer caudatum* *M.M. Shen* **holotype**

Mycelium *hyphae* thin-walled, 2.5–5.5 µm wide; *hyphal appressoria* *conidia*)18.5–27.0(–33.5) × 11.5–17.5 µm, length/width ratio 1.1–1.7(–2.2) *Chasmothecia* µm diam.; *peridium cells* irregularly polygonal, 4.5–24.5 µm diam., *appendages* 0.4–0.8 times as long as the chasmothecial diam., 73.5–174.0 × 7.5–14.5 µm, mostly somewhat undulate or almost nodulose, thick- *asci* saccate-clavate, 57.0–95.0 × 48.5–60.0 µm, length/width ratio 1.1– *ascospores* ellipsoid-ovoid, (13.0–)17.0–27.0 × 10.5–16.5 µm,

Additional material examined: **China**, *Acer* *M. Zang*

Host range and distribution: On *Acer caudatum*, Sapindaceae

Notes: *Sawadaea bomiensis* on *Acer caudatum*,

Sawadaea koelreuteriae *Microbiol.*

Basionym: *Uncinula koelreuteriae* *Bot. Mag. Tokyo* **27**:

Synonyms: *Erysiphe koelreuteriae* *Bull. Chin. Bot. Soc.*

Typhulochaeta koelreuteriae *Bull. Torrey Bot. Club.*

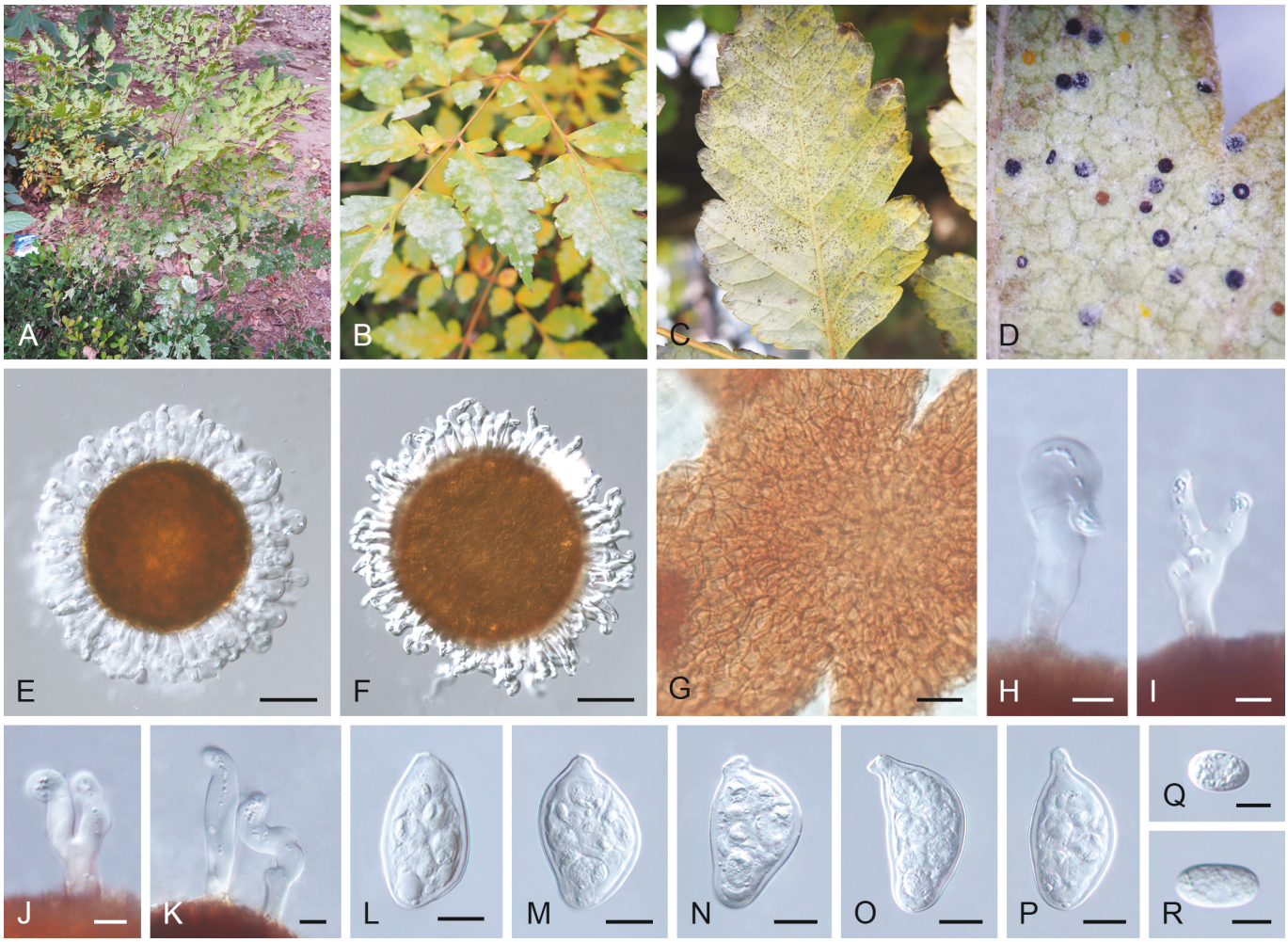

Fig. 12. *Sawadaea koelreuteriae* **C.** **D.–F, F.–H–K.** **L–P.** **Q, R.**
Scale bars: E, F = 50 µm; G–P = 20 µm; Q, R = 10 µm.

Typus: **China**, *Koelreuteria* [illegible] *S.X. Wei & L. Guo* [illegible] **holotype** [illegible]

Mycelium [illegible] *hyphae* [illegible] sinuous, 5.0–6.0 µm wide; *hyphal appressoria* [illegible] *micro-conidiophores* [illegible] 44.0–76.0 × 7.5–9.0 µm, foot-cells 19.5–49.5 × 6.0–8.5 µm; *micro-conidia* broad ellipsoid-ovoid, 18.5–28.5 × 13.0–18.0 µm, length/[illegible] *macro-conidiophores* 83.0–139.5 × 7.5–11.0 µm, arising from the mother cell, centrally or towards one septum, foot-cells cylindrical, straight, 43.5–97.5 × 7.0–9.0 µm, followed [illegible] *macro-conidia* [illegible] limoniform, fresh conidia 34.5–49.5 × 10.0–16.0 µm, length/width ratio 2.5–4.1, with fibrosin bodies; *germ tubes* [illegible] [illegible] *orthotubus* [illegible] *fibroidium* [illegible] *Chasmothecia* scattered, 135.5–209.0 µm diam.; *peridium cells* irregularly polygonal, 8.0–18.5 µm diam.; *appendages* [illegible] to seldom forked, often curved, 26.0–54.5 µm, 0.1–0.3 times as [illegible] [illegible] [illegible] *asci* [illegible] clavate-saccate, 56.0–89.5 × 31.0–53.0 µm, sessile or short-[illegible] *ascospores* [illegible] 16.5–23.0 × 13.0–16.5 µm, length/width ratio 1.2–1.4, colourless.

Additional materials examined: **China**, [illegible] *Koelreuteria paniculata*, [illegible] *L. Feng, L. Liu & R.J. Jiang* [illegible] *Koelreuteria paniculata*, 21 Oct. 2018, *S.R. Tang & L. Liu* (HMJAU-PM91891, ITS rDNA GenBank No.: OQ866179); Hubei [illegible] *Koelreuteria paniculata* [illegible] *S.R. Tang & L. Liu* [illegible] [illegible] *Koelreuteria paniculata*, *S.R. Tang & L. Liu* [illegible] ITS rDNA GenBank No.: OQ866180; HMJAU-PM91897, ITS rDNA GenBank No.: OQ866182, 28S rDNA GenBank No.: OQ866187; [illegible] [illegible] *Koelreuteria paniculata* [illegible] Oct. 2018, *S.R. Tang & L. Liu* [illegible] [illegible] *Koelreuteria paniculata*, 27 Oct. 2018, *S.R. Tang & L. Liu* [illegible] [illegible] *Koelreuteria paniculata* [illegible] *J. Feng* [illegible] *Koelreuteria paniculata*, *S.R. Tang & L. Liu* [illegible] [illegible] *Koelreuteria paniculata*, [illegible] *S.R. Tang & L. Liu* [illegible] [illegible] *Koelreuteria paniculata*, *S.R. Tang & L. Liu* [illegible] 28S rDNA GenBank No.: OQ866184; HMJAU-PM91898, ITS rDNA GenBank No.: OQ866183, 28S rDNA GenBank No.: OQ866188); [illegible] *Koelreuteria paniculata* [illegible] *S.R. Tang & L. Liu* [illegible]

