MYCOSPHERE 15(1): 473–653 (2024) www.mycosphere.org ISSN 2077 7019
Doi 10.5943/mycosphere/15/1/4

ARTICLE

Study on the diversity of rust pathogens from different hosts in Guizhou Province, China

Sun JE[1], Fu L[2], Norphanphoun C[3,4], Chen XJ[1,5], Yu LF[6], Hyde KD[3,4], McKenzie EHC[7], Wang Y[1*], Yang ZF[1*], and Liu FQ[1*]

[1] *College of Agriculture, Key Laboratory of Agricultural Microbiology of Guizhou Province, Guizhou University, Guiyang, Guizhou 550025, China*
[2] *Shandong Institute of Pomology, Tai'an, Shandong, 27100, China*
[3] *Center of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai, 57100, Thailand*
[4] *School of Science, Mae Fah Luang University, Chiang Rai, 57100, Thailand*
[5] *Guizhou Key Laboratory of Agricultural Biotechnology, Guizhou Academy of Agricultural Sciences, Guiyang, Guizhou 550006, China*
[6] *West Yunnan University, Lincang, 677000, China*
[7] *Landcare Research, Private Bag 92170, Auckland, New Zealand*

Citation – Sun JE, Fu L, Norphanphoun C, Chen XJ, Yu LF, Hyde KD, McKenzie EHC, Wang Y, Yang ZF, Liu FQ 2024 – Study on the diversity of rust pathogens from different hosts in Guizhou Province, China. Mycosphere 15(1), 473–653, Doi 10.5943/mycosphere/15/1/4

Abstract

Rust fungi are obligate plant pathogens that belong to *Basidiomycota*, *Puccinomycetes*, *Pucciniales*. Guizhou Province in Southwest China is rich in plant resources and has suitable climate conditions for plant disease development, but there are few studies on rust fungi. In this study over 300 plant samples with typical rust symptoms were collected from 33 counties in various regions of Guizhou Province. These samples come from 98 different host plants in 33 families. According to ITS-BLAST comparison results, the rust fungi belonged to 17 genera of 11 families in *Chaconiaceae* (*Mikronegeria*), *Coleosporiaceae* (*Coleosporium*), *Gymnosporangiaceae* (*Gymnosporangium*), *Melampsoraceae* (*Melampsora*), *Phakopsoraceae* (*Phakopsora*), *Phragmidiaceae* (*Gerwasia*, *Hamapora*, *Phragmidium*), *Pileolariaceae* (*Pileolaria*), Pucciniaceae (*Endophylum*, *Macropyxis*, *Puccinia*, *Uromyces*), *Pucciniastraceae* (*Pucciniastram*), *Tranzscheliaceae* (*Tranzschelia*), and *Uredinineae* incertae sedis (*Nyssopsora*, *Peridiopsora*). Phylogenetic analysis based on combined sequence data of ITS, LSU and *tef1α* loci, coupled with morphological evidence, support the species identification. Ninety-three species of rust fungi were obtained, comprising 29 novel taxa and 61 known species. Most of the rust species belonged to *Pucciniaceae* (48.9%), while the most prevalent host family infected was Rosaceae (21.9%). The Rosaceae are particularly susceptible to *Phragmidium* spp.

Keywords – Host jumping – Molecular phylogeny – Plant disease – Rust fungi – Taxonomy

INTRODUCTION

Pucciniales (*Basidiomycota*, *Puccinomycetes*) account for about 25% of basidiomycete fungi, and is one of the most abundant fungal groups (Aime & McTaggart 2021). Many rust species cause significant losses to economic crops and trees (Hiratsuka et al. 1992, Aime 2006). Currently, there are ca. 8,400 rust taxa reported in the world, parasitizing leaves, fruits and branches of plants, inhibiting normal growth and development of plants, and affecting their yield and quality (Aime et

---

Submitted: 16 October 2023; **Accepted:** 20 December 2023; **Published:** 6 March 2024

***Corresponding Author:** Yong Wang – e-mail – yongwangbis@aliyun.com,
Zai-Fu Yang – e-mail – zfyang@gzu.edu.cn,
Feng-Quan Liu – e-mail – fqliu20011@sina.com

Accepted by: Zhao Peng

al. 2018, Aime & McTaggart 2021, Zhao et al. 2021). According to Hennen & McCain (1993), the number of rust species in certain areas may equate to about 5–25% of plant species numbers. Wang et al. (2015) reported more than 35,000 higher plants species in China (454 families and 3,818 genera) and Zhao et al. (2021) estimated that perhaps 1700 to 8800 were infected by rust disease. According to Kolmer et al. (2009) and Fernandez et al. (2013), the hosts of rust fungi involve almost all families of plants, from ferns, gymnosperms to angiosperms.

Rust fungi are widely distributed in the world. Due to their complexity and diverse host conditions, the geographical distribution of various genera is significantly different. Most genera are widely distributed in the Northern Hemisphere, mainly in China, the European Union, the United States and Japan (Kern 1973, Wei 1988, Zhuang et al. 2012, Pscheidt & Rodriguez 2016, Tao et al. 2020, Zhao et al. 2021), such as *Phragmidium* and *Gymnosporangium*. A few are also distributed in tropical and subtropical areas, such as *Maravalia* and *Ravenelia* (De Carvalho & Hennen 2009, Ebinghaus et al. 2020). Compared with other genera, *Puccinia* has a more extensive geographical distribution (Zhuang et al. 1998, 2003, Berndt 2009, Carnegie et al. 2010, Roux et al. 2013, Kakishima et al. 2018, Zhao et al. 2021).

Some rust diseases caused by *Puccinia* spp. on wheat and *Melampsora lini* were reported as devastating pathogens and listed in the world's top ten fungal diseases (Dean et al. 2012). Several species of rust fungi cause serious harm to the economic value of agriculture and forestry. Many years ago, Harkness & Cooke (1878) reported *Uromyces fabae* as an important pathogen of leguminous crops threatening their growth. *Puccinia corticoids* was reported as an important pathogen of bamboo plants in China, Japan and India (Katumoto 1968, Cummins 1971, Gardner & Hodges 1989, He et al. 1990, Okane et al. 2020). *Phragmidium* spp. infect Rosaceae plants, especially *Rosa*, *Rubus*, and *Potentilla* and often cause serious disease (Yang et al. 2015, Pscheidt & Rodriguez 2016, Liu et al. 2018, 2019, 2020, Zhao et al. 2021). *Phragmidium mucronatum* and *P. tuberculatum* are common pathogens of ornamental roses in the world (Wahyuno et al. 2001, Wilson & Aime 2014). *Phragmidium rosae-roxburghii* was reported by Sun et al. (2022) as a pathogen of *Rosa roxburghii* in Guizhou Province, China, which mainly damages the stems, leaves and petioles. *Coleosporium* spp. cause rust diseases in many medicinal plants such as *Bletilla striata*, *Tetradium ruticarpum*, *Clematis florida*, and *Kalimeris indica*. Moreover, *Coleosporium* spp. are also found on *Pinus* plants and cause serious damage to young forests (Dai 1979, You et al. 2010, McTaggart & Aime 2018, Song 2019). *Gymnosporangium asiaticum*, *Tranzschelia discolor* and *T. pruni-spinosae* are rust disease pathogens on fruit trees including pear, apple, peach, etc. (Scholler et al. 2014, Tao et al. 2020). Other important rust pathogens include coffee rust (*Hemileia vastatrix*), soybean rust (*Phakopsora pachyrhizi*), toon rust (caused by *Nyssopsora cedralae* and *Phakopsora cheoana*), willow rust (*Melampsora salicis-sinicae*), chestnut powder rust (*Puccinastrum castaneae*) (Cummins & Hiratsuka 2003, Zhao et al. 2014, Zhuang et al. 2021).

The investigation of rust fungi in China began in the middle of the 19th century and a series of monographs and papers have been published. More than 1,200 rust taxa have been reported from China (Dai 1979, Zhuang et al. 1998, 2003, 2005, 2012, 2021, Ji et al. 2017, 2020, Zhao et al. 2021, Sun et al. 2022). Rust fungi have a complex life history and a variety of spore types (polymorphism). Since plant diseases caused by rust have always interfered with the development of human agricultural history, and most species have morphological similarity and unclear life cycle, their taxonomic research had attracted more and more attention from traditional morphological methods to multi-gene analyses and even genomics researches, and they have become a novel research hotspot (Aime et al. 2018, Ji et al. 2020, Aime & McTaggart 2021, Zhao et al. 2021).

Pathogens or other parasitic organisms generally have one or more fixed hosts. In order to adapt to the environment, they mutate or recombine so that they can infect or parasitize a new host, which is called "host jumping". Hart (1988) proposed for the first time that "host jumping" was the driving force for the diversity of rust fungi. Aime (2006) proposed that the phylogenetic relationship among rust fungi at the family level was related to the host plant. McTaggart et al. (2016) also believed that host transfer determined the diversity of rust fungi. According to the host coordination analysis, Aime et al. (2018) proposed that the host relationship of the rust life cycle could better reflect the relationship between the rust fungi.

The purposes of this study were as follows: (1) To understand the diversity and distribution of rust fungi in Guizhou Province. (2) To clarify the phylogenetic relationship of rust fungi based on three gene loci and their relationship with host plants in Guizhou Province. (3) To provide the description and illustration of the new taxa and new record of rust fungi in Guizhou Province.

MATERIALS AND METHODS

Sampling

Over 300 fresh rust fungal specimens were collected from different hosts in Guizhou Province, China. The hosts of these specimens belong to 33 plant families, Amaryllidaceae, Anacardiaceae, Apiaceae, Araceae, Araliaceae, Asteraceae, Cannaceae, Clusiaceae, Convolvulaceae, Elaeagnaceae, Fabaceae, Gentianaceae, Iridaceae, Lamiaceae, Liliaceae, Meliaceae, Moraceae, Orchidaceae, Oxalidaceae, Plantaginaceae, Poaceae, Polygonaceae, Ranunculaceae, Rhamnaceae, Rosaceae, Rubiaceae, Rutaceae, Salicaceae, Saxifragaceae, Urticaceae, Valerianaceae, Violaceae and Vitaceae. All samples were placed in envelopes and returned to the laboratory as described by Senanayake et al. (2020).

Microscopy observation

The spores from specimens were mounted in sterile water, on slides and observed using a Zeiss Scope 5 compound microscope (Axioscope 5, Jena, Germany), and photographed with an AxioCam 208 color (Jena, Germany) camera and saved as JPG files. Approximately 30 measurements were made of each feature using the ZEN 2.0 (blue edition) software. The rust specimens were deposited in the Herbarium of the Department of Plant Pathology, Agricultural College, Guizhou University (HGUP). According to Jayasiri et al. (2015) and Index Fungorum (2023), the Index Fungorum Registration Identifier and Facesoffungi number of the new species were obtained.

DNA extraction, PCR and Sequencing

Rust spores were scraped from fresh plant tissues using a sterilized scalpel. Total DNA of rust spores was extracted with a BIOMIGA Fungus Genomic DNA Extraction Kit (GD2416) following the manufacturer’s protocol. Three loci (ITS, LSU, *tef1α*) were amplified with the respective forward and reverse primers (Table 1). The PCR amplicons from purification and sequencing were carried out at Sangon Biotech (Chengdu, China).

Phylogenetic analyses

Newly generated sequences were deposited in GenBank. All the taxa used in the phylogenetic analyses are listed in Supplementary Tables 2–12. These sequences were compared with the GenBank database using the Basic Local Alignment Search Tool (BLAST), and available sequences of species in the genus containing ex-type or representative isolates were downloaded from GenBank following previous publications (Li et al. 2018, 2020, Vu et al. 2019, Chen et al. 2020, Chu et al. 2021). Alignments for the individual locus matrices were generated with the online version of MAFFT v. 7.307 (Katoh et al. 2019) and manually improved using AliView (Larsson 2014) for maximum alignment and minimum gaps. BioEdit v. 7.0.5 was used to inspect and manually improve the alignments wherever deemed necessary (Hall et al. 2011). Sequencematrix v. 1.7.8 was used to concatenate the aligned sequences (Vaidya et al. 2011).

Maximum likelihood (ML), maximum parsimony (MP) and Bayesian inference (BI) were used to place the newly discovered specimens into a phylogenetic framework and estimate phylogenetic relationships with other rust fungi. ML analysis was performed using IQ-TREE v. XXX (Nguyen et al. 2015, Trifinopoulos et al. 2016) on the IQ-TREE web server (http://iqtree.cibiv.univie.ac.at), using a model selected by auto with rapid bootstrap analysis followed by 1000 bootstrap replicates. The MP analysis was implemented to test the discrepancy of the ITS, LSU and *tef1α* dataset with PAUP v. 4.0b10 (Swofford 2002). Gaps (-) were treated as missing data, which were interpreted as uncertainty of multistate taxa. Phylogenetic trees were generated using the heuristic search option with tree bisection re-connection (TBR) branch swapping. "Maxtrees" was set to 5000, the tree length (TL), consistency index (CI), homoplasy index (HI), retention index (RI) and rescaled consistency index (RC) were calculated. Bayesian inference analysis was made with MrBayes v. 3.2.6 (Ronquist et al. 2012), with the best fitting substitution models using ModelFinder (Kalyaanamoorthy et al. 2017) for every single gene, and the two software were integrated into the PhyloSuite v.1.2.1 (Zhang et al. 2020). BI was performed using six Markov chain Monte Carlo runs for 5,000,000 generations, sampling every 1000 generations. The first 25% resulting trees were discarded as burn-in phase of each analysis.

Table 1 Primers used in this study.

Used genes	Primer	Sequence (5'–3')	Direction	Reference
ITS	Rust2inv	GATGAAGAACACAGTGAAA	Forward	Beenken et al. (2012)
	ITS4rust	CAGATTACAAATTTGGGCT	Reverse	Aime (2006)
LSU	No.4	ACCCGCTGAATTTAAGCATAT	Forward	Van der Auwera et al. (1994)
	No.11	CTCCTTGGTCCGTGTTTCAAGACGC	Reverse	Van der Auwera et al. (1994)
	LR6	CGCCAGTTCTGCTTACC	Forward	Vilgalys & Hester (1990)
	LR0R	ACCCGCTGAACTTAAGC	Reverse	Hopple (1994)
tef1α	EF1-728F	CAT CGA GAA GTT CGAGAA GG	Forward	Carbone & Kohn (1999)
	EF1-1567R	ACHGTRCCRATACCACCSATCTT	Reverse	Rehner & Buckley (2005)
	EF1-983F	GCYCCYGGHCAYCGTGAYTTYAT	Forward	Rehner & Buckley (2005)

Diversity Indices Analysis

Dominant Taxa

A taxon is defined as dominant if Pi > Camargo's index (1/S), where S represents species richness, which is the number of fungal taxa, and Pi is calculated as the number of isolates (Ni) that belong to a certain taxon (i) divided by the total number of isolates (N) (Camargo 1992, Kusari et al. 2013, Zhang et al. 2021).

RESULTS

Phylogenetic analyses

In this study, 304 rust samples were obtained from 33 plant families in Guizhou Province. Sixteen genera of the Pucciniales were determined, i.e., *Coleosporium* (Coleosporiaceae), *Endophylum* (Pucciniaceae), *Gerwasia* (Phragmidiaceae), *Gymnosporangium* (Gymnosporangiaceae), *Hamapora* (Phragmidiaceae), *Macropyxis* (Pucciniaceae), *Melampsora* (Melampsoraceae), *Mikronegeria* (Chaconiaceae), *Nyssopsora* (Uredinineae incertae sedis), *Peridiopsora* (Uredinineae incertae sedis), *Phragmidium* (Phragmidiaceae), *Phakopsora* (Phakopsoraceae), *Puccinia* (Pucciniaceae), *Pucciniastram* (Pucciniastracea), *Tranzschelia* (Tranzscheliaceae), *Uromyces* (Pucciniaceae). Eleven phylogenetic datasets were generated to evaluate taxonomic placement of these rust specimens in Guizhou Province (Figs 1–11).

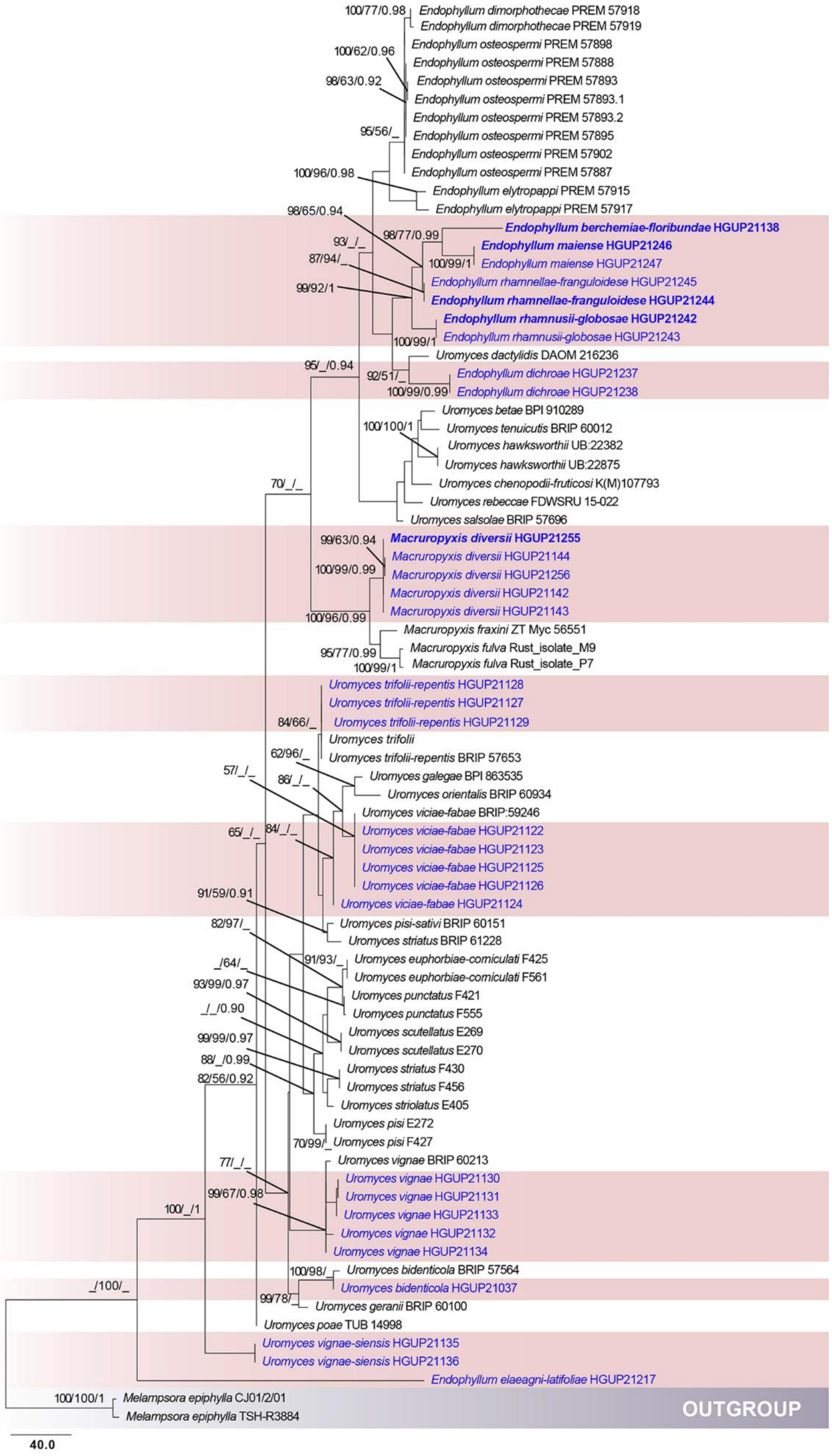

Figure 1 – Maximum parsimony tree of *Pucciniaceae* (excluding Puccinia) reconstructed from a two-locus dataset (ITS, LSU). RA ×ML bootstrap support values (ML ≥ 50%), MP bootstrap

support values (MP ≥ 50%) and Bayesian posterior probability (PP ≥ 0.90) are shown at the nodes (ML/MP/PP). The strains from this study are shown in blue. *Melampsora epiphylla* (CJ01/2/01 and TSH-R3884) was selected as outgroup.

Pucciniaceae

A total of 31 specimens of Pucciniaceae (*Puccinia* excluded) were obtained. The LSU gene fragment was also amplified to verify the accuracy of ITS comparison results and determined the taxonomic placement of these specimens by the analyses of combination of these two loci. Fifty-two DNA sequences of Pucciniaceae fungi (belonging to three genera) were downloaded from the GenBank database (Supplementary Table 2), with *Melampsora epiphylla* (CJ01/2/01) and *M. epiphylla* (TSH-R3884) as the outgroup. The software MrModeltest v.2.3 was used to select the best nucleic acid substitution model for the BI phylogenetic tree of two gene fragments: ITS: GTR+G; LSU: GTR+G. The two gene regions were spliced according to the ITS-LSU sequence (ITS = 1–648; LSU = 649–1252). The maximum likelihood (ML), maximum parsimony (MP) and Bayesian inference (BI) methods were run to yield the phylogenetic tree (Fig. 1).

The total character number of combined sequences was 1252, including 697 constants, 184 variables and parsimony uninformative, and 371 parsimony-informative characters. The maximum reduction method phylogenetic tree TL = 1217, CI = 0.631, RI = 0.845, RC = 0.533, HI = 0.439. There were 31 specimens of Pucciniaceae (excluding *Puccinia*) obtained by the preliminary comparison of ITS and these were mainly distributed in *Endophylum* (10 specimens), *Macropyxis* (5 specimens), and *Uromyces* (16 specimens).

Endophyllum

Specimen HGUP21138 is the first discovery of an *Endophylum* on *Berchemia floribunda* (Fig. 1). It formed an independent branch with specimens HGUP21246 and HGUP21247 from unknown plants, and the node support rate was (ML/MP/BI = 98/77/0.99). It is preliminarily judged that they may be two different species. Specimens HGUP21244 and HGUP21245 collected from *Rhamnella franguloides* plants formed a single branch, and the node support rate was (ML/MP/BI = 87/94/-), it was judged they were most likely a different species. Specimens HGUP21242 and HGUP21243 formed an independent branch with a high node support rate (ML/MP/BI = 100/99/1), and its kinship is distant. Specimens HGUP21237 and HGUP21238 are from *Dichroa febrifuga* plants and form a branch with a high support rate (ML/MP/BI = 100/99/0.99). However, the latter was a known species described by Raciborski (1909b) without nucleotide data. Specimen HGUP21217 is from *Elaeagnus elaeagnus*, which is different from the reported *Puccinia elaeagni* (on *Elaeagnus*) gathered in one branch with the node support rate (ML/MP/BI = -/100/-).

Macruropyxis

Specimens HGUP21255 and HGUP21256 collected from *Epipremnum aureum* and HGUP21142, HGUP21143, and HGUP21144 (from *Paederia foetida*), separated into one branch with high support rate (ML/MP/BI = 100/99/0.99), indicating that the five specimens are likely to be different species (Fig. 1).

Uromyces

As shown in Fig. 1, Specimens HGUP21122, HGUP21123, HGUP21124, HGUP21125, HGUP21126 (host is *Vicia faba*) are all similar to *U. viciae-fabae* gathered in one branch, the node support rate was (ML/MP/BI = 57/-/-), and the genetic distance was almost 0, indicating that the five specimens were probably *U. viciae-fabae*. Specimens HGUP21127, HGUP21128, HGUP21129 and *U. trifolii-repentis* (*Trifolium repens* rust) gathered in one branch, and the node support rate was (ML/MP/BI = 84/66/-). Their hosts were *Trifolium repens*, and they presumably belong to the same species. Specimens HGUP21130, HGUP21131, HGUP21132, HGUP21133, HGUP21134 were collected from *Phaseolus vulgaris*, and *U. vignae* (single spore rust of bean) gathered together, showing a very close genetic relationship. It is inferred that these five specimens are *U. vignae*. Specimens HGUP21135 and HGUP21136 were collected from *Vigna unguiculata*, although they formed an independent branch, they were different from the reported *U. vignae-sinensis* (cowpea monospora rust) from the same host, which may be the same species. Specimens HGUP21137 and *U. bidenticola* gathered into one branch, and the node support rate was (ML/MP/BI = 100/98/-). Both hosts were *Bidens bipinnata*, presumably the same species.

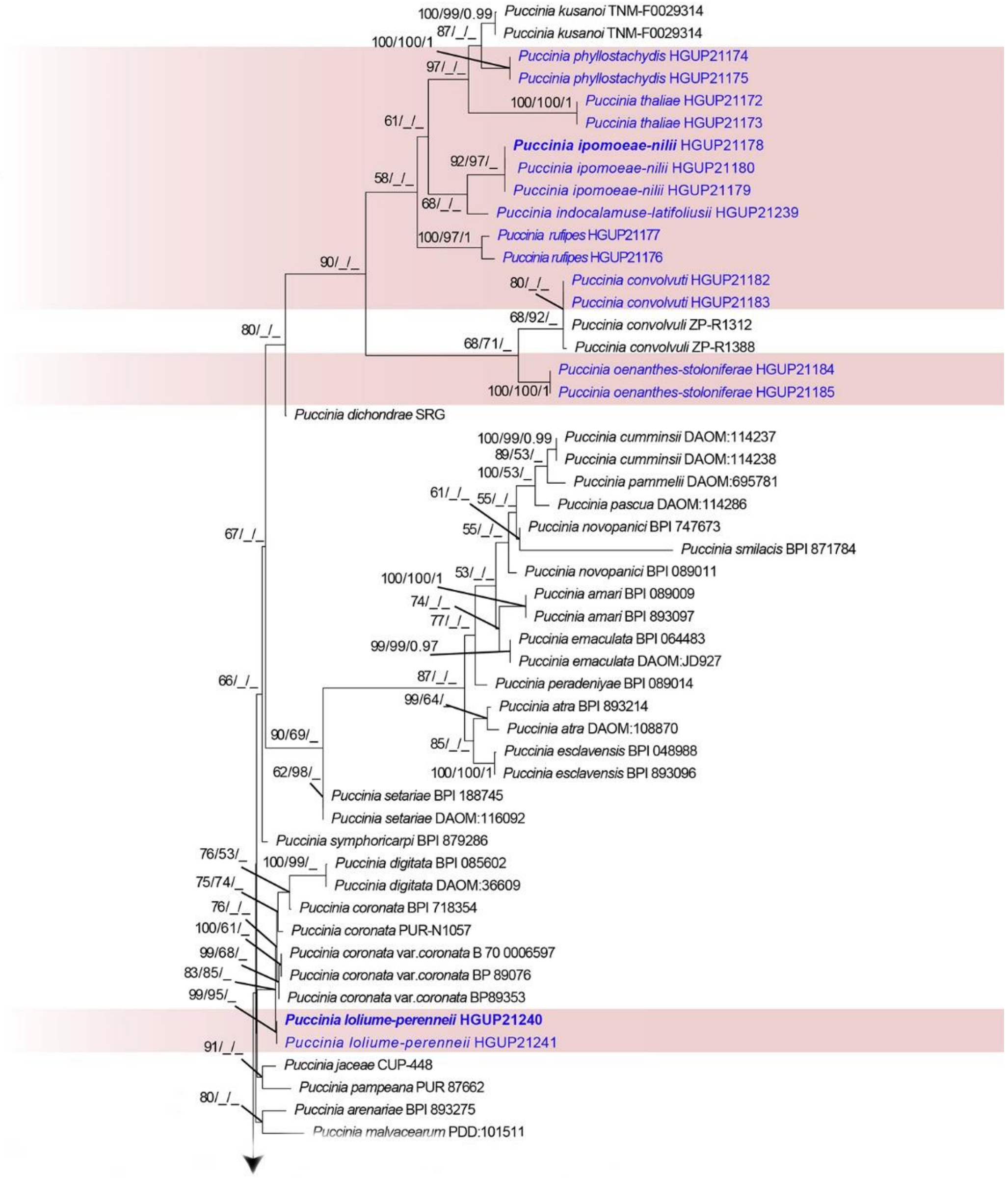

Figure 2 – Maximum likelihood tree of *Puccinia* reconstructed from a two-locus dataset (ITS, LSU). RA ×ML bootstrap support values (ML ≥ 50%), MP bootstrap support values (MP ≥ 50%) and Bayesian posterior probability (PP ≥ 0.90) are shown at the nodes (ML/MP/PP). The strains of this study are shown in blue. *Melampsora epiphylla* (CJ01/2/01 and TSH-R3884) was selected as outgroup.

Puccinia

In order to clarify the taxonomic status of 76 rust specimens preliminarily identified as *Puccinia*, LSU gene was amplified on the basis ITS gene. Based on these two gene fragments, 153 fungal sequences of *Puccinia* were downloaded from the GenBank database (Supplementary Table 3), with the out group being *Melampsora epiphylla* (CJ01/2/01) and *M. epiphylla* (TSH-R3884).

The best nucleic acid substitution model for BI of two gene fragments is: ITS: GTR+G; LSU: GTR+I+. According to the ITS-LSU sequence, the two genes were spliced (ITS = 1–594; LSU = 595–1134), and the phylogenetic trees of ML, MP and BI were constructed according to the above tree building methods. The total number of combined sequence sites is 1134, including 291 conservative sites, 155 highly variable non-reduced information sites and 688 reduced information sites. The maximum reduction method phylogenetic tree TL = 4147, CI = 0.366, RI = 0.776, RC = 0.284, HI = 0.634. Details of phylogenetic analyse of all *Puccinia* specimens in Table 2.

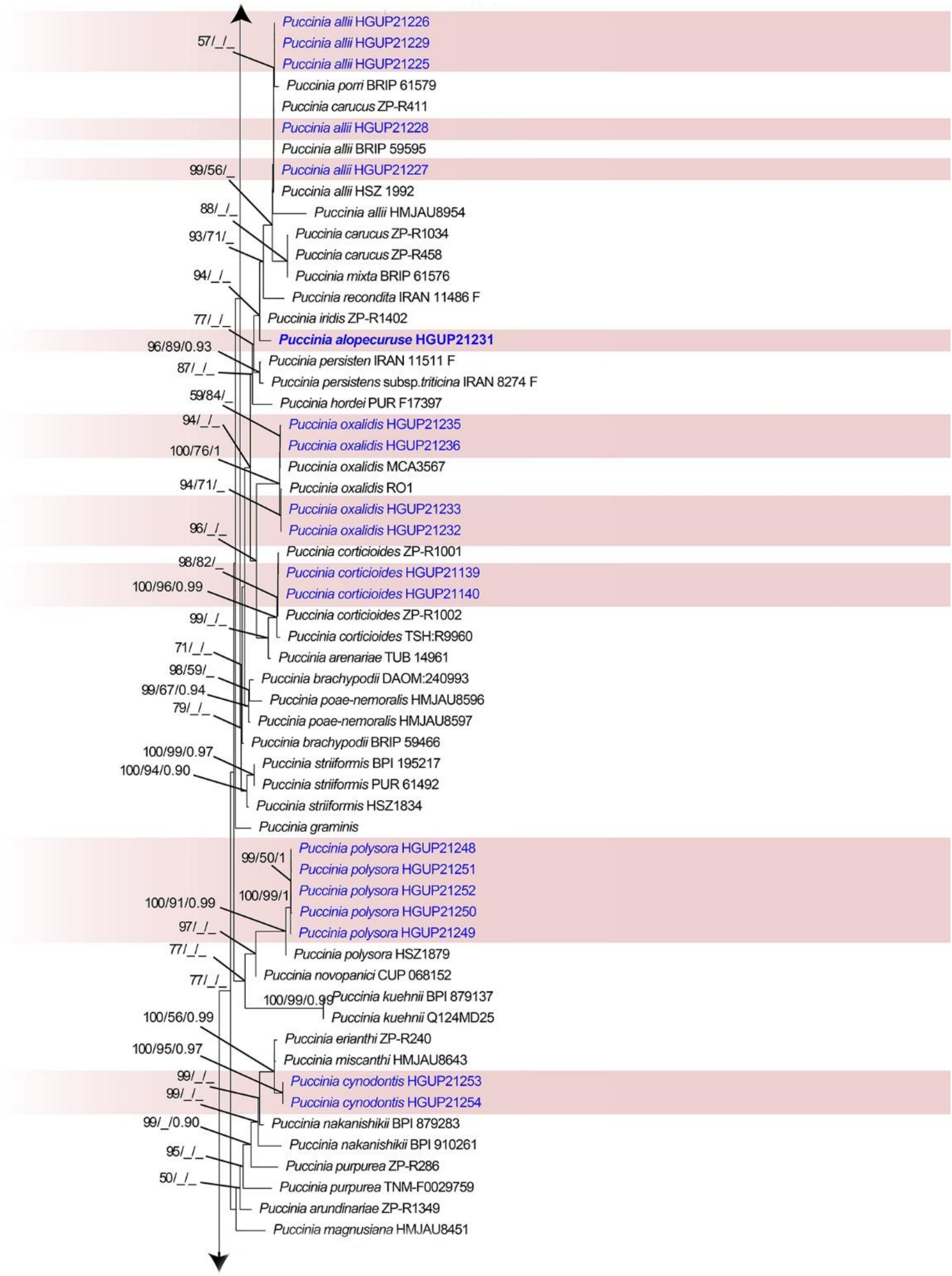

Figure 2 – Continued.

Phragmidiaceae

According to the preliminary identification of ITS, 41 specimens of rust belong to Phragmidiaceae. To determine their taxonomic status, LSU gene was further amplified. Seventynine Phragmidiaceae fungal sequences (Supplementary Table 4) were selected and downloaded from GenBank database (belonging to six genera), and the out groups was *Melampsora epiphylla* (CJ01/2/01) and *M. epiphylla* (TSH-R3884). The best nucleic acid substitution model for BI of two gene fragments is: ITS: GTR+I; LSU: GTR+G. After comparing ITS and LSU, splice them (ITS = 1-569; LSU = 570-1291), and construct ML, MP and BI phylogenetic trees according to the above tree building methods.

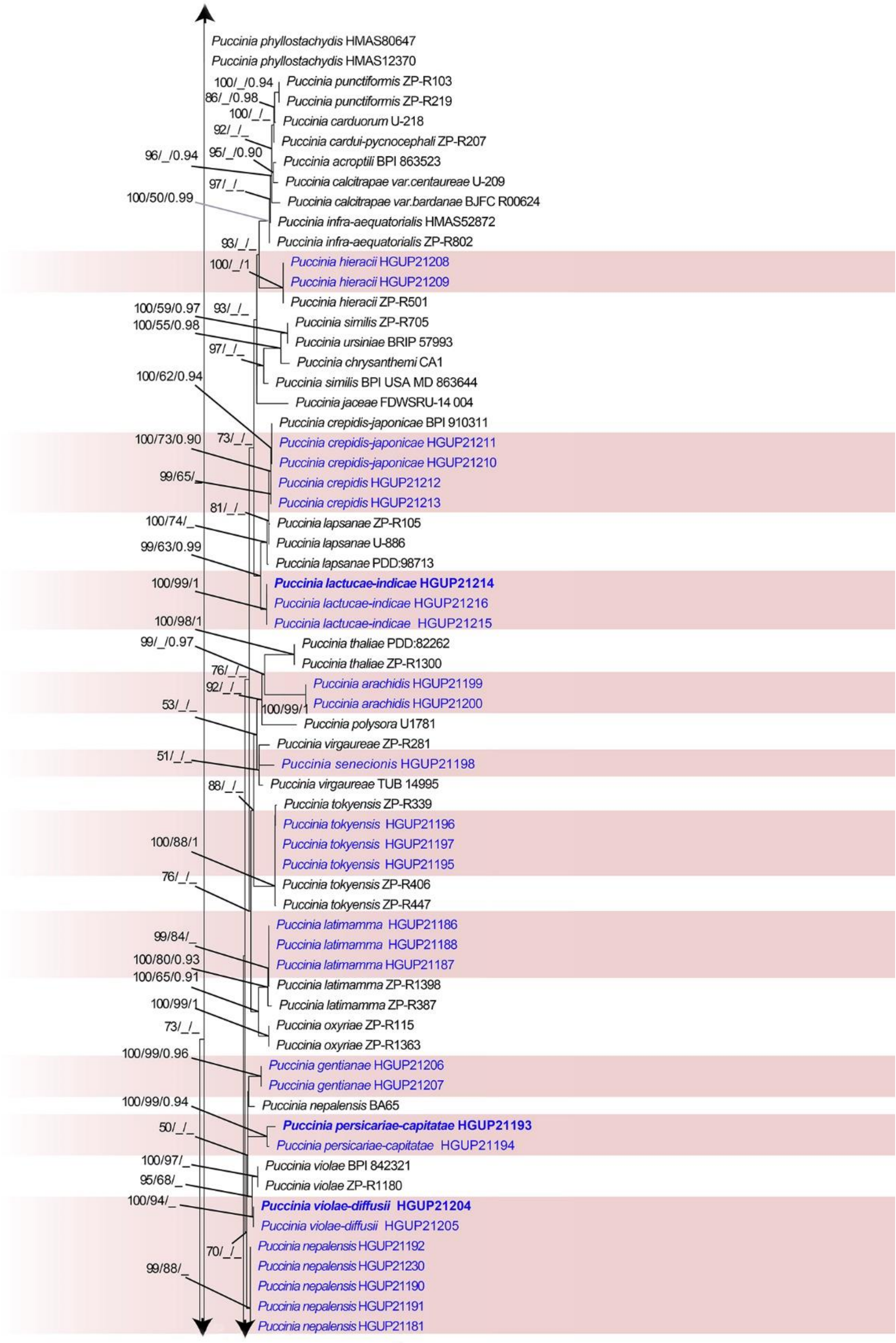

Figure 2 – Continued.

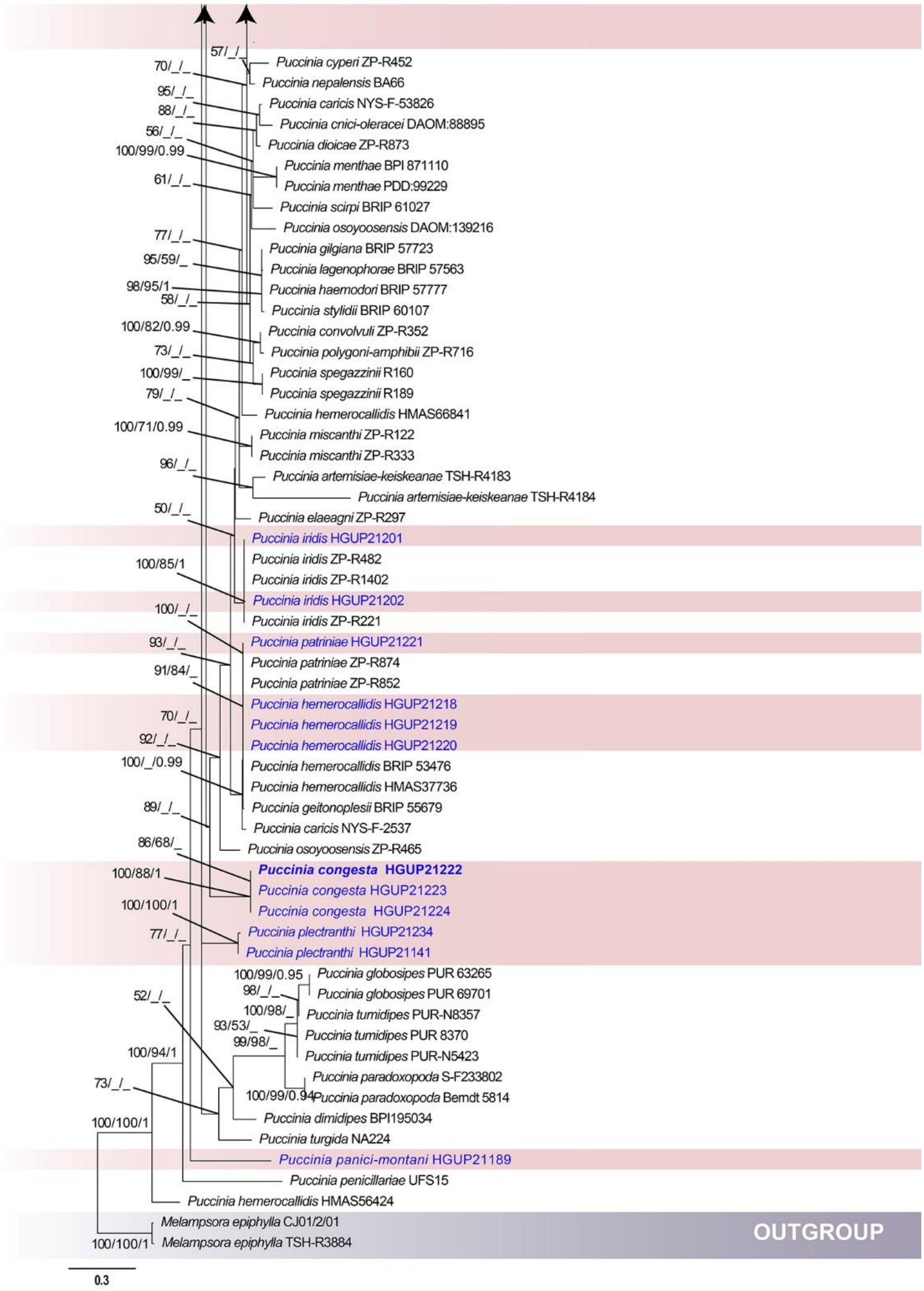

Figure 2 – Continued.