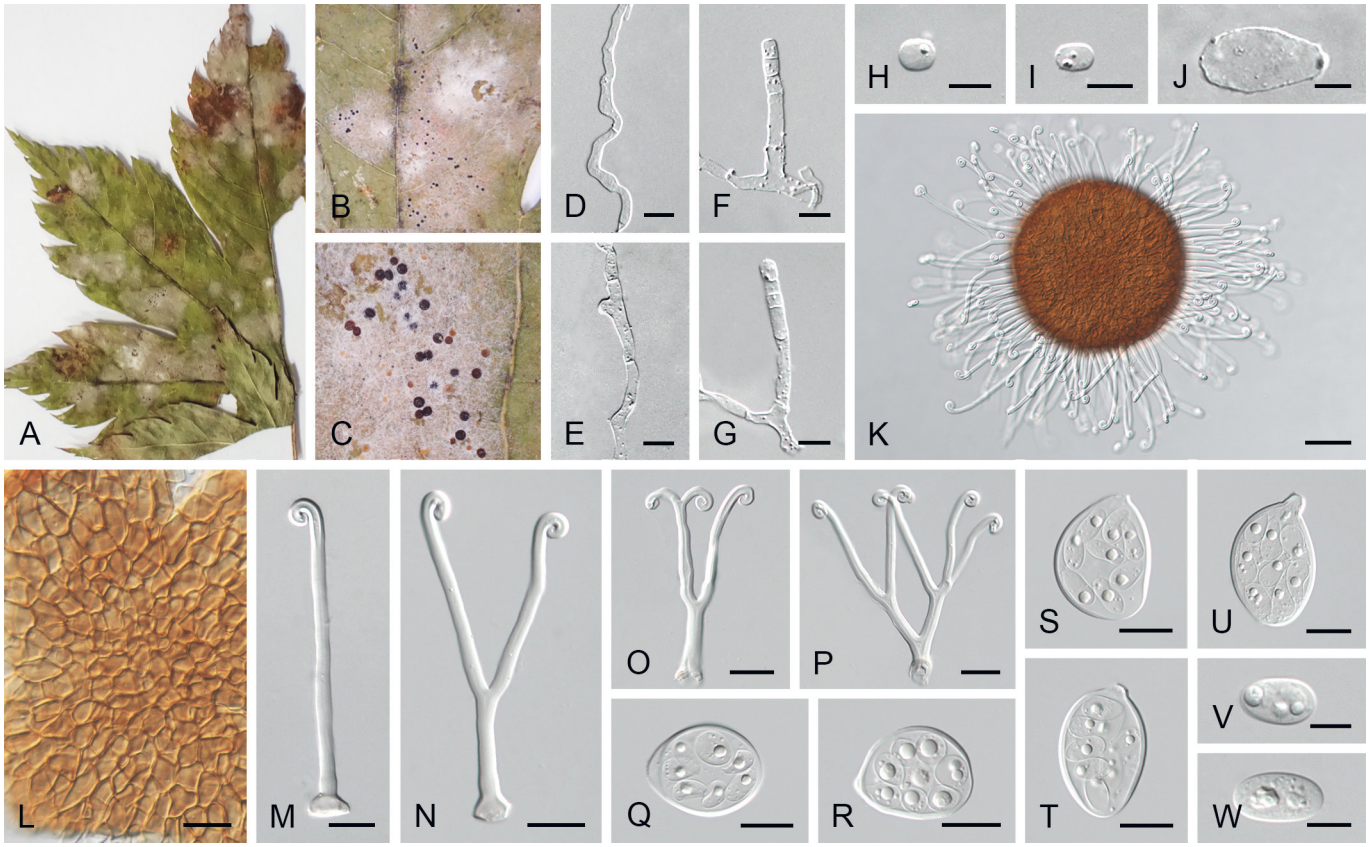

Fig. 13. *Sawadaea kovaliana* [illegible] **A–C.** [illegible] **D–F, G.** [illegible] **H, I.** [illegible] **J.** [illegible] **K.** [illegible] **L.** [illegible] **M–P.** [illegible] **Q–U.** [illegible] **V, W.** Ascospores. Scale bars: K = 50 µm; L–U = 20 µm; D–J, V, W = 10 µm.

Koelreuteria paniculata L.R. Tang & L. Liu
PM91894, ITS rDNA GenBank No.: OQ866181); Sichuan Province,
Koelreuteria paniculata L.R. Tang
& L. Liu

Host range and distribution: On *Koelreuteria bipinnata*, *paniculata*, *Koelreuteria* Sapindaceae

Notes: This species was first reported by Miyake (1913) and described as *Uncinula koelreuteriae*
Phyllactinia
Erysiphe E. koelreuteriae
Typhulochaeta
T. koelreuteriae.
Typhulochaeta
Erysiphe
Sawadaea
Sawadaea which was confirmed by molecular analyses. Liu *et al.*
S. koelreuteriae

sequences were obtained to confirm that this powdery mildew in *Koelreuteria* *Sawadaea*.

Sawadaea kovaliana *Ukrayins'k. Bot. Zhurn.* **47**

Typus: **Russia**
Aphelerpseudosieboldianum
2 Oct. 1989, *V.P. Heluta* **holotype**
sequence: GenBank No. OQ866167 (ITS+28S rDNA)].

Mycelium epiphyllous, forming distinct patches, confluent; *hyphae*
hyphal cell (16.5–)25.5–44.5 × 3.0–7.5(–9.5) µm; *hyphal appressoria*
micro-conidiophores 36.0–54.5 × 4.5–7.0 µm, foot-cells straight, cylindrical, 14.0–27.5 × 4.0–6.0 µm, basal septum sometimes elevated, up to 10.5 µm from the junction
micro-conidia
ellipsoid-ovoid, 7.5–10.5 × 5.0–8.5 µm, length/width ratio 1.1–
macro-conidiophores
macro-conidia
ellipsoid, 26.0–36.0 × 15.0–18.5 µm, length/width ratio 1.5–2.0. *Chasmothecia* gregarious, semiglobose, 146.0–218.0 µm diam.; *peridium cells* small, irregularly polygonal, about 4.0–27.5 µm diam.; *appendages*
(45.0–)98.5–135.5(–171.5) × 3.5–10.5 µm, 0.2–1.0 times as long

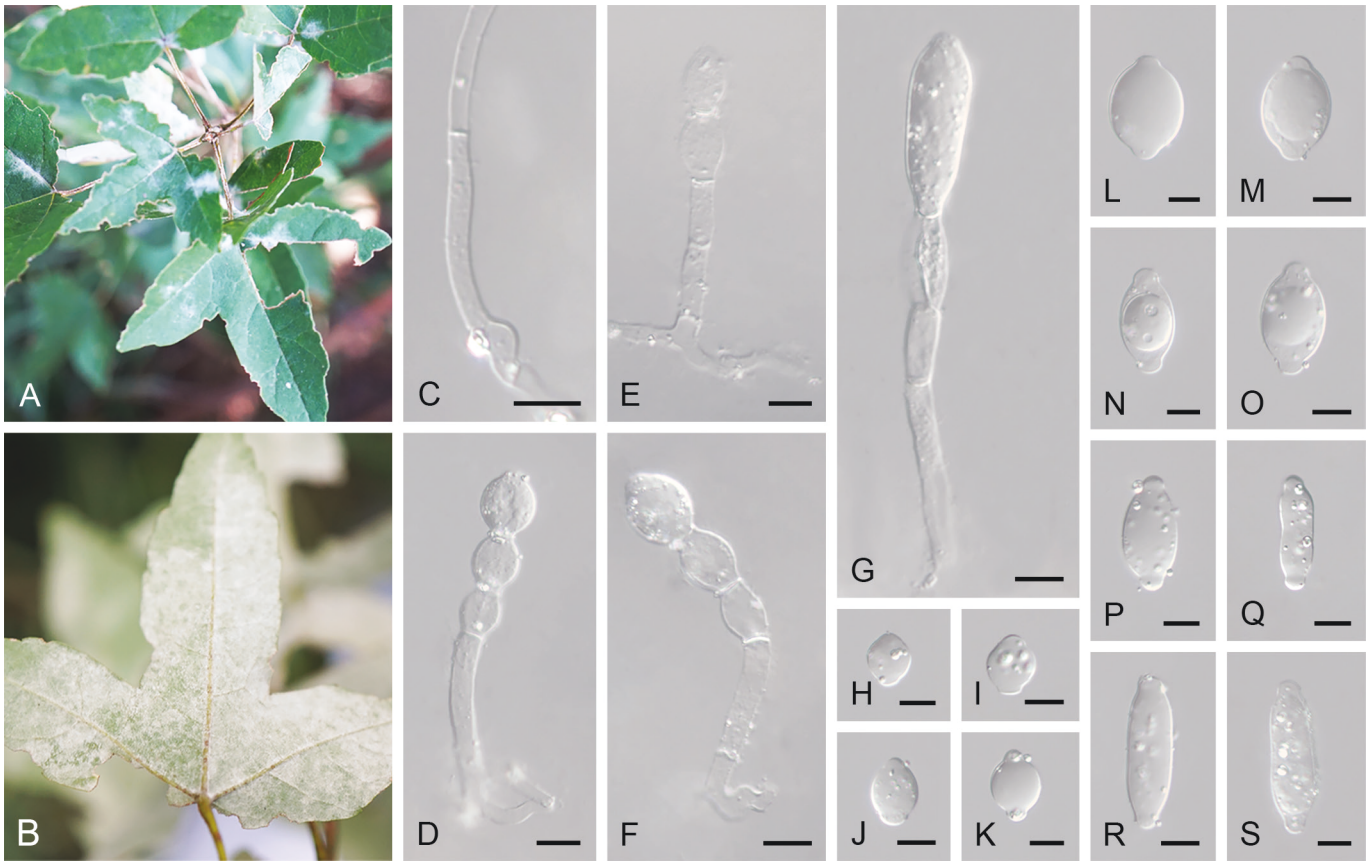

Fig. 14. *Sawadaea nankinensis* **A.** **B.** **C.** **D–F.** **G.** **H–K.** **L–S.** Macro-conidia. Scale bars = 10 µm.

asci 2
about 42.0–83 × 30.0–48.5 µm, length/width ratio 1.3–2.2, short-stalked, 5.0–13.5 × 6.5–11.5 µm, wall up to 3.5 µm thick, 8-spored; *ascospores*
11.5–24.0 × 8.0–14.0 µm, length/width ratio (1.0–)1.7–2.5(–2.9),

Additional material examined: **China**
Acer truncatum Y. Zhao
GenBank No.: OQ866168).