Phylogenetic analysis showed that the total number of combined sequence sites was 1291, including 501 conservative sites, 116 highly variable non-reduced information sites, and 694 reduced information sites. The maximum reduction method phylogenetic tree TL = 2636, CI = 0.506, RI = 0.850, RC = 0.430, HI = 0.493. The 41 specimens of Phragmidiaceae (Fig. 3) were mainly distributed in three genera with 26 specimens of *Phragmidium*; 8 specimens of *Gerwasia*; and 7 specimens of *Hamasora*. Details of phylogenetic analyse all Phragmidiaceae specimens in Table 2.

Coleosporiaceae

In order to accurately determine the taxonomic status of 40 specimens of rust fungus that have been preliminarily identified as Coleosporinaceae, we amplified the LSU gene, and selected and downloaded 124 fungal sequences corresponding to Coleosporinaceae in the GenBank database (belonging to seven genera) (Supplementary Table 5), and the out groups are *Melampsora epiphylla* (CJ01/2/01) and *M. epiphylla* (TSH-R3884). The best nucleic acid substitution model for BI is: ITS: GTR+G; LSU: GTR+I. After comparison, the ITS and LSU were spliced (ITS = 1-498; LSU = 499-992), and the phylogenetic trees of ML, MP and BI were constructed respectively. The phylogenetic analysis results showed that the total number of combined sequence sites was 992, including 542 conservative sites, 104 highly variable non-reduced information sites, and 346 reduced information sites. The maximum reduction method phylogenetic tree TL = 1001, CI = 0.613, RI = 0.865, RC = 0.530, HI = 0.386. According to the phylogenetic tree (Fig. 4), 41 specimens of Coleosporiaceae were preliminarily identified and only distributed in the genus *Coleosporium*. Details of the phylogenetic analyse of all *Coleosporium* specimens are in Table 2.

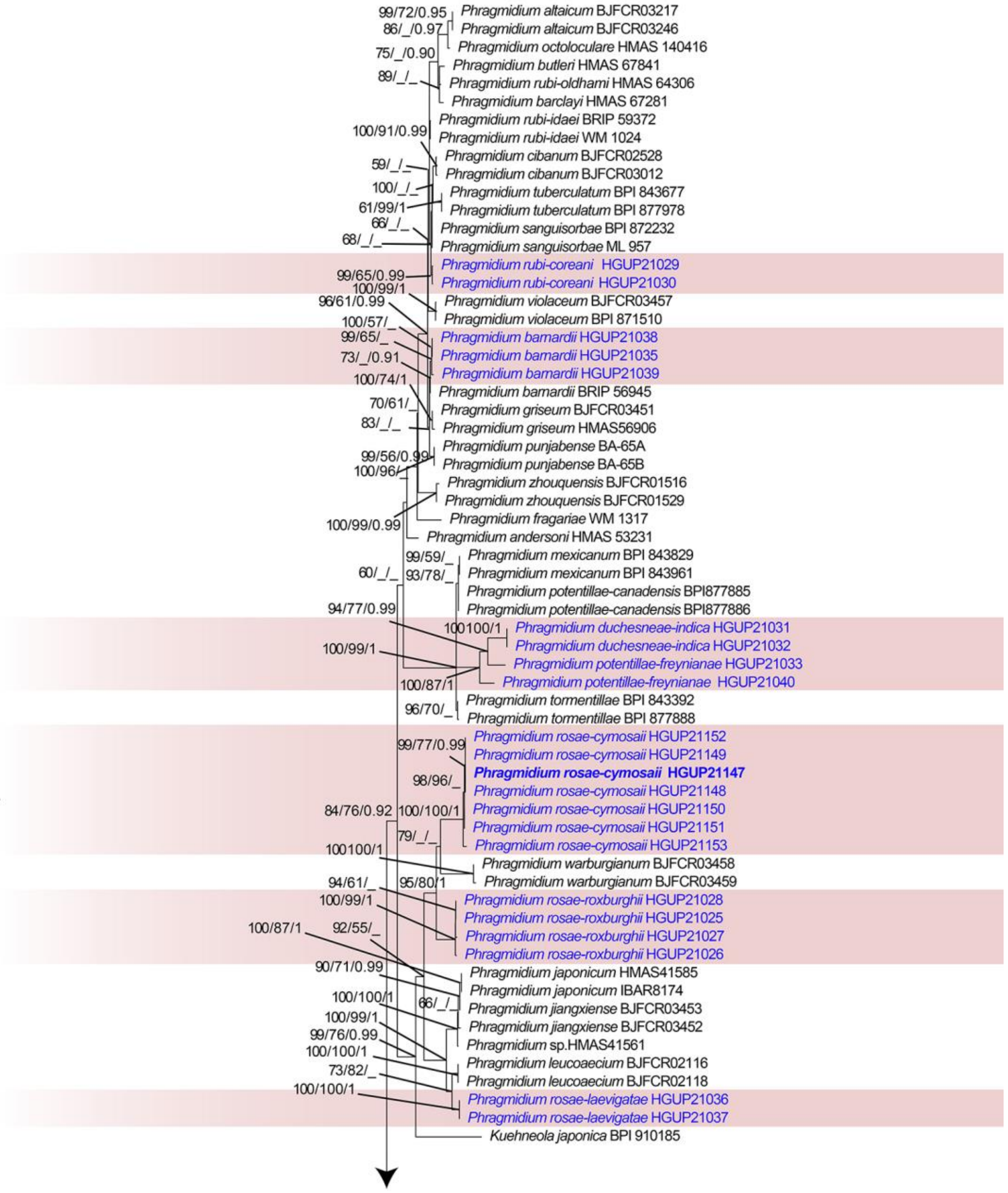

Figure 3 – Maximum likelihood tree of Phragmidiaceae reconstructed from a two-locus dataset (ITS, LSU). RA ×ML bootstrap support values (ML ≥ 50%), MP bootstrap support values (MP ≥

50%) and Bayesian posterior probability (PP ≥ 0.90) are shown at the nodes (ML/MP/PP). The strains from this study are shown in blue. *Melampsora epiphylla* (CJ01/2/01 and TSH-R3884) was selected as outgroup.

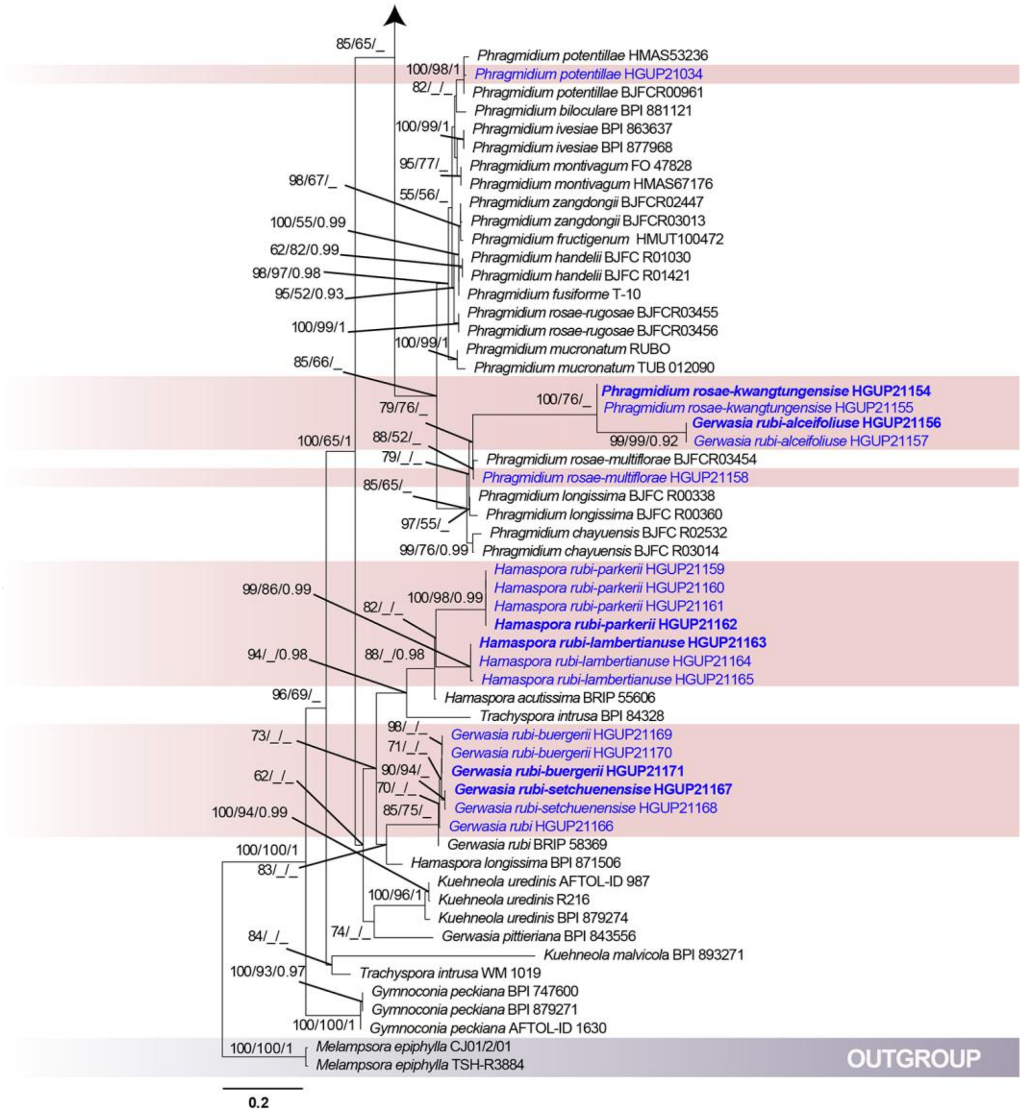

Figure 3 – Continued.

Pucciniastraceae

It has been preliminarily identified that four specimens belong to Pucciniastraceae. To clarify their classification status, LSU gene was amplified on the basis of ITS gene. Based on these two genes, 41 DNA sequences (belonging to seven genera) of the family were selected and downloaded from NCBI (Supplementary Table 6), and the out groups were *Gymnosporangium annuum* (BJFC-R01456) and *G. pleoporum* (BJFC-R02952). The best nucleic acid substitution model for BI of the two genes is GTR+I+. The two genes were spliced head-to-tail according to the ITS-LSU sequence (ITS = 1-439; LSU = 440-1004), and phylogenetic trees were constructed using MP, ML and BI methods respectively. In phylogenetic analysis, the total number of combined sequence sites is 1004, including 723 conservative sites, 37 highly variable non-reduced information sites, and 244 reduced information sites. The maximum reduction method phylogenetic tree TL = 520, CI = 0.675, RI = 0.844, RC = 0.570, HI = 0.325. According to the phylogenetic tree (Fig. 5), four specimens of Pucciniastraceae obtained through preliminary identification by ITS are distributed in the genus *Pucciniastrum*.

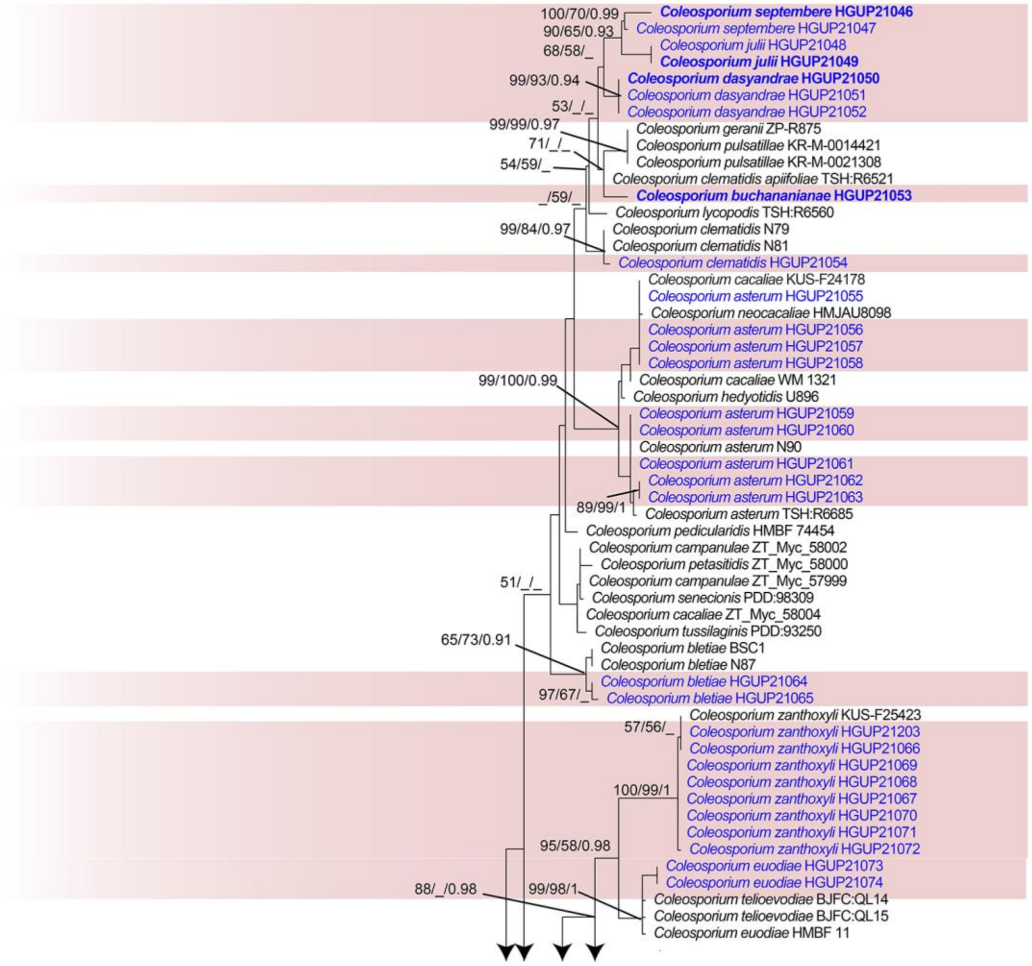

Figure 4 – Maximum parsimony tree of Coleosporinaceae reconstructed from a two-locus dataset (ITS, LSU). RA ×ML bootstrap support values (ML ≥ 50%), MP bootstrap support values (MP ≥ 50%) and Bayesian posterior probability (PP ≥ 0.90) are shown at the nodes (ML/MP/PP). The strains from this study are shown in blue. *Melampsora epiphylla* (CJ01/2/01 and TSH-R3884) was selected as outgroup.

Pucciniastrum

Specimens HGUP21108 and HGUP21109 are compatible with *P. circaeae* and *P. epilobii* and clustered into sister branches, showing a significant genetic difference and distant genetic relationship. Specimens HGUP21110 and HGUP21111 were collected from *Boehmeria nivea*, and are close to *P. corni*, *P. kusanoi*, *P. styracinum*, *P. yoshinagai*, *P. actinidiae* and *P. boehmeriae*, but node support rate (ML/MP/BI = 99/67/0.97), shows obvious genetic distance.

Phakopsoraceae

Molecular biological research was carried out on the five specimens of rust preliminarily identified as Phakopsoraceae. The relevant genes were amplified by PCR, the ITS and LSU sequence fragments were obtained, and compared in NCBI. The sequences of 32 taxa belonging to Phakopsoraceae (belonging to four genera) were selected and downloaded (Supplementary Table 7). The out groups were *Gymnosporangium asiaticum* (TNM F0027941) and *G. clavariiforme* (RSP05-32). The best nucleic acid substitution model for BI is: ITS: HKY+I+; LSU: GTR+I+. After comparing the two genes, the first and last splicing (ITS = 1-553; LSU = 554-1204) was performed according to the ITS-LSU sequence, and the phylogenetic tree was constructed using MP, ML and BI methods respectively. According to phylogenetic analysis, the total number of combined sequence sites is 1204, including 740 conservative sites, 116 highly variable non-simple information sites, and 348 simple information sites. The maximum reduction method phylogenetic tree TL = 940, CI = 0.735, RI = 0.824, RC = 0.606, HI = 0.264. According to the phylogenetic tree (Fig. 6), five Phakopsoraceae specimens identified by ITS are distributed in the genus *Phakopsora*.

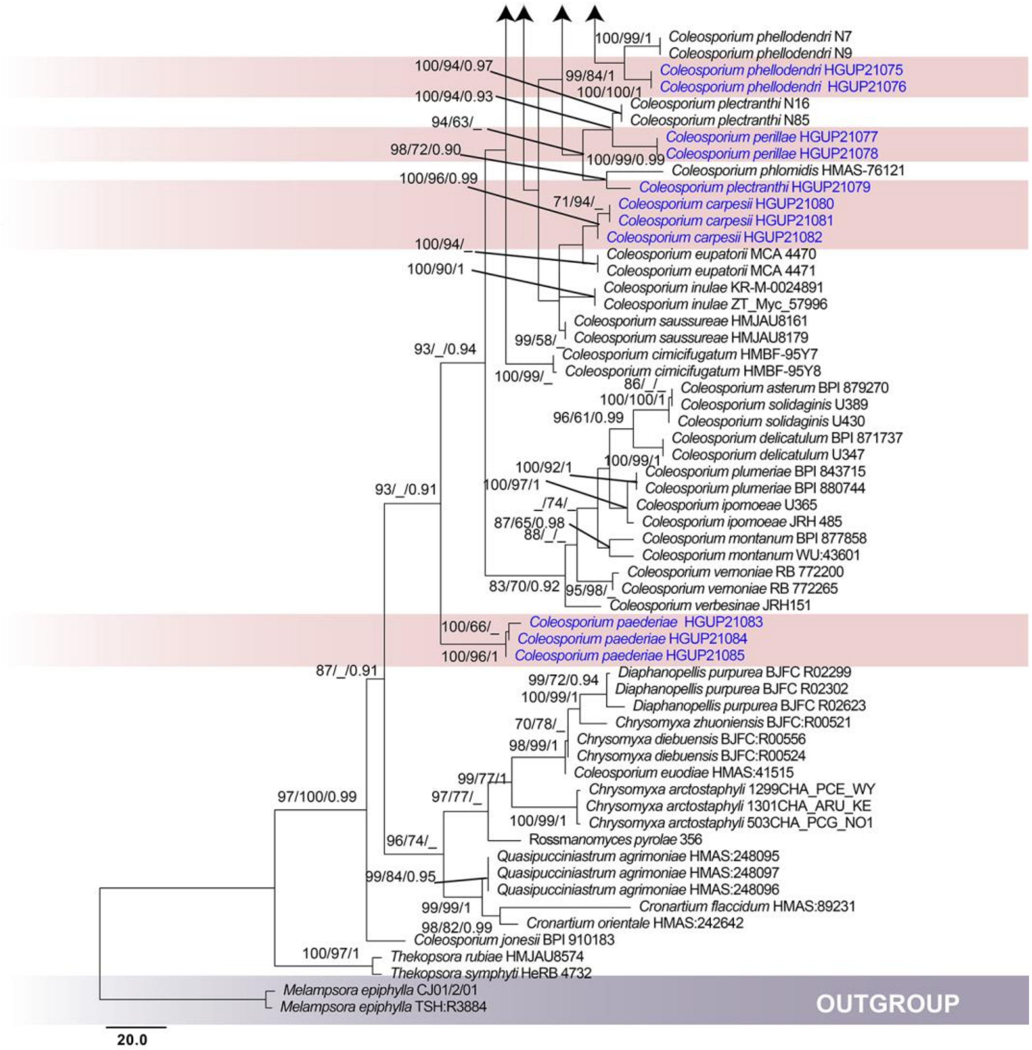

Figure 4 – Continued.

Phakopsora

Specimens HGUP21112, HGUP21113 and HGUP21114 (on *Cayratia japonica*) and specimens HGUP21115 and HGUP21116 (on *Parthenocissus tricuspidata*) clustered into sister branches (Fig. 6), and the node support rate was (ML/MP/BI = 95/90/1). At the same time, they also clustered into a single branch with a high support rate, showing a distinct genetic distance and a distant genetic relationship, and can be regarded as two independent species.

Melampsoraceae

Five specimens of Melampsoraceae rust fungus were obtained. To clarify the preliminary identification results of ITS, the related genes (LSU) were amplified by PCR. Based on these two genes, 48 sequences (belonging to two genera) of the family were downloaded from NCBI (Supplementary Table 8), and the out group was *Chrysomyxa empiri* (287CHE_ EMN_ SA1) and *C. monesis* (1309CHM_ MOU_ GR). The best nucleic acid substitution model for BI is GTR+I+. After sorting out the sequences, splice them according to the ITS-LSU sequence (ITS = 1-335; LSU = 336-714), and construct phylogenetic trees using MP, ML and BI methods respectively. Phylogenetic analysis showed that the total number of combined sequence sites was 714, including

469 conservative sites, 48 highly variable non-simple information sites and 197 simple information sites. The maximum reduction method phylogenetic tree TL = 492, CI = 0.628, RI = 0.807, RC = 0.506, HI = 0.372. According to the phylogenetic tree (Fig. 7), five Melampsoraceae specimens preliminarily identified by ITS are distributed in the genus *Melampsora*.

Table 2 Details of results in phylogenetic analyse of Coleosporiaceae (*Coleosporium*), Phragmidiaceae (*Gerwasia*, *Hamaspora*, *Phragmidium*), Pucciniaceae (*Puccinia*).

Family	Genus	Specimens	Host	Node support rate (ML/MP/BI)
Coleosporiaceae	*Coleosporium*	HGUP21054	*Clematis brevicaudata*	99/84/0.97
		HGUP21055-HGUP21061	*Aster ageratoides*	NA
		HGUP21062-HGUP21063	*A. indicus*	89/99/1
		HGUP21064-HGUP21065	*Bletilla striata*	65/73/0.91
		HGUP21066-HGUP21072, HGUP21203	*Zanthoxylum bungeanum*	100/99/1
		HGUP21073-HGUP21074	*Tetradium ruticarpum*	66/99/1
		HGUP21075-HGUP21076	*Phellodendron amurense*	100/100/1
		HGUP21077-HGUP21078	*Perilla frutescens*	99/84/0.97
		HGUP21079	*Camellia japonica*	98/72/0.90
		HGUP21080-HGUP21082	*Carpesium abrotanoides*	100/96/0.99
		HGUP21083-HGUP21085	*Paederia foetida*	100/96/1
Phragmidiaceae	*Gerwasia*	HGUP21156-HGUP21157	*Rubus* (*Ru*) *alceifolius*	99/99/0.92
		HGUP21166	*Ru. reflexus*	NA
		HGUP21167-HGUP21168	*Ru. setchuenensis*	90/94/-
		HGUP21169-HGUP21171	*Ru. buergeri*	85/75/-
	Hamaspora	HGUP21159-HGUP21162	*Ru. parkeri*	100/98/0.99
		HGUP21163-HGUP21165	*Ru. lambertianus*	99/86/0.99
	Phragmidium	HGUP21029-HGUP21030	*Ru. coreanus*	99/65/0.99
		HGUP21035, HGUP21038-HGUP21039	*Rubus* sp., *Ru. adenophorus*	99/65/-
		HGUP21031-HGUP21032	*Duchesnea indica*	100/100/1
		HGUP21033, HGUP21040	*Potentilla (Po) freyniana*	100/87/1
		HGUP21147-HGUP21153	*Rosa* (*Ro*) *cymosa*	100/100/1
		HGUP21025-HGUP21028	*Ro. Roxburghii*	100/99/1
		HGUP21036-HGUP21037	*Ro. Laevigata*	100/100/1

Table 2 Continued.

Family	**Genus**	**Specimens**	**Host**	**Node support rate (ML/MP/BI)**
		HGUP21034	*Po. Serpentina*	100/98/1
		HGUP21154-HGUP21155	*Ro. Kwangtungensis*	100/76/-
		HGUP21158	*Ro. Multiflorae*	88/52/1
Pucciniaceae	*Puccinia*	HGUP21174-HGUP21175	*Phyllostachys nuda*	100/100/1
		HGUP21172-HGUP21173	*Canna sativa*	100/100/1
		HGUP21178-HGUP21180	*Ipomoea nil*	92/97/-
		HGUP21239	*Indocalamus latifolia*	68/-/-
		HGUP21176-HGUP21177	*Imperata cylindrica*	100/97/1
		HGUP21182-HGUP21183	*Calystegia hederacea*	68/92/-
		HGUP21184-HGUP21185	*Oenanthe javanica*	95/90/1
		HGUP21240-HGUP21241	*Lolium perenne*	99/95/-
		HGUP21225-HGUP21229	*Allium sativum*	NA
		HGUP21231	*Alopecurus aequalis*	94/-/-
		HGUP21232-HGUP21233, HGUP21235-HGUP21236	*Oxalis sorrel*	100/76/1
		HGUP21139-HGUP21140	*Bamboo*	100/96/0.99
		HGUP21248-HGUP21252	*Zea mays*	100/99/1
		HGUP21253-HGUP21254	*Plantago asiatica*	100/95/0.97
		HGUP21208-HGUP21209	*Taraxacum mongolicum*	100/-/1
		HGUP21210-HGUP21211	*Youngia japonica*	100/62/0.94
		HGUP21212-HGUP21213	*Crepidiastrum sonchifolium*	99/65/-
		HGUP21214-HGUP21216	*Lactuca indica*	100/99/1
		HGUP21199-HGUP21200	*Arachis hypogaea*	100/99/1
		HGUP21198	*Senecio scandens*	51/-/-
		HGUP21195-HGUP21197	*Cryptotaenia japonica*	100/88/1
		HGUP21186-HGUP21188	*Pleuropterus multiflorus*	100/80/0.93
		HGUP21206-HGUP21207	*Gentiana macrophylla*	100/99/0.96
		HGUP21193-HGUP21194	*Persicaria capitata*	100/99/0.94
		HGUP21204-HGUP21205	*Viola diffusa*	100/94/-

Table 2 Continued.

Family	Genus	Specimens	Host	Node support rate (ML/MP/BI)
		HGUP21181, HGUP21190-HGUP21192, HGUP21230	*Rumex nepalensis*	99/88/-
		HGUP21201-HGUP21202	*Iris tectorum*	100/88/1
		HGUP21221	*Patrinia* (*Pa*) *villosa*	100/-/-
		HGUP21218-HGUP21220	*Hemerocallis fulva*	91/84/-
		HGUP21222-HGUP21224	*Persicaria posumbu*	100/88/1
		HGUP21141, HGUP21234	*Pa. foetida*	100/100/1
		HGUP21189	*Setaria plicata*	77/-/-

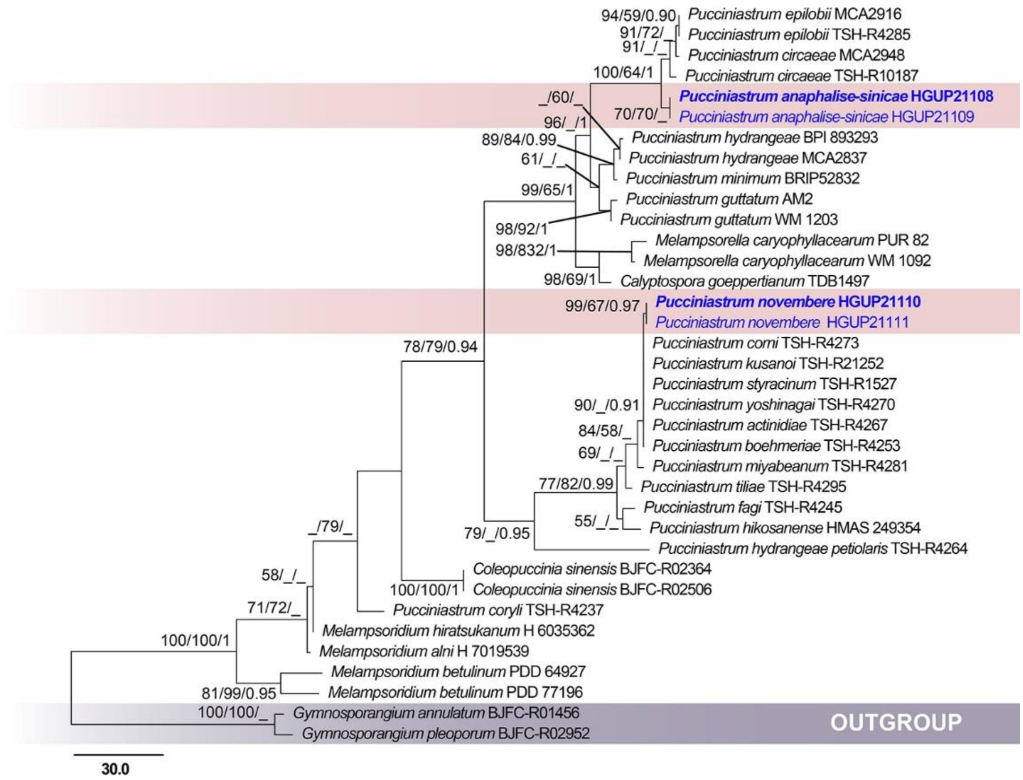

Figure 5 – Maximum parsimony tree of *Pucciniastraceae* reconstructed from a two-locus dataset (ITS, LSU). RA ×ML bootstrap support values (ML ≥ 50%), MP bootstrap support values (MP ≥ 50%) and Bayesian posterior probability (PP ≥ 0.90) are shown at the nodes (ML/MP/PP). The strains from this study are shown in blue. *Gymnosporangium annuum* (BJFC-R01456) and *G. pleoporum* (BJFC-R02952) were selected as outgroup.

Melampsora

Specimens HGUP21117 and HGUP21118 (on *Salix babylonica*) formed an independent branch (Fig. 7), and the node support rate was (ML/MP/BI = 100/99/0.99). There was a significant genetic distance between specimens and the neighboring species, and there was a distant genetic relationship. Specimens HGUP21119, HGUP21120 and HGUP21121 clustered together with

Melampsora coleosporioides with a qualified node support rate (ML/MP/BI = 91/-/-), and the genetic distance was close to 0, which was very likely to be the same species.

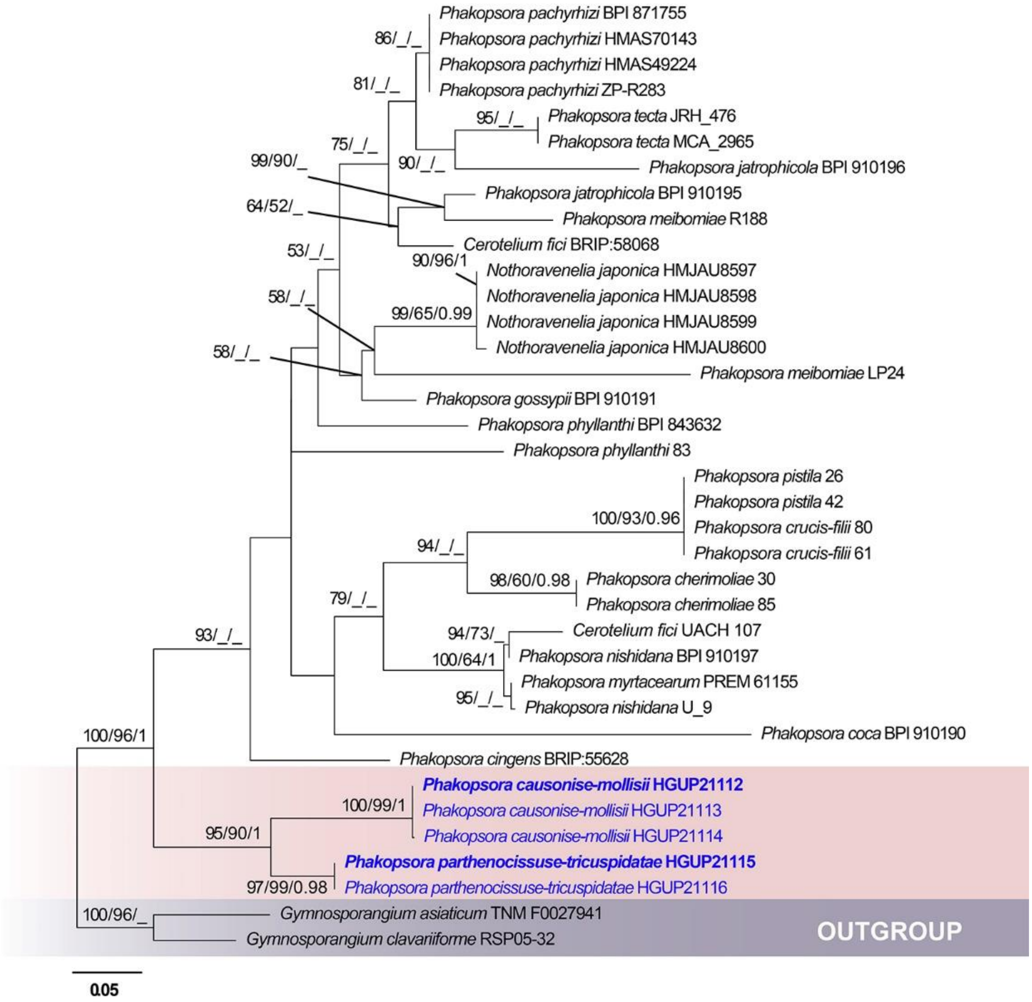

Figure 6 – Maximum likelihood tree of *Phakopsoraceae* reconstructed from a two-locus dataset (ITS, LSU). RA ×ML bootstrap support values (ML ≥ 50%), MP bootstrap support values (MP ≥ 50%) and Bayesian posterior probability (PP ≥ 0.90) are shown at the nodes (ML/MP/PP). The strains from this study are shown in blue. *Gymnosporangium asiaticum* (TNM F0027941) and *G. clavariiforme* (RSP05-32) was selected as outgroup.

Uredinineae incertae sedis

In order to accurately determine the taxonomic status of the nine specimens preliminarily identified as Uredinineae incertae sedis, we amplified the LSU gene, and selected and downloaded 26 fungal sequences corresponding to Uredinineae incertae sedis (belonging to five genera) in the GenBank database (Supplementary Table 9), with the out group *Phragmidium zangdongii* (BJFC-R02447 and BJFC-R03013). After comparison, the ITS and LSU were spliced (ITS = 1-399; LSU = 400-1063), and the phylogenetic trees of ML, MP and BI were constructed respectively. Phylogenetic analysis showed that the total number of combined sequence sites was 1063, including 564 conservative sites, 86 highly variable non-simple information sites, and 413 simple information sites. The maximum reduction method phylogenetic tree TL = 1265, CI = 0.603, RI = 0.812, RC = 0.489, HI = 0.396. According to the results of the phylogenetic tree (Fig. 8), the 9 specimens of Uredinineae incertae sedis identified are distributed in *Nyssopsora* (7 specimens) and *Periiopsora* (2 specimens).

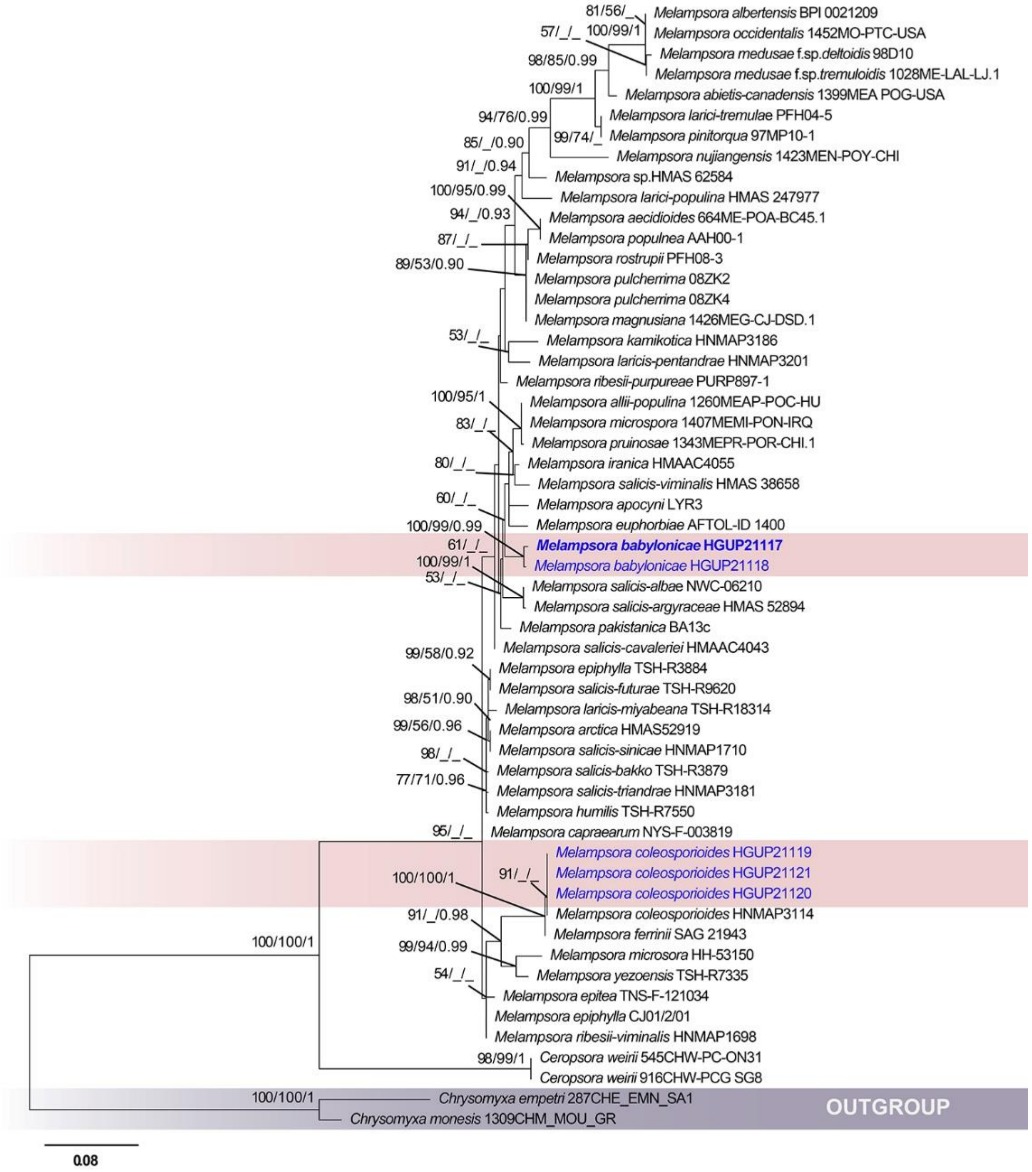

Figure 7 – Maximum likelihood tree of Melampsoraceae reconstructed from a two-locus dataset (ITS, LSU). RA ×ML bootstrap support values (ML ≥ 50%), MP bootstrap support values (MP ≥ 50%) and Bayesian posterior probability (PP ≥ 0.90) are shown at the nodes (ML/MP/PP). The strains from this study are shown in blue. *Chrysomyxa empiri* (287CHE_ EMN_ SA1) and *C. monesis* (1309CHM_ MOU_ GR) was selected as outgroup.

Nyssopsora

Specimens HGUP21103 and HGUP21104 (on *Acanthus ilicifolius*) with sufficient node support rate (ML/MP/BI = 99/80/0.99) along with *Nyssopsora koelreuteriae*, clustered into sister branches, showing a slightly distant genetic distance, with no close genetic relationship. Specimens HGUP21098, HGUP21099 and HGUP21100 from *Aralia elata* gathered together with specimens HGUP21101 and HGUP21102 (on *Toona sinensis*) with a high node support rate (ML/MP/BI = 100/99/0.99), with a relatively obvious genetic distance. Based on host and morphological characteristics, rust on *Toona sinensis* was reported as *N. cedrelae*, but specimens HGUP21101 and HGUP21102 are largely different from *N. cedrelae*.

Peridiopsora

Specimens HGUP21096 and HGUP21097 were collected from leaves of *Morus alba*. Although they were isolated into one branch, the node support rate was (ML/MP/BI =

100/99/0.99). According to the records, the pathogen of mulberry leaf rust is *Peridiopsora mori*, which is probably the same species.

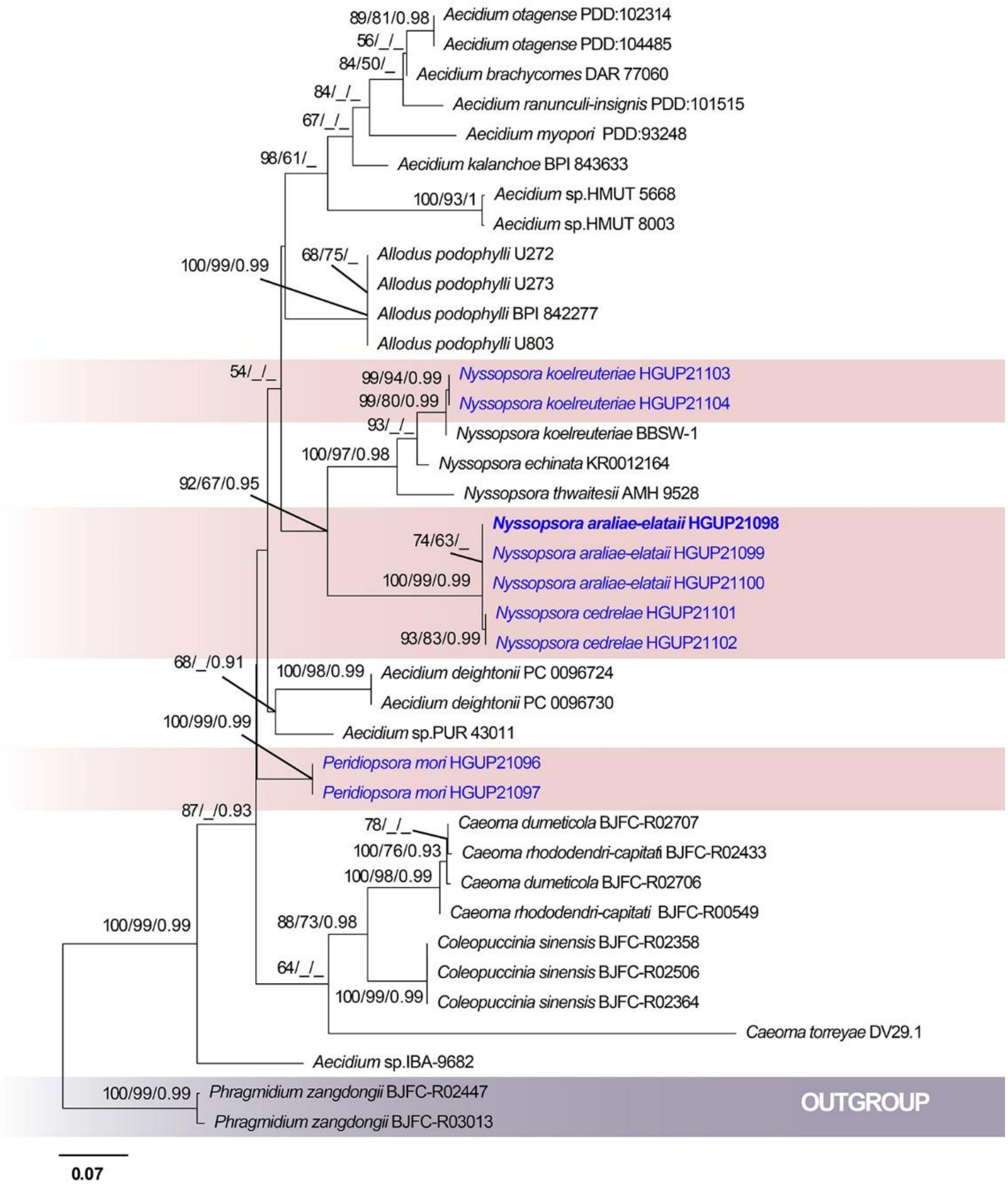

Figure 8 – Maximum likelihood tree of Uredinineae incertae sedis reconstructed from a two-locus dataset (ITS, LSU). RA ×ML bootstrap support values (ML ≥ 50%), MP bootstrap support values (MP ≥ 50%) and Bayesian posterior probability (PP ≥ 0.90) are shown at the nodes (ML/MP/PP). The strains from this study are shown in blue. *Phragmidium zangdongii* (BJFC-R02447 and BJFC-R03013) was selected as outgroup.

Chaconiaceae

According to the preliminary identification of ITS, three specimens of rust belong to Chaconiaceae. To determine their taxonomic status, LSU and SSU genes were further amplified. Based on these three gene fragments, DNA sequences of 22 Chaconiaceae (belonging to ten genera) were downloaded from NCBI (Supplementary Table 10), with the outgroup taxon *Septobasidium apiculatum* (DUKE: DAH (064)). The best nucleic acid substitution model for BI of three gene fragments is: ITS: HKY+G; LSU: GTR+G; SSU: HKY+I. According to the sequence of SSU-ITS-LSU, the three genes were spliced first and last (ITS = 1-485; LSU = 486-1150; SSU = 1151-2179), and the phylogenetic trees of ML, MP and BI were constructed respectively according to the above tree building methods. The total number of combined sequence sites is 2179, including 1508 conservative sites, 215 highly variable non-reduced information sites and 456 reduced information sites. The maximum reduction method phylogenetic tree TL = 1198, CI = 0.762, RI = 0.803, RC = 0.613, HI = 0.237. According to the phylogenetic tree (Fig. 9), the three Chaconiaceae specimens were preliminarily identified as in the genus *Mikronegeria*.

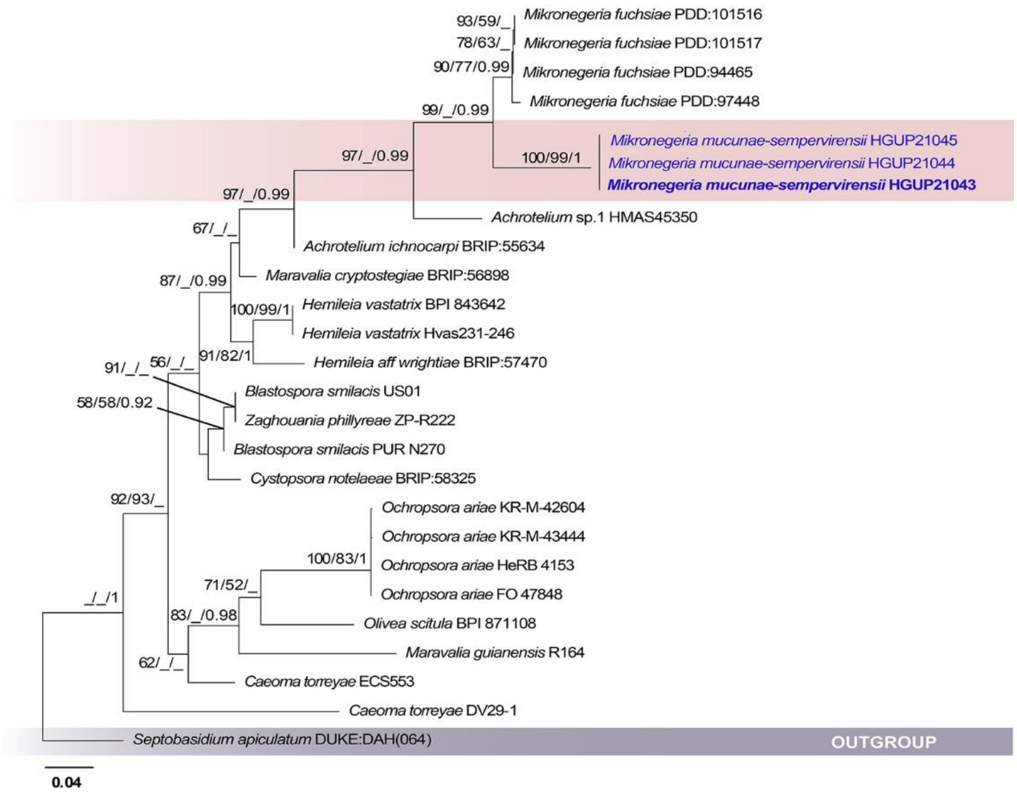

Figure 9 – Maximum likelihood tree of Chaconiaceae reconstructed from a two-locus dataset (ITS, LSU). RA ×ML bootstrap support values (ML ≥ 50%), MP bootstrap support values (MP ≥ 50%) and Bayesian posterior probability (PP ≥ 0.90) are shown at the nodes (ML/MP/PP). The strains from this study are shown in blue. *Septobasidium apiculatum* (DUKE: DAH (064)) was selected as outgroup.

Mikronegeria

Specimens HGUP21043, HGUP21044 and HGUP21045 (Fig. 9) clustered into a single branch with a high node support rate (ML/MP/BI = 100/99/1) and formed a sister branch with *Mikronegeria fuchsiae*, and maintained a relatively distant genetic relationship between the two taxa.

Gymnosporangiaceae

Ten specimens of Gymnosporangiaceae were obtained. To determine the genera and species taxonomic units of these specimens, molecular biological research was continued. The relevant genes were amplified by PCR, and the sequence fragments of ITS, LSU and *tef1α* were obtained. The sequences of 74 taxonomic units belonging to Gymnosporangiaceae (only one genus) were selected and downloaded from NCBI (Supplementary Table 11). After comparing the three genes, the first and last splicing (ITS = 1-488; LSU = 489-1046; *tef1α* = 1047-1626) was carried out according to the ITS-LSU-*tef1α* sequence, and the phylogenetic tree was constructed by MP, ML and BI methods respectively. According to phylogenetic analysis, the total number of combined sequence sites is 1626, including 952 conservative sites, 65 highly variable non-simple information sites and 609 simple information sites. The maximum reduction method phylogenetic tree TL =

1896, CI = 0.559, RI = 0.874, RC = 0.489, HI = 0.440. The ten specimens of Gymnosporangiaceae identified by ITS are all in the genus *Gymnosporangium* (Fig. 10).

Gymnosporangium

Specimens HGUP21086, HGUP21087, HGUP21088, and HGUP21089 were collected from leaves of pear while specimens HGUP21090, HGUP21091, and HGUP21092 were collected from *Chaenomeles speciosa*. Specimens HGUP21093, HGUP21094, and HGUP21095 were collected from apple. All ten specimens clustered together with *Gymnosporangium asiaticum* (Fig. 10) with sufficient node support rate (ML/MP/BI = 94/97/1).

Tranzscheliaceae

Three specimens of rust were preliminarily identified as Tranzscheliaceae. The relevant genes (ITS, LSU) were amplified by PCR, we selected and downloaded 20 DNA sequences in NCBI belonging to Tranzscheliaceae (belonging to two genera) (Supplementary Table 12). After comparing the two genes, the first and last splicing (ITS = 1-511; LSU = 512-1161) was performed according to the ITS-LSU sequence, and the phylogenetic tree was constructed using MP, ML and BI methods respectively. According to phylogenetic analysis, the total number of combined sequence sites is 1161, including 695 conservative sites, 111 highly variable non-simple information sites, and 355 simple information sites. The maximum reduction method phylogenetic tree TL = 701, CI = 0.835, RI = 0.886, RC = 0.740, HI = 0.164. The three specimens of Tranzscheliaceae obtained through preliminary identification are distributed in *Tranzschelia* (Fig. 11).

Tranzschelia

Specimens HGUP21105, HGUP21106 and HGUP21107 from *Prunus persica*, gathered in one branch along with *T. discolor* (Fig. 11), the node support rate was (ML/MP/BI = 99/99/1), and the genetic distance was very short, indicating that they are all the same species.

Taxonomy

Pucciniales T. Caruel, Atti della Reale Accademia dei Lincei, Memorie della Classe di Scienze Fisiche, Matematiche e Naturali Ser. 3, 10: 246 (1881)
Pucciniaceae Chevall. [as ‘Puccinieae’], Fl. gén. env. Paris (Paris) 1: 413 (1826)
Endophyllum Lév., Mémoires de la Société Linnéenne de Paris 4: 208 (1826)

Endophyllum berchemiae-floribundae J.E. Sun, Yong Wang bis & K.D. Hyde, sp. nov. Fig. 12

Index Fungorum number: IF901290; Facesoffungi number: FoF15357

Etymology – The name reflects the host *Berchemia floribunda*, from which the type specimen was collected.

Holotype – HGUP21138

Description – *Spermogonia*, *uredinia* and *aecia* not known. *Aecidioid telia* on leaves, abaxial, golden, rarely caulicolous, 1–2 cm long, peridium dehiscent at apex, no slits along the sides. *Aecidioid teliospores* 19–24 × 17–22 µm ($\overline{x}$ = 22.2 × 18.9 µm, n = 30), globose, inclusions pale to golden, scattered, wall 1.0–1.9 µm thick, colorless, echinulate.

Host – *Berchemia floribunda* (Rhamnaceae)

Material examined – CHINA, Guizhou Province, Guiyang city, 26°41′56″N, 106°66′85″W, 1160 m, 11 May 2021, on *Berchemia floribunda*, J.E. Sun, holotype HGUP21138.

Notes – *Berchemia floribunda* is an alternate host for the aecial stage of *Puccinia coronata* (Zhuang et al. 1998). However, in the phylogenetic analyses, specimen HGUP21138 did not group with *P. coronata*. Morphologically, however, they are different for teliospores (30–67 × 12–23 µm) (Zhuang et al. 1998). In phylogeny, this specimen was distant to other known species of *Endophylum*, *E. dimorphothecae*, *E. osteospermi* and *E. elytropappi* (Fig. 1). The aecidioid teliospores of *E. berchemiae-floribundae* are slightly smaller than those of *E. elytropappi* (25.5–26 × 20.5–21 µm; Wood & Crous 2005). We, thus, propose *E. berchemiae-floribundae* as a new taxon.

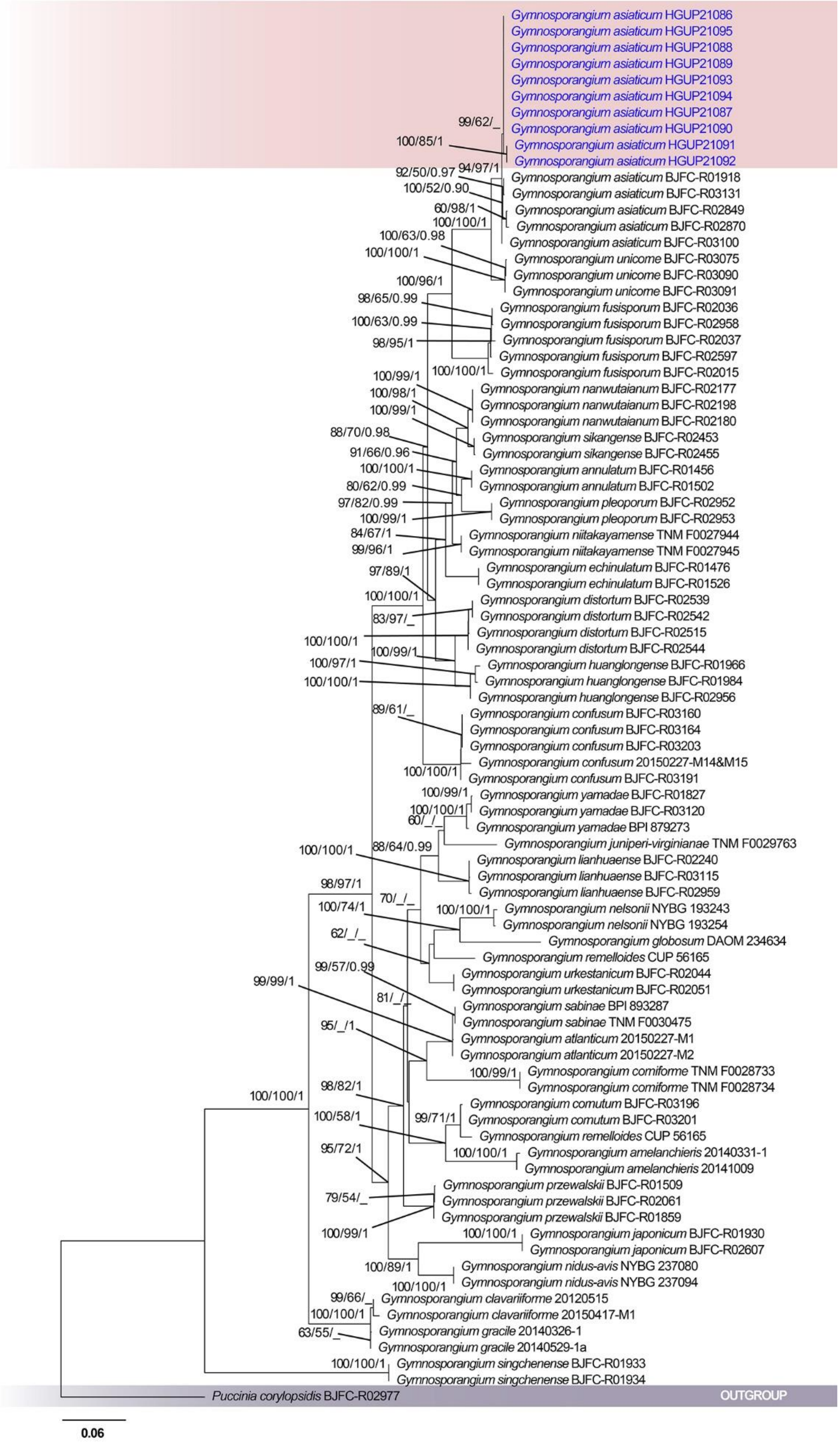

Figure 10 – Maximum likelihood tree of Gymnosporangiaceae reconstructed from a two-locus dataset (ITS, LSU, *tef1α*). RA ×ML bootstrap support values (ML ≥ 50%), MP bootstrap support values (MP ≥ 50%) and Bayesian posterior probability (PP ≥ 0.90) are shown at the nodes

(ML/MP/PP). The strains from this study are shown in blue. *Puccinia corylopsidis* (BJFC-R02977) was selected as outgroup.

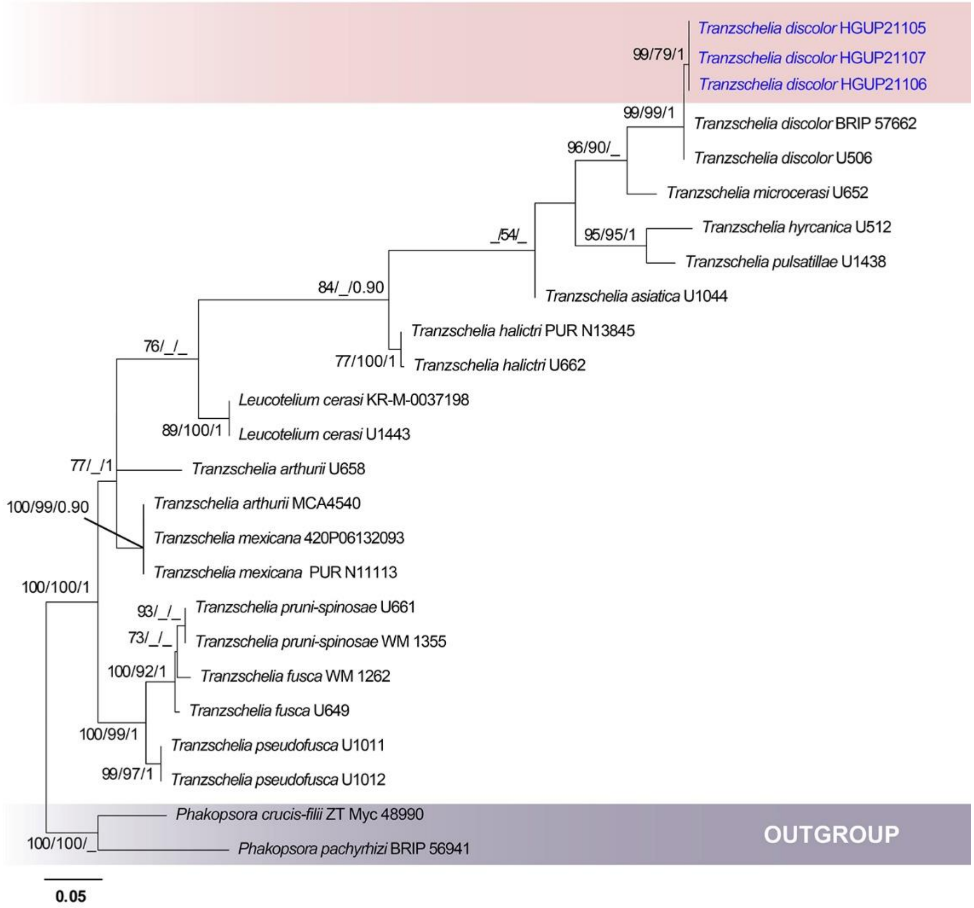

Figure 11 – Maximum likelihood tree of Tranzscheliaceae reconstructed from a two-locus dataset (ITS, LSU, TEF). RA ×ML bootstrap support values (ML ≥ 50%), MP bootstrap support values (MP ≥ 50%) and Bayesian posterior probability (PP ≥ 0.90) are shown at the nodes (ML/MP/PP). The strains from this study are shown in blue. *Phakopsora pachyrhizi* (BRIP 56941) and *P. crucis-filii* (ZT Myc 48990) was selected as outgroup.

Endophyllum maiense J.E. Sun, Yong Wang bis & K.D. Hyde, sp. nov. Fig. 13

Index Fungorum number: IF901291; Facesoffungi number: FoF15358

Etymology – The specific epithet "maiense" refers to the fungus being collected in May.

Holotype – HGUP21246

Description – *Spermogonia*, *uredinia* and *aecia* not known. *Aecidioid telia* produced on abaxial leaf surface, scattered, not surrounded by host epidermis, roestelioid, 1.0–4.0 mm diam., peridium dehiscent at apex, no slits along the sides, yellow. *Aecidioid teliospores* ellipsoidal or irregular, 17–23 × 13–17 µm ($\bar{x}$ = 19.9 × 14.3 µm, n = 30), inclusions light yellow; wall 1.4–2.4 µm thick, colorless, rugose.

Host – Unknown host

Material examined – CHINA, Guizhou Province, Guiyang city, 26°45′33″N, 106°65′80″W, 1121 m, 6 May 2022, unknown host, J.E. Sun, holotype HGUP21246; Guizhou Province, Guiyang city, 26°45′33″N, 106°65′80″W, 1121 m, 6 May 2022, unknown host, J.E. Sun, HGUP21247.

Notes – In the phylogenetic analysis specimens HGUP21246 and HGUP21247 formed an independent branch with high bootstrap support (ML/MP/BI: 100/99/1.00, Fig. 1), with a distant relationship to *Endophyllum dimorphothecae*, *E. elytropappi* and *E. osteospermi*. However, our specimens have smaller aecidioid teliospores than *E. dimorphothecae* (20–21× 16–17 µm), *E. elytropappi* (25.5–26 × 20.5–21 µm) and *E. osteospermi* (21.5–22.2 × 17–18 µm) (Wood & Crous 2005). Therefore, *E. maiense* is introduced as a new species based on morphological characters and phylogenetic evidences.

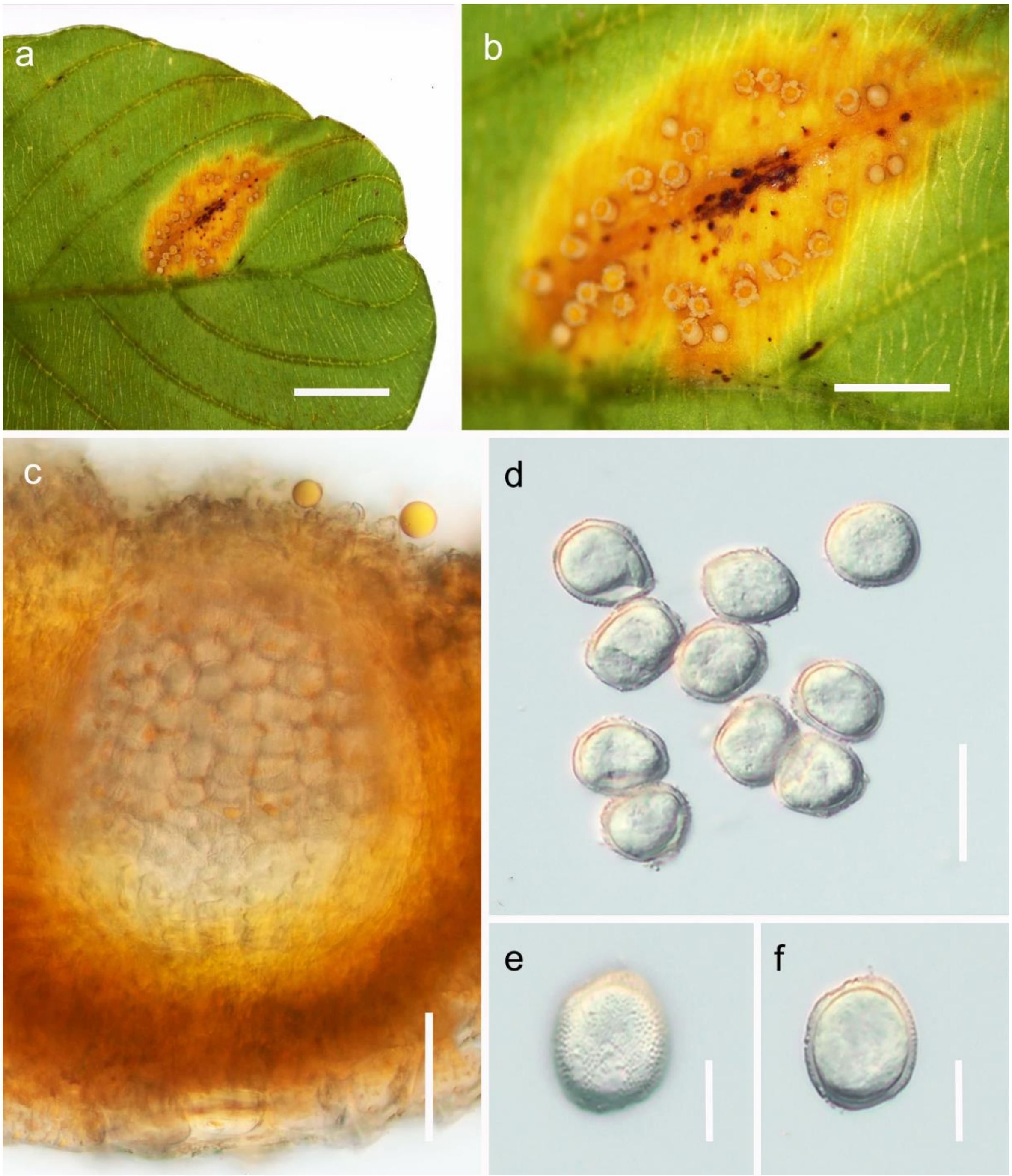

Figure 12 – *Endophyllum berchemiae-floribundae* (from holotype HGUP21138) on *Berchemia floribunda*. a–b Aecidioid telia on leaf. c Longitudinal section of aecidioid telium. d–f Aecidioid teliospores. Scale bars: a = 5 mm, b = 2 mm, c = 50 µm, d = 50 µm, e–f = 25 µm.

Endophyllum rhamnellae-franguloidese J.E. Sun, Yong Wang bis & K.D. Hyde, sp. nov.

Fig. 14

Index Fungorum number: IF901292; Facesoffungi number: FoF15359

Etymology – The name reflects the host *Rhamnella franguloides*, from which the type specimen was collected.

Holotype – HGUP21244

Description – *Spermogonia*, *uredinia* and *aecia* not known. *Aecidioid telia* produced on abaxial leaf surface, scattered, not surrounded by host epidermis, roestelioid, 1.0–4.0 mm diam., peridium dehiscent at apex, no slits along the sides, yellow. *Aecidioid teliospores* oblong to oval, 12–18 × 11–14 µm (x̅ = 14.2 × 12.5 µm, n = 30), inclusions light golden; wall 1.2–2.0 µm thick, colorless, rugose.

Host – *Rhamnella franguloides* (Rhamnaceae)

Material examined – CHINA, Guizhou Province, Duyun city, 25°36'61"N, 107°16'15"W, 1222 m, 2 May 2022, on *Rhamnella franguloides*, Y.J. Sun, holotype HGUP21244; Guizhou Province, Bijie city, 27°25'14"N, 106°14'17"W, 1200 m, 27 May 2022, on *R. franguloides*, J.E. Sun, HGUP21245.

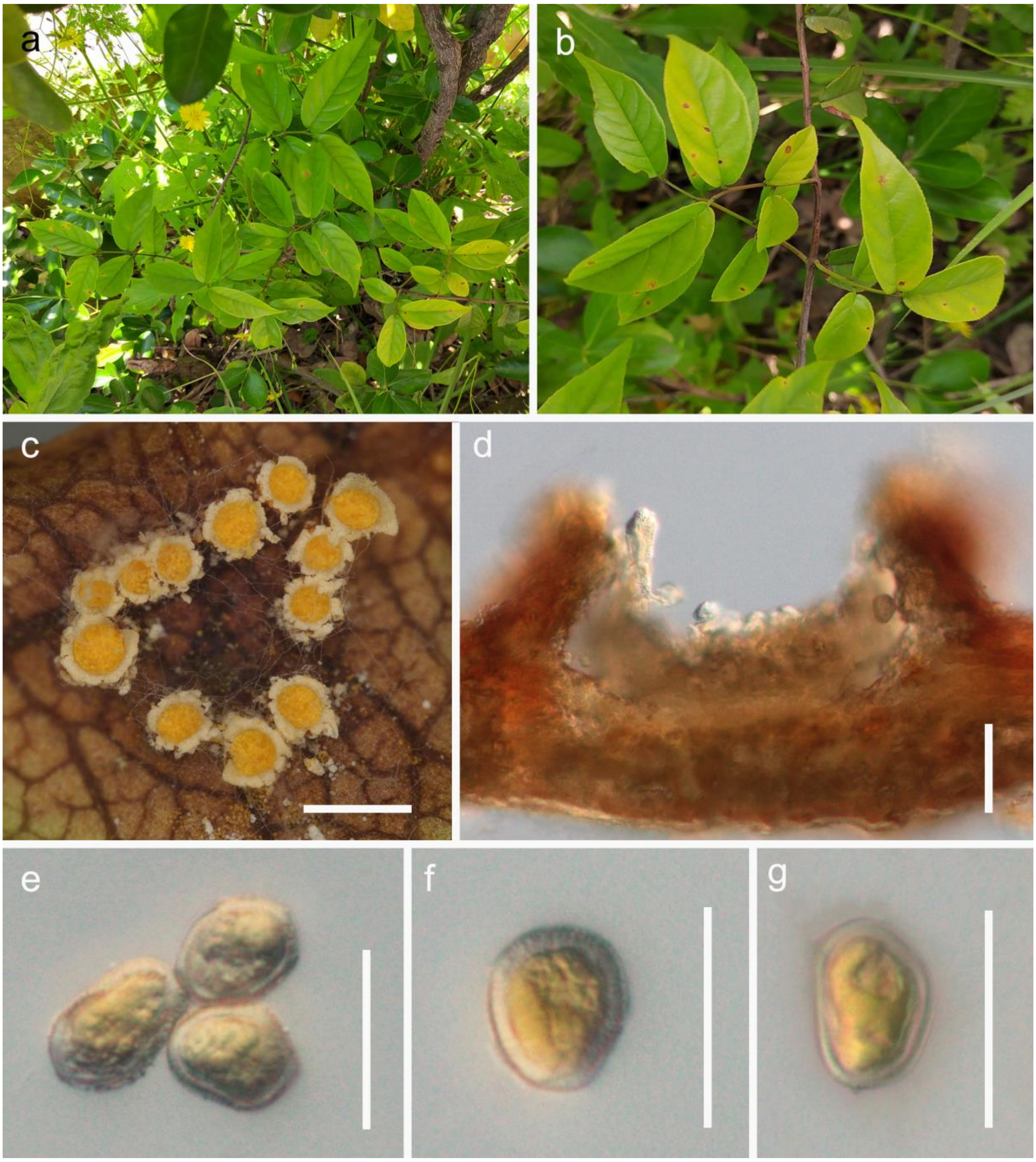

Figure 13 – *Endophyllum maiense* (from holotype HGUP21246). a–c Aecidioid telia on leaves. d Longitudinal section of aecidioid telium. e–g Aecidioid teliospores. Scale bars: c = 1 mm, d = 50 µm, e–g = 25 µm.

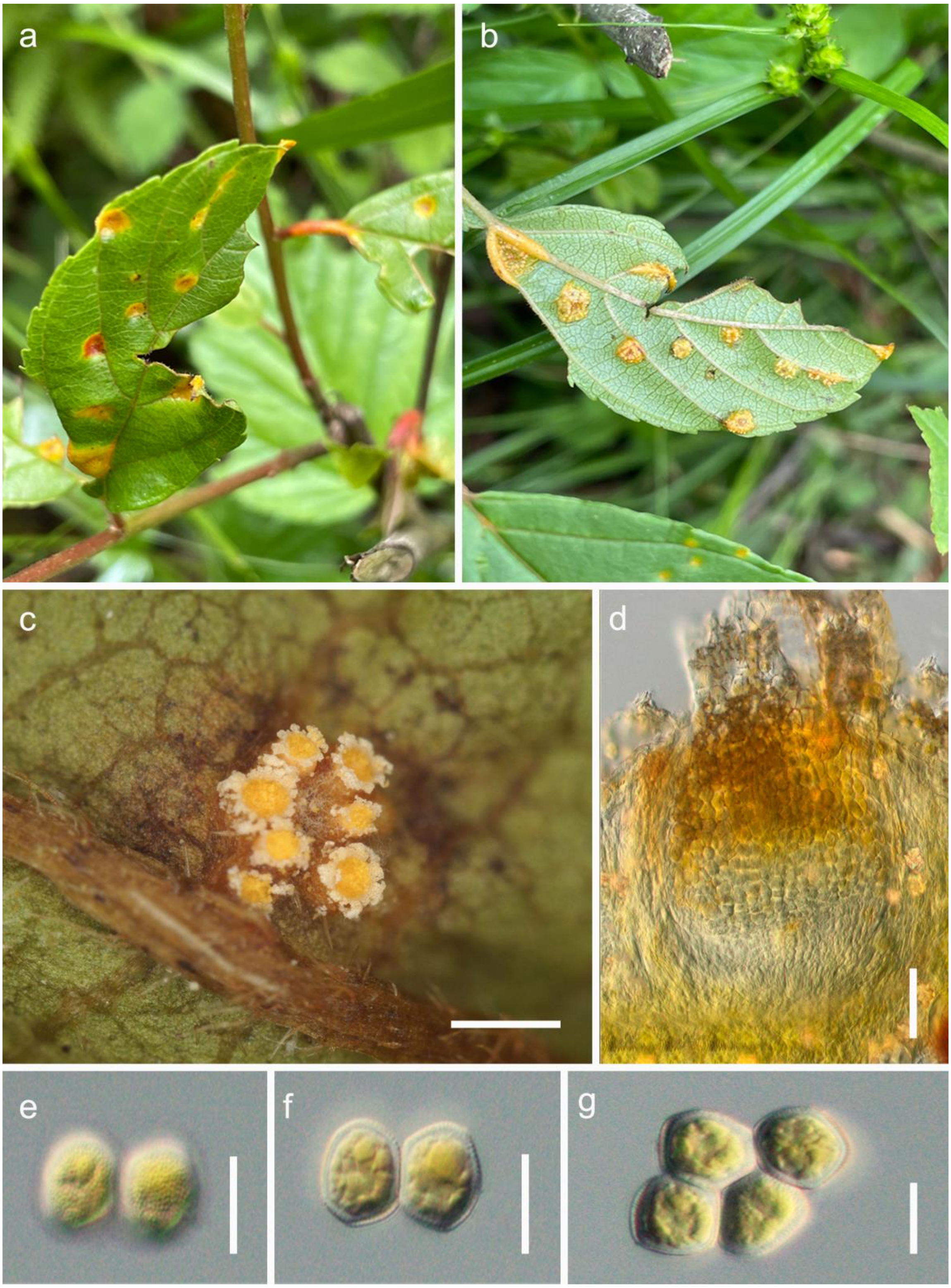

Figure 14 – *Endophyllum rhamnellai-franguloidese* (from holotype HGUP21244) on *Rhamnella franguloides*. a–c Aecidioid telia on leaves. d Longitudinal section of aecidioid telium. e–g Aecidioid teliospores. Scale bars: c = 1 mm, d = 50 µm, e–g = 12.5 µm.

Notes – *Rhamnella franguloides* is an alternate host for aecia of *Puccinia coronata* (Zhuang et al. 1998), but the present fungus is phylogenetically different. Morphologically, it differs from *P. coronata* by smaller aecidioid teliospores (30–67 × 12–23 µm; Zhuang et al. 1998). In the phylogenetic analysis, *Endophyllum rhamnellae-franguloidese* (HGUP21244, HGUP21245) formed a single branch close to *E. elytropappi* and *E. dichroae* (Fig. 1), *E. rhamnellae-*

franguloidese has smaller aecidioid teliospores than *E. dichroae* (23–35 × 18–22 µm), and *E. elytropappi* (25.5–26 × 20.5–21 µm) (Wood & Crous 2005, Zhuang et al. 2012). Hence, based on both morphology and phylogeny, we identify our specimens as a new species

Endophyllum rhamnusii-globosae J.E. Sun, Yong Wang bis & K.D. Hyde, sp. nov. Fig. 15

Index Fungorum number: IF901293; Facesoffungi number: FoF15360

Etymology – The name reflects the host *Rhamnus globosa*, from which the type specimen was collected.

Holotype – HGUP21242

Description – *Spermogonia*, *uredinia* and *aecia* not known. *Aecidioid telia* produced on abaxial leaf surface, scattered, not surrounded by host epidermis, obvious boundary, roestelioid, 1.0–3.0 mm diam., peridium dehiscent at apex, no slits along the sides, yellow. *Aecidioid teliospores* oblong to oval, 13–18 × 10–17 µm (x̅ = 16.2 × 14.4 µm, n = 30), inclusions golden; wall 1.8–2.5 µm thick, colorless, rugose.

Host – *Rhamnus globosa* (Rhamnaceae)

Material examined – CHINA, Guizhou Province, Duyun city, 25°36'81"N, 107°16'25"W, 1224 m, 2 May 2022, on *Rhamnus globosa*, Y.J. Sun, holotype HGUP21242; Guizhou Province, Duyun city, 25°36'81"N, 107°16'25"W, 1224 m, 2 May 2022, on *Rhamnus globosa*, Y.J. Sun, HGUP21243.

Notes – *Rhamnus globosa* is an alternate host for the aecial stage of *Puccinia coronata* (Zhuang et al. 1998). However, our specimens did not group with *P. coronata* in the phylogenetic analyses, and the two species differ by smaller aecidioid teliospores (30–67 × 12–23 µm) in morphology (Zhuang et al. 1998). Phylogenetically, our specimens formed an independent clade with high support (Fig. 1), and distant to the other species. *Endophyllum rhamnusii-globosae* has smaller aecidioid teliospores than *E. dichroae* (23–35 × 18–22 µm) and *E. elytropappi* (25.5–26 × 20.5–21 µm) (Wood & Crous 2005, Zhuang et al. 2012).

Endophyllum dichroae Racib., Bull. int. Acad. Sci. Lett. Cracovie, Cl. sci. math. nat. Sér. B, sci. nat. 3: 274 (1909) Fig. 16

MycoBank number: MB178778

Description – *Spermogonia*, *uredinia* and *aecia* not found. *Aecidioid telia* produced on the abaxial leaf surface, scattered, not surrounded by host epidermis, obvious boundary, roestelioid, 0.5–1.5 mm diam., peridium dehiscent at apex, no slits along the sides, yellow. *Aecidioid teliospores* ellipsoidal or irregular, 21–28 × 19–24 µm (x̅ = 24.6 × 21.4 µm, n = 30), inclusions light yellow; wall 1.8–2.6 µm thick, colorless, rugose.

Host – *Dichroa febrifuga* (Hydrangeaceae).

Material examined – CHINA, Guizhou Province, Panzhou city, 25°61′29″N, 104°82′39″W, 1893 m, 2 Aug 2022, on *Dichroa febrifuga*, J.E. Sun, HGUP21237, HGUP21238.

Notes – *Endophyllum dichroae* was described on an unknown host by Raciborski (1909b), with large aecidioid teliospores (28–38 × 18–20 µm). Our specimens formed a branch with high support rate. When comparing our specimens with the description of Zhang et al. (2012) of *E. dichroae* on the same host plant, the aecidioid teliospores are similar in size (21–28 × 19–24 µm *vs.* 23–35 × 18–22 µm) in morphology. We, therefore, name our collections as *E. dichroae*.