Host range and distribution: On *Acer* (*pseudosieboldianum*, *truncatum*) *Sapindaceae*

Notes:
Sawadaea kovaliana
Sawadaea kovaliana
Sawadaea
S. taii *S. kovaliana*
S. taii. *Acer sieboldianum*,
S. kovaliana , *Acer Palmatala*
S. taii *Platanoidea*
S. taii *S. kovaliana*

kovaliana.
A. truncatum *Acer*
Platanoidea *S.*
kovaliana
be re-amplified to determine its accuracy). Braun & Cook (2012) *S. bicornis* *Acer pseudosieboldianum* *kovaliana* . *Sawadaea bicornis*
S. kovaliana

Sawadaea nankinensis
Mycoscience **49**
Basionym: *Uncinula nankinensis* *Contr. Biol. Lab. Sci. Soc. China, Bot. Ser.*, **6**
Synonyms: *Erysiphe nankinensis*
Schlechtendalia **40**

Typus: **China** *Acer buergerianum* ,
F.L. Tai [**lectotype**
holectotype

Mycelium
hyphae straight or somewhat sinuous, 3.0–7.0 µm; *hyphal appressoria*

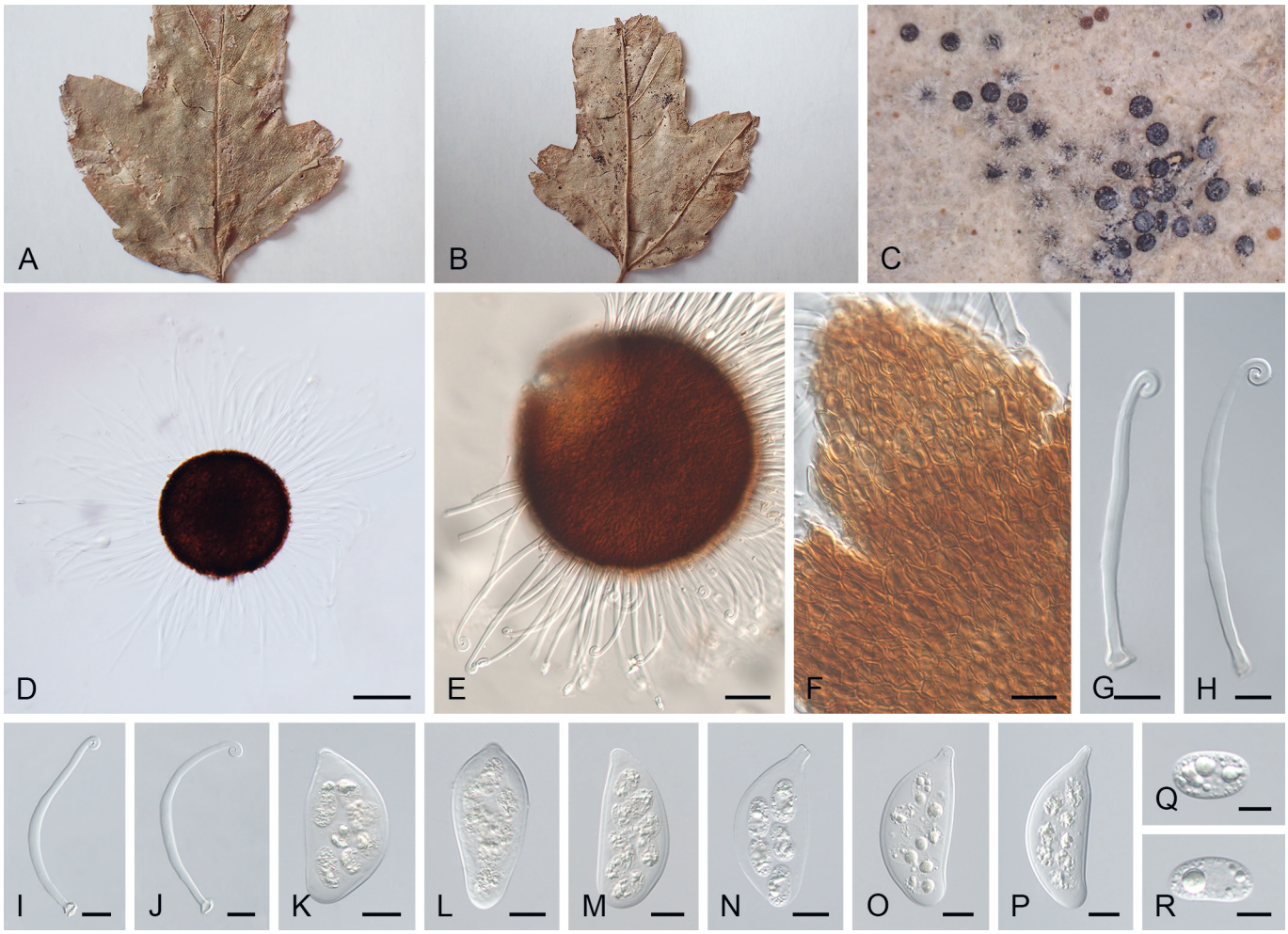

Fig. 15. *Sawadaea nankinensis* **A.** **B.** **C.** **D, E.** **G–J.** **K–P.** **Q, R.** Ascospores. Scale bars: D = 100 µm; E = 50 µm; F–P = 20 µm; Q, R = 10 µm.

micro-conidiophores 27.0–59.5 × 5.0–6.5 µm, foot-cells straight, cylindrical, basal septum sometimes elevated, up to 19.5 µm from *micro-conidia*
almost globose, 12.0–21.0 × 10.0–20.0 µm, length/width ratio *macro-conidiophores* 90.0–140.0 × 7.0–10.0 µm, followed
macro-conidia
47.0 × 11.0–18.5 µm, length/width ratio 1.3–3.9. *Chasmothecia* hypophyllous, scattered to ± gregarious, large, 233.5–319.5 µm diam. (av. 285.5 µm), globose-lenticular, basal part becoming finally concave; *peridium cells*
17.0(–23.5) µm diam.; *appendages*
145.0–286.0 × 5.0–12.5 µm, appendages about 0.5–1.0(–1.2)
asci
100.0(–116.0) × 31.0–52.0 µm, length/width ratio 1.7–3.2 (av. 2.3), mostly short-stalked, stalk about 7.5–17.5(–24.5) × 6.5–10.5(–12.0) µm, rarely sessile, (2–)5–8-spored; *ascospores*
ovoid, 18.0–27.0 × 11.0–15.5 µm, length/width ratio 1.2–2.0(–2.4)

Additional materials examined: **China**,
Acer buergerianum, 21 Oct. 2019, *D.N. Jin & X.Y. Wang*
Acer buergerianum, 24 Oct. *D.N. Jin & X.Y. Wang*
OQ866173); Jiangsu Province, Nanjing City, on *Acer buergerianum*, 29 Oct. 1954, *R.Y. Zheng*
Acer buergerianum, *D.L. Liu*

Host range and distribution: On *Acer buergerianum*, *Sapindaceae*,

Notes: This species was firstly reported as *Uncinula nankinensis*
Sawadaea,
not mentioned. Only the macro-conidia were described, with germ
orthotubus
Fibroidium
Acer sinopurpurascens
Erysiphe, *Uncinula*
Erysiphe
E. nankinensis *et al.*
Acer buergerianum
sequences for the first time. Phylogenetic trees were constructed
Sawadaea *Sawadaea*
nankinensis. Moreover, Zheng & Yu (1987) did not find any conidia
in size than previously reported, viz., 233.5–319.5 µm. Zheng *et al.*

Acer buergerianum

Sawadaea negundinis *J. Fac. Agric., Hokkaido Imp. Univ., Sapporo*38
Synonyms: *Uncinula negundinis* *et al.*,
Fungus diseases on cultivated plants of Jilin Province
Sawadaea bicornis

Typus: **Japan** *Acer negundo*, 21 Oct. 1922, *Y. Homma* (**holotype**)

Mycelium
hypha
3.5–5.0 µm wide; *hyphal appressoria*
micro-conidiophores 22.5–48.5 × 4.5–7.5 µm, foot-cells 17.0–32.5 × 4.5–7.5 µm, followed by 1–3 shorter cells , basal septum elevated, 4.5–11.0 µm from the junction with the mother *micro-conidia* ellipsoid-ovoid, 7.0–12.5(–17.5) × 5.0–10.0(–13.0) µm, length/width ratio 1.1–2.0, with fibrosin bodies; *macro-conidiophores* 30.5–86.0 × 6.0–10.5 µm, arising from the middle or
× 6.0–10.5 µm, followed by 1–3(–4) shorter cells and catenescent *macro-conidia*
18.5–31.0 × 11.0–23. 5 µm, length/width ratio 1.1–1.8(–2.9), with fibrosin bodies; *germ tubes*
long, about 10.0–67.5 × 2.5–6.0 µm, *orthotubus*
Fibroidium *Chasmothecia*
247.5 µm diam.; *peridium cells*
5.0–21.0 µm diam.; *appendages*
deeply cleft, first branching point near the middle of the stalk,
60.5–114.5 × 4.0–13.0 µm, appendages about 0.4–1 times as long
asci
ovoid, subglobose or irregular, 66.0–82.0 × 30.5–33.0 µm, length/width ratio 2.1–2.6, sessile or short-stalked, 5.5–12.5 × 4.5–9.0 µm
ascospores
almost globose, subcylindrical or irregular, 18.0–20.5 × 10.5–13.5 µm, length/width ratio 1.3–1.8, colourless.

Additional materials examined: **China**,
Acer negundo *S.Y. Liu & F.Y. Zhao*
(HMJAU 02219, ITS rDNA GenBank No.: OR711904, 28S rDNA
Acer negundo *Liu*
Acer negundo *F.Y. Zhao, J.N. Li & J.S. Lu*
Acer negundo, *F.Y. Zhao, V.N. Nguyen, J.N. Li & J.S. Lu*
Acer negundo *S.Y. Liu, S. Takamatsu, G.X. Guan & L. Zhao*
Acer triflorum, *L.L. Yang*

OR708548, 28S rDNA GenBank No.: MT462443); Jilin Province, [illegible] *Acer pictum* [illegible] *mono*, 24 Oct. 2010, *W.T. Jiang* (HMJAU 00746, ITS rDNA GenBank No.: OR711903, 28S [illegible]
[illegible] *Acer negundo*, [illegible] *S.Y. Liu & G.X. Guan* [illegible]
[illegible] *Acer negundo*, [illegible] *G.X. Guan* [illegible]
[illegible] *Acer negundo*, [illegible] *G.X. Guan & J. Feng* [illegible] OQ866174); Jilin Province, Changchun City, on *Acer negundo*, [illegible] *G.X. Guan & J. Feng* [illegible] rDNA GenBank No.: OQ866162); Jilin Province, Changchun City, [illegible] *Acer negundo*, [illegible] *G.X. Guan & J. Feng* [illegible] PM92117, ITS rDNA GenBank No.: OQ866175); Jilin Province, [illegible] *Acer negundo*, [illegible] *G.X. Guan & J. Feng* (HMJAU-PM92118, ITS rDNA GenBank No.: OQ866176); [illegible] *Acer triflorum*, [illegible] *G.X. Guan & J. Feng* [illegible] OQ866177); Jilin Province, Gongzhuling City, on *Acer negundo*, *P.K. Qi* [illegible] *Acer triflorum*, 4 Oct. [illegible] *S.Y. Liu, S. Takamatsu, P.L. Qiu & J. Feng* [illegible] ITS+28S rDNA GenBank No.: OQ866161); Jilin Province, Yanbian [illegible] *Acer negundo*, 13 Oct. 2011, *W.T. Jiang* [illegible] ITS rDNA GenBank No.: OR708549, 28S rDNA GenBank No.: [illegible] **Russia** [illegible] *Acer negundo*, 28 Oct. 2018, *T.S. Bulgakov* [illegible] HMJAU-PM92126, ITS+28S rDNA GenBank No.: OQ866163).