Endophyllum elaeagni-latifoliae (Petch) Gokhale, Thirum. & Patel, Current Science 24 (4): 126 (1955) Fig. 17

MycoBank number: MB297184

Description – *Spermogonia*, *uredinia* and *aecia* not found. *Aecidioid telia* produced on abaxial leaf surface, scattered, obvious boundary, roestelioid, 2.0–6.0 mm diam., peridium dehiscent at apex, no slits along the sides, brown-black. *Aecidioid teliospores* ellipsoidal or oblong to irregular, 20–30 × 14–20 µm (x̅ = 22.2 × 16.9 µm, n = 30), inclusions pale white to yellow; wall 1.4–2.0 µm thick, colorless, verrucose.

Host – *Elaeagnus pungens* (Elaeagnaceae).

Material examined – CHINA, Guizhou Province, Guiyang city, 26°65'86"N, 106°67'42"W, 1213 m, 21 Aug 2021, on *Elaeagnus pungens*, J.E. Sun, HGUP21217.

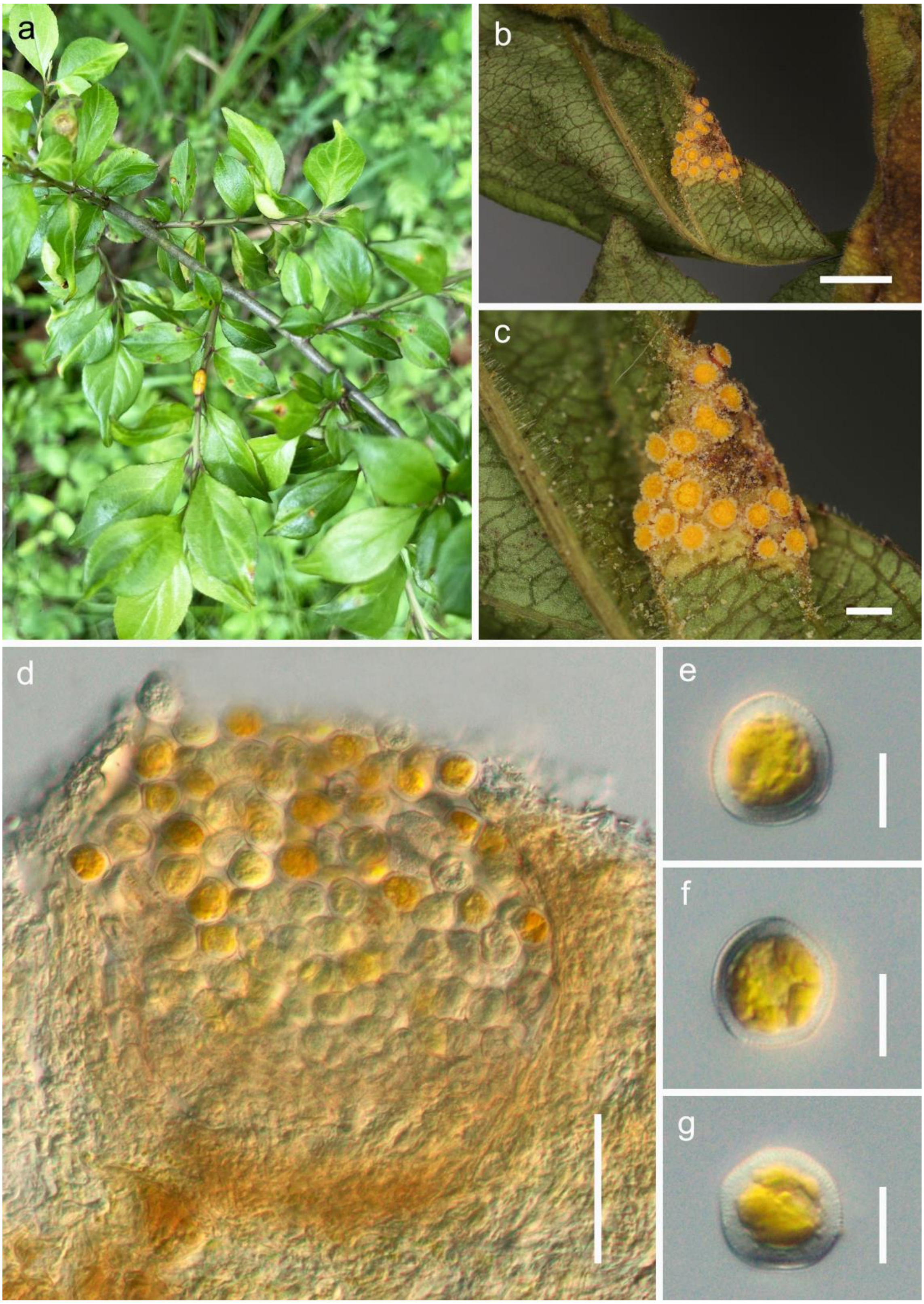

Figure 15 – *Endophyllum rhamnusii-globosae* (from holotype HGUP21242) on *Rhamnus globosa*. a–c Aecidioid telia on leaves. d Longitudinal section of aecidioid telium. e–g Aecidioid teliospores. Scale bars: b = 2 mm, c = 0.5 mm, d = 50 µm, e–g = 12.5 µm.

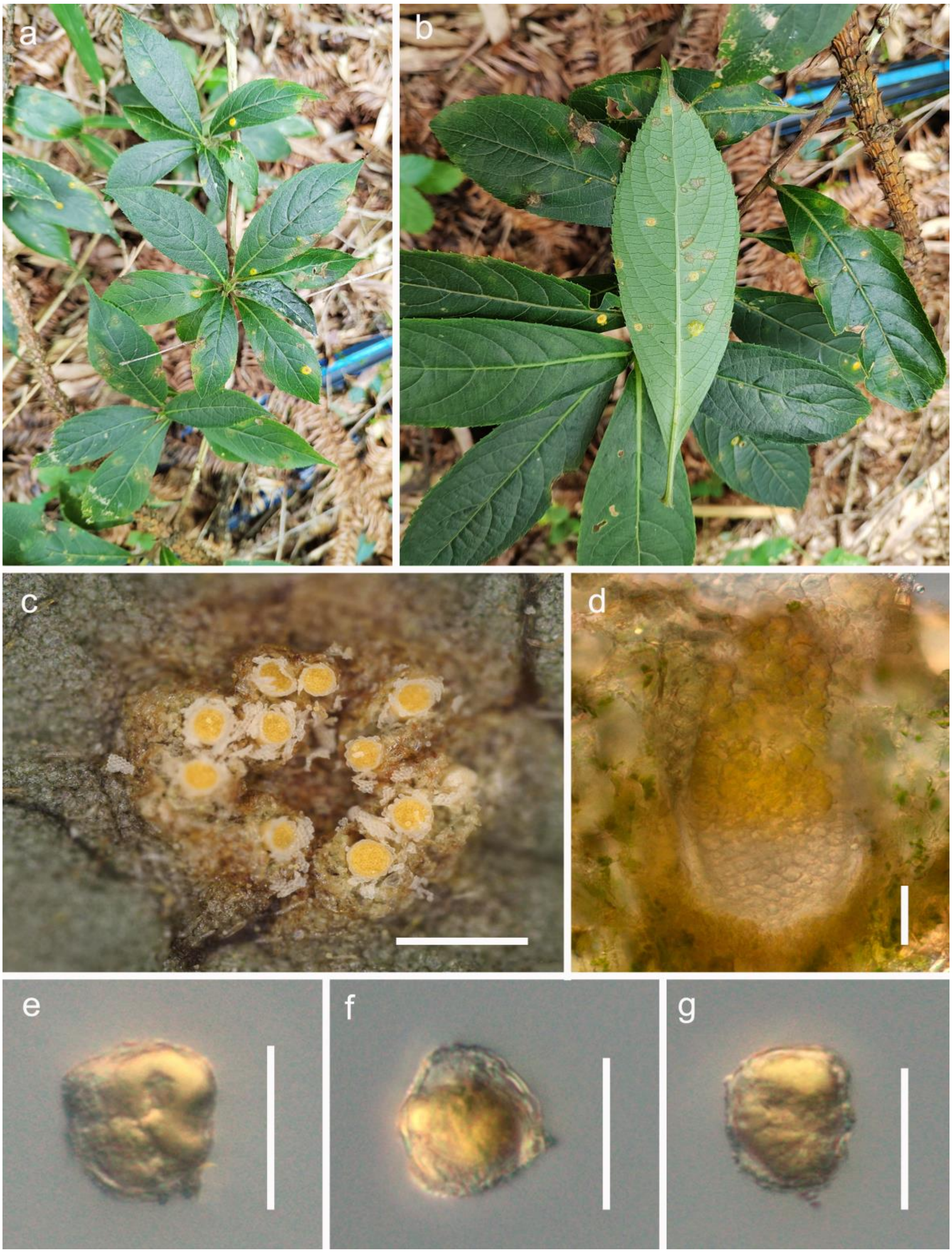

Figure 16 – *Endophyllum dichroae* (HGUP21237) on *Dichroa febrifuga*. a–c Aecidioid telia on leaves. d Longitudinal section of aecidioid telium. e–g Aecidioid teliospores. Scale bars: c = 0.5 mm, d = 50 µm, e–g = 25 µm.

Notes – The telial stage of *Endophyllum elaeagni-latifoliae* and *Puccinia elaeagni* were described on *Elaeagnus* sp. (Zhuang et al. 2003, 2012), although unfortunately with no molecular data. When comparing our specimen with the description of *E. elaeagni-latifoliae*, they are similar in morphology (aecidioid teliospores: 17–25 × 14–20 µm; wall: 1.5–2.0 µm) (Zhuang et al. 2012). We, therefore, confirm our specimen as *E. elaeagni-latifoliae*, through morphological characters, and provide its nucleotide data.

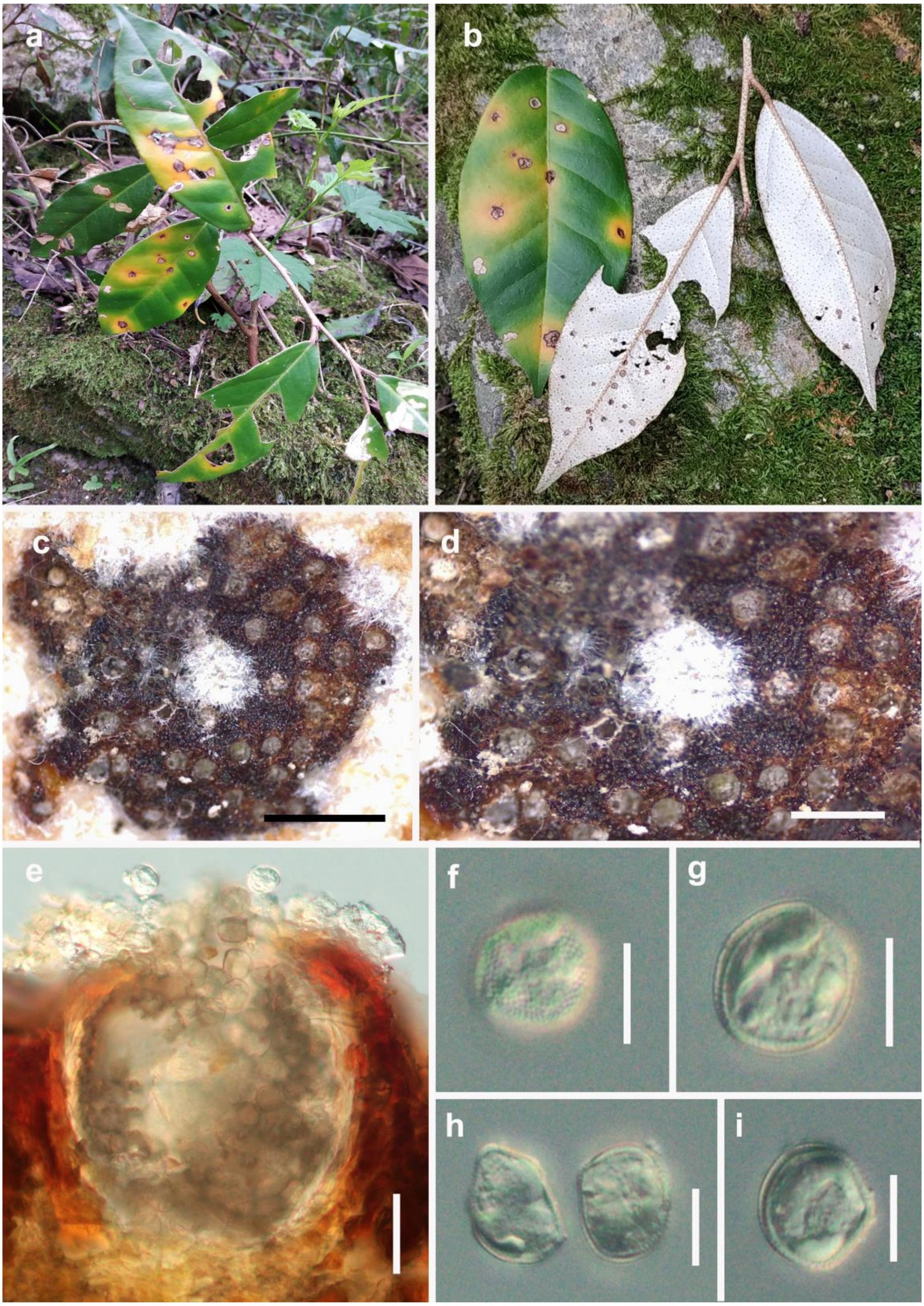

Figure 17 – *Endophyllum elaeagni-latifoliae* (from HGUP21217) on *Elaeagnus pungens*. a–d Aecidioid telia on leaves. e Longitudinal section of aecidioid telium. f–i Aecidioid teliospores. Scale bars: c = 2 mm, d = 1 mm, e = 50 µm, f–i = 12.5 µm.

Macruropyxis Azbukina, Misc. Rep. Res. Inst. nat. Resour., Tokyo: 20 (1972).

Macruropyxis diversii J.E. Sun, Yong Wang bis & K.D. Hyde, sp. nov. Figs 18, 19

Index Fungorum number: IF901294; Facesoffungi number: FoF15361

Etymology – Name reflects the diverse hosts, *Epipremnum aureum* and *Paederia foetida*, from which the type specimen was collected.

Holotype – HGUP21255

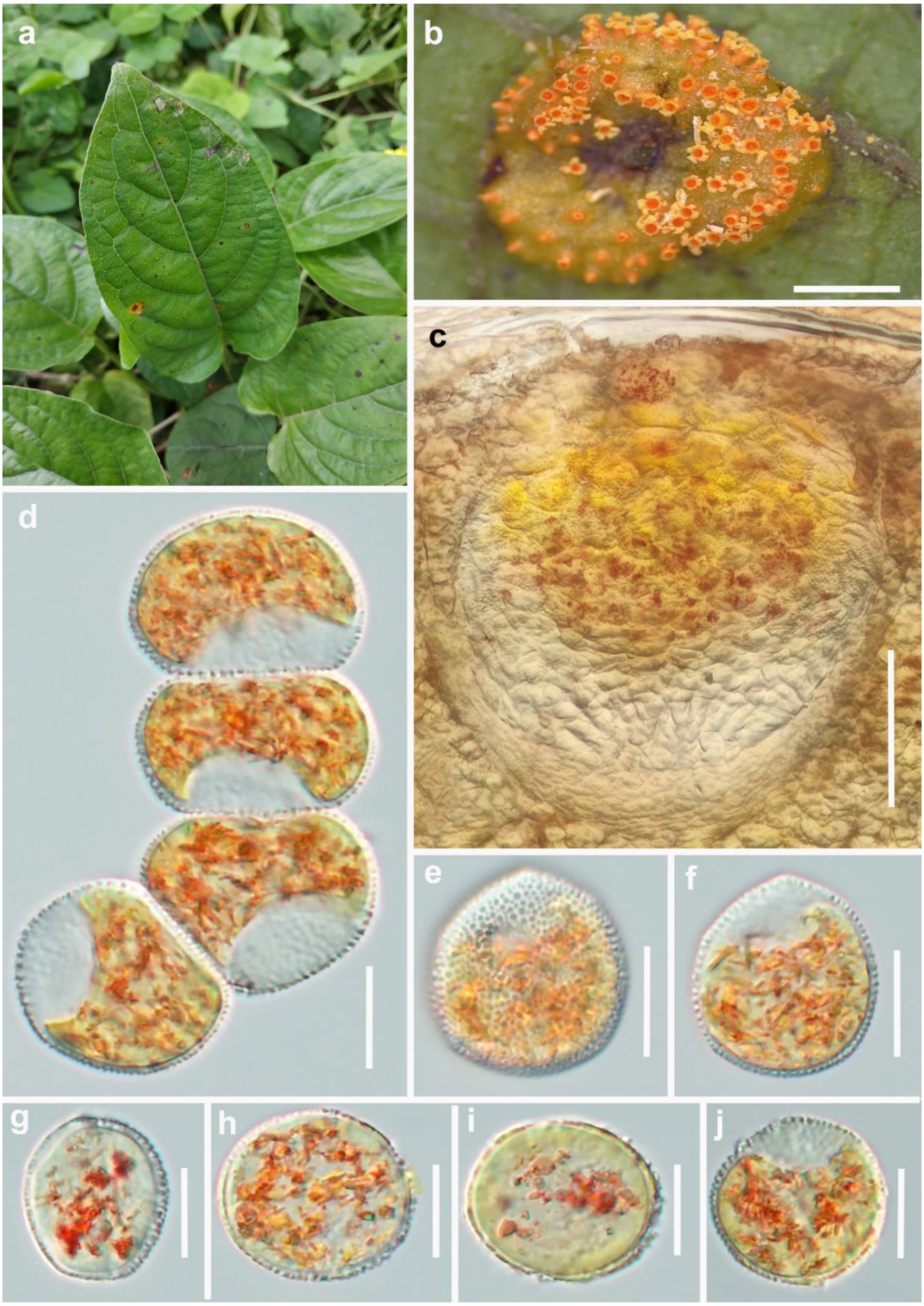

Figure 18 – *Macruropyxis diversii* (from holotype HGUP21255) on *Epipremnum aureum*. a–b Aecia on leaves. c Longitudinal section of aecium. d–j Aeciospores. Scale bars: b = 2 mm, c = 50 µm, d–j = 10 µm.

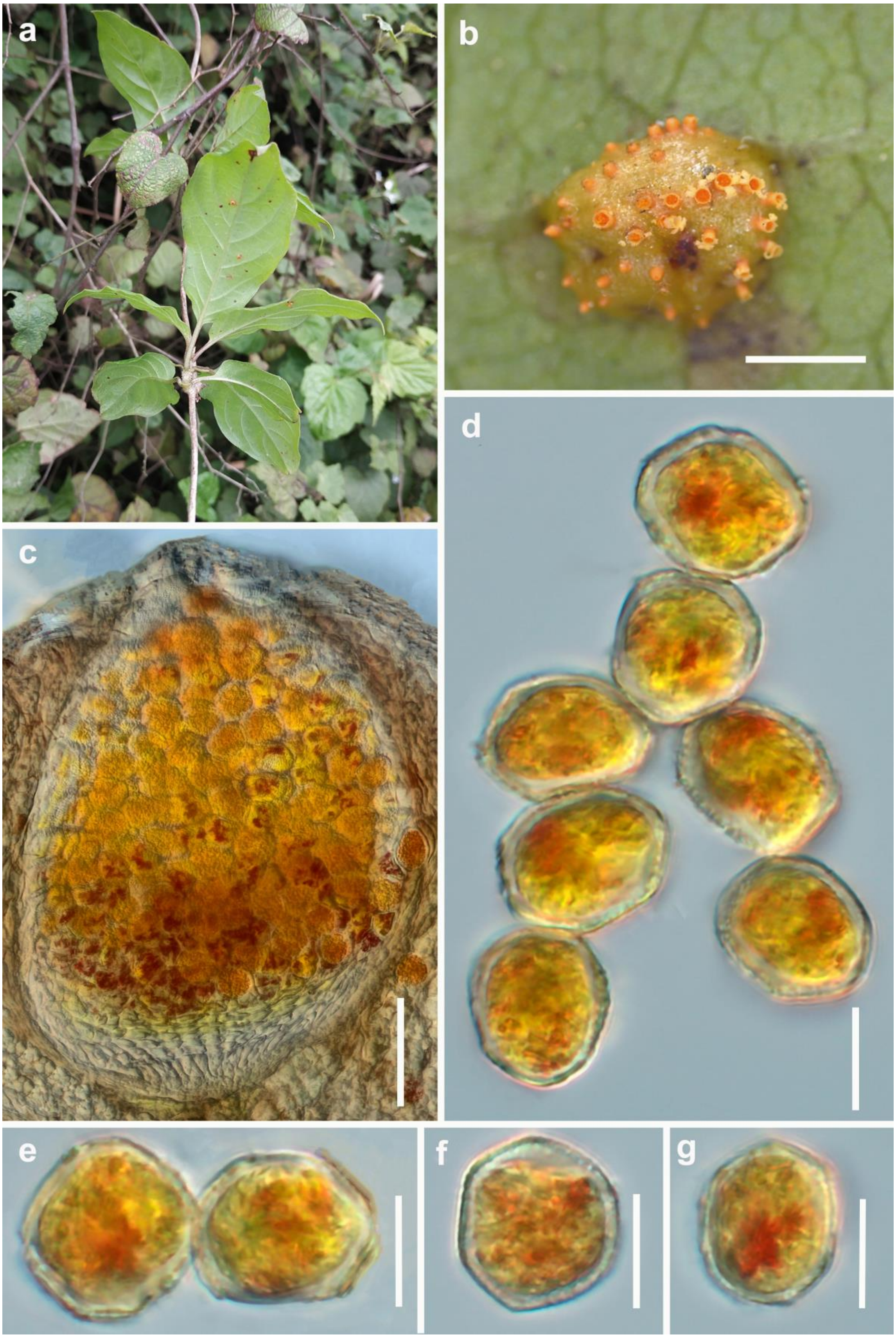

Figure 19 – *Macruropyxis diversii* (from HGUP21144) on *Paederia foetida*. a–b Aecia on leaves. c Longitudinal section of aecium. d–g Aeciospores. Scale bars: b = 5 mm, c = 50 µm, d–g = 10 µm.

Description – *Spermogonia*, *uredinia* and *telia* not found. *Aecia* produced on abaxial leaf surface, yellow or golden, 2.0–4.0 mm long, peridium dehiscent at apex, no slits along the sides.

Aeciospores 17–22 (15–18) × 14–20 (11–14) µm (x̅ = 18.1 × 16.2 µm, n = 30), globose or oval, yellow or golden with light brownish red; wall 0.7–1.2 (1.2–1.7) µm thick, colorless, densely and minutely echinulate. forming a golden sphere, faint yellow to golden, 1.0–1.5 mm diam, peridium dehiscent at apex.

Hosts – *Epipremnum aureum* (Araceae), *Paederia foetida* (Rubiaceae)

Material examined – CHINA, Guizhou Province, Guiyang city, 26°44'75"N, 106°58'69"W, 1001 m, 3 May 2021, on *Epipremnum aureum*, J.E. Sun, holotype HGUP21255; Guizhou Province, Zunyi city, 27°66'54"N, 107°52'97"W, 792 m, 14 May 2021, on *E. aureum*, J.E. Sun, HGUP21256; Guiyang city, 26°44'74"N, 106°58'68"W, 980 m, 3 May 2021, on *Paederia foetida*, J.E. Sun, HGUP21144; Guiyang city, 26°45′20″N, 106°65′60″W, 1110 m, 6 May 2022, on *P. foetida*, J.E. Sun, HGUP21142, HGUP21143.

Notes – The specimens on *Epipremnum aureum* (HGUP21255, HGUP21256) have slightly wider aeciospores than those on *Paederia foetida* (HGUP21142, HGUP21143, HGUP21144) (14–20 µm *vs.* 11–14 µm). However, phylogenetic analyses showed that all five specimens separated into one branch with a high support rate (Fig. 1). The comparison of DNA base composition supports the five specimens are likely to be the same species (1/478 in ITS and 1/572 in LSU). Moreover, they kept a distant relationship with *Macruropyxis fulva* (rust isolates M9 and P7) (Martin et al. 2017). Although without the description of morphological characteristics of aeciospores for *M. fulva*, we introduce our specimens as new to science, by phylogenetic analyses with nucleotide data from Martin et al. (2017).

Uromyces (Link) Unger, Exanth. Pflanzen (Wien): 277 (1833)

Uromyces viciae-fabae (Pers.) J. Schröt., Hedwigia 14: 98 (1875) Fig. 20

MycoBank number: MB281700

Description – *Spermogonia* and *aecia* not observed. *Uredinia* and *telia* produced on abaxial leaf surface, stems and petioles, powdery, surrounding by host epidermis, pulverulent, cinnamon-brown, 1.0 × 2.5 mm diam. *Urediniospores* 26–38 × 19–31 µm (x̅ = 32.5 × 25.5 µm, n = 30), globose, ellipsoidal, or obovoid, colorless to light brown; wall 1.4–3.1 µm thick, colorless to pale brown. *Teliospores* aseptate, 30–43 × 16–27 µm (x̅ = 38.5 × 21.5 µm, n = 30), oval or subglobose, pale brown, brown to honey-brown, wall 0.5–2.1 µm thick, colorless, echinulate. Pedicel 18–57 µm long, colorless to pale brown.

Host – *Vicia faba* (Fabaceae), broad bean (common name).

Material examined – CHINA, Guizhou Province, Guiyang city, 27°30'75"N, 106°98'11"W, 865 m, 9 Apr 2021, on *Vicia faba*, J.E. Sun, HGUP21122, HGUP21123; Guiyang city, 26°64'84"N, 106°18'27"W, 1287 m, 29 Apr 2022, on *V. faba*, J.E. Sun, HGUP21124; Zunyi city, 27°40'24"N, 106°24'44"W, 1092 m, 30 Apr 2022, on *V. faba*, J.E. Sun, HGUP21125, HGUP21126.

Notes – Based on the phylogenetic tree, the collected specimens gathered in one branch of *U. viciae-fabae*, the node support rate was (ML/MP/BI=57/-/-; (Fig. 1)), and the genetic distance was almost 0, indicating that the five specimens were *U. viciae-fabae*. Morphologically, the five specimens match *U. viciae-fabae* as described by Zhuang et al. (2003). Thus, we named our specimens as *U. viciae-fabae.*

Uromyces trifolii-repentis (Castagne) Liro, Acta Soc. Fauna Flora fenn. 29(no. 6): 11 (1906) [1906-1908] Fig. 21

MycoBank number: MB203477

Description – *Spermogonia* and *aecia* not observed. *Uredinia* and *telia* produced on abaxial leaf surface, powdery, surrounding by host epidermis, pulverulent, cinnamon-brown, 0.5–1.0 mm diam. *Urediniospores* globose to oval, or subglobose, 22–27 × 19–26 µm (x̅ = 24.8 × 21.5 µm, n = 30), inclusions pale brown, to cinnamon-brown; wall 1.0–1.9 µm thick, pale brown, echinulation. *Teliospores* aseptate, 23–28 × 17–23 µm (x̅ = 24.7 × 19.9 µm, n = 30), oval, honey-brown to brown; wall smooth, 1.4–2.5 µm thick, cinnamon-brown; pedicel 19–39 µm long, colorless to pale brown.

Host – *Trifolium repens* (Fabaceae).

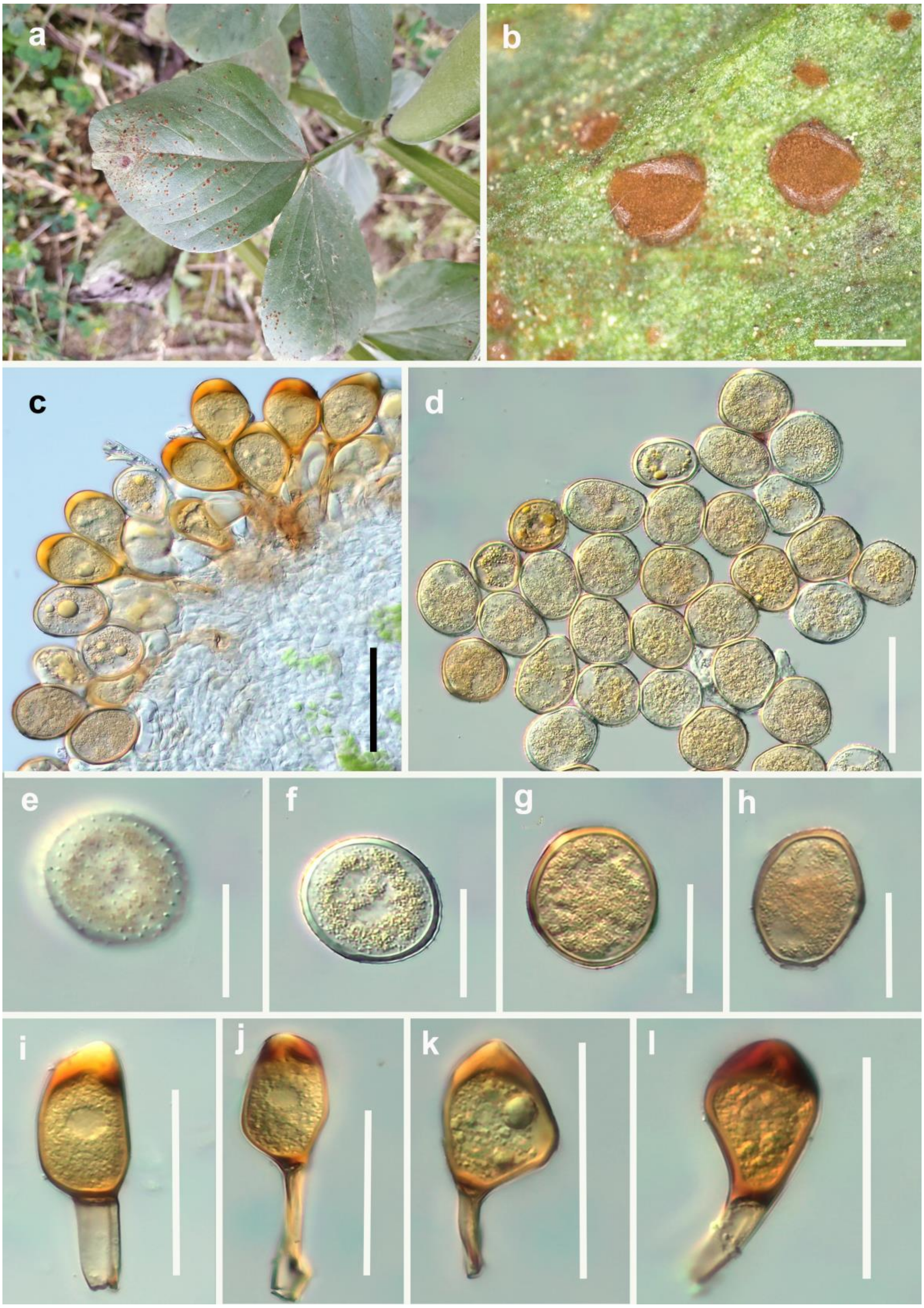

Figure 20 – *Uromyces viciae-fabae* (from HGUP21122) on *Vicia faba.* a–b Uredinia and telia on leaves. c Longitudinal section of uredinium and telium. d–h Urediniospores. i–l Teliospores. Scale bars: b = 2 mm, c–d, i–l = 25 µm, e–h = 12.5 µm.

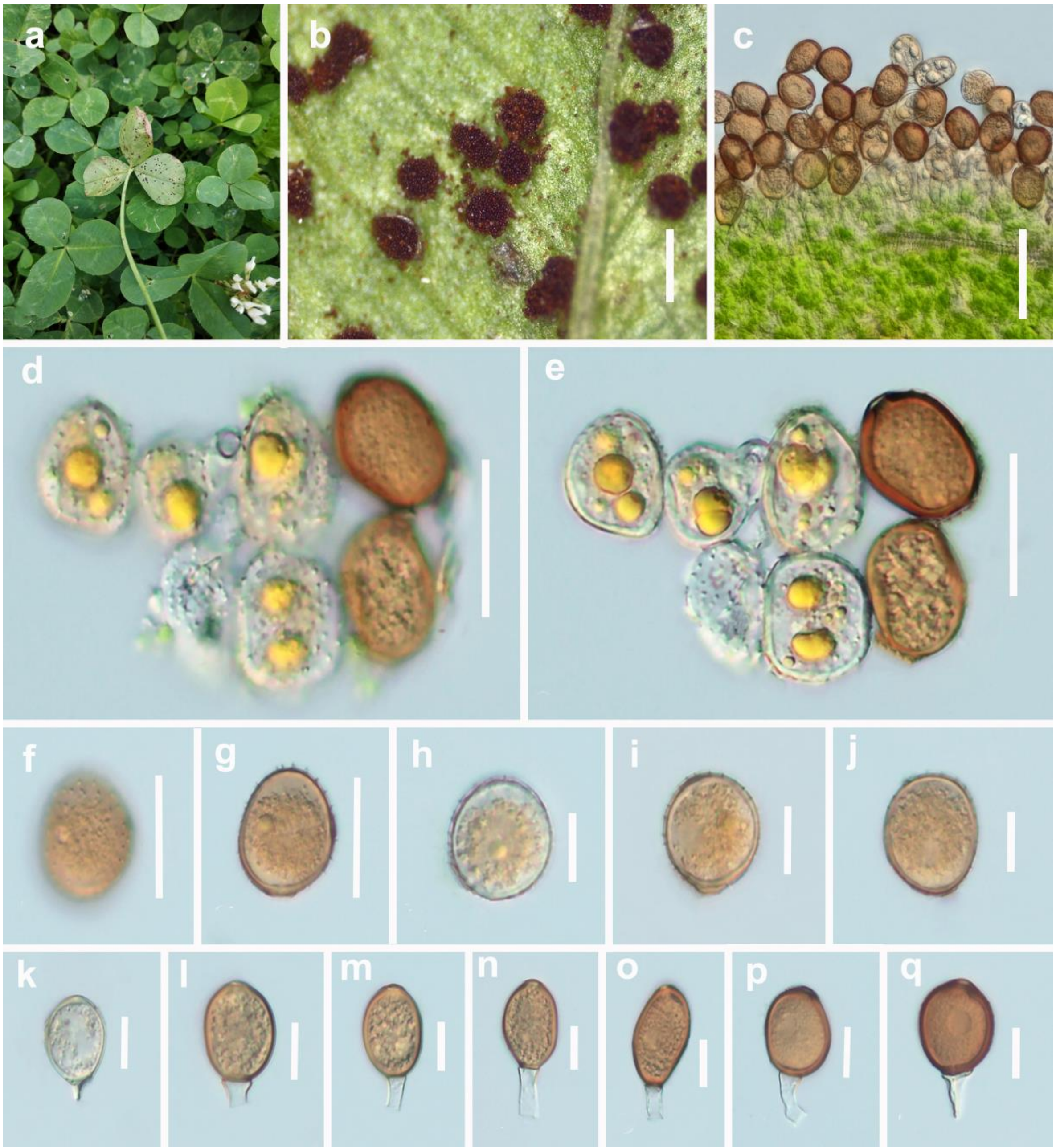

Figure 21 – *Uromyces trifolii-repentis* (HGUP21127) on *Trifolium repens*. a–b Uredinia and telia on leaves. c Longitudinal section of uredinium and telium. d–j Urediniospores. k–q Teliospores. Scale bars: b = 1 mm, c = 50 µm, d–q = 25 µm.

Material examined – CHINA, Guizhou Province, Bijie city, 27°06'87"N, 105°24'29"W, 1201 m, 21 Mar 2021, on *Trifolium repens*, J.E. Sun, HGUP21127; Guiyang city, 26°41'55"N, 106°66'82"W, 1135 m, 11 May 2021, on *T. repens*, J.E. Sun, HGUP21128, HGUP21129.

Notes – Phylogenetic investigations revealed that our collections and *Uromyces trifolii-repentis* gathered in one branch, and the node support rate was (ML/MP/BI=84/66/-; Fig. 1). Morphological characters of urediniospores and teliospores from our specimens are similar to *U. trifolii-repentis* as described by Zhuang et al. (2003). Hence, based on both morphology and phylogeny, we identify our specimens as *U. trifolii-repentis*.

Uromyces vignae Barclay, J. Asiat. Soc. Bengal, Pt. 2, Nat. Sci. 60: 211 (1891) Fig. 22

MycoBank number: MB231908

Description – *Spermogonia* and *aecia* not found. *Uredinia* and *telia* produced on abaxial leaf surface, powdery, surrounding by host epidermis, pulverulent, cinnamon-brown, 0.5–1.5 mm diam. *Urediniospores* globose to oval, or subglobose, 22–27 × 19–26 µm (x̅ = 24.5 × 23.3 µm, n = 30), inclusions light brown, to cinnamon-brown; wall 1.0–1.9 µm thick, light brown, echinulate. *Teliospores* aseptate, 27–35 × 22–28 µm (x̅ = 30.5 × 24.8 µm, n = 30), oval, honey-brown to chocolate-brown; wall smooth, 1.7–3.4 µm thick, chocolate-brown; pedicel 19–39 µm long, colorless to pale brown.

Host – *Phaseolus vulgaris* (Fabaceae)

Material examined – CHINA, Guizhou Province, Guiyang city, 27°4409'26"N, 106°98'90"W, 724 m, 22 Jun, 2021, on *Phaseolus vulgaris,* J.E. Sun, HGUP21131; Panzhou city, 25°89'60"N, 104°84'32"W, 802 m, 19 Jul 2021, on *P. vulgaris,* J.E. Sun, HGUP21130; Zunyi city, 27°66'44"N, 106°41'45"W, 1105 m, 10 Jun 2022, on *P. vulgaris*, J.E. Sun, HGUP21132; Guiyang city, 26°97'94"N, 106°44'96"W, 1145 m, 25 Jun, 2022, on *P. vulgaris*, J.E. Sun, HGUP21133; Bijie city, 25°16'40"N, 105°65′05″W, 1503 m, 4 Aug 2022, on *P. vulgaris*, J.E. Sun, HGUP21134.

Notes – Our specimens collected from kidney beans and *U. vignae* (single spore rust of bean) gathered together in the phylogenetic analysis (Fig. 1). Moreover, upon a detailed comparison of our specimens and the description of *U. vignae* in Zhuang et al. (2003), The morphological similarities were not significant. Based on these findings, we name our collections as *U. vignae*.

Uromyces vignae-sinensis Miura, Flora of Manchuria and East Mongolia, III Cryptogams, Fungi (Industr. Contr. S. Manch. Rly 27): 268 (1928) Fig. 23

MycoBank number: MB255386

Description – *Spermogonia* and *aecia* not found. *Uredinia* and *telia* produced on abaxial leaf surface, powdery, surrounding by host epidermis, powdery, cinnamon-brown, 0.5–1.0 mm diam. *Urediniospores* globose to oval, or subglobose, 21–27 × 17–23 µm (x̅ = 23.5 × 19.3 µm, n = 30), inclusions light brown to cinnamon-brown; wall 1.0–2.0 µm thick, cinnamon, echinulate. *Teliospores* aseptate, 25–33 × 21–27 µm (x̅ = 28.8 × 24.3 µm, n = 30), oval, honey-brown to chocolate-brown; wall smooth, 1.5–2.7 µm thick, chocolate-brown; pedicel 17-35 µm long, colorless to pale brown.

Host – *Vigna unguiculata* (Fabaceae)

Material examined – CHINA, Guizhou Province, Tongren city, 28°16'04"N, 108°33'47"W, 805 m, 4 Sep 2021, on *Vigna unguiculata*, J.E. Sun, HGUP21135, HGUP21136.

Notes – *Uromyces vignae-sinensis* was initially identified as the cowpea monospora rust, but unfortunately, we were unable to obtain nucleotide data for comparison. Therefore, our specimens formed an independent branch in the phylogenetic analysis. When compared with the description of Zhuang et al. (2003), our specimens are similar to the urediniospores and teliospores of *U. vignae-sinensis*. Therefore, we name the collections as *U. vignae-sinensis*.

Uromyces bidenticola Arthur, Mycologia 9 (2): 71, 1917 Fig. 24

MycoBank number: MB101940

Description – *Spermogonia*, *telia* and *aecia* not found. *Uredinia* produced on abaxial leaf surface, pulverulent, surrounded by host epidermis, cinnamon-brown, 0.5–1.0 mm diam. *Urediniospores* globose to oval, or subglobose, 21–28 × 17–22 µm (x̅ = 25.2 × 19.5 µm, n = 30), inclusions colorless or light-brown to cinnamon-brown; wall 1.5–2.2 µm thick, colorless to cinnamon, echinulate.

Host – *Bidens pilosa* (Asteraceae)

Material examined – CHINA, Guizhou Province, Liupanshui city, 26°34'46"N, 104°48'25"W, 1850 m, 25 Sep 2021, on *Bidens pilosa*, J.E. Sun, HGUP21037.

Notes – In the phylogenetic analysis, our specimen and *Uromyces bidenticola* (Bidens bipinnata monospora rust) clustered together with robust bootstrap support (Fig. 1). The morphological characteristics of our collection are similar to the description by Zhuang et al. (2003). We, therefore, propose our collections as *U. bidenticola*.

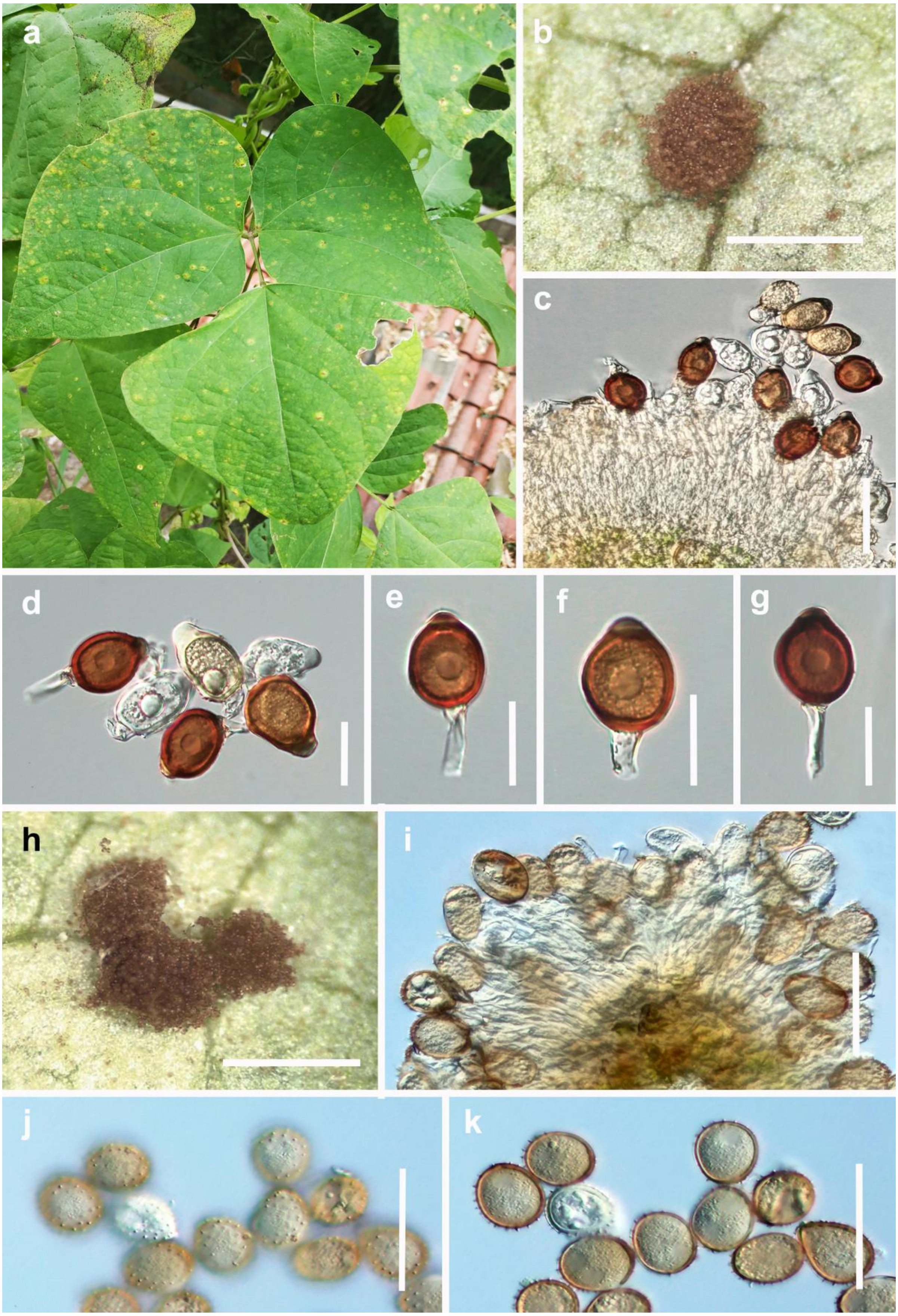

Figure 22 – *Uromyces vignae* (from HGUP21130) on *Phaseolus vulgaris*. a–b Telia on leaves. c Longitudinal section of telium. d–g Teliospores. h Uredinia on leaves. i Longitudinal section of uredinium. j–k Urediniospores. Scale bars: b, h = 1 mm, c = 50 µm, d–g, i–k = 25 µm.

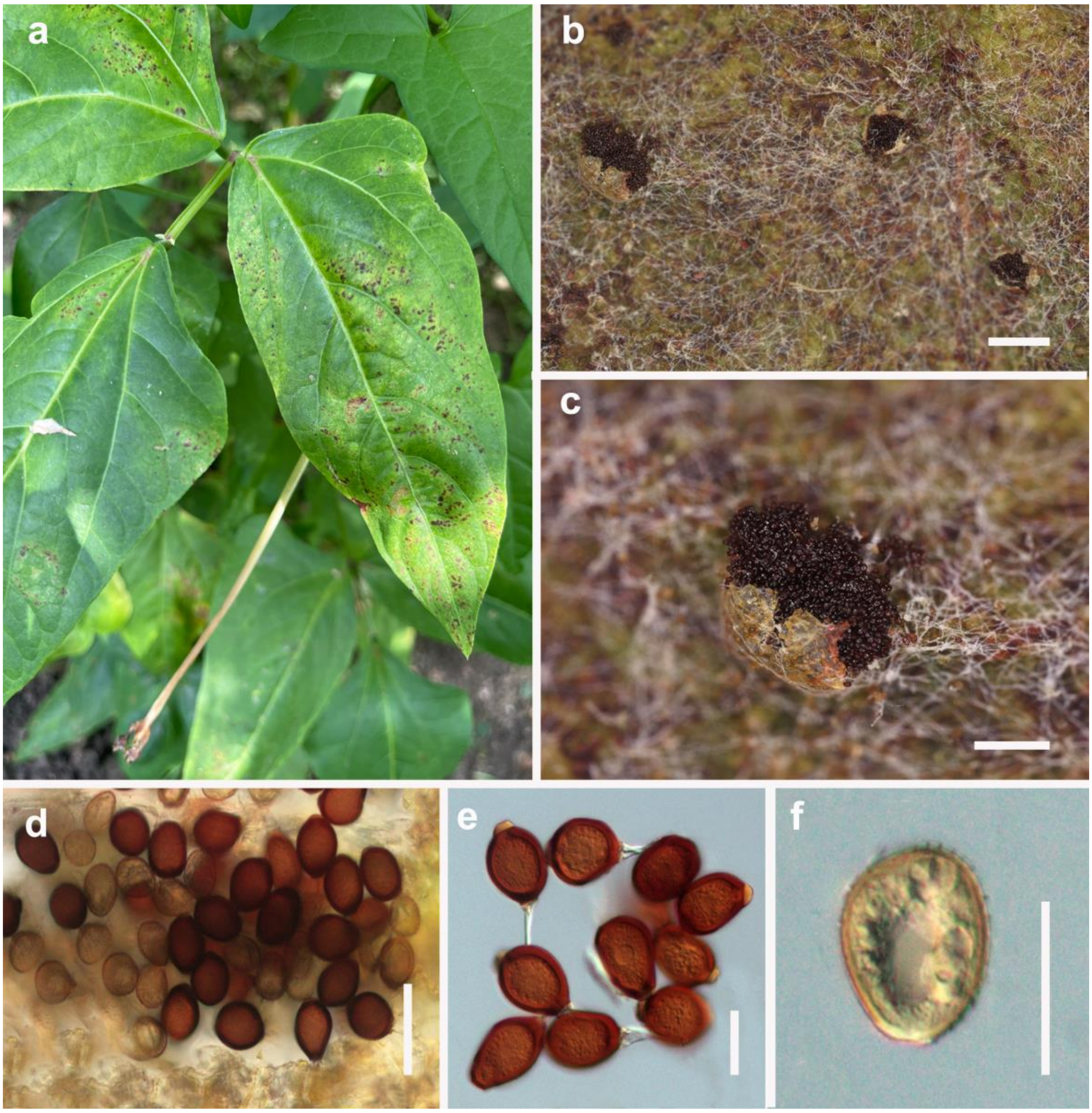

Figure 23 – *Uromyces vignae-sinensis* (from HGUP21135) on *Vigna unguiculata*. a–c Telia and uredinia on leaves. d Longitudinal section of telium and uredinium. e Teliospores. f Urediniospore. Scale bars: b = 1 mm, c = 0.5 mm, d = 50 µm, e–f = 25 µm.

Puccinia Pers., Synopsis methodica fungorum: 225 (1801)

Puccinia ipomoeae-nilii J.E. Sun, Yong Wang bis & K.D. Hyde, sp. nov. Fig. 25

Index Fungorum number: IF901295; Facesoffungi number: FoF15362

Etymology – Name reflects the host *Ipomoea nil*, from which the type specimen was collected.

Holotype – HGUP21178

Description – *Spermogonia*, *aecia* and *telia* unknown. *Uredinia* produced on abaxial leaf surface, surrounded by host epidermis, oblong or oval, chocolate-brown spot, pulverulent, 1.0–1.5 mm diam. *Urediniospores* globose, ellipsoidal, or fusiform, 24–30 × 19–23 µm ($\bar{x}$ = 26.8 × 20.5 µm, n = 30), pale to light brown, brown; wall 1.4–2.0 µm thick, colorless, densely, and minutely echinulate.

Host – *Ipomoea nil* (Convolvulaceae)

Material examined – CHINA, Guizhou Province, Duyun city, 27°26'05"N, 107°38'91"W, 842 m, 23 Jun 2021, on *Ipomoea nil*, J.E. Sun, holotype HGUP21178; Guizhou Province, Duyun city, 27°26'05"N, 107°38'91"W, 842 m, 23 Jun 2021, on *I. nil*, J.E. Sun, HGUP21179; Guizyang city, 26°43'75"N, 106°67′79″W, 1110 m, 24 May 2021, on *I. nil*, J.E. Sun, HGUP21180.

Notes – Two *Puccinia* species, *P. convolvuli* and *P. heitoensis*, have been described on Convolvulaceae (Zhuang et al. 2005). In phylogeny, our specimens were in an independent branch with support (Fig. 2). *Puccinia ipomoeae-nilii* show 98.76% (321/325 bp including 1 bp of gaps) and 67.25% (267/397 bp) sequence similarity with *P. convolvuli* of ITS and LSU sequences, respectively. The urediniospores of *P. ipomoeae-nilii* are morphologically similar to those of *P. convolvuli* although the urediniospore wall of *P. convolvuli* is slightly thicker (1.4–2.0 µm *vs.* 2.0–3.0 µm) (Zhuang et al. 2005). Based on distinct phylogeny and morphology, *P. ipomoeae-nilii* is introduced as a novel taxon.

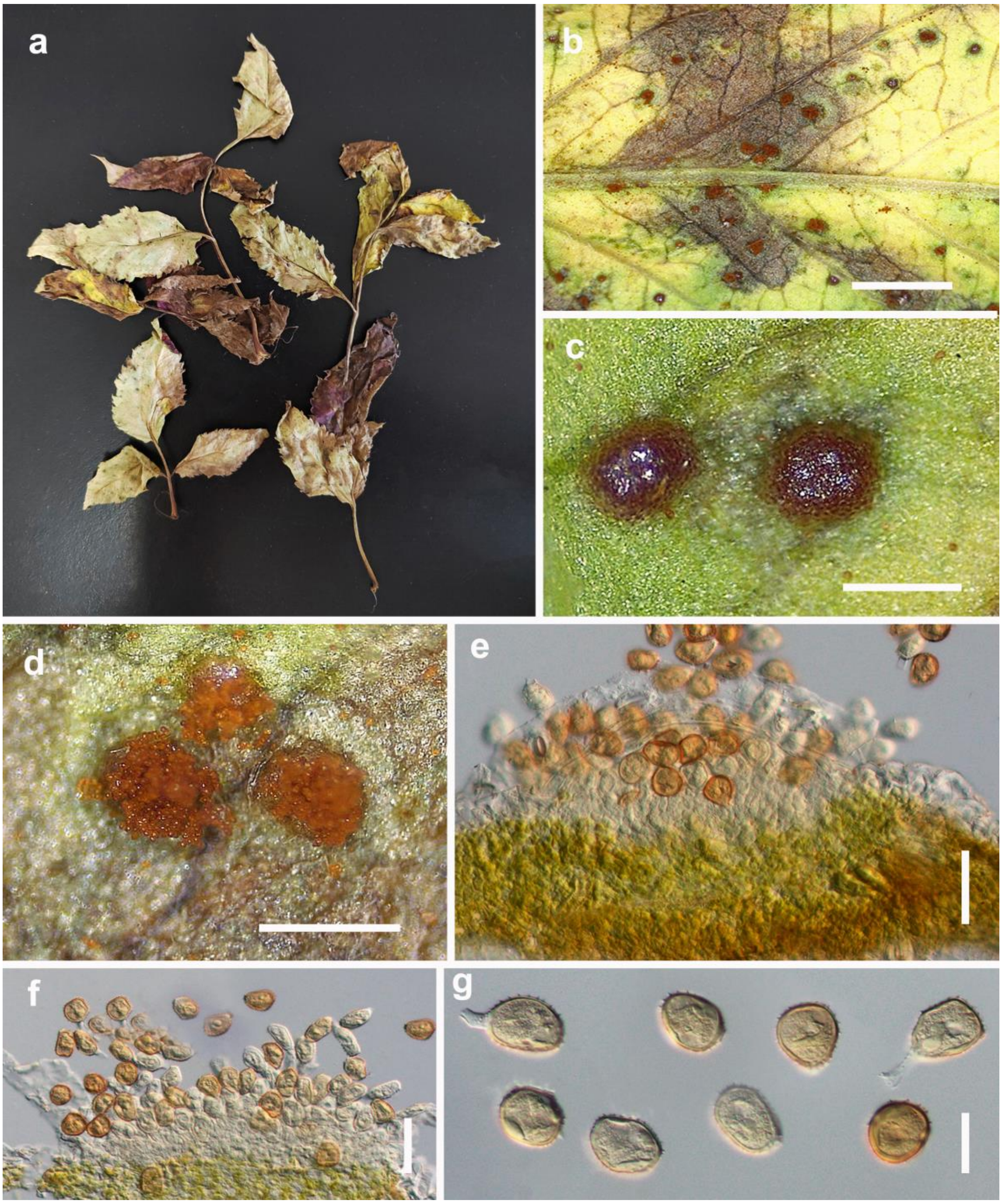

Figure 24 – *Uromyces bidenticola* (from HGUP21137) on *Bidens pilosa*. a–d Uredinia on leaves. e–f Longitudinal section of uredinia. g Urediniospores. Scale bars: b = 5 mm, c–d = 1 mm, e–f = 50 µm, g = 25 µm.

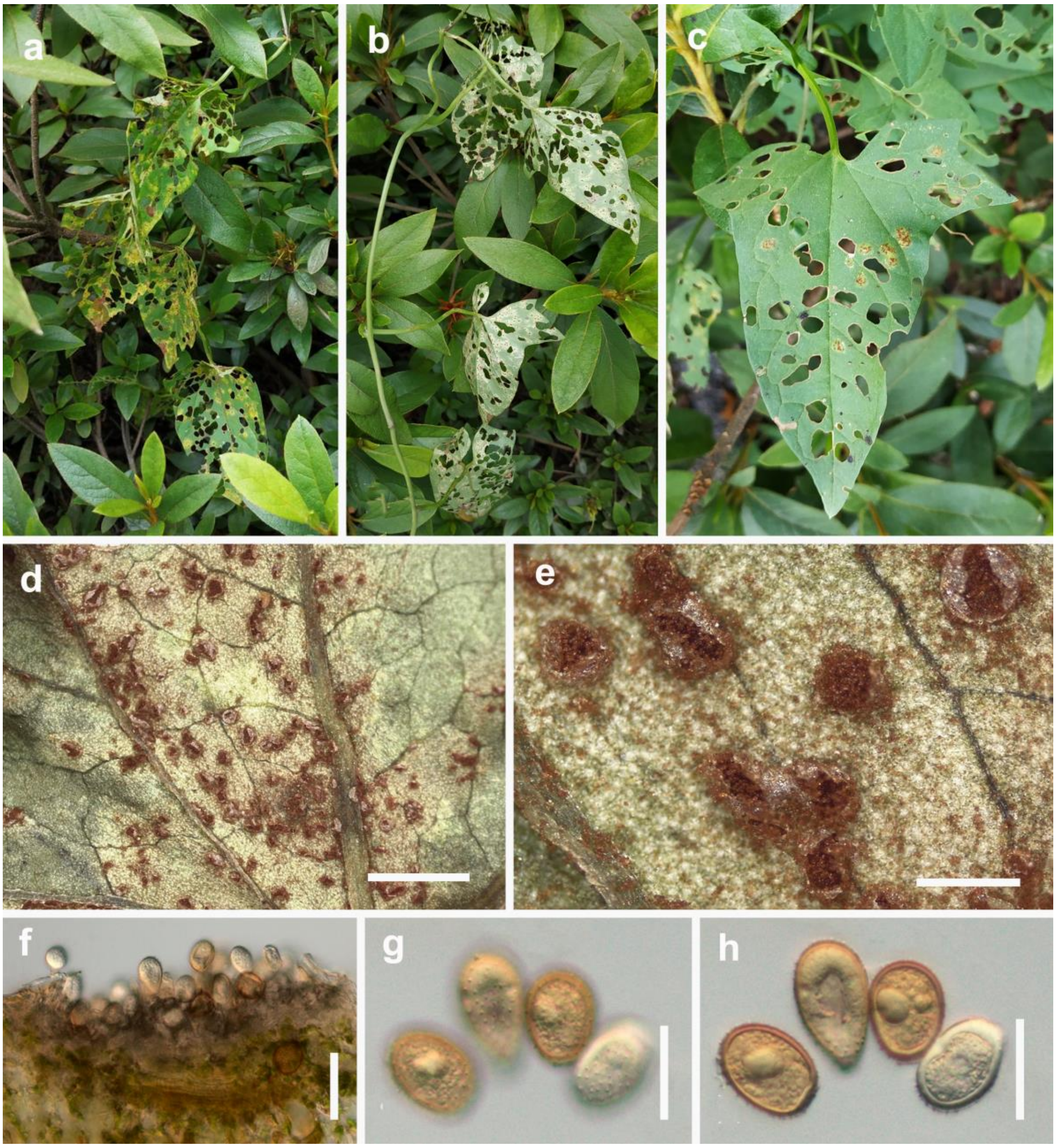

Figure 25 – *Puccinia ipomoeae-nilii* (from holotype HGUP21178) on *Ipomoea nil*. a–e Uredinia on leaves. f Longitudinal section of uredinium. g–h Urediniospores. Scale bars: d = 5 mm, e = 1 mm, f = 50 µm, g–h = 25 µm.

Puccinia indocalamuse-latifoliusii J.E. Sun, Yong Wang bis & K.D. Hyde, sp. nov.

Fig. 26

Index Fungorum number: IF901296; Facesoffungi number: FoF15385

Etymology – The name reflects the host *Indocalamus latifolius*, from which the type specimen was collected.

Holotype – HGUP21239

Description – *Spermogonia*, *aecia* and *telia* unknown. *Uredinia* produced on abaxial leaf surface, surrounded by host epidermis, oblong to oval, or irregular, light brown spot, pulverulent, 1.0–1.5 mm diam. *Urediniospores* globose or ovoid, 22–27 × 19–26 µm ($\bar{x}$ = 24.5 × 23.3 µm, n = 30), pale to light brown or brown, 1–3 equatorial germ pores; wall 1.0–2.0 µm thick, colorless, densely and minutely echinulate.

Host – *Indocalamus latifolius* (Bambusoideae, Poaceae)

Material examined – CHINA, Guizhou Province, Zunyi city, 27°66'53"N, 107°52'98"W, 780 m, 14 May 2021, on *Indocalamus latifolius*, J.E. Sun, holotype HGUP21239.

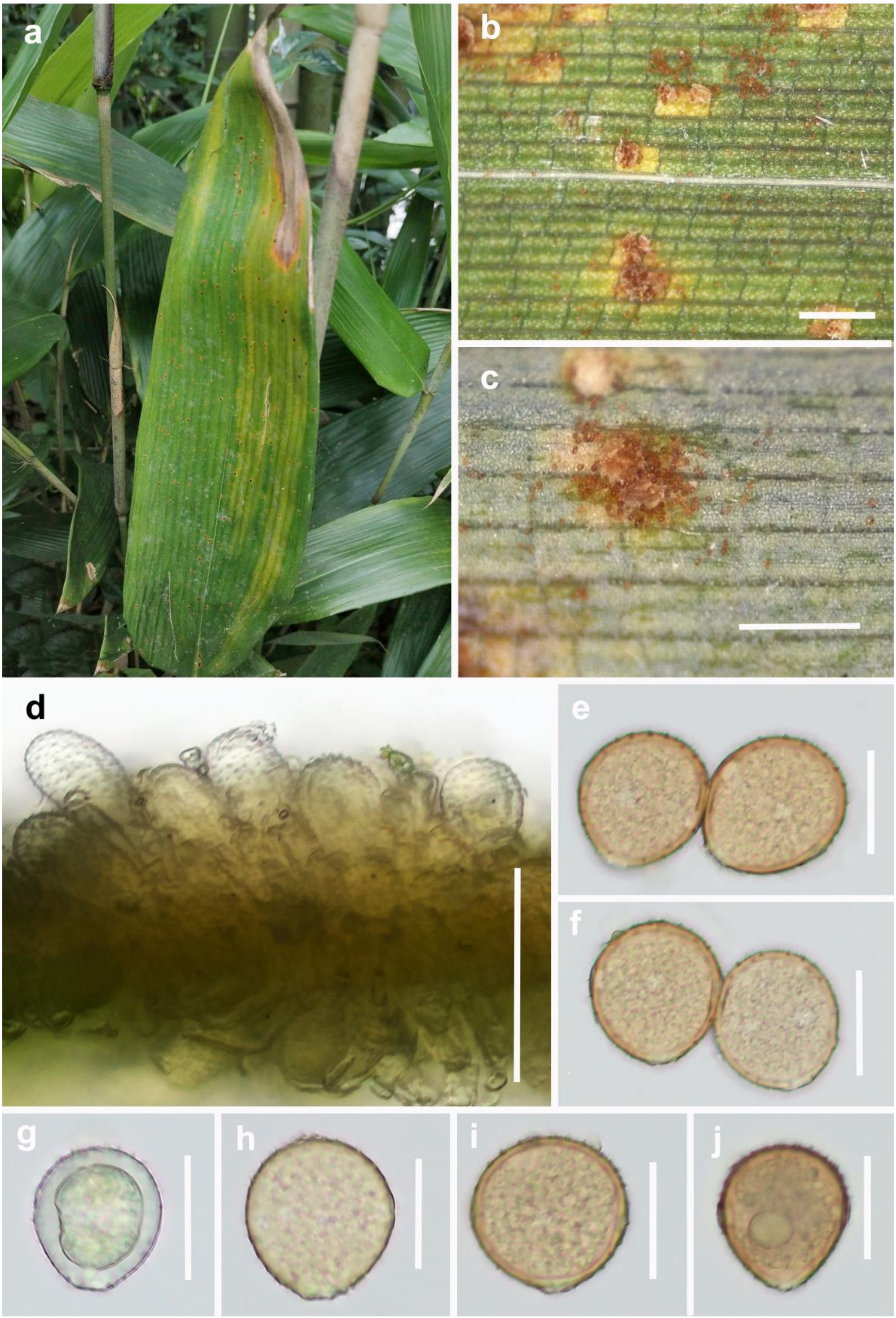

Figure 26 – *Puccinia indocalamuse-latifoliusii* (from holotype HGUP21239) on *Indocalamus latifolius*. a–c Uredinia on leaves. d Longitudinal section of uredinium. e–j Urediniospores. Scale bars: b = 5 mm, c = 1 mm, d = 50 µm, e–j = 25 µm.

Notes – Several *Puccinia* species occur on plants of the Bambusoideae subfamily. These species include *P. arundinis-donacis*, *P. bambusicola*, *P. lophatheri*, *P. phyllostachydis*, *P. polliniicola*, *P. sinarundinariae*, and *P. brachystachyicola*, as documented by Zhuang et al. (1998). In our phylogenetic analyses, a new species *P. indocalamuse-latifoliusii*, collected from *Indocalamus latifolius* (Bambusoideae), was found to be sister to *P. ipomoeae-nilii* (Fig. 2). Additionally, *P. indocalamuse-latifoliusii* can be differentiated from *P. arundinis-donacis* by its smaller urediniospores (22–27 × 19–26 µm *vs.* 26–34 × 14–21 µm). It has fewer germ pores than *P. lophatheri* (1–3 *vs.* 3–4), and smaller urediniospores than *P. phyllostachydis* (22–27 × 19–26 µm *vs.* 26–35 × 24–29 µm) with fewer germ pores (1–3 *vs.* 4–5). It differs from *P. polliniicola* in smaller urediniospores (22–27 × 19–26 µm *vs.* 28–38 × 23–30 µm) and fewer germ pores (1–3 *vs.* 4–6) (Zhuang et al. 1998). Therefore, we consider the new collection as a novel species.

Puccinia lolii-perennae J.E. Sun, Yong Wang bis & K.D. Hyde, sp. nov. Fig. 27

Index Fungorum number: IF901297; Facesoffungi number: FoF15363

Etymology – The name reflects the host *Lolium perenne*, from which the type specimen was collected.

Holotype – HGUP21240

Description – *Spermogonia*, *aecia* and *telia* unknown. *Uredinia* produced on the leaf surface and stems, adaxial, surrounded by host epidermis, ellipsoidal to elongate, golden, pulverulent, 1.0–2.0 mm diam. *Urediniospores* ellipsoidal, ovoid, or subglobose, 14–20 × 12–16 µm ($\bar{x}$ = 17.8 × 13.7 µm, n = 30), inclusions golden; wall 1.6–2.6 µm thick, colorless, regularly verrucose.

Host – *Lolium perenne* (Poaceae)

Material examined – CHINA, Guizhou Province, Guiyang city, 26°45'22"N, 106°65'65"W, 1013 m, 13 Jul 2021, on *Lolium perenne*, J.E. Sun, holotype HGUP21240; Guizhou Province, Duyun city, 26°45'88"N, 106°98'43"W, 854 m, 22 Jun 2021, on *L. perenne*, J.E. Sun, HGUP21241.

Notes – In the phylogenetic analysis, our specimens independently gathered in one branch, and the node support rate was (ML/MP/BI=99/95/-; Fig. 2), reflecting a relatively long genetic distance. The urediniospores of *P. loliume-perenneii* are smaller than those of *Puccinia coronata* (20–30 × 16–24 µm) and *P. graminis* (21–40 × 13–23 µm), which were reported from *Lolium* sp., *L. multiflorum* and *L. temulentum* (Zhuang et al. 1998). Therefore, *P. loliume-perenneii* is introduced as a new species.

Puccinia alopecuruse J.E. Sun, Yong Wang bis & K.D. Hyde, sp. nov. Fig. 28

Index Fungorum number: IF901298; Facesoffungi number: FoF15365

Etymology – The name reflects the host genus, *Alopecurus*, from which the type specimen was collected.

Holotype – HGUP21231

Description – *Spermogonia*, *aecia* and *telia* unknown. *Uredinia* hypophyllous, surrounded by host epidermis, ellipsoidal to oval, golden, pulverulent, 1.0–3.0 mm diam. *Urediniospores* ellipsoidal, ovoid, or subglobose, 21–28 × 16–21 µm ($\bar{x}$ = 23.8 × 18.5 µm, n = 30), inclusions pale or yellow to red; wall 2.1–2.6 µm thick, colorless.

Host – *Alopecurus aequalis* (Poaceae)

Material examined – CHINA, Guizhou Province, Guiyang city, 27°12'42"N, 107°13'48"W, 1082 m, 9 Apr 2021, on *Alopecurus aequalis*, J.E. Sun, holotype HGUP21231.

Notes – *Puccinia alopecuruse* is the first *Puccinia* species reported to be associated with *Alopecurus aequalis* (Cummins 1971, Zhuang et al. 1998). The urediniospores of our specimen were similar to those of *P. coronata* (21–28 × 16–21 µm *vs.* 20–30 × 16–24 µm; Zhuang et al. 1998). In the phylogenetic analysis, *P. alopecuruse* was found to be closely related to *P. iridis* (ZP-R1402) (Fig. 2) on *Iris* spp. *Puccinia alopecuruse* has smaller urediniospores than *P. iridis* (21–28 × 16–21 µm *vs.* 25–40 × 18–27 µm; Zhuang et al. 1998). Therefore, *P. alopecuruse* is introduced as a new species based on morphological characters and phylogenetic evidence.

Puccinia lactucae-indicae J.E. Sun, Yong Wang bis & K.D. Hyde, sp. nov. Fig. 29

Index Fungorum number: IF901299; Facesoffungi number: FoF15364

Etymology – Name reflects the host *Lactuca indica*, from which the type specimen was collected.

Holotype – HGUP21214

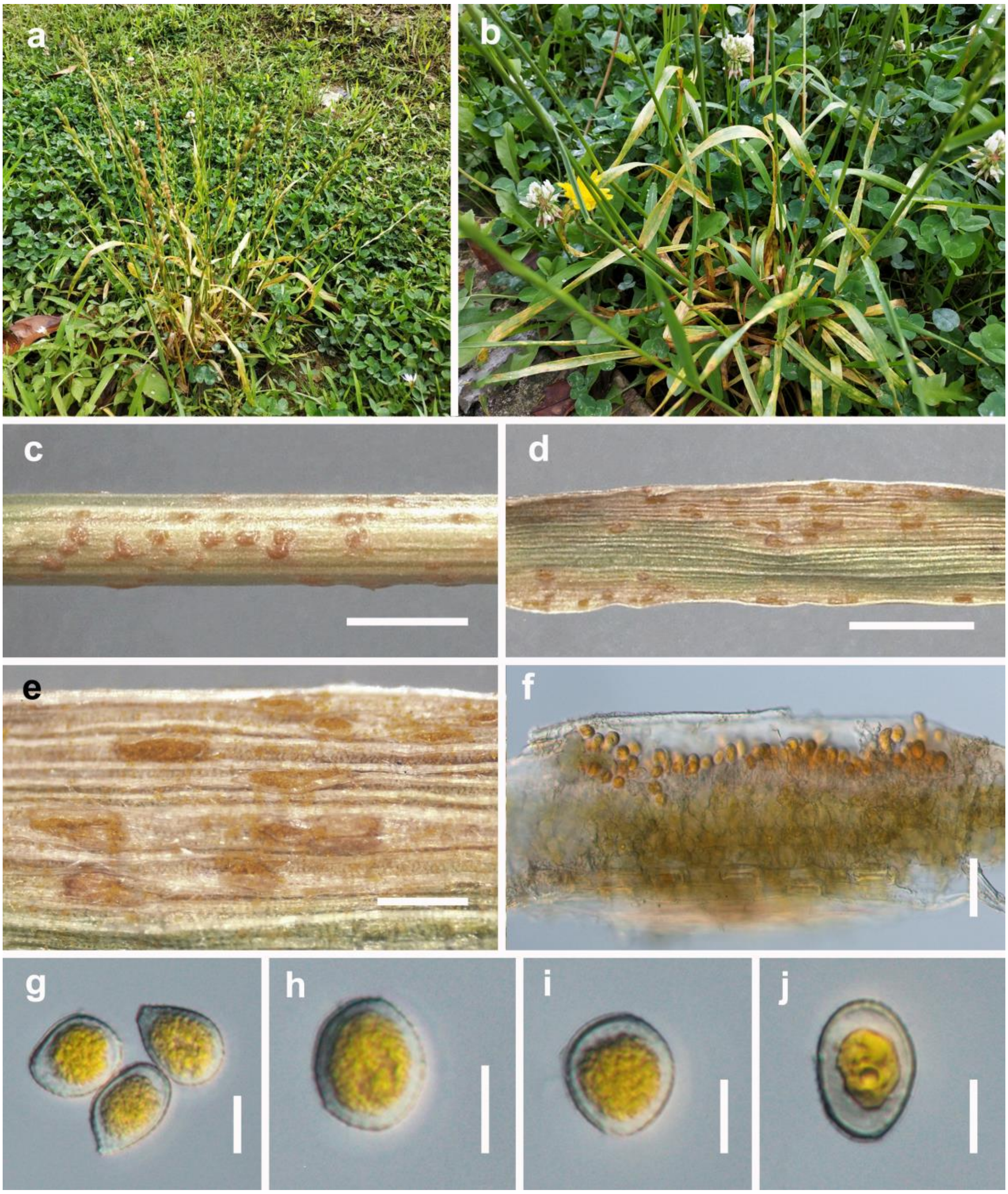

Figure 27 – *Puccinia loliume-perenneii* (from holotype HGUP21240) on *Lolium perenne*. a–e Uredinia on leaves and stems. f Longitudinal section of uredinium. g–j Urediniospores. Scale bars: c–d = 5 mm, e = 1 mm, f = 50 µm, g–j = 12.5 µm.

Description – *Spermogonia* unknown. *Aecia* abaxial, circular or subglobose, golden, 0.1–0.5 mm diam. *Aeciospores* ellipsoidal or subglobose, 22–30 × 16–22 µm (x̄ = 25.6 × 20.4 µm, n = 30), inclusions light golden; wall 1.9–2.8 µm thick. *Uredinia* abaxial, scattered, surrounded by host epidermis, circular spot, light brown, pulverulent, 0.5–1.0 mm diam. *Urediniospores* globose or ellipsoidal, 19–26 × 17–22 µm (x̄ = 21.6 × 19.9 µm, n = 30), cinnamon-brown; wall 1.3–1.6 µm thick, densely and minutely echinulate. *Telia* abaxial, circular or subcircular, chocolate-brown, pulverulent, 0.5–1.0 mm. *Teliospores* ellipsoidal to cylindrical, 2-celled, constricted at septum, chocolate-brown to gray-brown, 28–35 × 22–29 µm ($\overline{x}$ = 31.6 × 24.4 µm, n = 30); wall 1.9–2.7 µm thick; pedicels not swollen at the base, fragile, colorless.

Host – *Lactuca indica* (Asteraceae)

Material examined – CHINA, Guizhou Province, Zunyi city, 27°67'15"N, 106°39'77"W, 1029 m, 27 May 2022, on *Lactuca indica*, J.E. Sun, holotype HGUP21214; Guizhou Province, Zunyi city, 27°66'88"N, 106°48'63"W, 1043 m, 10 Jun 2022, on *L. indica*, J.E. Sun, HGUP21215; Panzhou city, 25°61'40"N, 104°82'05"W, 1862 m, 4 Aug 2022, on *L. indica*, X.J. Chen, HGUP21216.

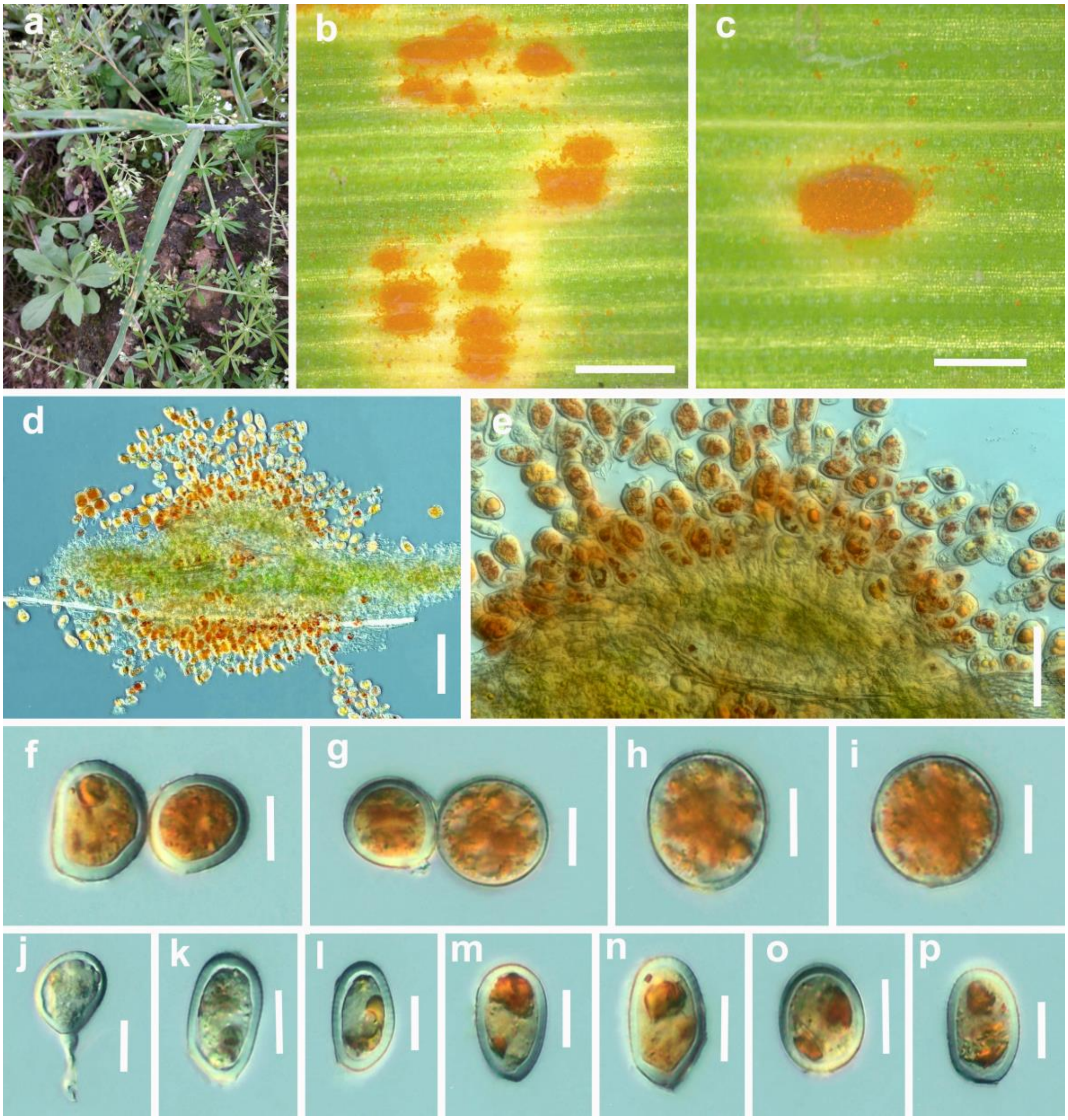

Figure 28 – *Puccinia alopecuruse* (from holotype HGUP21231) on *Alopecurus aequalis*. a–c Uredinia on leaves. d–e Longitudinal section of uredinia. f–p Urediniospores. Scale bars: b = 2 mm, c = 1 mm, d = 100 µm, e = 50 µm, f–p = 12.5 µm.

Notes – *Puccinia lactucae-indicae* is the third species known on *Lactuca indica*, after *P. lactucae-debilis* and *P. minussensis* (Zhuang et al. 2005). It is similar to *P. lactucae-debilis* in morphology of urediniospores (19–26 × 17–22 µm *vs.* 20–27 × 16–23 µm) and teliospores (28–35 × 22–29 µm *vs.* 25–36 × 18–25 µm). However, it can be distinguished by the larger aeciospores (22–30 × 16–22 µm *vs.* 14–22 × 12–16 µm). *Puccinia lactucae-indicae* formed a distinct clade

(ML/MP/BI = 100/99/1; Fig. 2) in the phylogenetic tree. Therefore, we identified *P. lactucae-indicae* as a new species.