Host range and distribution: On *Acer negundo*, *pictum* [illegible] *monotriflorum* (Sapindaceae [illegible]

Notes: [illegible] *Sawadaea* [illegible] *Acer negundo* [illegible] *Sawadaea bicornis*, *S. negundinis*, [illegible] *S. tulasnei*. *Acer negundo* [illegible] [illegible] *S. bicornis* [illegible] *S. negundinis* [illegible] [illegible] *S. bicornis*, [illegible] *Sawadaea negundinis* [illegible] [illegible] *et al.* [illegible] *et al.* [illegible] [illegible] *Acer negundo* [illegible] [illegible] *bicornis* [illegible] [illegible] *negundo* were identified as *S. bicornis* [illegible] *S. negundinis* [illegible]

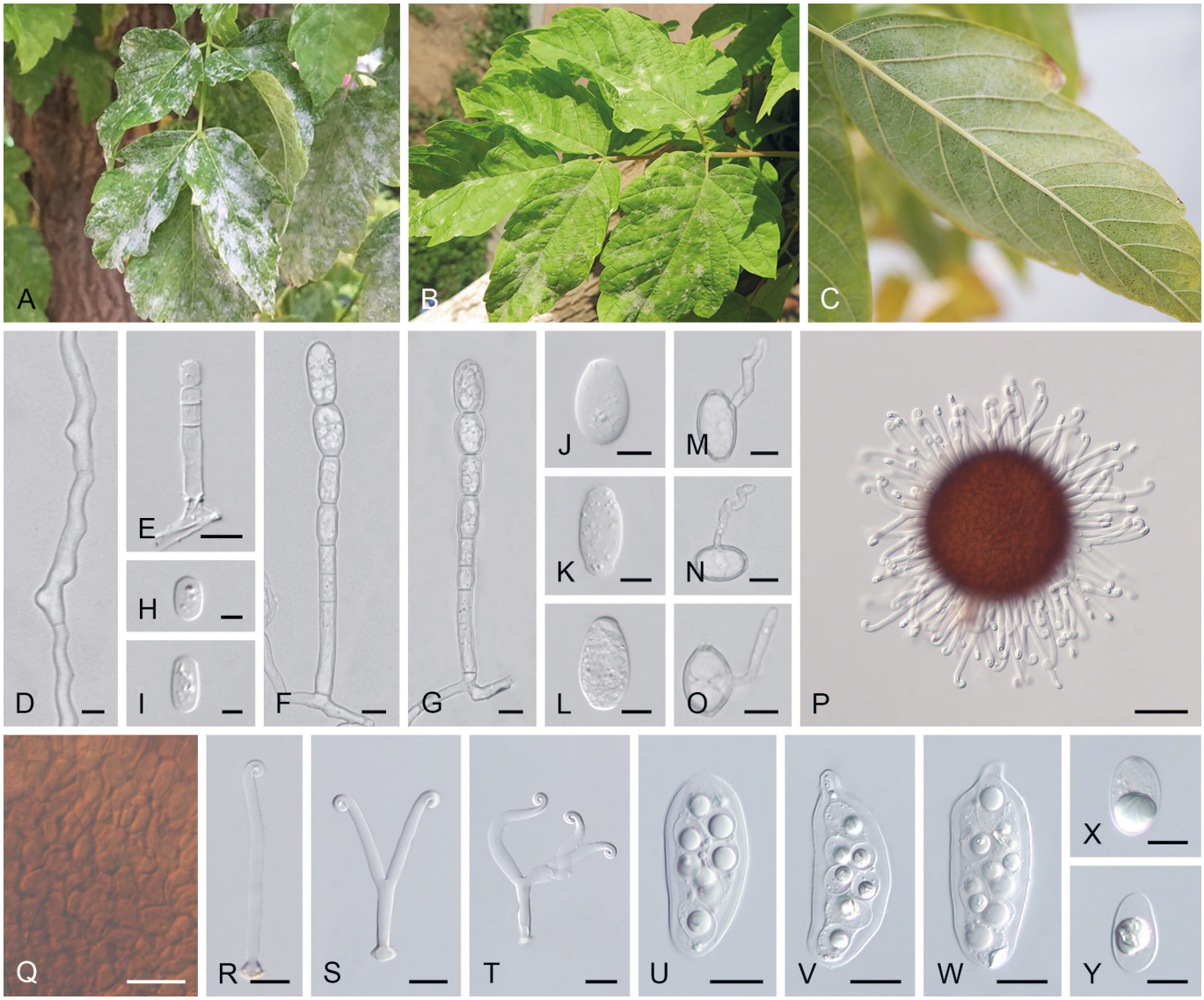

Fig. 16. *Sawadaea negundinis* [illegible] **B** [illegible] **C** [illegible] **D**, [illegible] **E**, [illegible] **G** [illegible] **H, I** [illegible] **J–L** [illegible] **M–O** [illegible] **P** [illegible] **R–T** [illegible] **U–W** [illegible] **X, Y.** Ascospores. Scale bars: P = 50 µm; F, G, Q–W = 20 µm; D, E, J–O, X, Y = 10 µm; H, I = 5 µm.

et al.
found significant differences between chasmothecial appendages of *S. negundinis* and *S. bicornis*. *S. negundinis*
S. bicornis
S. bicornis
S. bicornis
S. negundinis
A. negundo. *S. bicornis* *polyphaga* in

Sawadaea polyfida *Acta Microbiol. Sin.* **20**
Basionym: *Uncinula polyfida* *Hanking J.* **11**
Synonym: *Sawadaea polyfida* *japonica*
Mycotaxon **22**

Typus: **China** *cer amplum*
catalpifolium (≡ *A. catalpifolium*) **lectotype**

Mycelium *hyphae* straight to sinuous, septate, branched, thin-walled, 3.0–5.0 µm, *hyphal appressoria*
micro-conidiophores 26.0–39.0 × 5.0–7.5 µm, arising from the upper
× 5.0–7.0 µm, basal septum sometimes elevated, followed by 1–2 *micro-conidia* in shape, ellipsoid-ovoid, 7.5–9.5 × 6.0–9.0 µm, length/width ratio 1.1–1.3, (av. 1.2), with fibrosin bodies; *macro-conidiophores*

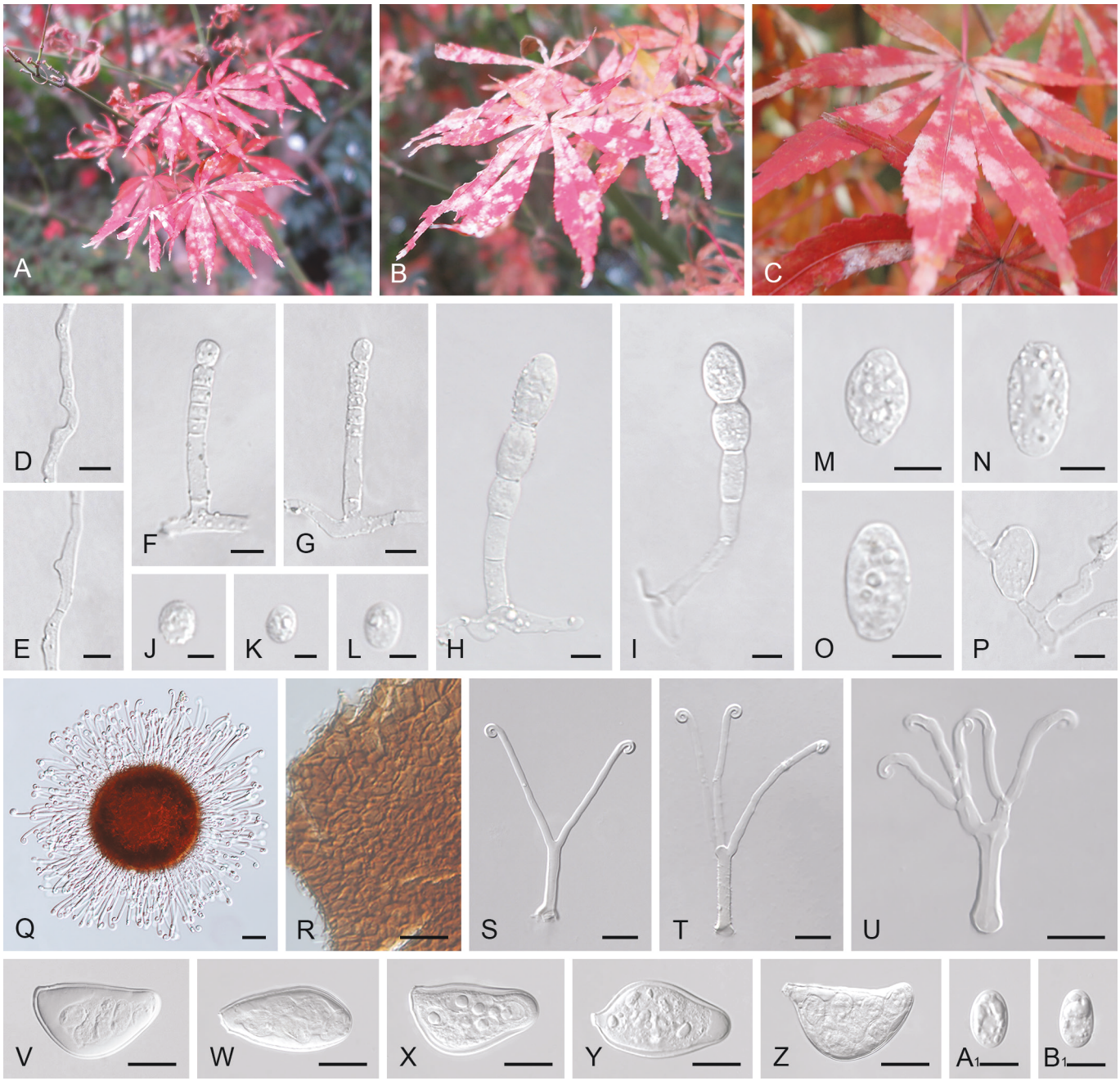

Fig. 17. *Sawadaea polyfida* **A–C.** **D, E.** **F, G.** **H, I.** **J–L.** **M–O.** **P.** **Q.** **R–U.** **V–Z.** **A1, B1.** Ascospores. Scale bars: Q = 50 µm; R–Z = 20 µm; D–I, M–P, A1, B1 = 10 µm; J–L = 5 µm.