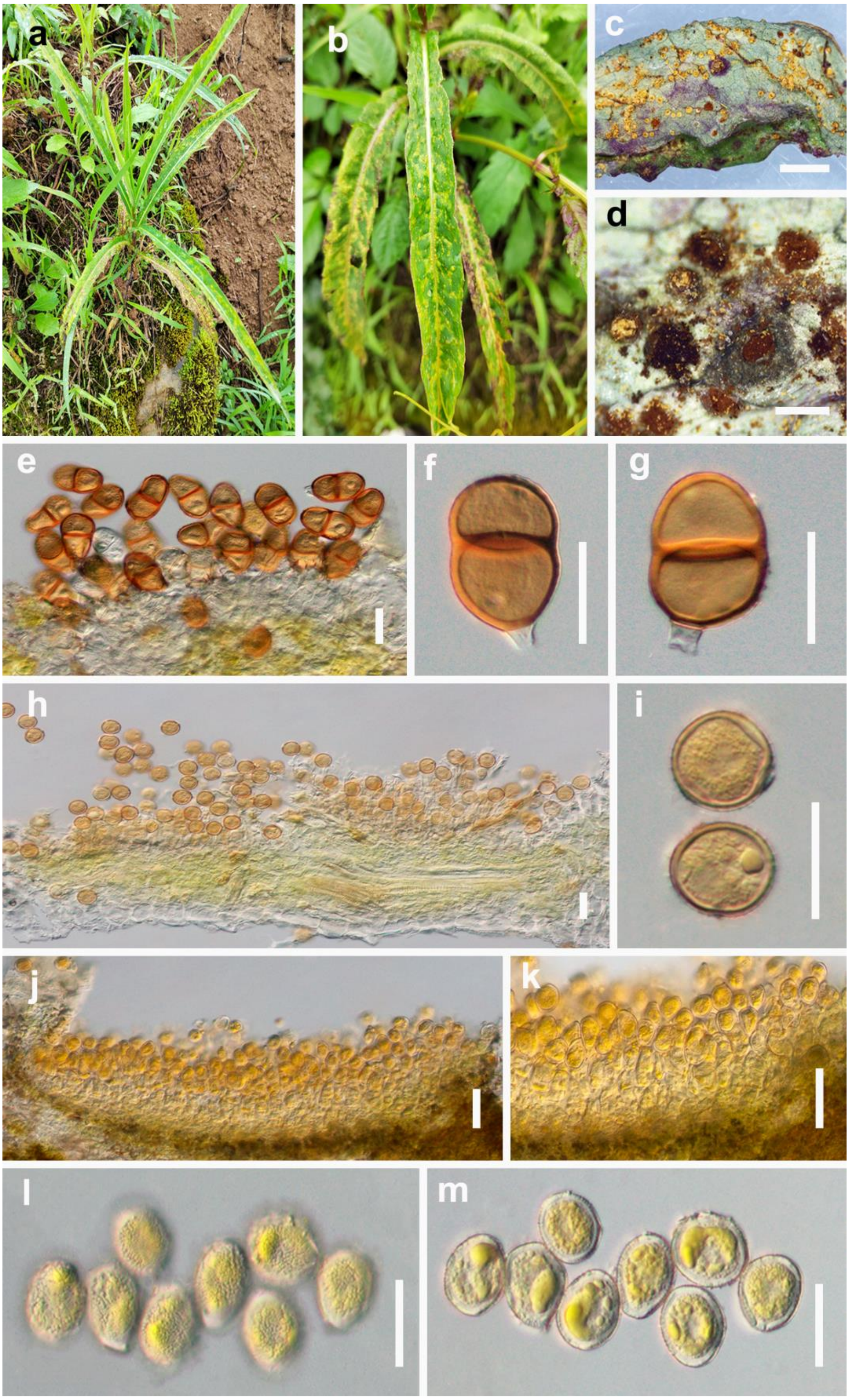

Figure 29 – *Puccinia lactucae-indicae* (from holotype HGUP21214) on *Lactuca indica*. a–d Aecia, uredinia and telia on leaves. e Longitudinal section of telium. f–g Teliospores. h Longitudinal

section of uredinium. i Urediniospores. j–k Longitudinal section of aecium. l–m Aeciospores. Scale bars: c = 5 mm, d = 1 mm, e, h, j–k = 50 µm, f–g, i, l–m = 25 µm.

Puccinia persicariae-capitatae J.E. Sun, Yong Wang bis & K.D. Hyde, sp. nov. Fig. 30

Index Fungorum number: IF901300; Facesoffungi number: FoF15366

Etymology – The name reflects the host *Persicaria capitata*, from which the type specimen was collected.

Holotype – HGUP21193

Description – *Spermogonia* and *aecia* unknown. *Uredinia* abaxial, scattered, surrounded by host epidermis, ellipsoidal or globose, golden, pulverulent, 1.0–2.5 mm diam. *Urediniospores* ellipsoidal or globose, 15–19 × 12–17 µm ($\bar{x}$ = 17.2 × 14.4 µm, n = 30), pale to light-golden; wall 0.9–1.4 µm thick, colorless to light brown, densely and minutely echinulate. *Telia* abaxial, centralized, ellipsoidal, or globose, chocolate-brown, pulverulent, 1.0–2.5 mm diam. *Teliospores* clavate or ellipsoidal, 2–celled, constricted at the septum, 24–36 × 13–18 µm ($\bar{x}$ = 30.8 × 16 µm, n = 30), cinnamon-brown to chocolate-brown; wall 0.9–1.6 µm thick, pedicels not swollen at the base,10–25 µm long, colorless.

Host – *Persicaria capitata* (Polygonaceae)

Material examined – CHINA, Guizhou Province, Liupanshui city, 26°34'46"N, 104°48'25"W, 1850 m, 25 Sep 2021, on *Persicaria capitata*, X.Y. Zhang, holotype HGUP21193; Guizhou Province, Liupanshui city, 26°34'46"N, 104°48'25"W, 1850 m, 25 Sep 2021, on *P. capitata*, X.Y. Zhang, HGUP21194.

Notes – In the phylogenetic analysis, *Puccinia persicariae-capitatae* grouped in a clade (Fig. 2) distant from other species. *Puccinia polygonicola* with telial and uredinial stages and *P. congesta* with the telial stage, occur on *Persicaria capitata* (Zhuang et al. 2005). Morphologically, it can be distinguished from *P. polygonicola* by smaller urediniospores (17–30 × 15–23 µm) and teliospores (30–53 × 15–23 µm). It also has smaller teliospores than *P. congesta* (30–55 × 12–23 µm; Zhuang et al. 2005). Therefore, based on both morphology and phylogenetic analyses, *P. persicariae-capitatae* is introduced as a new species.

Puccinia violae-diffusii J.E. Sun, Yong Wang bis & K.D. Hyde, sp. nov. Fig. 31

Index Fungorum number: IF901301; Facesoffungi number: FoF15367

Etymology – The name reflects the host *Viola diffusa*, from which the type specimen was collected.

Holotype – HGUP21204

Description – *Spermogonia* and *aecia* unknown. *Uredinia* and *telia* produced on the leaf surface, hypophyllous, scattered, surrounded by host epidermis, circular spot, chocolate-brown, pulverulent, 0.1–0.5 mm diam. *Urediniospores* globose or ellipsoidal, 18–22 × 13–19 µm ($\bar{x}$ = 19.8 × 16.4 µm, n = 30), cinnamon-brown; wall 1.2–2.0 µm thick, cinnamon-brown, densely and minutely echinulate. *Teliospores* ellipsoidal to cylindrical, 1–2-celled (mostly 2-celled), constricted at the septum, chocolate-brown to gray-brown, 20–30 × 13–20 µm ($\bar{x}$ = 22.6 × 16.4 µm, n = 30); wall 1.3–2.1 µm thick; pedicels not swollen at the base, 8–20 µm long, colorless, regularly echinulate.

Host – *Viola diffusa* (Polygonaceae)

Material examined – CHINA, Guizhou Province, Liupanshui city, 26°34'46"N, 104°48'27"W, 1840 m, 25 Sep 2021, on *Viola diffusa*, X.Y. Zhang, holotype HGUP21204.

Notes – In phylogeny, *P. violae-diffusii* grouped with HGUP21205 (on *Oplismenus undulatifolius*) in one branch (Fig. 2). However, the urediniospores of *P. violae-diffusii* are smaller than those of HGUP21205 (21–26 × 19–25 µm, the latter is probably *P. flaccida* (Zhang et al. 2005). *Puccinia violae* is also known on *Viola diffusa* with telial and uredinial stages. However, *P. violae-diffusii* has smaller urediniospores than *P. violae* (20–35 × 17–30 µm) and smaller teliospores (30–45 × 17–23 µm) (Zhuang et al. 2005). Hence, we propose *P. violae-diffusii* as a novel taxon, distinct from *P. violae* and other related taxa.

Figure 30 – *Puccinia persicariae-capitatae* (from holotype HGUP21193) on *Persicaria capitata*. a–d Uredinia and telia on leaves. e–f Longitudinal section of uredinium and telium. g–h Urediniospores. i Longitudinal section of telium. j–k Teliospores. Scale bars: b = 5 mm, c = 2 mm, d = 1 mm, e, f, i = 50 µm, g–h, j–k = 20 µm.

Figure 31 – *Puccinia violae-diffusii* (from holotype HGUP21204) on *Viola diffusa*. a–c Uredinia and telia on leaves. d Longitudinal section of uredinium and telium. e Urediniospore. f Teliospore. Scale bars: b = 5 mm, c = 1 mm, d = 50 µm, e = 20 µm, f = 12.5 µm.

Puccinia flaccida Berk. & Broome, Journal of the Linnean Society. Botany 14: 91 (1873) Fig. 32

MycoBank number: MB149013

Description – *Spermogonia*, *aecia* and *telia* not found. *Uredinia* abaxial, scattered, surrounded by host epidermis, circular spot, chocolate-brown, pulverulent, 0.1–0.5 mm diam. *Urediniospores* globose or ellipsoidal, 21–26 × 19–25 µm ($\bar{x}$ = 22.6 × 21.7 µm, n = 20), pale; wall 1.2–2.0 µm thick, colorless, echinulate.

Host – *Oplismenus undulatifolius* (Poaceae)

Material examined – CHINA, Guizhou Province, Liupanshui city, 26°04'39"N, 104°51'13"W, 1252 m, 19 Jul 2021, on *Oplismenus undulatifolius*, J.E. Sun, HGUP21205.

Notes – Although HGUP21205 grouped with *P. violae-diffusii* (HGUP21204 on *Viola diffusa*) in one branch (Fig. 2), the urediniospores are of different sizes (see *P. violae-diffusii* for discussion). *Puccinia flaccida* is known on *Oplismenus undulatifolius* (Zhuang et al. 2005) but, unfortunately, without DNA data. The urediniospores of our specimen are similar in size to *P. flaccida* (23–29 × 18–24 µm; Zhang et al. 2005). Therefore, we designate the collection as *P. flaccida*.

Puccinia phyllostachydis Kusano, Journal of the College of Agriculture Imperial University of Tokyo 8 (1): 38 (1908) Fig. 33

MycoBank number: MB160813

Description – *Spermogonia*, *aecia* and *telia* not found. *Uredinia* hypophyllous, surrounded by host epidermis, oblong to oval, or irregular, cinnamon-brown to chocolate-brown, pulverulent, 0.5–1.0 mm diam. Paraphyses capitate, 40–80 × 15–30 µm, wall thickened at apex, 5.0–11.0 µm. *Urediniospores* ellipsoidal or globose, 26–35 × 24–29 µm ($\bar{x}$ = 31.3 × 26.5 µm, n = 30), inclusions yellowish-brown; wall 2.4–3.4 µm thick, colorless, densely and minutely echinulate.

Host – *Phyllostachys nuda* (Bambusoideae, Poaceae)

Material examined – CHINA, Guizhou Province, Zunyi city, 27°40'10"N, 106°24'34"W, 1001 m, 6 May 2022, on *Phyllostachys nuda*, Y.Q. Yang, HGUP21174, HGUP21175.

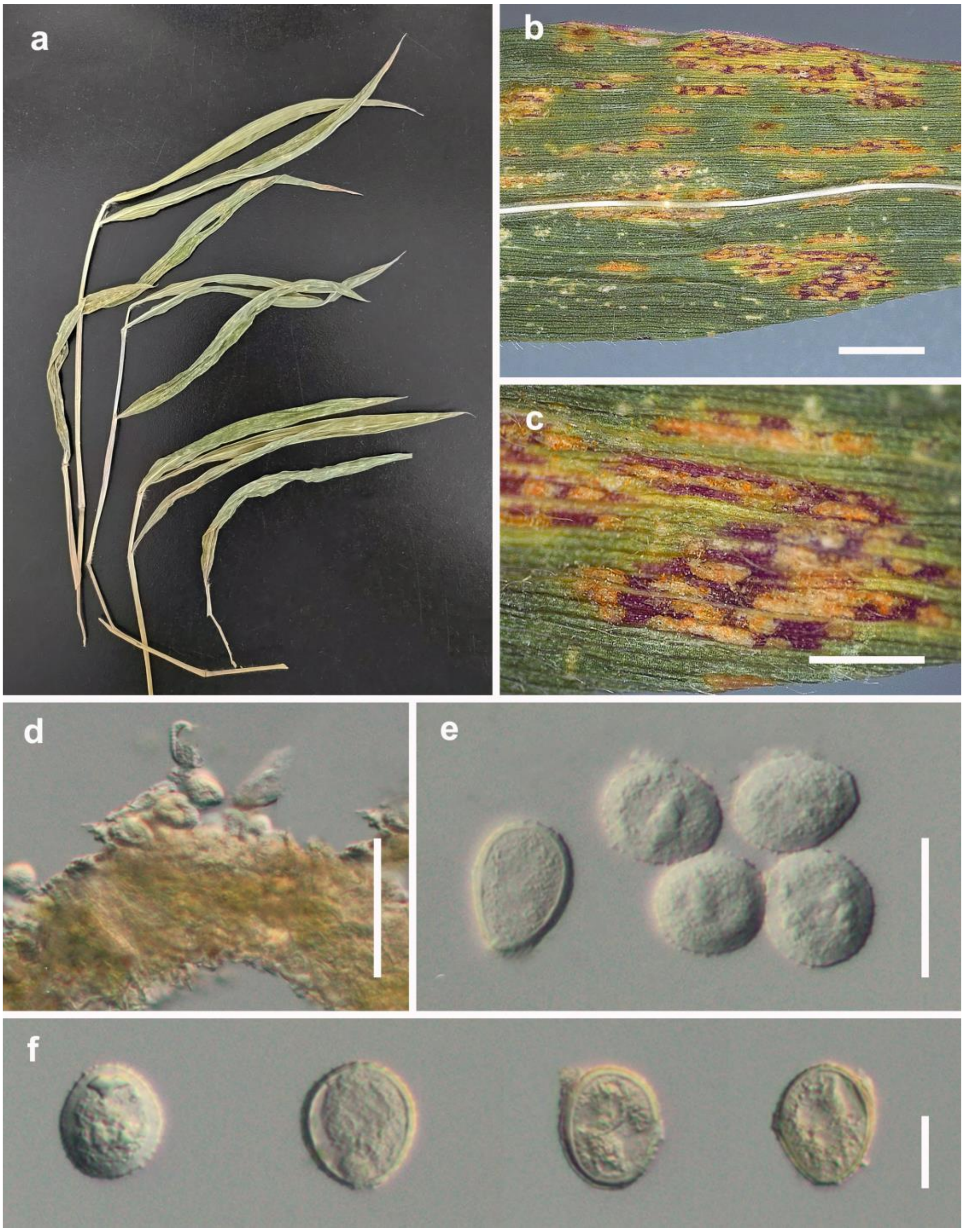

Figure 32 – *Puccinia flaccida* (from HGUP21205) on *Oplismenus undulatifolius*. a–c Uredinia on leaves. d Longitudinal section of uredinium. e–f Urediniospores. Scale bars: b = 5 mm, c = 2 mm, d = 50 µm, e = 25 µm. f = 12.5 µm.

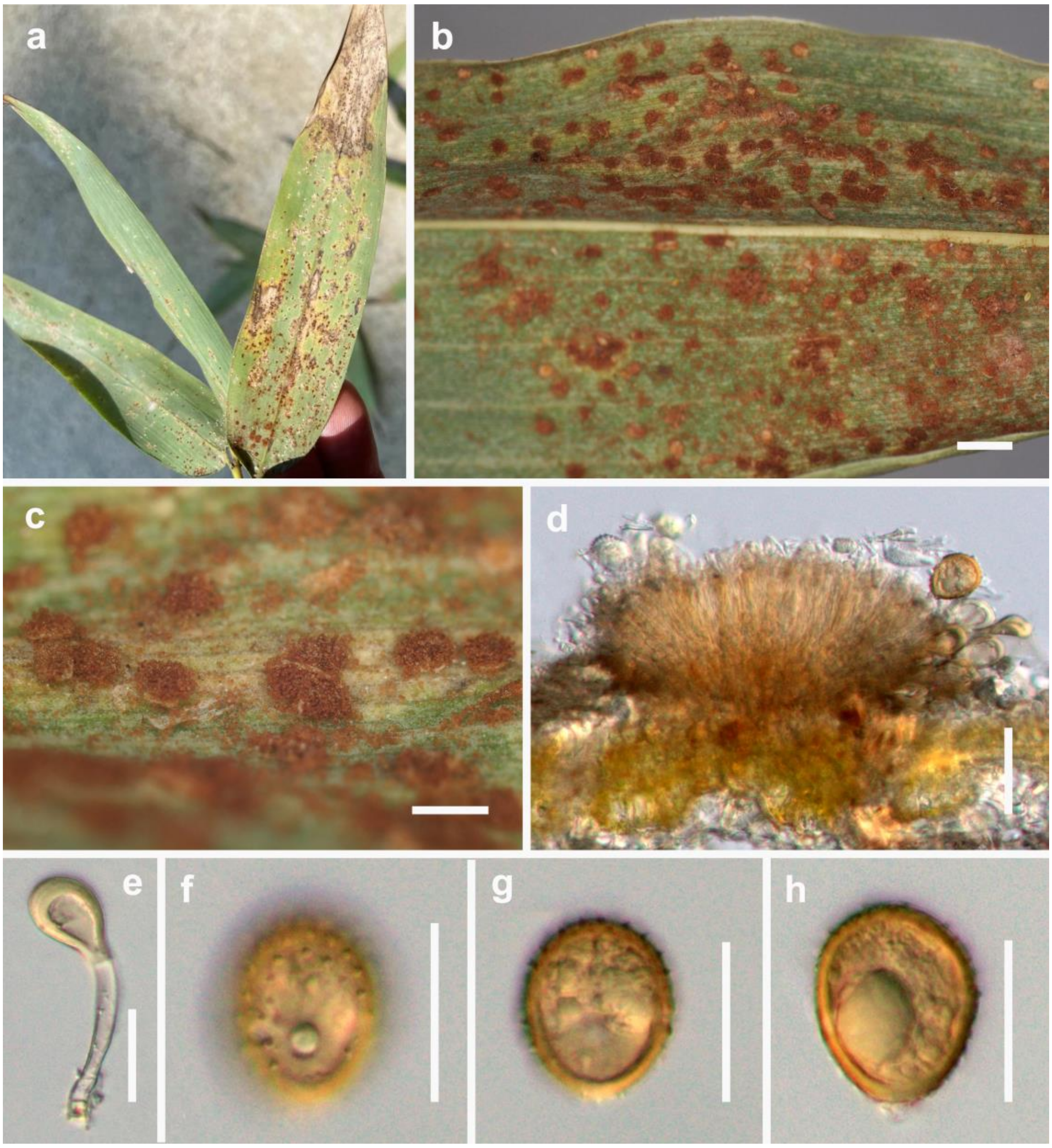

Figure 33 – *Puccinia phyllostachydis* (from HGUP21174) on *Phyllostachys nuda*. a–c Uredinia on leaves. d Longitudinal section of uredinium. e Paraphysis. f–h Urediniospores. Scale bars: b = 1 mm, c = 0.5 mm, d = 50 µm, e–h = 25 µm.

Notes – Four species of *Puccinia*, namely *P. phyllostachydis*, *P. longicornis*, *P. nigroconoidea*, and *P. scabrida* have been reported on *Phyllostachys* spp. (Zhuang et al. 1998). Upon comparison with the description provided by Zhuang et al (1998), Our specimens closely resemble the urediniospores of *P. phyllostachydis* (26–34× 23–28 *vs.* 26–35 × 24–29 µm; Zhuang et al. 1998). Therefore, we name the collection as *P. phyllostachydis*.

Puccinia thaliae Dietel, Hedwigia 38: 250 (1899) Fig. 34

MycoBank number: MB170747

Description – *Spermogonia*, *aecia* and *telia* not found. *Uredinia* hypophyllous, surrounded by host epidermis, oblong to oval, or irregular, yellow spot, pulverulent, 0.1–1.0 mm diam. *Urediniospores* ellipsoidal or globose, 24–38 × 18–24 µm ($\bar{x}$ = 31.1 × 21.3 µm, n = 30), inclusions yellow; wall 2.2–3.2 µm thick, colorless, densely and minutely echinulate.

Host – *Canna indica* (Cannaceae)

Material examined – CHINA, Guizhou Province, Xingyi city, 25°21'22"N, 105°30'12"W, 1024 m, 22 Jul 2022, on *Canna indica*, X.J. Chen, HGUP21172, HGUP21173.

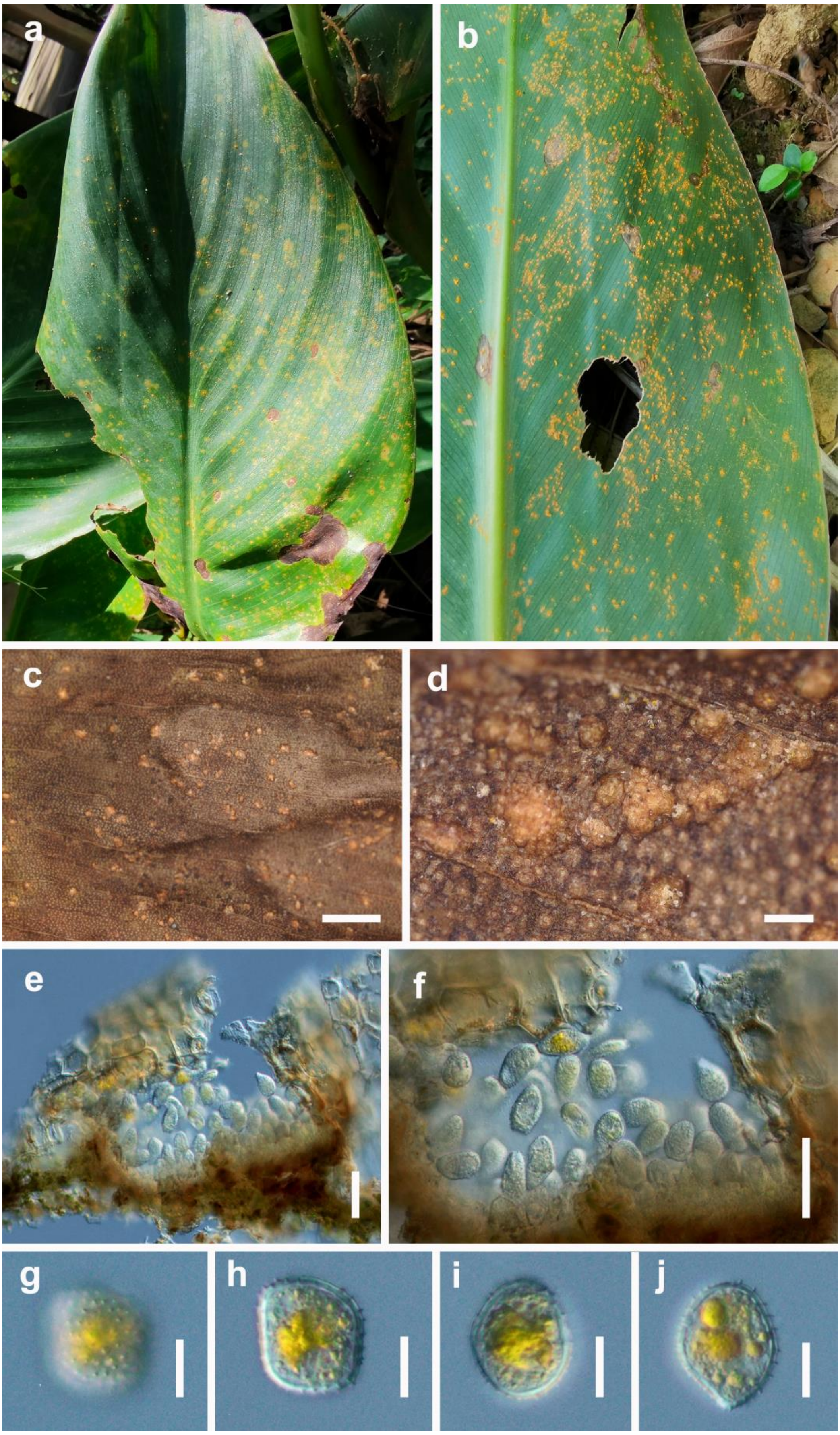

Figure 34 – *Puccinia thaliae* (from HGUP21172) on *Canna indica*. a–d Uredinia on leaves. e–f Longitudinal section of uredinium. g–j Urediniospores. Scale bars: c = 2 mm, d = 0.5 mm, e = 100 µm, f = 50 µm, g–j = 12.5 µm.

Notes – *Puccinia thaliae* occurs on *Canna indica* and is the most common and geographically diverse species in China. Our specimens match the description of *P. thaliae* (Zhuang et al. 2005). We, therefore, name our collections as *P. thaliae* based on morphology and their host.

Puccinia rufipes Dietel, Bot. Jb. 32: 48 (1902) Fig. 35

MycoBank number: MB246867

Description – *Spermogonia*, *telia* and *aecia* not found. *Uredinia* on the abaxial leaf surface, not surrounded by host epidermis, long-oval or elongate, bright brown to purplish-red, pulverulent, 1.0–7.0 mm diam. Paraphyses capitate, 50–65 × 14–23 µm, wall thickened at apex, 5.0–11.0 µm. *Urediniospores* globose or ellipsoidal, 25–36 × 18–27 µm ($\bar{x}$ = 31.2 × 22.9 µm, n = 30), golden or cinnamon-brown; wall 1.4–2.4 µm thick, cinnamon-brown, densely and minutely verrucose.

Host – *Imperata cylindrica* (Poaceae)

Material examined – CHINA, Guizhou Province, Liupanshui city, 25°61'40"N, 104°82'58"W, 1856 m, 4 Aug 2022, on *Imperata cylindrica*, J.E. Sun, HGUP21176; Duyun city, 27°66′02″N, 107°13'07"W, 1034 m, 10 Jun 2022, on *I. cylindrica*, W.M. Luo, HGUP21177.

Notes – *Puccinia rufipes* and *P. microspora* have been described on *Imperata cylindrica* (Zhuang et al. 1998). Unfortunately, nucleotide data is not available for either species in NCBI. Phylogenetic analyses show that our specimens had a distant relationship to other *Puccinia* species with high bootstrap support (Fig. 2). *Puccinia rufipes* has larger urediniospores than *P. microspora* (25–36 × 18–27 µm *vs*. 20–30 × 18–20 µm). Zhuang et al. (1998) gave similar measurements to those found in the current study for the paraphyses (50–65 × 14–23 µm *vs*. 40–65 × 14–23 µm) and for the urediniospores (25–36 × 18–27 µm vs. 26–35 × 18–25 µm). On the basis of morphology and host information, we identify our collections as *P. rufipes*.

Puccinia convolvuli (Pers.) Castagne, Observ. Uréd. 1: 16 (1842) Fig. 36

MycoBank number: MB211846

Description – *Spermogonia*, *uredinia* and *telia* not found. *Aecia* produced on the abaxial leaf surface, scattered, obvious boundary, roestelioid, 2.0–6.0 mm diam., peridium dehiscent at apex, no slits along the sides, yellow. *Aeciospores* ellipsoidal or oblong, 17–25 × 14–20 µm ($\bar{x}$ = 21.8 × 16.7 µm, n = 30), inclusions pale to yellow; wall 1.3–2.1 µm thick, colorless, irregularly verrucose.

Host – *Calystegia hederacea* (Convolvulaceae)

Material examined – CHINA, Guizhou Province, Guiyang city, 26°43'4"N, 106°67'80"W, 1108 m, 24 May 2021, on *Calystegia hederacea*, J.E. Sun, HGUP21182; Guiyang city, 28°15'81"N, 108°33'49"W, 813 m, 4 Sep 2021, on *C. hederacea*, J.E. Sun, HGUP21183.

Notes – *Puccinia convolvuli* was introduced from *Calystegia hederacea* by Castagne (1842). Descriptions and illustrations of the aecia and aeciospores of this taxon were provided by Zhuang et al. (2005). The morphologies of our collections resemble the aeciospores size of *P. convolvuli* (17–25 × 14–20 µm *vs*. 18–25 × 15–20 µm). Furthermore, the phylogenetic analyses demonstrated that our specimens, along with two other specimens (ZP-R1312, ZP-R1388), form a group with *P. convolvuli* (Fig. 2). We, therefore, identify our collections as *P. convolvuli*.

Puccinia oenanthes-stoloniferae S. Ito ex Tranzschel, Obzor Rzhavchinnykh Gribov SSSR: 299 (1939) Fig. 37

MycoBank number: MB337960

Description – *Spermogonia*, *aecia* and *telia* not found. *Uredinia* hypophyllous, surrounded by host epidermis, oblong to oval, or irregular, yellow, pulverulent, 0.5–1.0 mm diam. *Urediniospores* ellipsoidal or ovoid, 19–27 × 15–22 µm ($\bar{x}$ = 22.9 × 17.9 µm, n = 30), inclusions pale to yellow; wall 1.7–2.2 µm thick, colorless, densely and minutely echinulate.

Host – *Oenanthe javanica* (Apiaceae)

Material examined – CHINA, Guizhou Province, Duyun city, 26°76'88"N, 106°48'46"W, 799 m, 22 Jun 2021, on *Oenanthe javanica*, J.E. Sun, HGUP21184, HGUP21185.

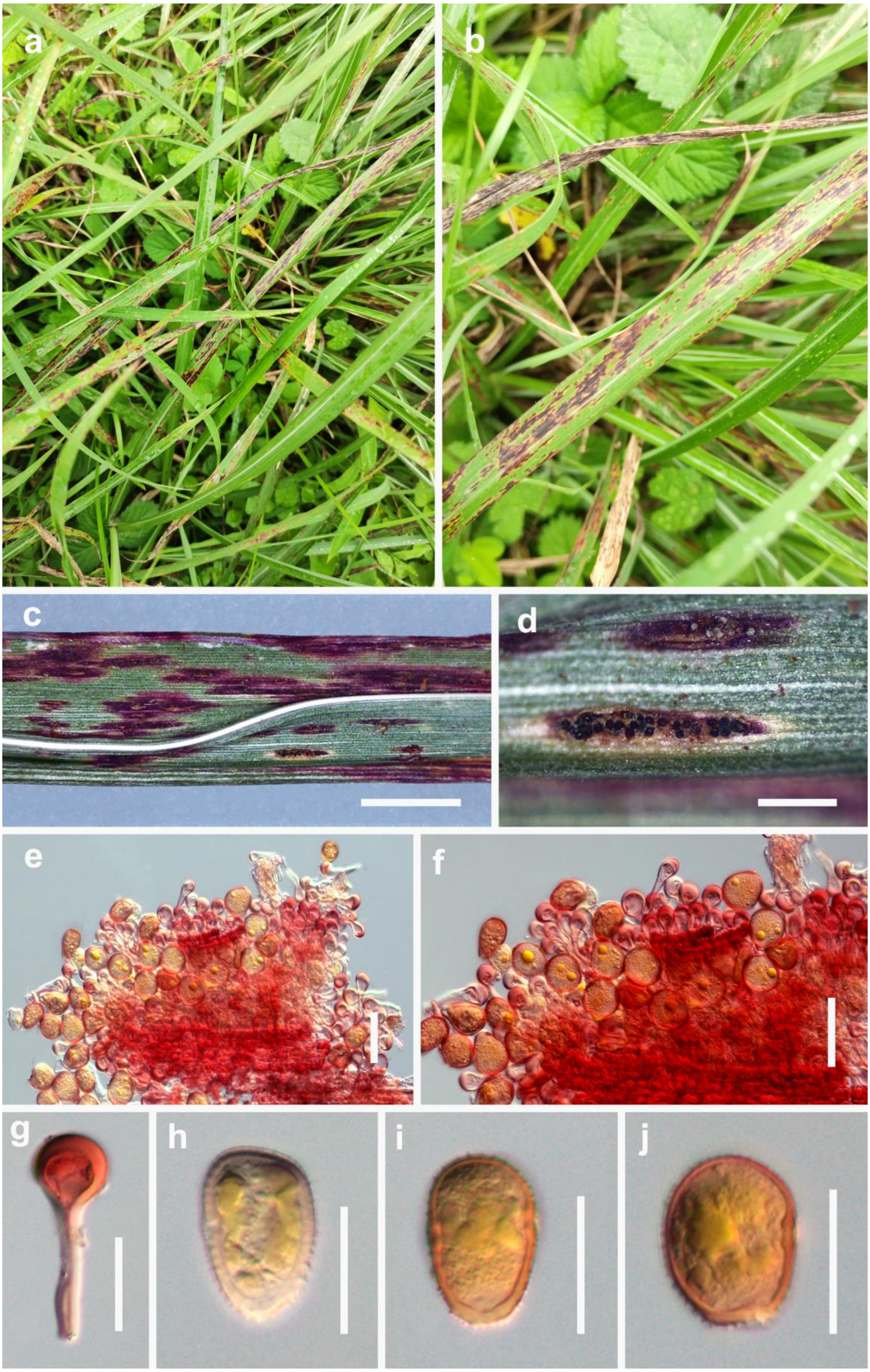

Figure 35 – *Puccinia rufipes* (from HGUP21176) on *Imperata cylindrica*. a–d Uredinia on leaves. e–f Longitudinal section of uredinium. g Paraphysis. h–j Urediniospores. Scale bars: c = 5 mm, d = 1 mm, e = 100 µm, f = 50 µm, g–j = 25 µm.

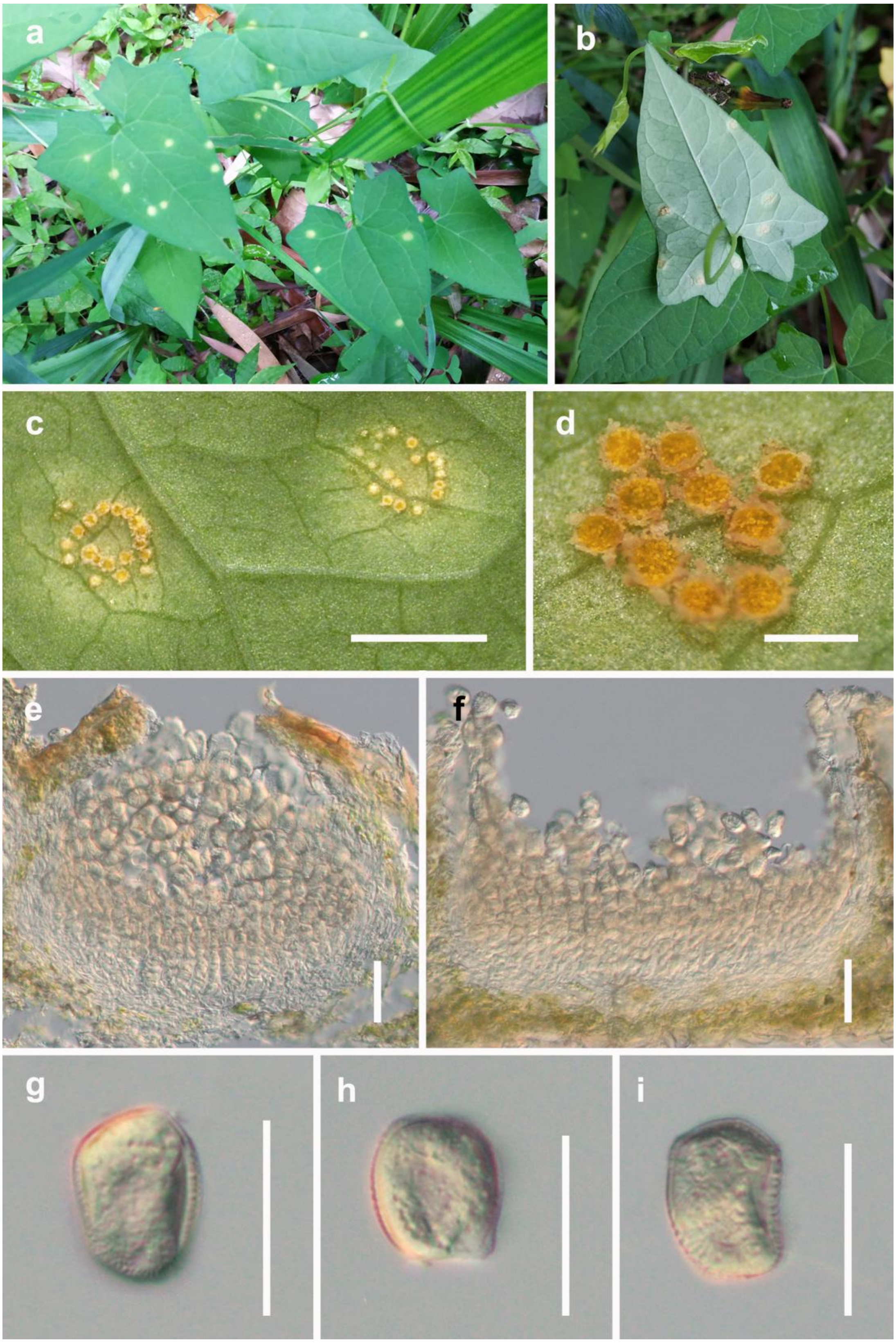

Figure 36 – *Puccinia convolvuli* (from HGUP21182) on *Calystegia hederacea*. a–d Aecia on leaves. e–f Longitudinal section of aecia. g–i Aeciospores. Scale bars: c = 5 mm, d = 2 mm, e–f = 50 µm, g–i = 25 µm.

Notes – Based on multi-locus phylogenetic analyses, our specimens formed a distinct branch with strong support in the phylogenetic tree (Fig. 2). The morphology of our collections closely resembles that of *Puccinia oenanthes-stoloniferae* as described by Zhuang et al. (2005). In light of these findings and shared morphological features and phylogenetic placement, we propose our collections as *P. oenanthes-stoloniferae*. By establishing the presence of *P. oenanthes-stoloniferae* in our collections and providing its DNA data, we add valuable information to the knowledge of this common species in China, contributing to its taxonomic and genetic studies.

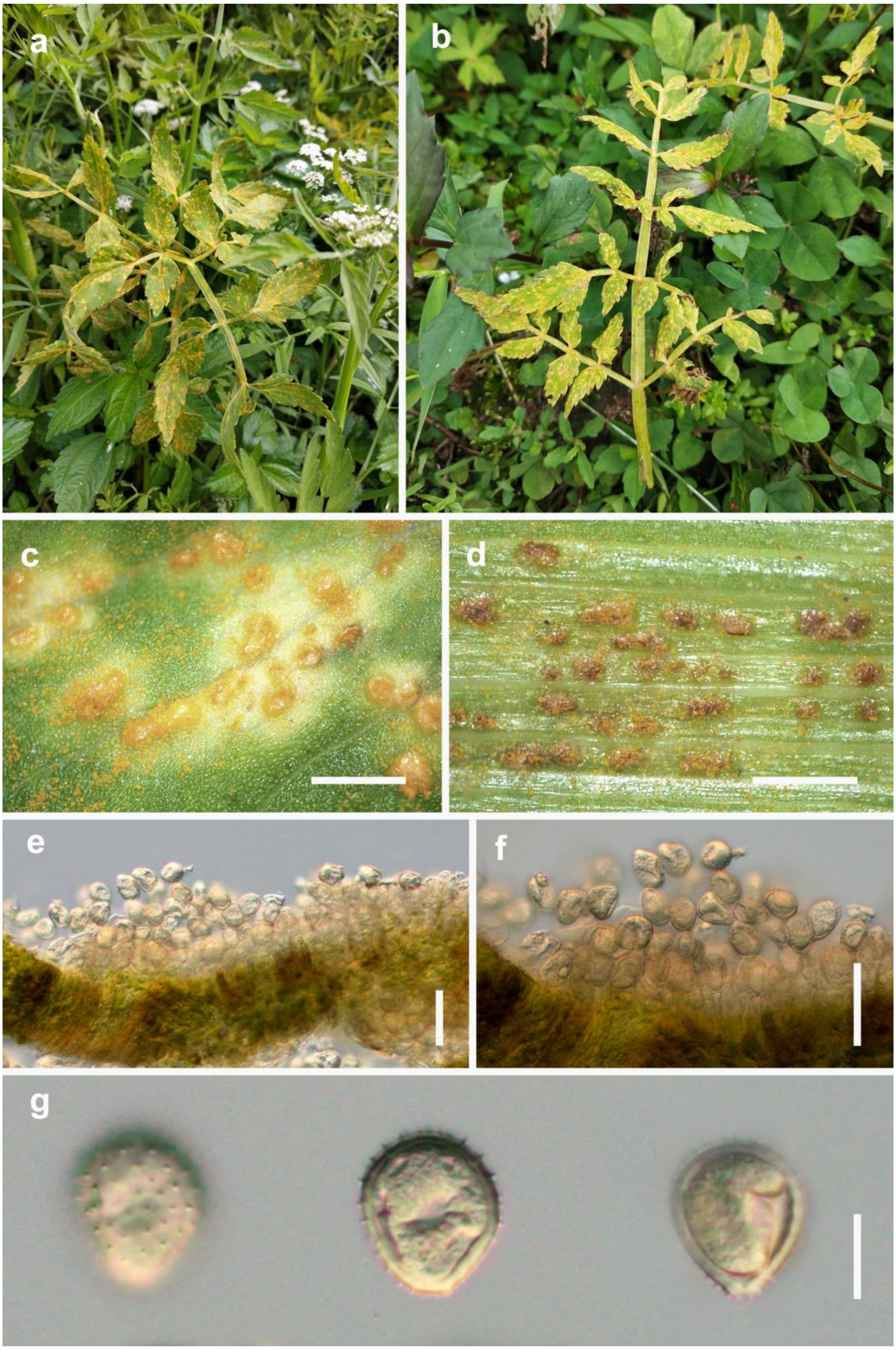

Figure 37 – *Puccinia oenanthes-stoloniferae* (from HGUP21184) on *Oenanthe javanica*. a–d Uredinia on leaves. e–f Longitudinal section of uredinium. g Urediniospores. Scale bars: c–d = 2 mm, e–f = 50 µm, g = 12.5 µm.