× 5.5–9.0 µm, arising from the mother cell, foot-cells cylindrical, straight, 16.0–30.5 × 5.0–8.5 µm, followed by 1–2 shorter cells and [illegible] *macro-conidia* [illegible] × 11.5–15.5 µm, length/width ratio 1.5–2.0 (av. 1.7), with fibrosin [illegible] *germ tubes* [illegible] (*orthotubus*) [illegible] *fibroidium* [illegible] *Chasmothecia* scattered to ± gregarious, 129.5–276.5 µm diam.; *peridium cells* irregularly polygonal, 4.0–24.5 µm diam., arranged ± radially; *appendages* [illegible] apex, apices uncinate to circinate, 28.0–162.5 × 3.5–8.5(–12.5) µm, 0.2–0.9 times as long as the chasmothecial diam., thick-[illegible] *asci* 8–38, ellipsoid-obovoid, saccate-clavate, (41.0–)70.0–110.0 × (20.0–)46.5–61.5 µm, length/width ratio 1.1–2.3 (av. 1.8), wall thick, 1.8–4.0 µm, almost sessile or with a stalk, 8.5–36.0 × 9.0–17.0 µm, [illegible] *ascospores* ellipsoid-ovoid, 12.5–33.0 × 9.5–19.0 µm, length/width ratio 1.1–2.2 (av. 1.7), colourless.

Additional materials examined: **China**, [illegible] *Acer palmatum*, 28 [illegible] *S.R. Tang & L. Liu* [illegible] *Acer palmatum* [illegible] *dissectum*, 28 [illegible] *S.R. Tang & L. Liu* [illegible] [illegible] *cer palmatum* [illegible] *Y. Zhang & D.N. Ji* [illegible] *cer palmatum* [illegible] *S.R. Tang & L. Liu* [illegible] [illegible] *Acer palmatum*, 6 [illegible] 2 *Z.Y. Zhang & D.N. Jin* [illegible] *cer palmatum* [illegible] *Z.Y. Zhang & D.N. Jin* [illegible] No.: OR863613); Jilin Province, Wangqing, on *Acer* [illegible] 0 *Y.C. Yang et al.* [illegible] *er palmatum*, 7 Oct. 2020, *Z.Y. Zhang & D.N. Jin* [illegible] GenBank No.: OR701408); Jiangsu Province, Suzhou City, Qiantang [illegible] *cer palmatum*, 9 Oct. 2020, *Z.Y. Zhang & D.N. Jin* (HMJAU-PM92138, ITS+28S rDNA GenBank No.: OR701409); [illegible] *Acer palmatum*, 7 [illegible] *Z.Y. Zhang & X.Y. Wang* [illegible] *er palmatum* [illegible] *R. Tang & L. Liu* [illegible] [illegible] *Acer amplum* subsp. *catalpifolium* [illegible] *F. Tao* (HMAS13624, 28S rDNA GenBank No.: OQ874975); Yunnan [illegible] *Acer palmatum* [illegible] *Y. Zhang & D.N. Jin* [illegible] [illegible] *palmatum*, 13 Oct. 2020, *Z.Y. Zhang & D.N. Jin* [illegible] ITS+28S rDNA GenBank No.: OR701411). **USA**, [illegible] *Acer palmatum*, 2 [illegible] *M. Bradshaw* [illegible] rDNA GenBank No.: OR166384); Boston, on *Acer palmatum*, 2 [illegible] *M. Bradshaw* [illegible] OR166379); Boston, on *Acer circinatum* [illegible] *M. Bradshaw* (FH00941966, ITS rDNA GenBank No.: OR166376).

Host range and distribution: On *Acer* (*amplum* [illegible] *catalpifolium* [illegible] *japonicum*, *micranthum*, *negundo*, *palmatum* [illegible] *palmatum*, *palmatum* [illegible] *amoenum* [≡ *amoenum*] *palmatum* [illegible] *matsumurae* [≡ *amoenum* var. *matsumurae*] *pseudosieboldianum* [≡ *takesimense*] *shirasawanum*, *sieboldianum*, *stachyophyllum* [≡ *tetramerum*] *tschonoskii* var. *australe* [≡ *australe*] *tenuifolium*) *Sapindaceae*, [illegible] [illegible]

Notes: [illegible] *Uncinula polyfida* [illegible] *Acer amplum* [illegible] *catalpifolium* [illegible] *Acer* [illegible] *A. palmatum* var. *palmatum* [illegible] *matsumurae* [illegible] *japonica* [illegible] *A. palmatum* [illegible] *matsumurae* (≡ *A. palmatum* var. *matsumurae*) [illegible] (100–)150–200 µm diam. However, owing to the strong variability of [illegible] *S. polyfida* [illegible] the Chinese type and Japanese collections is difficult. Hence, Braun [illegible] *S. polyfida* . *Sawadaea polyfida* [illegible] [illegible] *S. polyfida* [illegible] [illegible] *Acer* sect. *Palmata* (*A. circinatum* [illegible] *A. japonicum*, *A. palmatum* [illegible] *A. pseudosieboldianum* [illegible] *A. shirasawanum*, *A. sieboldianum*, and *A. tenuifolium*) [illegible] *Acer* [illegible] *Palmata* [illegible] [illegible] *polyfida* [illegible] *Acer circinatum* [illegible] *A. circinata* [illegible] *Palmata* [illegible] Asia. On the other hand, there are some sequences retrieved from *S. polyfida* on *Acer* [illegible] *A. amplum* [illegible] *catalpifolium* [illegible] *Platanoidea*) *A. micranthum* and *A. tschonoskii* var. *australe* (*Micrantha*) *A. negundo* [illegible] *Negundo*) *A. stachyophyllum* [illegible] *Arguta*) *Sawadaea polyfida* on *A. pseudosieboldianum* (≡ *A. takesimense*) [illegible] [illegible] *et al.* [illegible] *et al.*) [illegible] introduction of this species in Europe (Switzerland). Other records [illegible] [illegible] *S. polyfida* [illegible] [illegible] *A. amplum* [illegible] *catalpifolium* [illegible] [illegible] [illegible] *S. polyfida* [illegible] *et al.* [illegible] [illegible] [illegible] [illegible] would be useful for a further clarification of the phylogeny and [illegible] [illegible] *platanoides* [illegible] [illegible] *polyfida* [illegible] [illegible] are not enough for further attempts. So we tentatively identified it as *S. polyfida*. Further study is needed to confirm if *S. polyfida* [illegible] [illegible] *A. platanoides* .

Sawadaea taii [illegible] ***sp. nov.*** [illegible] [illegible]

Etymology: [illegible] [illegible]

Typus: **China**, [illegible] [illegible] *Acer truncatum* [illegible] *S.Y. Liu, S. Takamatsu, G.X. Guan & L. Zhao* [holotype [illegible] isotype

Diagnosis: *C. bomiensis*

Mycelium *hyphae* septate, branched, thin-walled, 17.0–34.5 × 1.5–6.5 µm; *hyphal appressoria* *micro-conidiophores* 34.0–43.0 × 4.0–5.5 µm, a septum, foot-cells cylindrical, straight, 15.5–31.5 × 4.0–5.5 µm, basal septum sometimes elevated, to 9.5 µm away from the junction *micro-conidia* 5.0–12.0 × 4.0–9.0 µm, length/width ratio 1.0–1.9 (av. > 1), with fibrosin bodies; *macro-conidiophores* 38.0–50.5 × 5.5–8.0 µm, a septum, foot-cells cylindrical, straight, 21.5–39.0 × 5.5–8.0 µm, *macro-conidia* variable in shape, ellipsoid-ovoid, 15.0–28.0 × 11.0–15.5 µm, length/width ratio 1.1–1.9 (av. > 1.5), with fibrosin bodies; *germ tubes* *thotubus* *Fibroidium* *Chasmothecia* gregarious, (115.0–)142.5–185.0(–226.0) µm diam.; *peridium cells* irregularly polygonal, 4.5–17.5 µm diam., arranged ± *appendages*

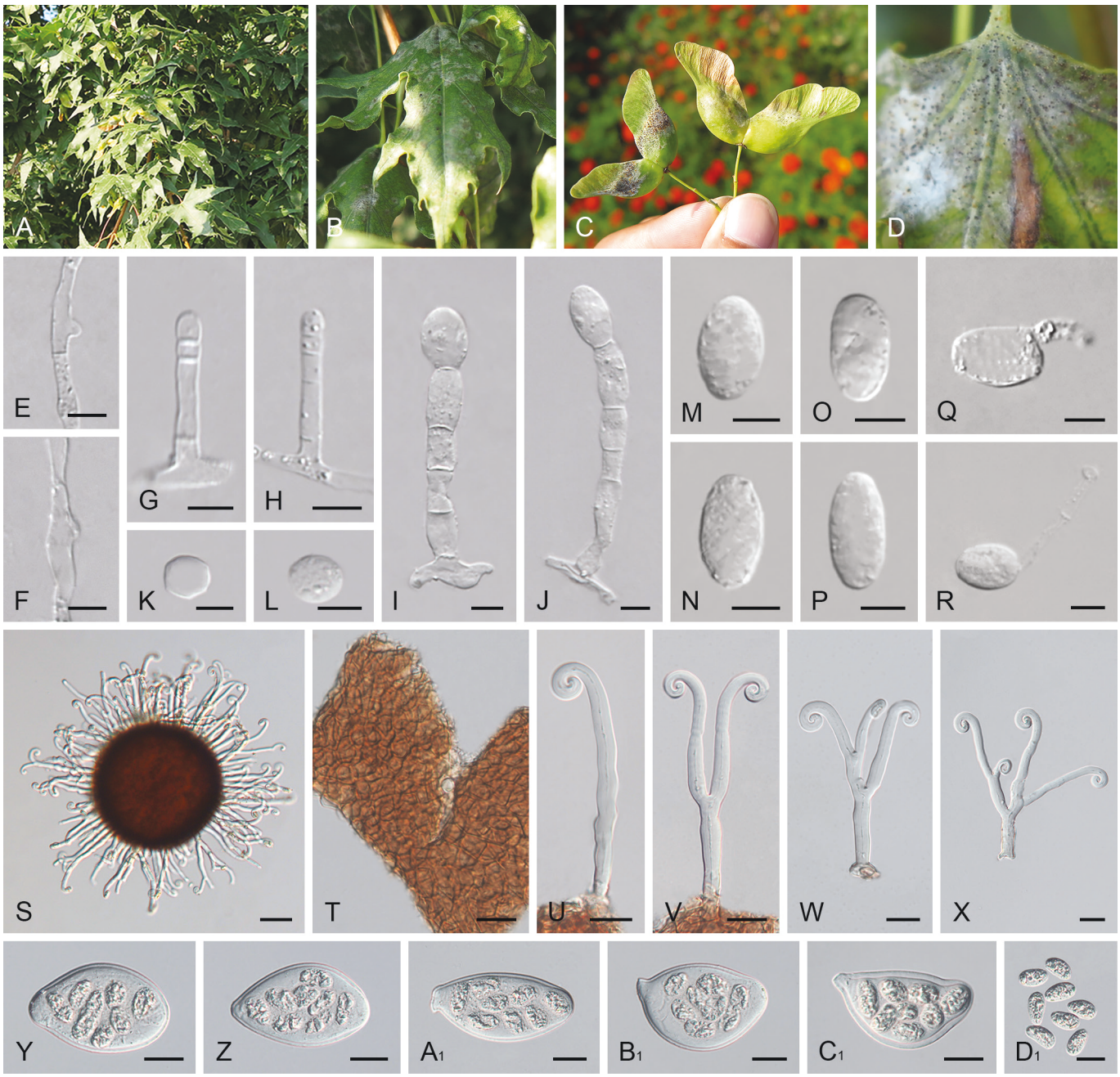

Fig. 18. *Sawadaea taii sp. nov.* **A.** **E, F.** **G, H.** **I, J.** **K, L.** **M–P.** **Q, R.** **S.** **T.** **U–X.** **Y–C1.** **D1.** Ascospores. Scale bars: S = 100 µm; T–C1 = 20 µm; E–R, D1 = 10 µm.

70.0–167.5(–225.0) × 4.0–14.0 µm, 0.4–1.3 times (av. 0.8) as
asci
× 47.5–68.0 µm, length/width ratio 1.2–1.7 (av. 1.4), wall thick, 1.5–7.0 µm, short-stalked or almost sessile, stalk length up to 7.0 µm, *ascospores* ellipsoid-ovoid, 16.0–23.5 × 12.5–15.5 µm, length/width ratio 1.1–1.8 (av. 1.4), colourless.

Additional materials examined: **China**,
Liquidambar formosana, 21 Oct. 2018, *S.R. Tang & L. Liu*
Acer truncatum, *T.Z. Liu*
rDNA GenBank No.: OQ866158); Jilin Province, Changchun City, *Acer truncatum*, *L.L. Yang*
Acer truncatum, 2 Oct. 2018, *S. Takamatsu, S.Y. Liu, P.L. Qiu & J. Feng*
Q.M. Wang
OR841072); Yunnan Province, Weixi Lisu Autonomous County, on *Acer barbinerve*, *S.J. Han*
GenBank No.: OQ866169).

Host range and distribution: On *Acer* (*barbinerve*, *truncatum*) *Sapindaceae*, *Liquidambar formosana*, *Hamamelidaceae*,

Notes: *Sawadaea* *Hamamelidaceae* is reported in this study for the first time. *Sawadaea taii*
S. bomiensis
S. bomiensis *Sawadaea taii*
S. acerina *Acer tataricum* *ginnala*,
tataricum
further attempts. So we tentatively identified them as *S. taii*. study is needed to confirm if *S. taii* *tataricum*.

Sawadaea tulasnei *Fac. Agric. Hokkaido Univ.*
Basionym: *Uncinula tulasnei* *Fungi Rhen. Exs.*
Synonyms: *U. aceris* *tulasnei* *Mem. Torrey Bot. Club*
U. bicornis *tulasnei* *Mycologia*
Erysiphe varium *Scleromyc. Suec.*

Typus: **Germany**, *Acer platanoides*,
Fungi Rhen. Exs., Suppl., Fasc. III,
lectotype
isolectotypes *Fungi Rhen. Exs., Suppl.*
epitype
Germany,
J. Kruse

Mycelium *hyphae* straight to sinuous, septate, branched, thin-walled, 12.5–45.5 × 2.0–6.5 µm; *hyphal appressoria*
micro-conidiophores 24.0–53.0 × 4.5–7.0 µm, arising from the mother cell, centrally or
× 4.0–7.5 µm, basal septum sometimes elevated, to 9 µm from
micro-conidia ovoid, 6.5–14.0 × 4.0–9.0 µm, length/width ratio 1.0–2.3 (av. 1.4), with fibrosin bodies; *macro-conidiophores* 27.0–96.0(–141.0) × 5.0–9.5(–11.0) µm, arising from the mother cell centrally or not centrally, foot-cells cylindrical, straight, 13.0–51.0 × 5.0–10.0 µm, basal septum sometimes elevated, to 15 µm from the junction
macro-conidia ovoid, 14.0–49.5(–59.5) × 10.5–17.5(–26.0) µm, length/width ratio 1.0–4.1 (av. 1.7), with fibrosin bodies; germ tubes terminal, *orthotubus* *fibroidium*
Chasmothecia scattered to ± gregarious, 170.0–234.5 µm diam. (av. > 200 µm); *peridium cells*
18.5(–25.5) µm diam., arranged ± radially; *appendages*
× 5.5–11.0 µm, 0.3–1.5 times (av. 0.7) as long as the chasmothecial
asci
105.5 × (27.5–)40.0–69.0 µm, length/width ratio 1.3–3.0 (av. 1.7), wall thick, to 5.6 µm, short-stalked or almost sessile, stalked length up to 14.6 µm, 8-spored; *ascospores* ellipsoid-ovoid, 18.5–30.0 × 14.0–18.5 µm, length/width ratio 1.2–2.0 (av. 1.6), colourless.

Additional materials examined: **Canada**, Ontario, Niagara Region, *Acer platanoides* *S.V. Ilyukhin*
PM92145, ITS+28S rDNA GenBank No.: OQ866165); Ontario, *Acer platanoides*
S.V. Ilyukhin (HMJAU-PM92146); Ontario, Niagara *Acer platanoides*, *S.V. Ilyukhin* (HMJAU-PM92147, 28S rDNA GenBank No.: OQ866193). **Russia**,
Acer platanoides, *T.S. Bulgakov*
PM92148, ITS rDNA GenBank No.: OQ866178); Rostov region, *Acer platanoides*
T.S. Bulgakov
Acer platanoides, 24 Oct. 2018, *T.S. Bulgakov*
Acer platanoides, *T.S. Bulgakov*
ITS+28S rDNA GenBank No.: OQ866166). **USA**, *Acer platanoides*, *A. Pfister*
GenBank No.: OR166381); Boston, on *Acer platanoides*,
M. Bradshaw
OR166380).

Host range and distribution (phylogenetically proven hosts): On *Acer* (*platanoides* , *macrophyllum*, *tataricum*)

Notes: *Sawadaea tulasnei* *Acer* *platanoides* *tulasnei* is largely confined *et al.* *et al.* *S. tulasnei* *A. macrophyllum* (*Acer* *Macrophylla*) *A. tataricum* (*Ginnala* *et al.* *S. tulasnei* is not strictly confined to *A. platanoides* (s *Platanoidea* *S. tulasnei* on *Acer* (*crataegifolium* , *japonicum* , *macrophyllum* , *miyabei* , *monspessulanum* s *cinerascens* [≡ *cinerascens*] *palmatum*, *A. pictum* s *mayrii* [≡ *mayrii*] *A. pictum* s *mono* [≡ *mono*] *platanoides*, *stevenii*, *tataricum* s *tataricum*, *tataricum* s *ginnala* [≡ *ginnala*] *truncatum*, *ukurunduense*

A. cappadocicum d *A. monspessulanum* s *turcomanicum* (≡ *A. turcomanicum*) *et al.* *S. tulasnei*

Acer *crataegifolium* (*Sawadaea bifida* s *A. pictum* s *mayrii* s *mono* (*S. bifida*) *A. palmata* (*S. taii*) *A. tataricas* *ginnala* (*S. acerina*, *S. bifida*) *A. truncatum* (*S. kovaliana* , *S. taii*) *Sawadaea* *Acer* p *A. japonicum* d *A. miyabei* *et al.* *S. bicornis* d *S. tulasnei* *A. monspessulanum* from Turkey. The latter record is doubtful and in need of confirmation