Puccinia allii (DC.) F. Rudolphi, Linnaea 4: 392 (1829) Fig. 38

MycoBank number: MB146618

Description – *Spermogonia* and *aecia* not found. *Uredinia* on abaxial leaf surface, scattered, surrounded by host epidermis, circular spot, light brown, pulverulent, 0.5–1.5 mm diam. *Urediniospores* ellipsoidal or subglobose, 25–35 × 17–23 µm ($\bar{x}$ = 29.5 × 21.1 µm, n = 30), inclusions golden; wall 2.2–2.8 µm thick, colorless. *Telia* on abaxial leaf surface, linear or irregular, chocolate-brown to black, 1.0–2.5 mm diam. *Teliospores* ellipsoidal to cylindrical, 2-celled, constricted at septum, golden, 35–75 × 15–25 µm ($\bar{x}$ = 52.2 × 18.1 µm, n = 30); apical wall thickened, 1.2–2.8 µm; pedicels not swollen at base, fragile, colorless.

Host – *Allium sativum* (Amaryllidaceae)

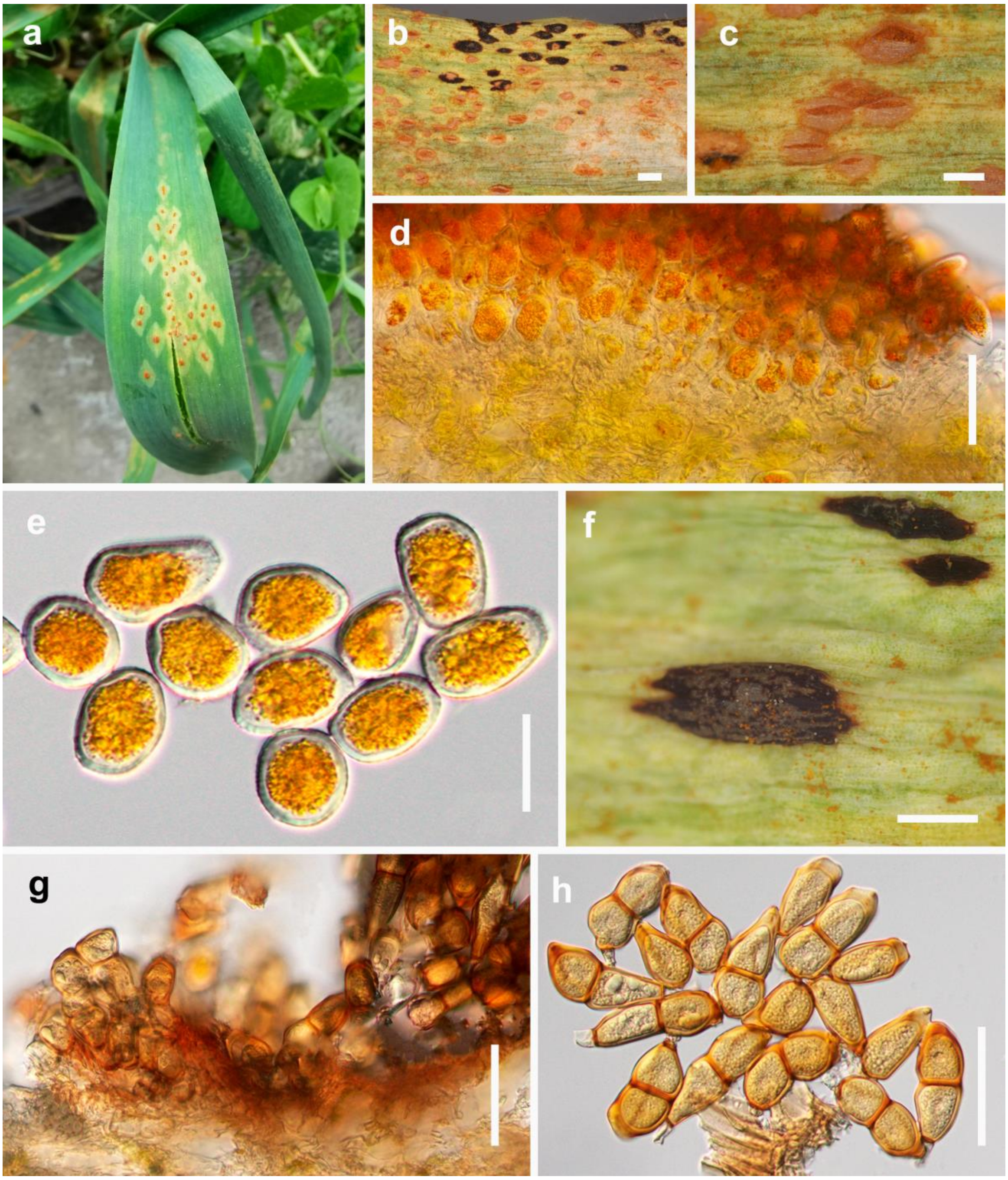

Figure 38 – *Puccinia allii* (from HGUP21226) on *Allium sativum*. a–b Uredinia and telia on leaves. c Uredinia on leaves. d Longitudinal section of uredinium. e Urediniospores. f Telia on leaves.

g Longitudinal section of telium. h Teliospores. Scale bars: b = 2 mm, c, f = 0.5 mm, d, g = 50 µm, e, h = 25 µm.

Material examined – CHINA, Guizhou Province, Guiyang city, 26°90'78"N, 106°71'75"W, 1002 m, 7 Apr 2022, on *Allium sativum*, J.E. Sun, HGUP21225; Bijie city, 25°61'40"N, 104°74'28"W, 1450 m, 19 Apr 2022, on *A. sativum*, X.J. Chen, HGUP21226, HGUP21227; Zunyi city, 27°40'24"N, 106°24'44"W, 1092 m, 30 Apr 2022, on *A. sativum*, J.E. Sun, HGUP21228; Guiyang city, 26°90′65″N, 106°71'12"W, 1315 m, 7 Apr 2022, on *A. sativum*, Y.K. He, HGUP21229.

Notes – *Puccinia allii* is a common pathogen, with uredinial and telial stages found on *Allium* spp. throughout the world. Our specimens grouped with *P. allii* (BRIP 59595, HSZ 1992, HMJAU8954), along with three other species in the phylogenetic tree (Fig. 2). Descriptions and illustrations for the urediniospores and teliospores of *P. allii* were provided by Zhuang et al. (2005). The morphology from our collection (HGUP21226) is similar to the urediniospores and teliospores of species *P. allii*. We, therefore, identified our collections as *P. allii*.

Puccinia oxalidis Dietel & Ellis, Hedwigia 34: 291 (1895) Fig. 39

MycoBank number: MB191096

Description – *Spermogonia*, *aecia* and *telia* not found. *Uredinia* on the abaxial leaf surface, not surrounded by host epidermis, no obvious boundary, irregular, golden, pulverulent, 1.0–3.0 mm diam. *Urediniospores* globose or ellipsoidal to ovoid, 19–26 × 18–25 µm ($\bar{x}$ = 22.9 × 22 µm, n = 30), inclusions pale or golden; wall 1.0–1.6 µm thick, colorless rough.

Host – *Oxalis corniculata* (Oxalidaceae)

Material examined – CHINA, Guizhou Province, Guiyang city, 26°41'53"N, 106°66'81"W, 1145 m, 11 May 2021, on *Oxalis corniculata*, J.E. Sun, HGUP21232, HGUP21233; Zunyi city, 27°76'88"N, 107°48'46"W, 740 m, 14 May 2021, on *O. corniculata*, J.E. Sun, HGUP21235, HGUP21236.

Notes – *Puccinia oxalidis* was originally identified from *Oxalis* sp. by Dietel (1895). In the phylogenetic analysis, our specimens clustered with *P. oxalidis* (MCA3567 and RO1) (Fig. 2), with high bootstrap values. Morphologically the urediniospores from our collections closely resemble the urediniospores of *P. oxalidis* (15–23 × 14–20 µm) as described by Zhuang et al. (2005). We, thus, identify our collections as *P. oxalidis*.

Puccinia corticioides Berk. & Broome, Journal of the Linnean Society. Botany 16: 52 (1877) Fig. 40

MycoBank number: MB237523

Description – *Spermogonia*, *aecia* and *telia* not found. *Uredinia* produced on stems, nearly oval, pulverulent, 1.0–3.0 mm diam., with big centralized yellowish or golden spot. *Urediniospores* subglobose or obovoid, 16–25 × 14–20 µm ($\bar{x}$ = 19.4 × 15.2 µm, n = 30), golden; wall 1.6–2.3 µm thick, colorless, rugose.

Host – Bamboo (Bambusoideae, Poaceae)

Material examined – CHINA, Guizhou Province, Liupanshui city, 26°34'23"N, 104°08'12"W, 1810 m, 10 May 2021, on bamboo, J.E. Sun, HGUP21139, HGUP21140.

Notes – *Puccinia corticioides* was initially assigned to *Stereostratum* (Magnus 1899). However, Okane et al. (2020) proposed reviving the binomial *P. corticioides* to replace *S. corticioides* though inoculation experiments and further nucleotide sequence analyses. Our specimens and *P. corticioides* formed a well-supported clade in the phylogenetic tree (Fig. 2). They have similar morphology to *P. corticioides* with urediniospores (16–25 × 14–20 µm vs. 19–26 ×15–21 µm) (Okane et al. 2020). We confirm the specimens as *P. corticioides*.

Puccinia polysora Underw., Bulletin of the Torrey Botanical Club 24: 86, 1897 Fig. 41

MycoBank number: MB179511

Description – *Spermogonia*, *aecia* and *telia* not found. *Uredinia* produced on abaxial leaf surface, surrounded by host epidermis, ellipsoidal, oblong to oval, cinnamon-brown, pulverulent, 1.0–5.0 mm diam. *Urediniospores* ellipsoidal, ovoid, or subglobose, 21–30 × 21–25 µm ($\overline{x}$ = 26.5 × 22.8 µm, n = 30), inclusions pale or yellow to cinnamon-brown; wall 1.7–3.1 µm thick, colorless, densely, and minutely echinulate.

Host – *Zea mays* (Poaceae)

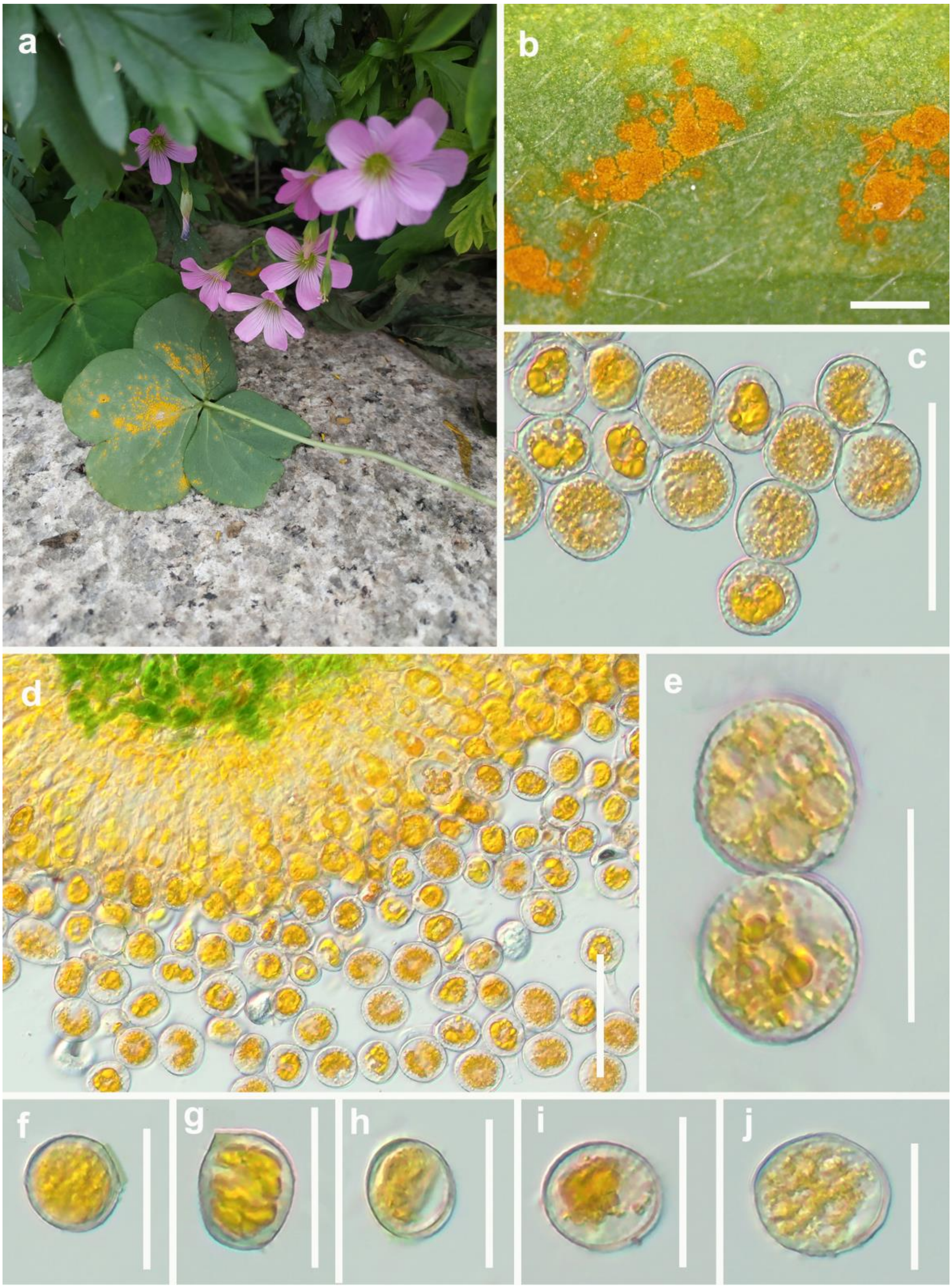

Figure 39 – *Puccinia oxalidis* (from HGUP21232) on *Oxalis corniculata*. a–b Uredinia on leaves. d Longitudinal section of uredinium. c, e–j Urediniospores. Scale bars: b = 1 mm, d = 50 µm, c, e = 25 µm, f–j = 12.5 µm.

Material examined – CHINA, Guizhou Province, Duyun city, 26°76'88"N, 106°48'46"W, 813 m, 22 Jun 2021, on *Zea mays*, J.E. Sun, HGUP21248; Panzhou city, 25°89'60"N, 104°84'32"W, 802 m, 19 Jul 2021, on *Z. mays*, J.E. Sun, HGUP21249; Liupanshui city, 26°07'09"N, 106°08'23"W, 1413 m, 14 Jul 2021, on *Z. mays*, J.E. Sun, HGUP21250; Tongren city, 28°16'10"N, 108°33'74"W, 787 m, 4 Sep 2021, on *Z. mays*, J.E. Sun, HGUP21251; Zunyi city, 27°66'02"N, 106°40'67"W, 1056 m, 10 Jun 2022, on *Z. mays*, J.E. Sun, HGUP21252.

Notes – Our specimens are phylogenetically close to *Puccinia polysora* (HSZ1879) (Fig. 2). The specimens show 94.95% (377/397 bp including 9 bp of gaps) and 86.76% (394/454 bp including 60 bp of gaps) sequence similarities with *P. polysora* for ITS and LSU sequences, respectively. Our collections are morphologically similar to *P. polysora* although they have shorter urediniospores (21–30 µm *vs.* 28–38 µm) (Zhuang et al. 2005). Thus, we identify the collections as *P. polysora*

Figure 40 – *Puccinia corticioides* (from HGUP21139) on bamboo. a–c Uredinia on stems. d–e Longitudinal section of uredinium. f–g Urediniospores. Scale bars: b = 5 mm, c = 2 mm, d = 100 µm, e = 50 µm, f–g = 25 µm.

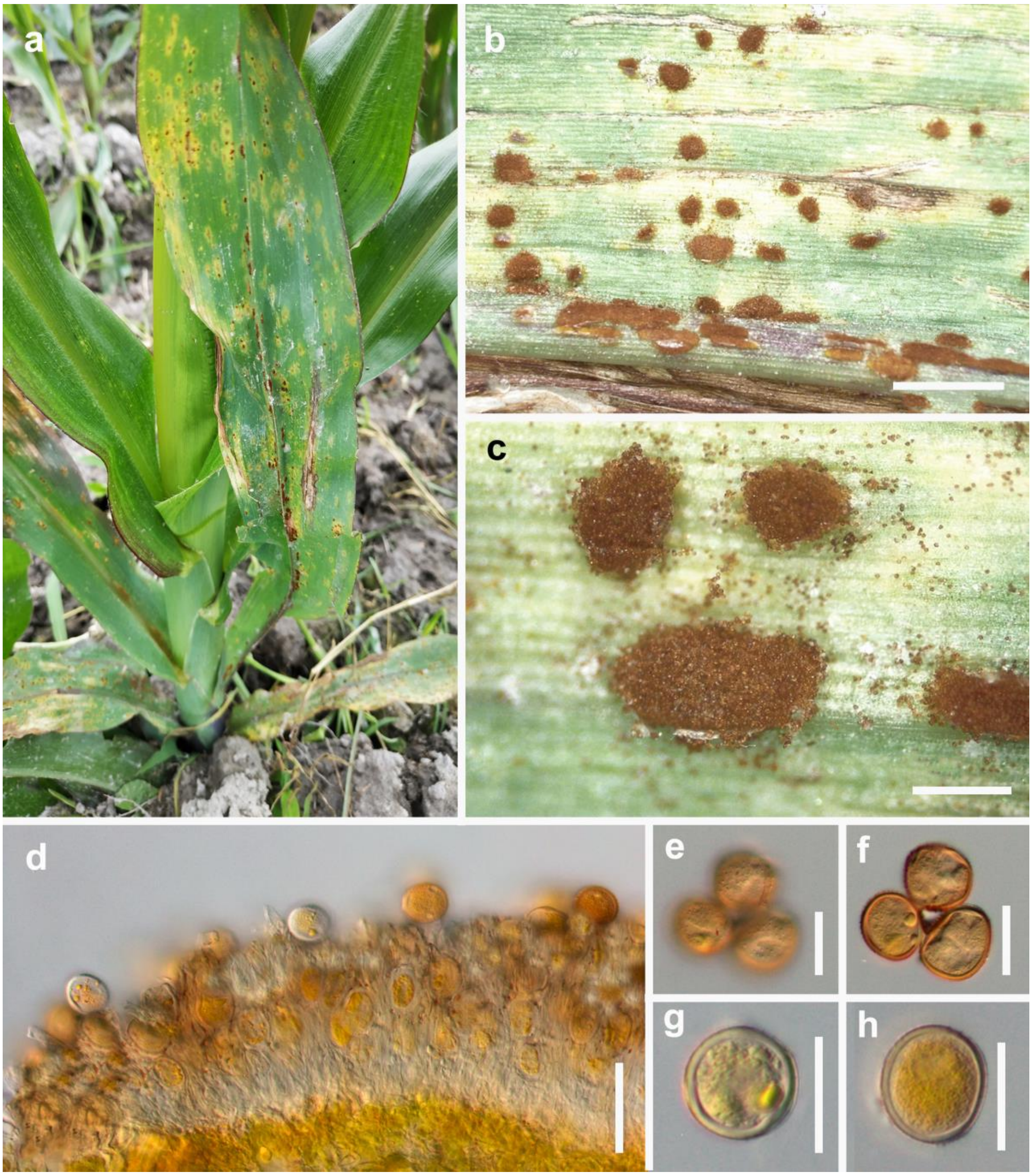

Figure 41 – *Puccinia polysora* (from HGUP21248) on *Zea mays*. a–c Uredinia on leaves. d Longitudinal section of uredinium. e–h Urediniospores. Scale bars: b = 5 mm, c = 1 mm, d = 50 µm, e–h = 25 µm.

Puccinia cynodontis Lacroix ex Desm., Plantes Crypt. de France: no. 655 (1859) Fig. 42

MycoBank number: MB224089

Description – *Spermogonia*, *uredinia* and *telia* not found. *Aecia* produced on abaxial leaf surface, scattered, obvious boundary, roestelioid, 1.0–5.0 mm diam., peridium dehiscent at apex, no slits along the sides, yellow. *Aeciospores* globose or subglobose, 20–26 × 19–25 µm ($\overline{x}$ = 24.2 × 21.4 µm, n = 30), inclusions golden; wall 1.3–2.1 µm thick, colorless, rough.

Host – *Plantago asiatica* (Plantaginaceae)

Material examined – CHINA, Guizhou Province, Guizhou city, 26°6145'38"N, 106°65'43"W, 1118 m, 3 May 2022, on *Plantago asiatica*, J.E. Sun, HGUP21253, HGUP21254.

Notes – Morphological characters of aeciospores from our collections are similar to *P. cynodontis* which was designated by Zhuang et al. (2005). The uredinial and telial stages of this rust occur on the grass, *Cynodon dactylon*, as described by Zhuang et al. (2005). Based on morphology we identify our collections as *P. cynodontis*.

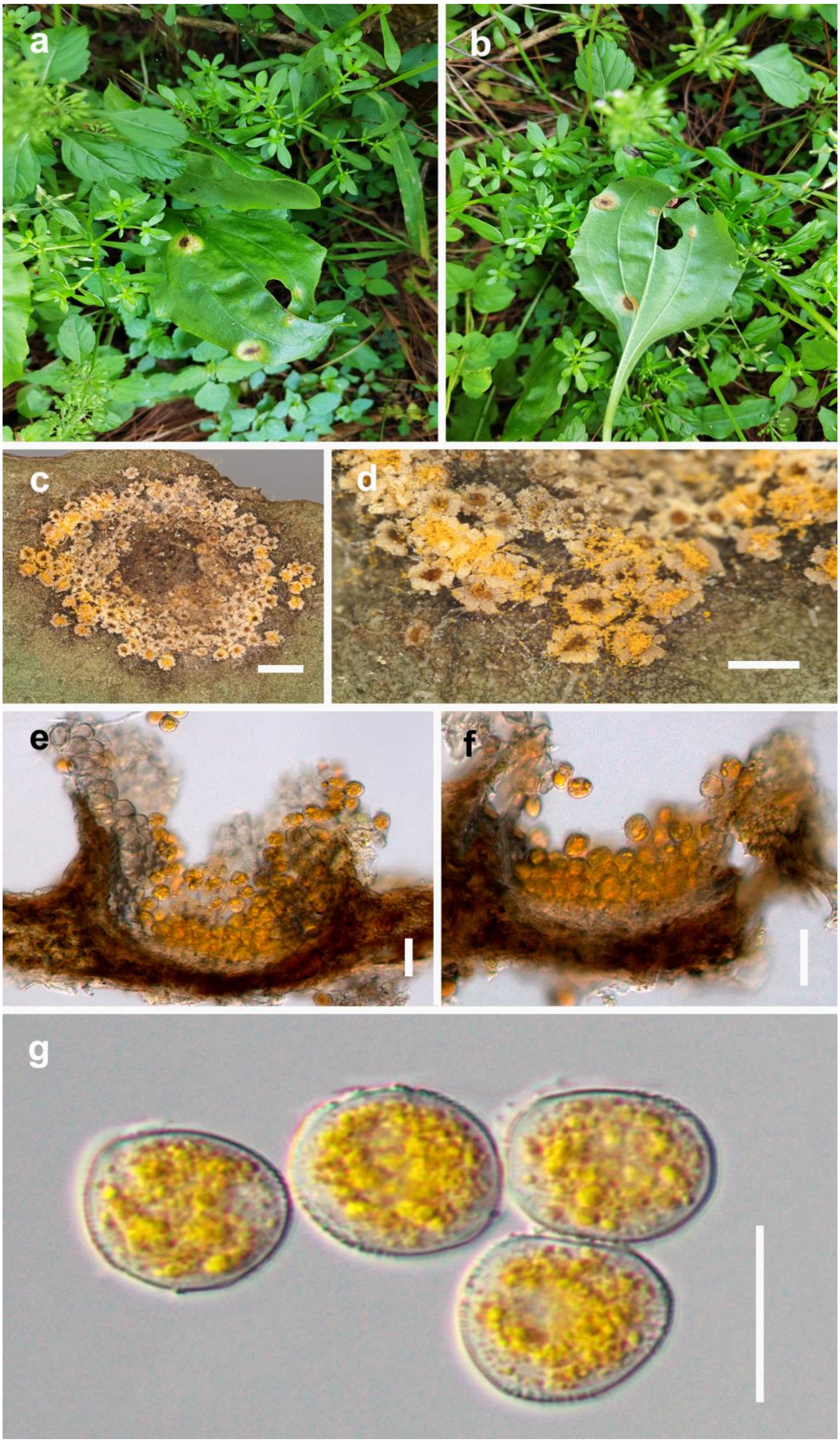

Figure 42 – *Puccinia cynodontis* (from HGUP21253) on *Plantago asiatica*. a–d Aecia on leaves. e–f Longitudinal section of aecia. g Aeciospores. Scale bars: c = 1 mm, d = 0.5 mm, e–f = 50 µm, g = 25 µm.

Puccinia hieracii (Röhl.) H. Mart., Prodromus Flora Mosquensis Ed. 2: 226, 1817. Fig. 43

MycoBank number: MB245124

Description – *Spermogonia*, *aecia* and *telia* not found. *Uredinia* produced on abaxial leaf surface, scattered, not surrounded by host epidermis, circular spot or irregular, chocolate-brown, pulverulent, 1.0–3.0 mm diam. *Urediniospores* globose or ellipsoidal, 23–31 × 19–25 µm ($\bar{x}$ = 26.5 × 23.5 µm, n = 30), cinnamon-brown to brown; wall 1.7–3.1 µm thick, densely, and minutely echinulate.

Host – *Taraxacum mongolicum* (Asteraceae)

Material examined – CHINA, Guizhou Province, Zunyi city, 27°67'16"N, 106°39'77"W, 1020 m, 26 May 2022, on *Taraxacum mongolicum*, J.E. Sun, HGUP21208; Panzhou city, 25°89'60"N, 104°84'33"W, 805 m, 19 Jun 2021, on *T. mongolicum*, J.E. Sun, HGUP21209.

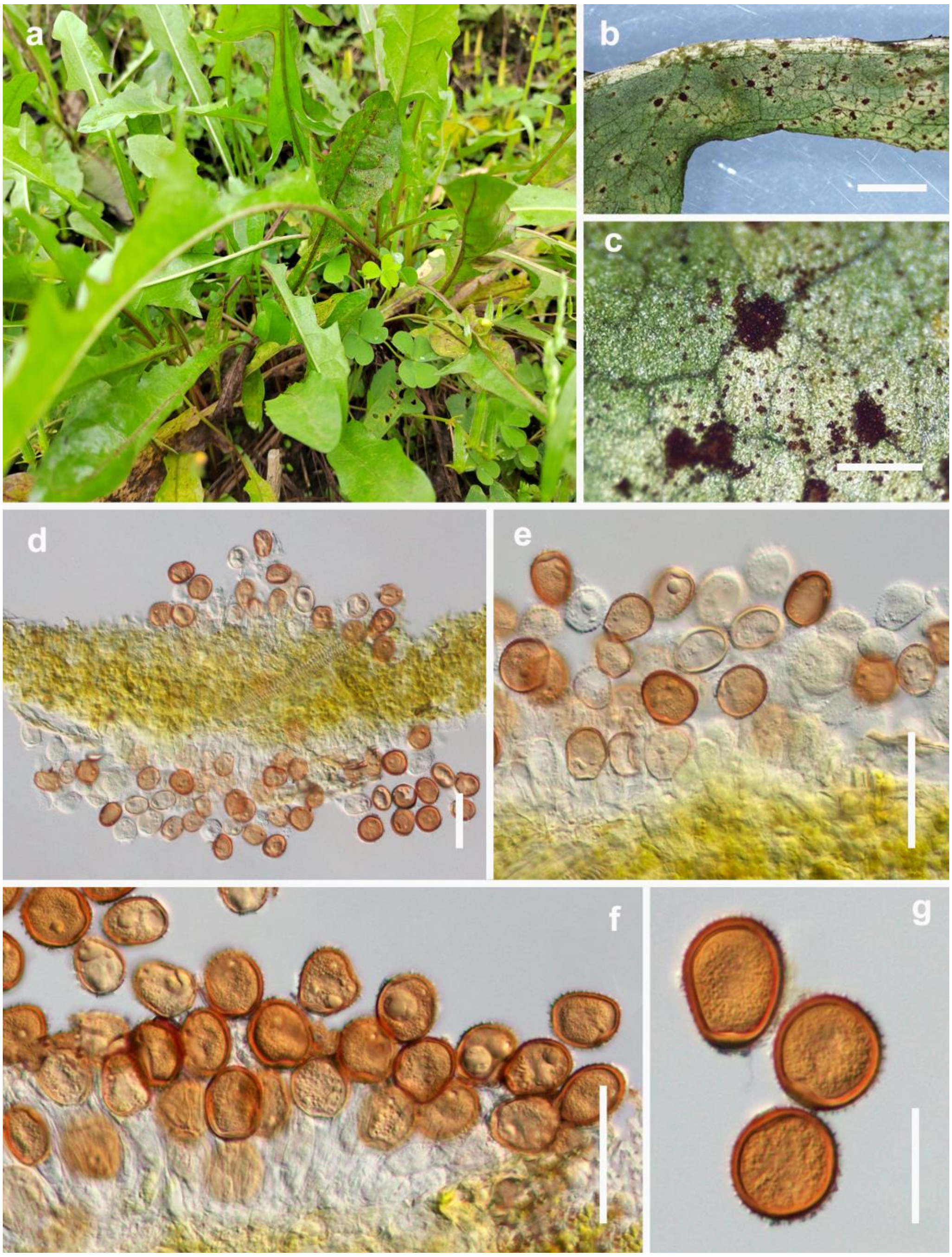

Figure 43 – *Puccinia hieracii* (from HGUP21208) on *Taraxacum mongolicum*. a–c Uredinia on leaves. d–f Longitudinal section of uredinium. g Urediniospores. Scale bars: b = 5 mm, c = 1 mm, d–f = 50 µm, g = 25 µm.

Notes – Phylogenetic analyses show that our specimens grouped with *P. hieracii* with high support (ML/MP/PP: 100/-/1; Fig. 2). Morphologically our collections have similar uredinia and urediniospores (23–31 × 19–25 µm *vs.* 25–29 × 20–25 µm) to *P. hieracii* (Zhuang et al. 2012). Based on both morphology and phylogenetic analyses, we confirm our collections as *P. hieracii*.

Puccinia crepidis-japonicae (Lindr.) Dietel, Annales Mycologici 6: 226 (1908) Fig. 44

MycoBank number: MB233934

Description – *Spermogonia*, *aecia* and *telia* not found. *Uredinia* produced on abaxial leaf surface and stems, scattered, surrounded by host epidermis, circular spot or ellipsoidal, cinnamon-brown, pulverulent, 0.5–1.5 mm diam. *Urediniospores* globose or ellipsoidal, 17–23 × 15–20 µm (x̄ = 20.5 × 18.1 µm, n = 30), cinnamon-brown; wall 1.2–2.0 µm thick, densely, and minutely echinulate.

Host – *Youngia japonica* (Asteraceae)

Material examined – CHINA, Guizhou Province, Guiyang city, 26°45'33"N, 106°65'80"W, 1121 m, 6 May 2022, on *Youngia japonica*, J.E. Sun, HGUP21210, HGUP21211.

Notes – Our specimens formed an independent basal clade in the phylogenetic tree (Fig. 2), with a close relationship to *Puccinia crepidis-japonicae* (BPI 910311). Our collections are similar to *P. crepidis-japonicae* in the dimensions of urediniospores (16–27 × 16–22 µm) as described by Zhuang et al. (2005). *Puccinia crepidis-japonicae* occurred only on *Youngia* sp. In China (Zhuang et al. 2005), and our specimens were also collected from *Y. japonica*. Hence, we named our collections as *P. crepidis-japonicae*.

Puccinia crepidis J. Schröt., Kryptogamen-Flora von Schlesien 3-1(3): 319 (1887) Fig. 45

MycoBank number: MB247358

Description – *Spermogonia*, *aecia* and *telia* not found. *Uredinia* produced on abaxial leaf surface, scattered, not surrounded by host epidermis, circular spot, chocolate-brown, pulverulent, 0.5–1.0 mm diam. *Urediniospores* globose or subglobose, 20–25 × 16–23 µm (x̄ = 22.6 × 19.6 µm, n = 30), cinnamon-brown; wall 1.4–2.3 µm thick, densely and minutely echinulate.

Host – *Crepidiastrum sonchifolium* (Asteraceae)

Material examined – CHINA, Guizhou Province, Guiyang city, 26°44'99"N, 106°65'01"W, 1105 m, 16 Jul 2022, on *Crepidiastrum sonchifolium*, J.E. Sun, HGUP21212, HGUP21213.

Notes – *Puccinia crepidis* occurs often on *Crepidiastrum* sp. and *Crepis* sp., but there is no nucleotide data in NCBI. In the phylogenetic analysis, our specimens grouped in an independent clade, closely related to *P. lapsanae* and *P. crepidis-japonicae* with 99% ML, 65% MP bootstrap support (Fig. 2). Morphologically urediniospore dimensions from our collections are similar to those of *P. crepidis* which was designated by Zhuang et al. (2005). Hence, we identified our collections as *P. crepidis*.

Puccinia arachidis Speg., Anales de la Sociedad Científica Argentina 17 (2): 90 (1884)
Fig. 46

MycoBank number: MB182957

Description – *Spermogonia*, *aecia* and *telia* not found. *Uredinia* amphigenous, surrounded by host epidermis, ellipsoidal to oval, or irregular, cinnamon-brown to chocolate-brown, pulverulent, 1.0–2.0 mm diam. *Urediniospores* ellipsoidal or ovoid, 21–30 × 17–23 µm (x̄ = 25.8 × 19.6 µm, n = 30), inclusions pale to cinnamon-brown; wall 1.5–2.2 µm thick, colorless, densely and minutely echinulate.

Host – *Arachis hypogaea* (Fabaceae)

Material examined – CHINA, Guizhou Province, Xingyi city, 24°92'20"N, 105°58'60"W, 1002 m, 26 Jul 2021, on *Arachis hypogaea*, X.J. Chen, HGUP21199, HGUP21200.

Notes – *Puccinia arachidis* occurs on *Arachis hypogaea*. However, telia and teliospores of *P. arachidis* have not been reported in China. Morphologically, our description is similar to that reported by Zhuang et al. (2005). The specimens phylogenetically grouped an independent clade with high bootstrap support (Fig. 2). Based on the morphology and its host, we identified our collections as *P. arachidis*.

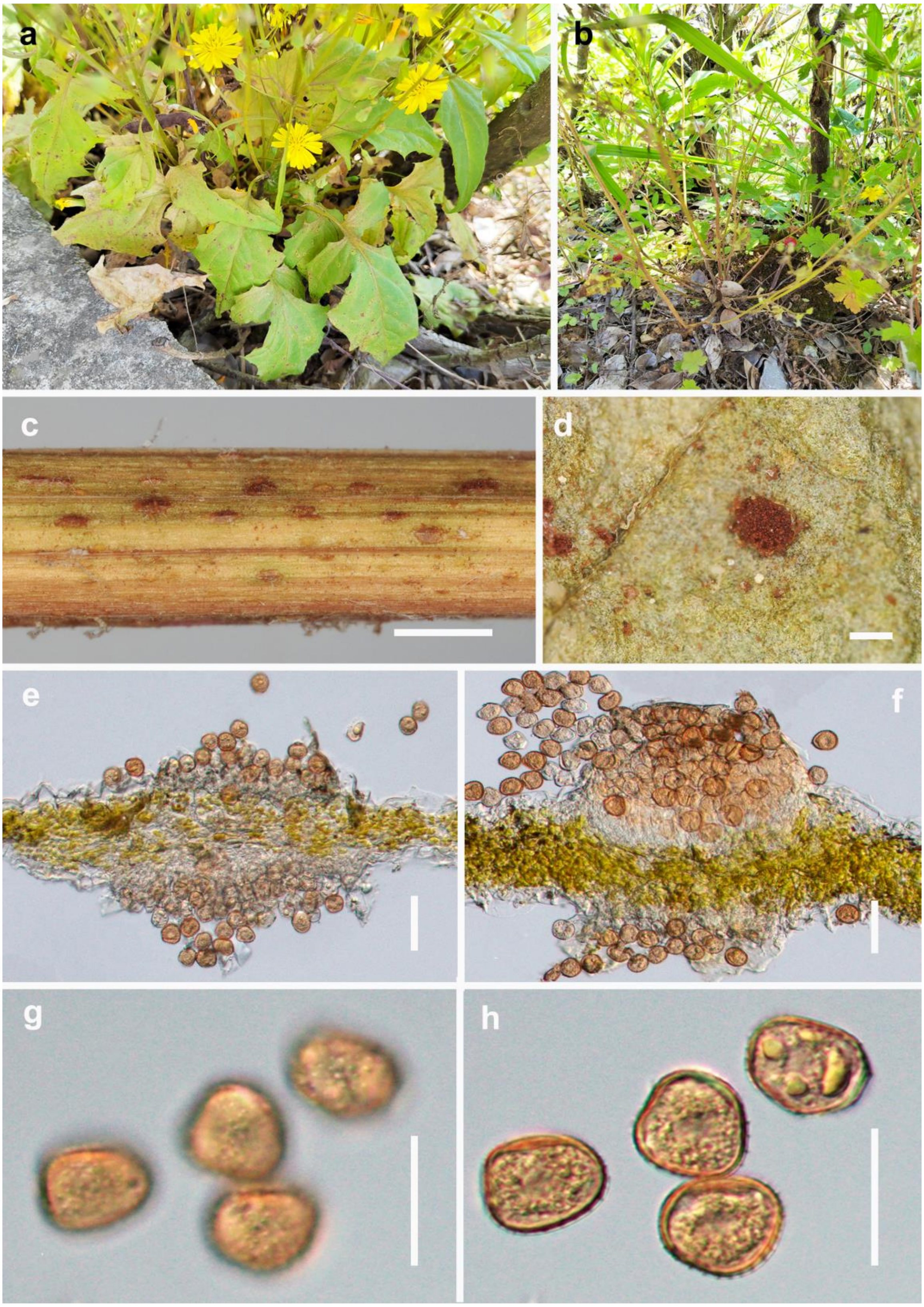

Figure 44 – *Puccinia crepidis-japonicae* (from HGUP21210) on *Youngia japonica*. a–d Uredinia on leaves and stems. e–f Longitudinal section of uredinia. g–h Urediniospores. Scale bars: c = 1 mm, d = 0.5 mm, e–f = 50 µm, g–h = 25 µm.