A. truncatum *S. tulasnei* *Sawadaea* *A. truncatum* *S. taii* *S. tulasnei*

Takamatsuella *Taxonomic manual of the Erysiphales (powdery mildews)*

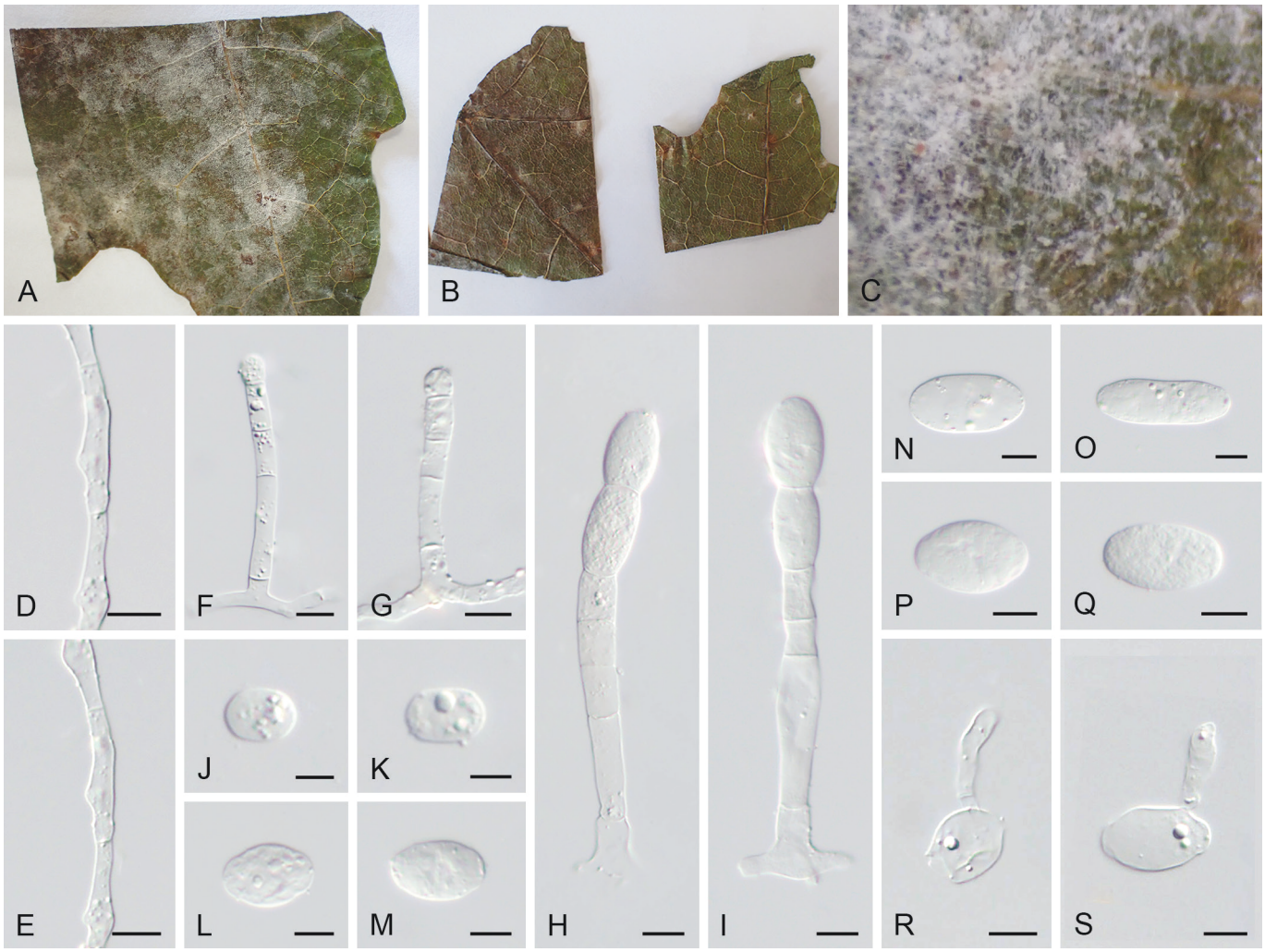

Fig. 19. *Sawadaea tulasnei* **A.** **B.** **C.** s **D, E.** **F, G.** **H, I.** **J–M.** **N–Q.** **R, S.** bars: D–I, N–S = 10 µm; J–M = 5 µm.

Type species: *Takamatsuella circinata*
A. Shi (≡ *Uncinula circinata*

Takamatsuella circinata
Taxonomic manual of the Erysiphales (powdery mildews)
Basionym: *Uncinula circinata* *Bot.*
Synonym: *Erysiphe circinata*
Schlechtendalia

Typus: **USA**, *Acer spicatum* ,
Peck [**ectotype** **isolectotype**]

Mycelium
hyphae
sparingly branched, hyaline, thin-walled, smooth, 2.5–8.0 µm
hyphal appressoria
conidiophores 27.0–107.5 × 5.0–8.0 µm, arising from mother cells,
20.0–41.0(–56.5) × 5.0–9.5 µm, basal septum sometimes elevated, to 10.5 µm from the junction with the mother cell, followed by 1–3
conidia
ellipsoid-ovoid, 17.0–29.0 × 9.5–13.5 µm, length/width ratio
Chasmothecia
(148.5–)236.5–298.5(–318.0) µm diam., hemispherical to lenticular, flattened or slightly concave in the lower half with age; *peridium cells* inconspicuous, irregularly polygonal, about 3.5–27.5 µm diam.; *appendages*
below the equator, stiff to flexuous, simple, rarely forked, apices tightly uncinate to circinate, 31.0–245.0 × 3.0–8.5 µm, about 0.2–1.0
asci
clavate-saccate, 48.5–100.0 × 20.0–48.0 µm, length/width ratio (1.6–)2.0–3.4 (av. 2.3), sessile or stalked, stalk 5.0–14.5 × 6.0–11.5 µm, (4–)6–8-spored; *ascospores* ellipsoid-ovoid, 13.0–26.0 × 11.0–15.0 µm, length/width ratio 1.1–2.5 (av. 1.6), colourless.

Additional materials examined: **China**,
Acer sp., 29 Oct. 1954, *B.N. Jiang*
Acer wilsonii , 15 Oct. 1978, *R.Y. Zheng & Y.Q. Lai* **USA** *Acer pycnanthum*
M. Bradshaw
OR166378); New Hampshire, on *Acer rubrum*, *W.G. Farlow* *Acer spicatum* , 12 Oct. 1968, *C.T. Rogerson & S.J. Smith*
OR166377); Washington, on *Acer* *J.B. Norton*

Host range and distribution (Braun & Cook 2012): On *Acer* (*lasycarpum* , *glabrum*, *nigrum*, *pensylvanicum*, *pycnanthum*, *rubrum*, *saccharinum*, *saccharum*, *spicatum*, *wilsonii*) *Sapindaceae*; Asia (China), North America (Canada [Manitoba, Ontario, Quebec],

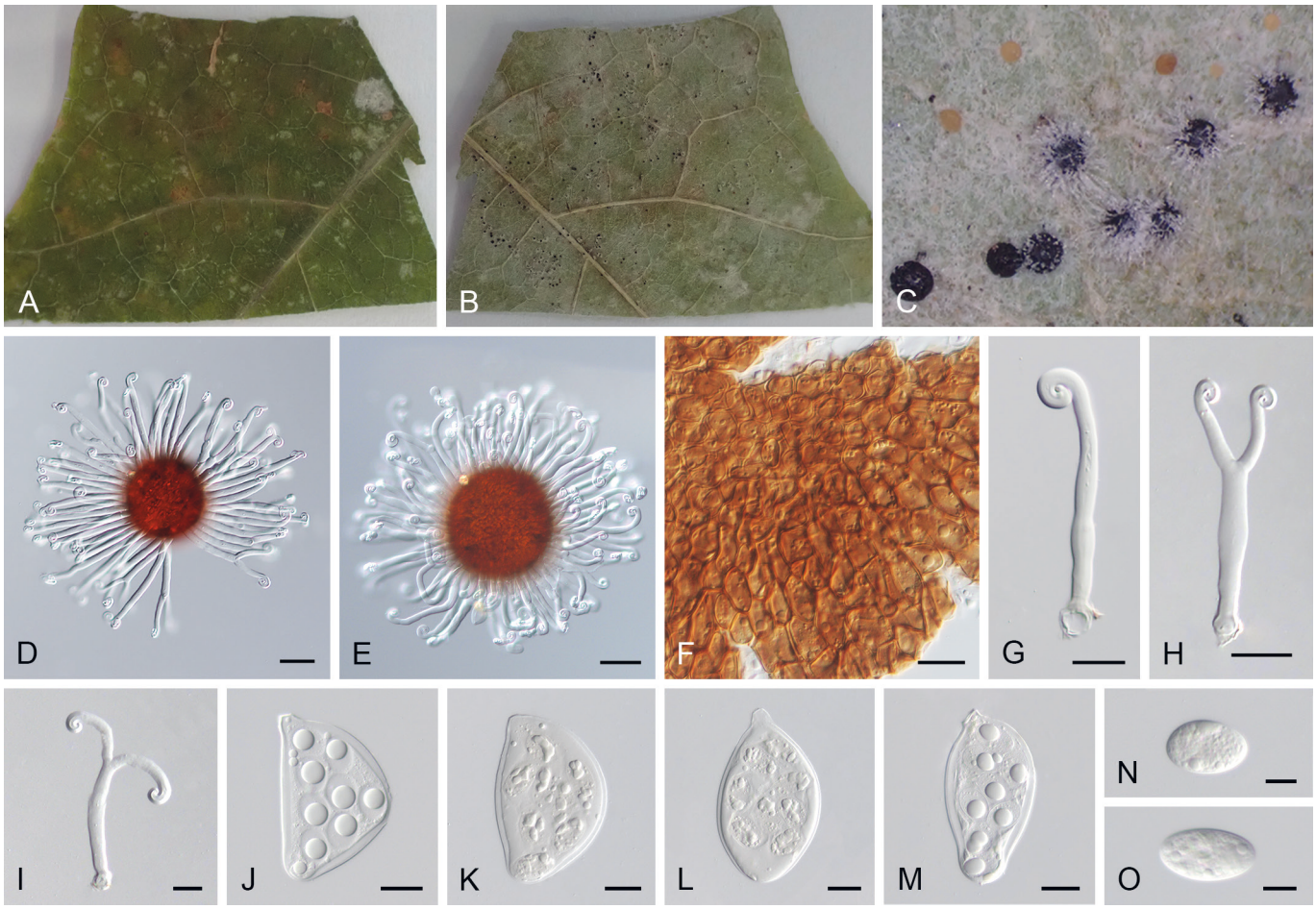

Fig. 20. *Sawadaea tulasnei* **A.** **B.** **C.** **D**, **E.** **F–I.** **J–M.** **N, O.** Ascospores. Scale bars: D, E = 50 µm; F–M = 20 µm; N, O = 10 µm.

Notes *Uncinula circinata* *Acer spicatum* , *U. bicornis* *U. circinata* *Erysiphe* et al. *Sawadaea* *U. circinata* *U. circinata* *Takamatsuella* *U. circinata* *Uncinula circinata* *circinata* *U.* *circinata* (*Acer wilsonii*, *Acer wilsonii*.

T. circinata can confirm the distribution of *T. circinata* The confirmation of molecular sequences in China requires further *Acer griseum* *circinata* *Uncinula* *Erysiphe* *E. circinata* *A. griseum* remains unclear and unconfirmed.

DISCUSSION

Since Homma (1937) updated the classification of *Sawadaea*, *S. bicornis*, *S. negundinis* *S. tulasneii* *S. aesculi* et al. *S. bomiensis* , *S. polyfida* *S. bifida* *S. kovaliana*

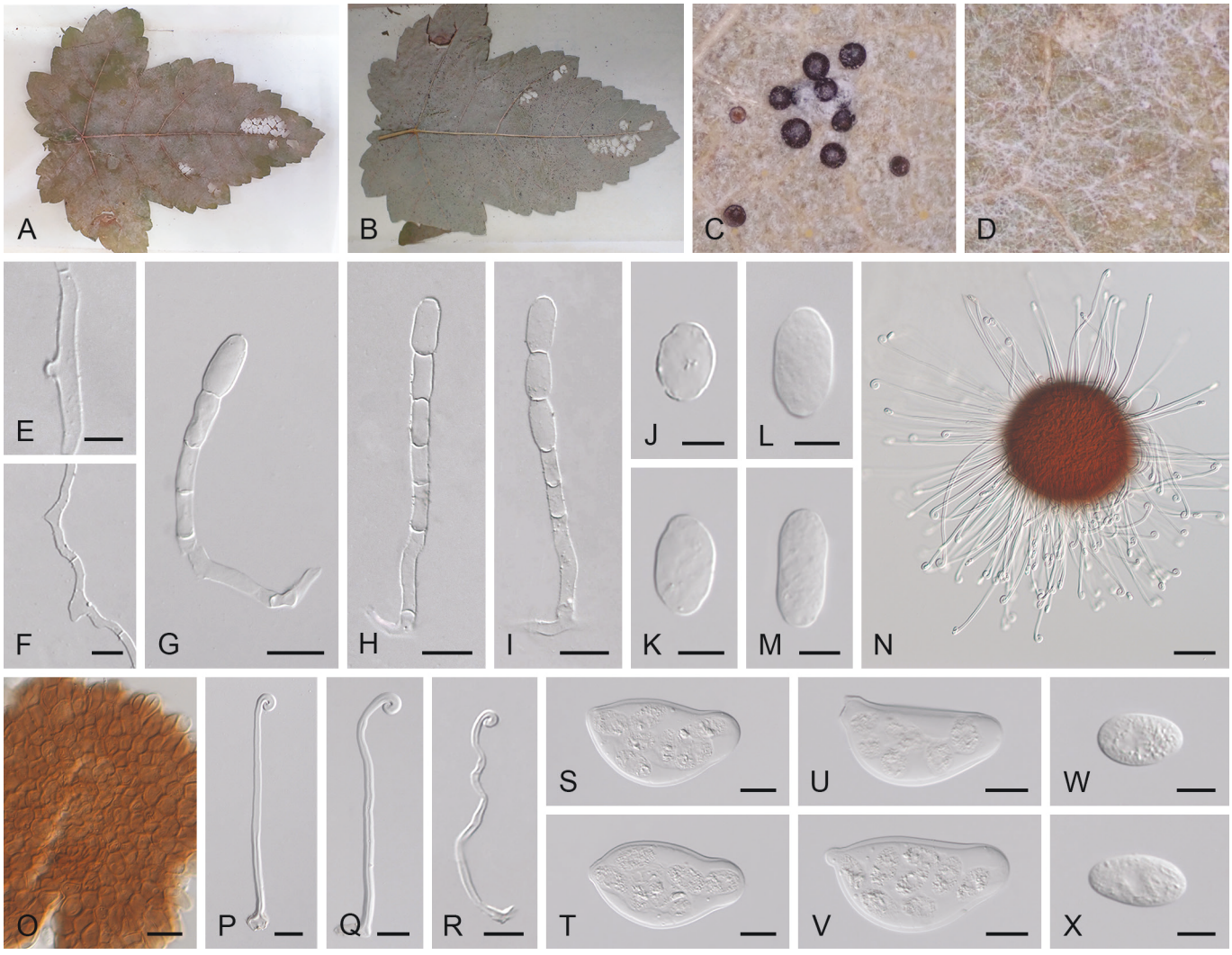

Fig. 21. *Takamatsuella circinata* **A.** **B.** **C, D.** **E, F, I–M.** **O–R.** **S–V.** **W, X.** Ascospores. Scale bars: N = 50 µm; G–I, O–V = 20 µm; E, F, J–M, W, X = 10 µm.

[illegible] *et al.* [illegible] *Uncinula nankinensis* [illegible] *Sawadaea*, [illegible] *Uncinula koelreuteriae* [illegible] *Sawadaea.* [illegible] *Sawadaea* [illegible] *S. bifida* [illegible] *S. kovaliana* clarified the two names and allowed us [illegible] *S. acerina*, [illegible] *S. aceris-arguti*, [illegible] *S. taii.*

[illegible] an important role in the reflection of the phylogenetic relationships [illegible] *Sawadaea* [illegible] *Takamatsuella* [illegible] *Takamatsuella* [illegible] *Sawadaea.* [illegible] *Takamatsuella circinata* [illegible] only species in the genus, and confirmed from China based on morphological examinations, although phylogenetic confirmation is [illegible]

Sawadaea [illegible] *Acer* [illegible] *S. koelreuteriae* [illegible] *Koelreuteria*, [illegible] *S. aesculi* [illegible] *Aesculus* [illegible] *S. taii* [illegible] *Acer* (*Sapindaceae* [illegible]) [illegible] *Liquidambar* (*Hamamelidaceae*) [illegible] *Erysiphe necator*, [illegible] *Vitaceae*, [illegible] *Carica papaya* (*Caricaceae*) [illegible] *et al.* [illegible]

[illegible] *Sawadaea* [illegible] *Acer* [illegible] *Acer* [illegible] *Koelreuteria*, *Aesculus* [illegible] *Liquidambar* [illegible] *Acer buergerianum* (*S. nankinensis*) [illegible] *Koelreuteria puniculata* (*S. koelreuteriae*) [illegible] *Aesculus chinensis* (*S. aesculi*) [illegible] *Acer* [illegible] (*S. polyfida* , *S. negundinis*, *S. bifida* [illegible] *Sawadaea* [illegible] *S. bicornis*, *S. polyfida* [illegible] *S. tulasnei* [illegible] *S. tulasnei* [illegible]

[illegible] *Sawadaea* [illegible] *S. acerina*, *S. bicornis*, *S. koelreuteriae*, [illegible] *S. nankinensis* , [illegible] clades are not yet sufficiently supported, e.g., the two species *S. bifida* [illegible] *S. negundinis* [illegible] *et al.* [illegible] *S. bifida*, [illegible] *Acer pictum*, [illegible] *Acer* [illegible] *Platanoidea*) [illegible] *S. bifida* [illegible] + *S. negundinis* cluster (Clade 6) that possibly reflects an additional cryptic species, [illegible] *S.* [illegible] *tulasnei* ” [illegible] *Sawadaea* [illegible] *Acer crataegifolium* [illegible] *A. rufinerve*, [illegible] *Acer* [illegible] *Macrantha* [illegible] *Sawadaea* [illegible] *A. ginnala* [illegible] *Ginnala*) [illegible] cases, the identities of the host plants should be checked to confirm identifications.

[illegible] *Sawadaea tulasnei* [illegible] *S. bifida* [illegible] *S. acerina* [illegible] *S. taii*. *Sawadaea bicornis* [illegible] *et al.* [illegible] subclades, one of these is largely confined to *Acer campestre* [illegible] *S. bicornis*) [illegible] *A. platanoides* [illegible] *Acer* [illegible] *Platanoidea.* [illegible] *A. negundo* [illegible] *A. pseudoplatanus* [illegible] *Acer* [illegible] "*forma speciales*" [illegible] "*forma specialis*" [illegible] as such they do not have types that make such names verifiable. "*Forma speciales*" [illegible] difficult. As such it is not surprising that results by different authors have often been contradictory, difficult to understand, and hard to [illegible] *Erysiphe* [illegible] *neolycopersici* [illegible] *et al.* [illegible] *Pseudoidium neolycopersici*) [illegible] render these races objectively verifiable. In addition, the genetic [illegible] such cases warrants the application of an official rank covered by the [illegible] "*formae*" [illegible] [illegible] century and the first half of the 20[th] [illegible] "*formae*" [illegible] 1910). Jaczewski (1927) was the first author in powdery mildews [illegible] "*formae*" [illegible] "*formae*" [illegible]

reflected in well-supported clades/subclades and are accompanied
gh
Tes ls ph f
Sawadaea s Th *Sawadaea* n *Alectryon excelsus* (Sapindaceae) g
S. negundinis t *et al.* P
s *S. bifida* s *S. negundinis* m
n *negundinis* h
g
S *Sawadaea* d *Takamatsuella* v
Parauncinula , *Blumeria* *Cystotheca* n
come to a phylogenetic tree that reflects a more realistic evolutionary
h *Sawadaea* . g
p *S. koelreuteriae* b
g *S. koelreuteriae* is
d *Podosphaera tridactyla* s *S. koelreuteriae* *S. nankinensis* p
w *Blumeria* *Cystotheca* g
Parauncinula g
S. koelreuteriae *S. nankinensis* .
S. koelreuteriae e
Blumeria *Cystotheca* g
n
d *Sawadaea* p
g *Sawadaea* i g
n
research, mainly by means of molecular analyses. Our analyses
g *Sawadaea* in
Sawadaea p
Asia, makes identifications based on morphology more difficult and requires well-developed holomorphs. Confirmations of identifications
n
Acer n
identifications difficult in this region. Furthermore, *Acer* p
Sawadaea p
A. pictum s *mono* *A. truncatum*. *Acer negundo* s
n
Sawadaea
s *S. bicornis* f *polyphaga*, *S. negundinis*, d *S. polyfida*.

ACKNOWLEDGEMENTS

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study. This work was financially supported by the National Natural
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DECLARATION ON CONFLICT OF INTEREST

The authors declare that there is no conflict of interest.

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