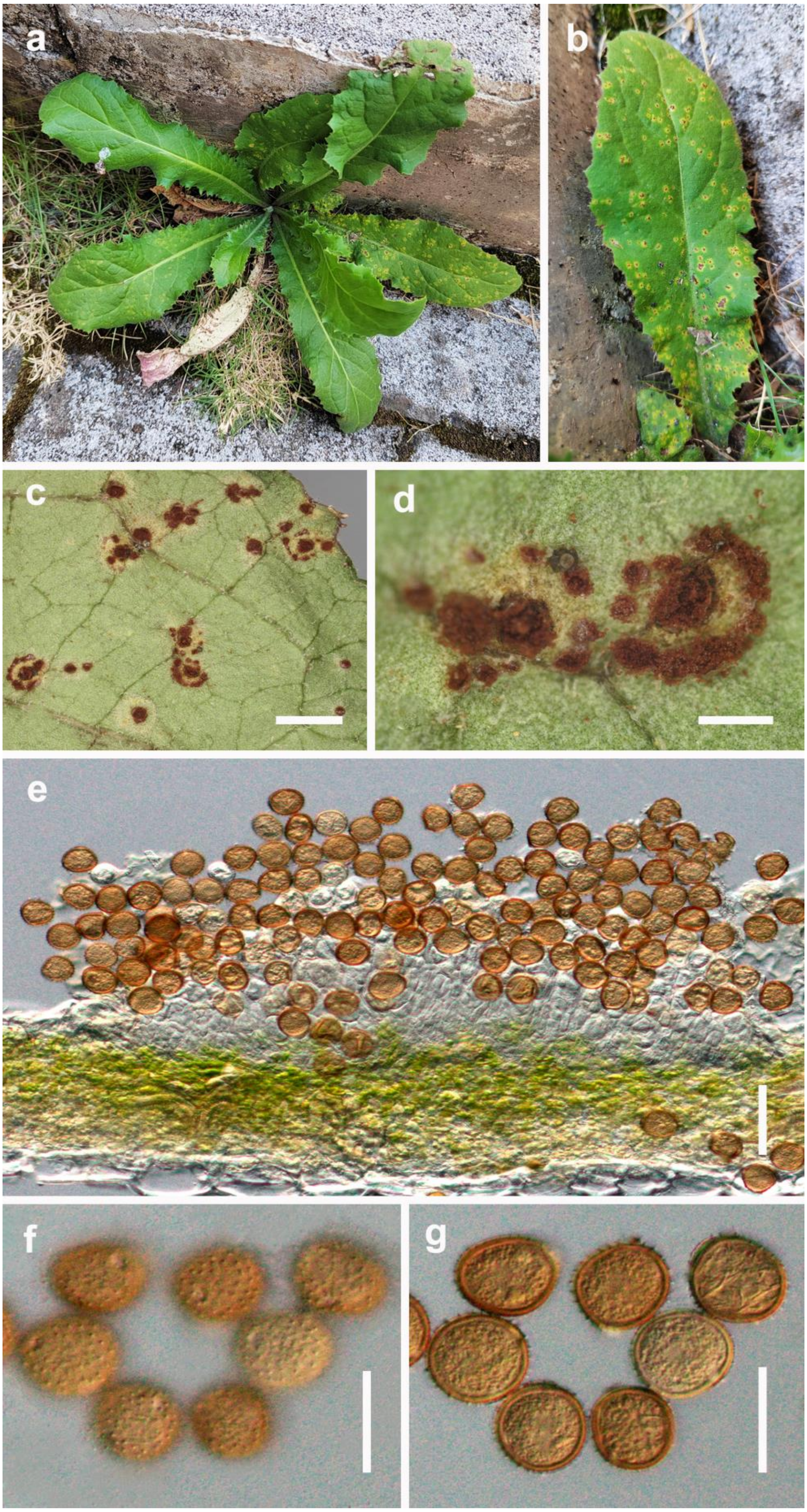

Figure 45 – *Puccinia crepidis* (from HGUP21212) on *Crepidiastrum sonchifolium*. a–d Uredinia on leaves. e Longitudinal section of uredinium. f–g Urediniospores. Scale bars: c = 2 mm, d = 0.5 mm, e = 50 µm, f–g = 25 µm.

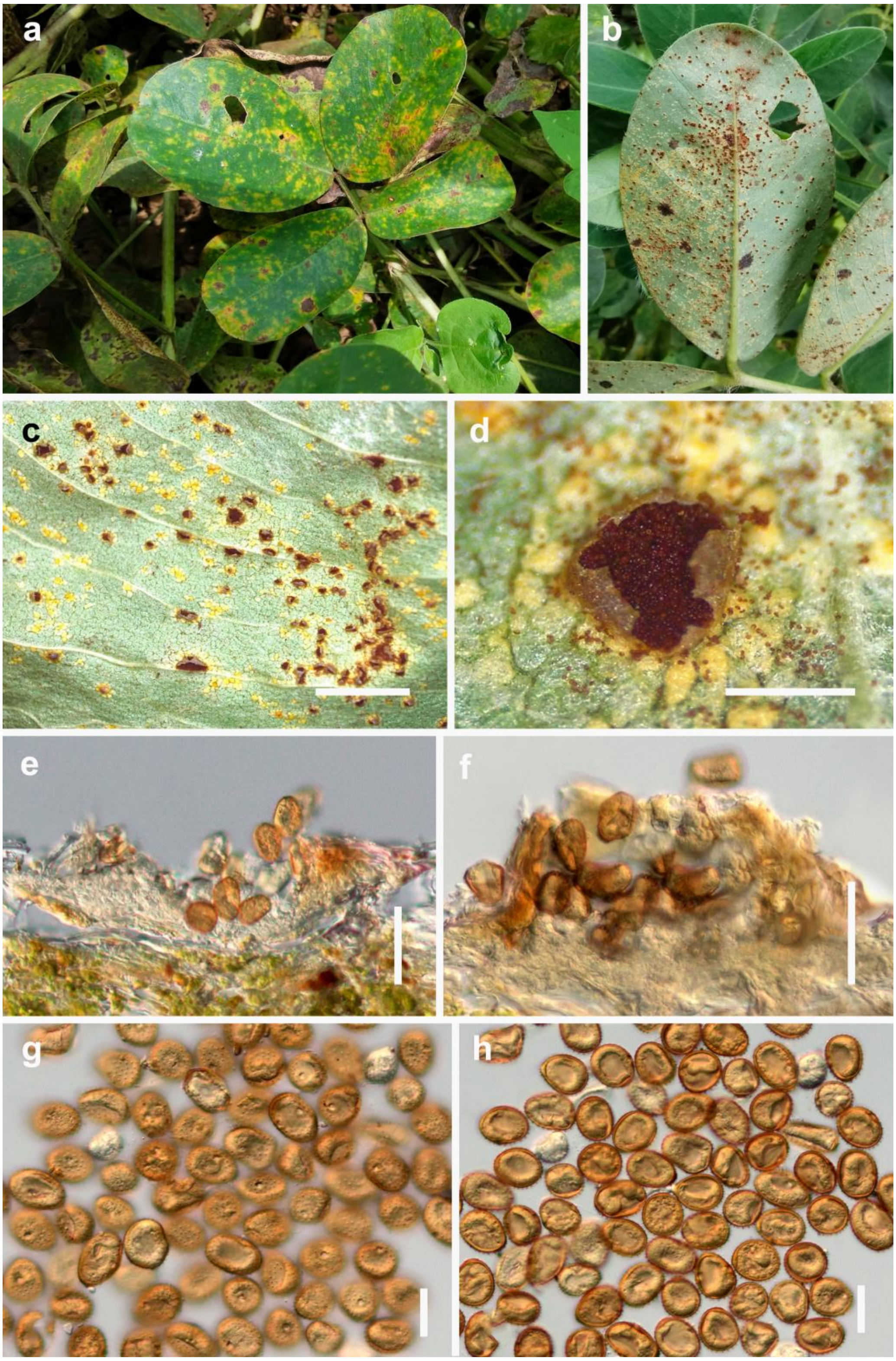

Figure 46 – *Puccinia arachidis* (from HGUP21199) on *Arachis hypogaea*. a–d Uredinia on leaves. e–f Longitudinal section of uredinia. g–h Urediniospores. Scale bars: c = 5 mm, d = 1 mm, e–h = 50 µm, g–h = 25 µm.

Puccinia senecionis Lindr., Acta Societatis pro Fauna et Flora Fennica 26 (5): 12 (1904).

Fig. 47

MycoBank number: MB227908

Description – *Spermogonia*, *uredinia* and *telia* not found. *Aecia* produced on abaxial leaf surface, scattered, not surrounded by host epidermis, obvious boundary, roestelioid, 1.0–5.0 mm diam., peridium dehiscent at apex, no slits along the sides, yellow. *Aeciospores* ellipsoidal or subglose, 17–22 × 15–19 µm ($\overline{x}$ = 20 × 17.3 µm, n = 30), yellow; wall 0.8–1.3 µm thick, colorless, rugose.

Host – *Senecio scandens* (Asteraceae)

Material examined – CHINA, Guizhou Province, Tongren city, 27°74'78"N, 108°83'05"W, 560 m, 23 May 2022, *Senecio scandens*, Y.R. Sun, HGUP21198.

Notes – Our specimen independently gathered in one branch, with a low node support rate (ML/MP/BI=51/-/-), showing obvious genetic distance. Morphologically our collection is similar to *P. senecionis* as reported by Zhuang et al. (1998). On the basis of both morphology and phylogenetic analyses, we identify our collection as *P. senecionis*.

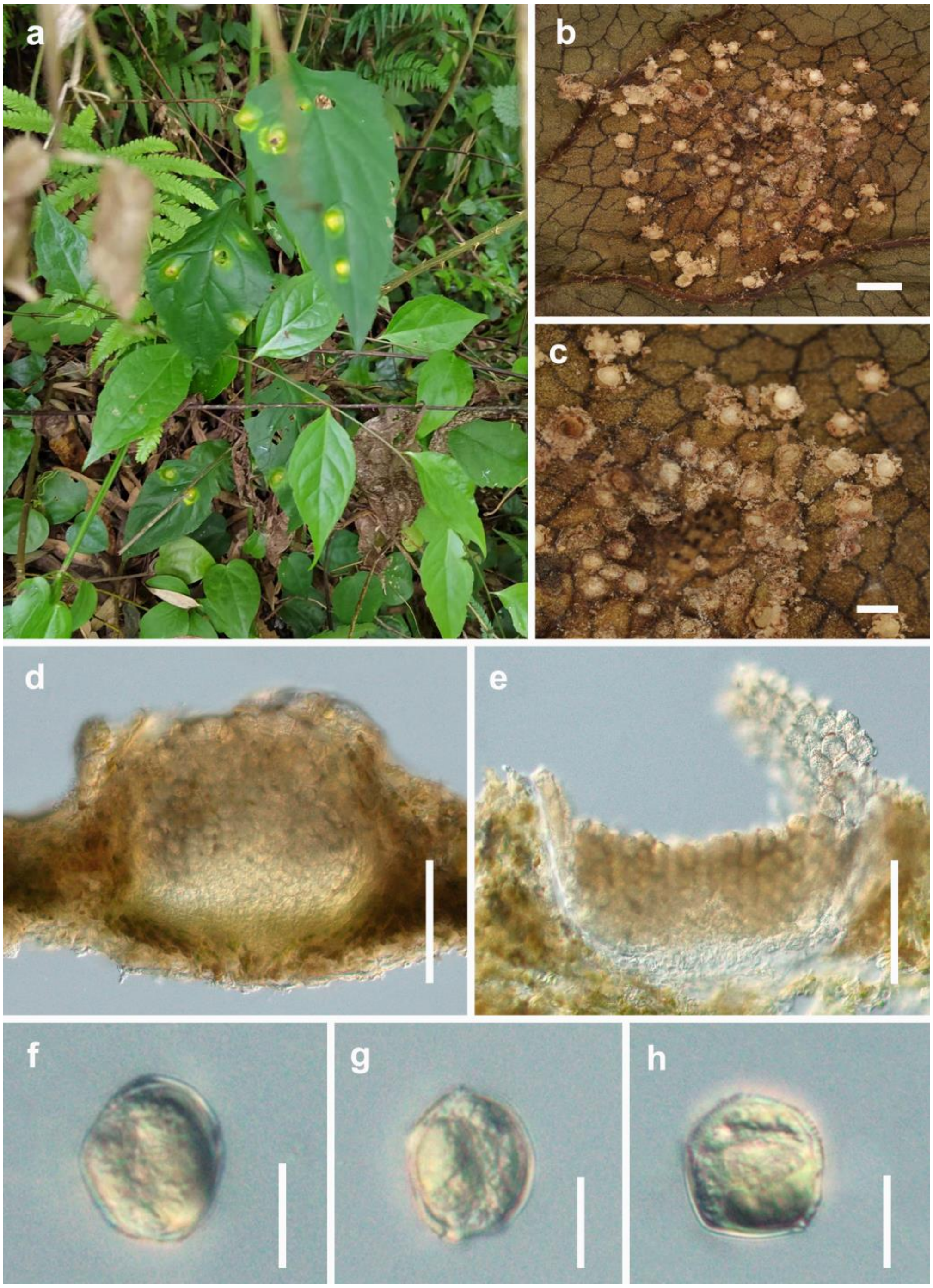

Figure 47 – *Puccinia senecionis* (from HGUP21198) on *Senecio scandens*. a–c Aecia on leaves. d–e Longitudinal section of aecia. f–h Aeciospores. Scale bars: b = 1 mm, c = 0.5 mm, d–e = 50 µm, f–h = 12.5 µm.

Puccinia tokyensis P. Syd. & Syd., Monographia Uredinearum 1 (5): 377 (1902) Fig. 48

MycoBank number: MB166521

Description – *Spermogonia*, *aecia* and *telia* not found. *Uredinia* hypophyllous, surrounded by host epidermis, ellipsoidal to oval, yellow, pulverulent, 1.0–2.0 mm diam. *Urediniospores* ellipsoidal or ovoid, 20–26 × 16–23 µm ($\bar{x}$ = 23.3 × 19.1 µm, n = 30), inclusions pale to light-golden; wall 1.4–2.3 µm thick, colorless, densely, and minutely echinulate.

Host – *Cryptotaenia japonica* (Apiaceae)

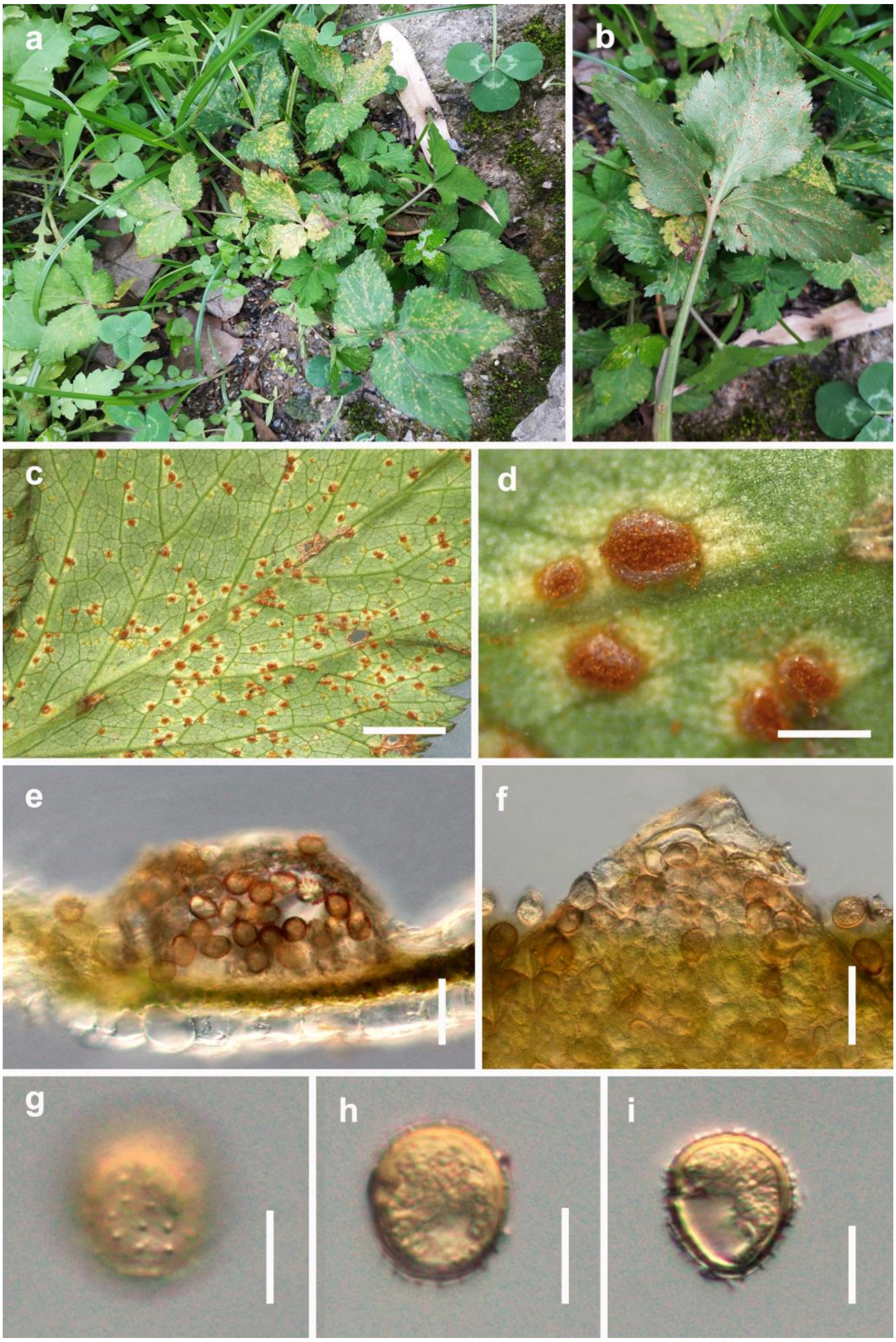

Figure 48 – *Puccinia tokyensis* (from HGUP21195) on *Cryptotaenia japonica*. a–d Uredinia on leaves. e–f Longitudinal section of uredinia. g–i Urediniospores. Scale bars: c = 5 mm, d = 1 mm, e–f = 50 µm, g–i = 12.5 µm.

Material examined – CHINA, Guizhou Province, Guiyang city, 26°43'94"N, 106°67'94"W, 1115 m, 24 May 2021, on *Cryptotaenia japonica*, J.E. Sun, HGUP21195; Zunyi city, 27°67'29"N, 106°39'93"W, 1004 m, 27 May 2022, on *C. japonica*, J.E. Sun, HGUP21196; Guiyang city, 26°98'37"N, 106°45'39"W, 1111 m, 24 Mar 2022, on *C. japonica*, J.E. Sun, HGUP21197.

Notes – *Puccinia tokyensis* was found mainly on *Cryptotaenia japonica*, including spermogonial, aecial, uredinial and telial stages by Zhuang et al. (2005). In the phylogenetic analysis our specimens cluster with *P. tokyensis* (ZP-R339, ZP-R406 and ZP-R447) with good support (Fig. 2). The urediniospores are similar to those of *P. tokyensis* as described by Zhuang et al. (2005). Hence, based on both morphology and phylogeny, we identify our collections as *P. tokyensis*.

Puccinia latimamma J.Y. Zhuang & S.X. Wei, Mycosystema: 154 (2000) Fig. 49

MycoBank number: MB467374

Description – *Spermogonia*, *aecia* and *telia* not found. *Uredinia* hypophyllous, surrounded by host epidermis, oblong to oval, cinnamon-brown, pulverulent, 1.0–2.0 mm diam. *Urediniospores* ellipsoidal or ovoid, 20–28 × 17–22 µm ($\bar{x}$ = 24.7 × 19.9 µm, n = 30), inclusions pale to cinnamon-brown; wall 1.0–1.6 µm thick, colorless, densely, and minutely echinulate.

Hosts – *Pleuropterus multiflorus* (Polygonaceae)

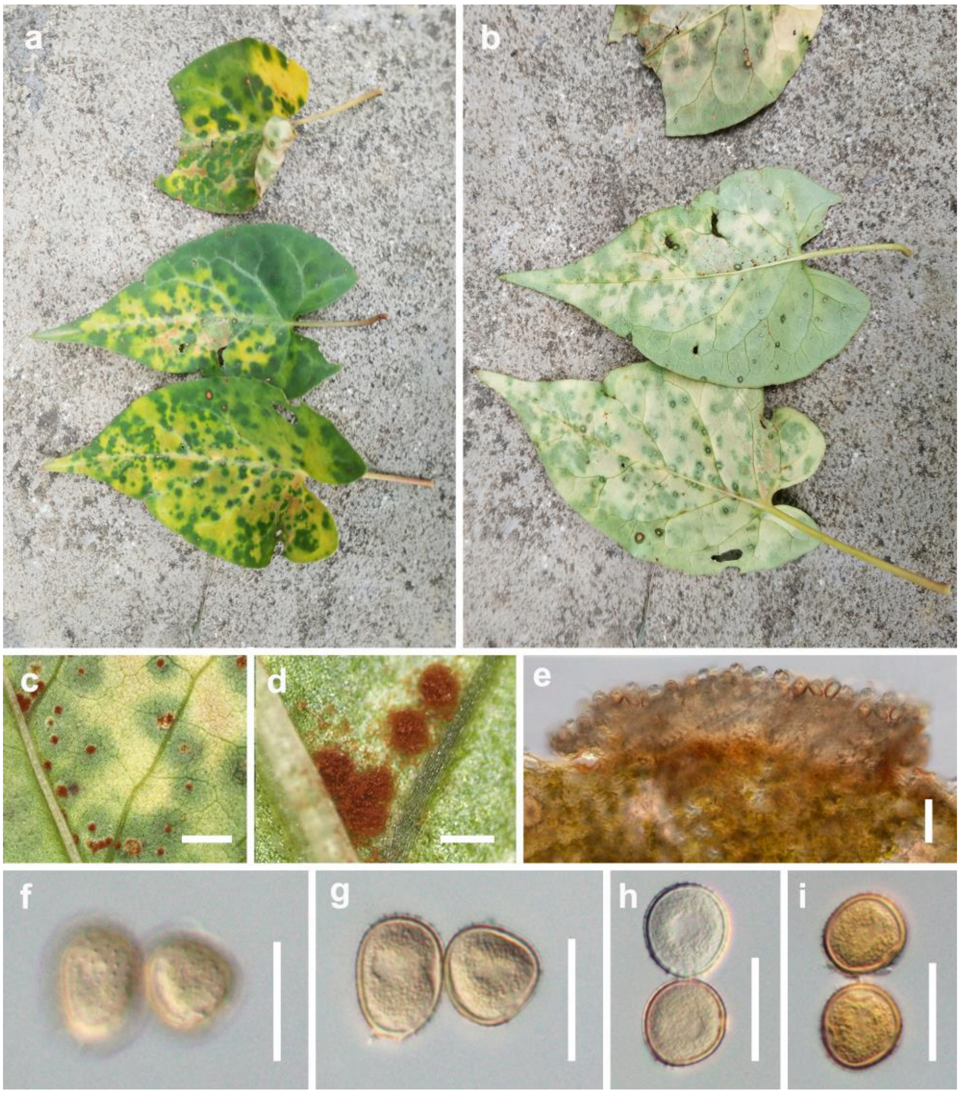

Figure 49 – *Puccinia latimamma* (from HGUP21186) on *Pleuropterus multiflorus*. a–d Uredinia on leaves. e Longitudinal section of uredinium. f–i Urediniospores. Scale bars: c = 5 mm, d = 1 mm, e = 50 µm, f–i = 25 µm.

Material examined – CHINA, Guizhou Province, Guiyang city, 26°43'75"N, 106°67'79"W, 1121 m, 24 May 2021, on *Pleuropterus multiflorus*, J.E. Sun, HGUP21186; Liupanshui city, 26°04'56"N, 104°52'10"W, 1335 m, 17 Jul 2021, on *P. multiflorus*, J.E. Sun, HGUP21187; Zunyi city, 27°66'19"N, 106°40'89"W, 1072 m, 10 Jun 2022, on *P. multiflorus*, J.E. Sun, HGUP21188.

Notes – In the multiple loci phylogenetic analysis (Fig. 2), our specimens clustered with *Puccinia latimamma* (ZP-R1398, ZP-R387). Morphologically our collections are similar to *P. latimamma* although they have wider uredinia (1.0–2.0 mm *vs*. 0.2–0.5 mm) (Zhuang et al. 2005). Based on both morphology and phylogenetic analyses, we identify our collections as *P. latimamma*.

Puccinia gentianae (F. Strauss) Mart., Deutschl. Flora, Edn 2: 131 (1824) Fig. 50

MycoBank number: MB147173

Description – *Spermogonia* and *aecia* not found. *Uredinia* produced on abaxial leaf surface, scattered, surrounded by host epidermis, circular spot, light brown, pulverulent, 0.5–1.0 mm diam. *Urediniospores* globose or ellipsoidal, 24–30 × 23–28 µm ($\bar{x}$ = 27 × 24.9 µm, n = 30), cinnamon-brown; wall 1.7–2.4 µm thick, densely and minutely echinulate. *Telia* produced on abaxial leaf surface, circular or subglobose, chocolate-brown, pulverulent, 0.5–1.0 mm. *Teliospores* ellipsoidal to cylindrical, 2-celled, constricted at the septum, chocolate-brown to gray-brown, 34–41 × 23–30 µm ($\bar{x}$ = 38.2 × 26.9 µm, n = 30); wall 2.3–3.3 µm thick; pedicels not swollen at the base, fragile, colorless.

Host – *Gentiana macrophylla* (Gentianaceae)

Material examined – CHINA, Yunnan Province: Dali city, 26°44'35"N, 99°96'18"W, 2227 m, 28 Oct 2021, on *Gentiana macrophylla*, X.J. Chen, HGUP21206, HGUP21207.

Notes – *Puccinia gentianae* was recorded on *Gentiana algida*, *G. crassicaulis*, *G. lhakangensis* and *G. macrophylla* (Zhuang et al. 2005), although without nucleotide data. Our specimens phylogenetically grouped in a separated clade with high bootstrap support (Fig. 2). The urediniospores (24–30 × 23–28 µm *vs*. 22–33 × 18–26 µm) and teliospores (34–41 × 23–30 µm *vs*. 28–43 × 23–30 µm) of our specimens are quite similar to those of *P. gentianae* as illustrated and described by Zhuang et al. (2005). Thus, we identified our collections as *P. gentianae*.

Puccinia congesta Berk. & Broome, Journal of the Linnean Society. Botany 14: 91 (1875) Figs 51, 52

MycoBank number: MB206356

Description – *Spermogonia*, *aecia* and *uredinia* not found. *Telia* produced on abaxial leaf surface, circular or subcircular, chocolate-brown, pulverulent, 0.5–1.0 mm diam. *Teliospores* ellipsoidal to cylindrical, 1–2-celled, constricted at the septum, chocolate-brown to gray-brown, 35–45 × 15–21 µm ($\bar{x}$ = 39.8 × 17.7 µm, n = 30); wall 1.8–2.7 µm thick; pedicels not swollen at the base, 50–110 µm long, colorless.

Hosts – *Persicaria posumbu* (Polygonaceae), Polygonaceae

Material examined – CHINA, Guizhou Province, Guiyang city, 26°65'97"N, 106°67'65"W, 1354 m, 21 Aug 2021, on *Persicaria posumbu*, J.E. Sun, HGUP21222, HGUP21223; Duyun city, 25°83'00"N, 107°32'59"W, 781 m, 20 Jul 2022, on Polygonaceae, J.E. Sun, HGUP21224.

Notes – Two *Puccinia* species, *P. polygonicola* and *P. congesta*, occur on *Persicaria posumbu* (Zhuang et al. 2005), but there is no DNA data in NCBI. In comparison with the description of Zhuang et al. (2005), our specimens are similar to the teliospores (35–45 × 15–21 µm *vs*. 30–55 × 12–23 µm) of *P. congesta*. In the phylogenetic analysis, the specimens grouped a clade (Fig. 2) with a distant relationship to other species. Therefore, we name the collections as *P. congesta*.

Puccinia nepalensis Barclay & Dietel, Hedwigia 29: 265 (1890) Fig. 53

MycoBank number: MB214101

Description – *Spermogonia*, *aecia* and *telia* not found. *Uredinia* hypophyllous, surrounded by host epidermis, oblong to oval, cinnamon-brown, pulverulent, 1.0–3.0 mm diam. *Urediniospores* ellipsoidal or ovoid, some irregular, 25–34 × 22–29 µm ($\bar{x}$ = 28.3 × 24.9 µm, n = 30), inclusions pale to cinnamon-brown; wall 1.4–2.6 µm thick, colorless, densely and minutely echinulate.

Host – *Rumex nepalensis* (Polygonaceae)

Material examined – CHINA, Guizhou Province, Kaili city, 26°95'91"N, 108°67'75"W, 721 m, 24 Mar 2022, on *Rumex nepalensis*, X.J. Chen, HGUP21190, HGUP21191; Guiyang city, 26°44'02"N, 106°67'92"W, 1006 m, 24 May 2021, on *R. nepalensis*, J.E. Sun, HGUP21192; Duyun city, 26°76'45"N, 106°48'42"W, 852 m, 24 Mar 2022, on *R. nepalensis*, X.J. Chen, HGUP21181, HGUP21230.

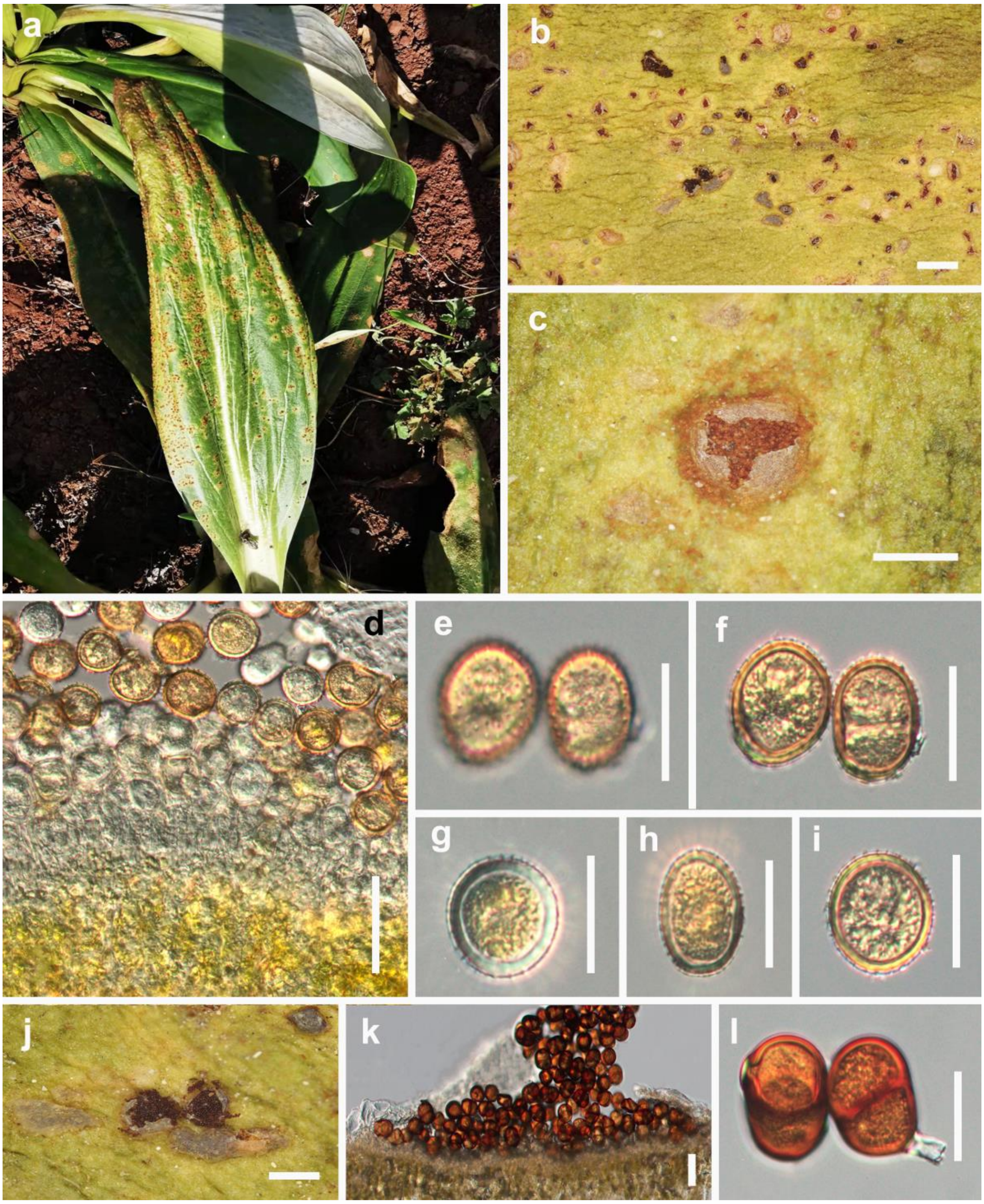

Figure 50 – *Puccinia gentianae* (from HGUP21206) on *Gentiana macrophylla*. a–b Uredinia and telia on leaves. c Uredinium on leaf. d Longitudinal section of uredinium. e–i Urediniospores.

j Telia on leaf. k Longitudinal section of telium. l Teliospores. Scale bars: b = 5 mm, c, j = 1 mm, d, k = 50 µm, e–i, l = 25 µm.

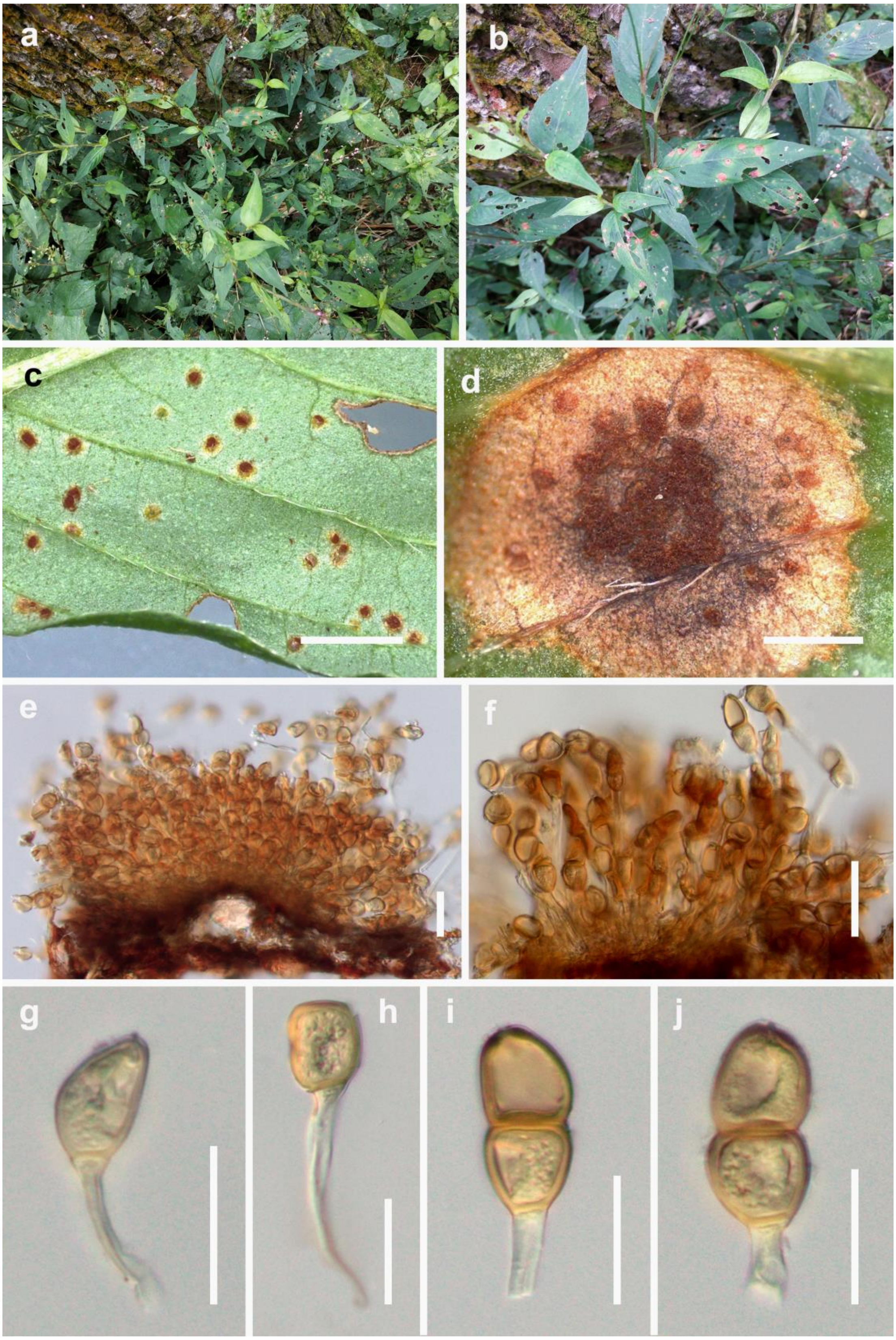

Figure 51 – *Puccinia congesta* (from HGUP21222) on *Persicaria posumbu*. a–d Telia on leaves. e–f Longitudinal section of telia. g–j Teliospores. Scale bars: c = 5 mm, d = 1 mm, e–f = 50 µm, g–j = 25 µm.

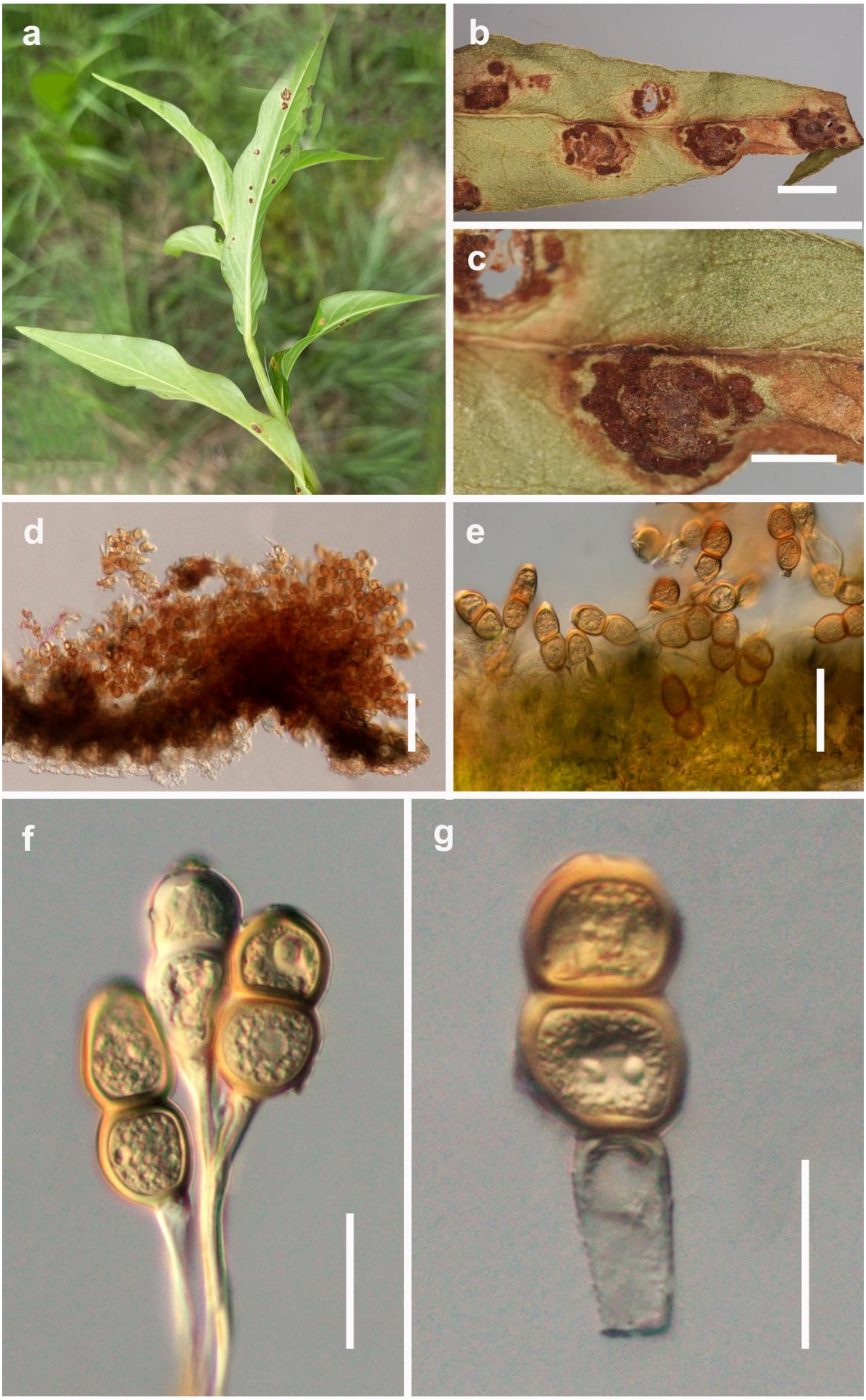

Figure 52 – *Puccinia congesta* (from HGUP21224) on Polygonaceae. a–c Telia on leaves. d–e Longitudinal section of telia. f–g Teliospores. Scale bars: b–c = 2 mm, d = 100 µm, e = 50 µm, f–g = 25 µm.

Notes – *Puccinia nepalensis* has been reported on *Rumex nepalensis* from China, India and Pakistan (Dietel 1890, Zhuang et al. 2005). Our specimens had a node support rate of ML/MP/BI=99/88/- in the phylogenetic tree (Fig. 2). Morphologically, our collections resemble *P. nepalensis* in the dimension of uredinia (2.0–3.0 mm) and urediniospores (20–30 × 18–25 µm) (Zhuang et al. 2005). Hence, we identify our collections as *P. nepalensis*.

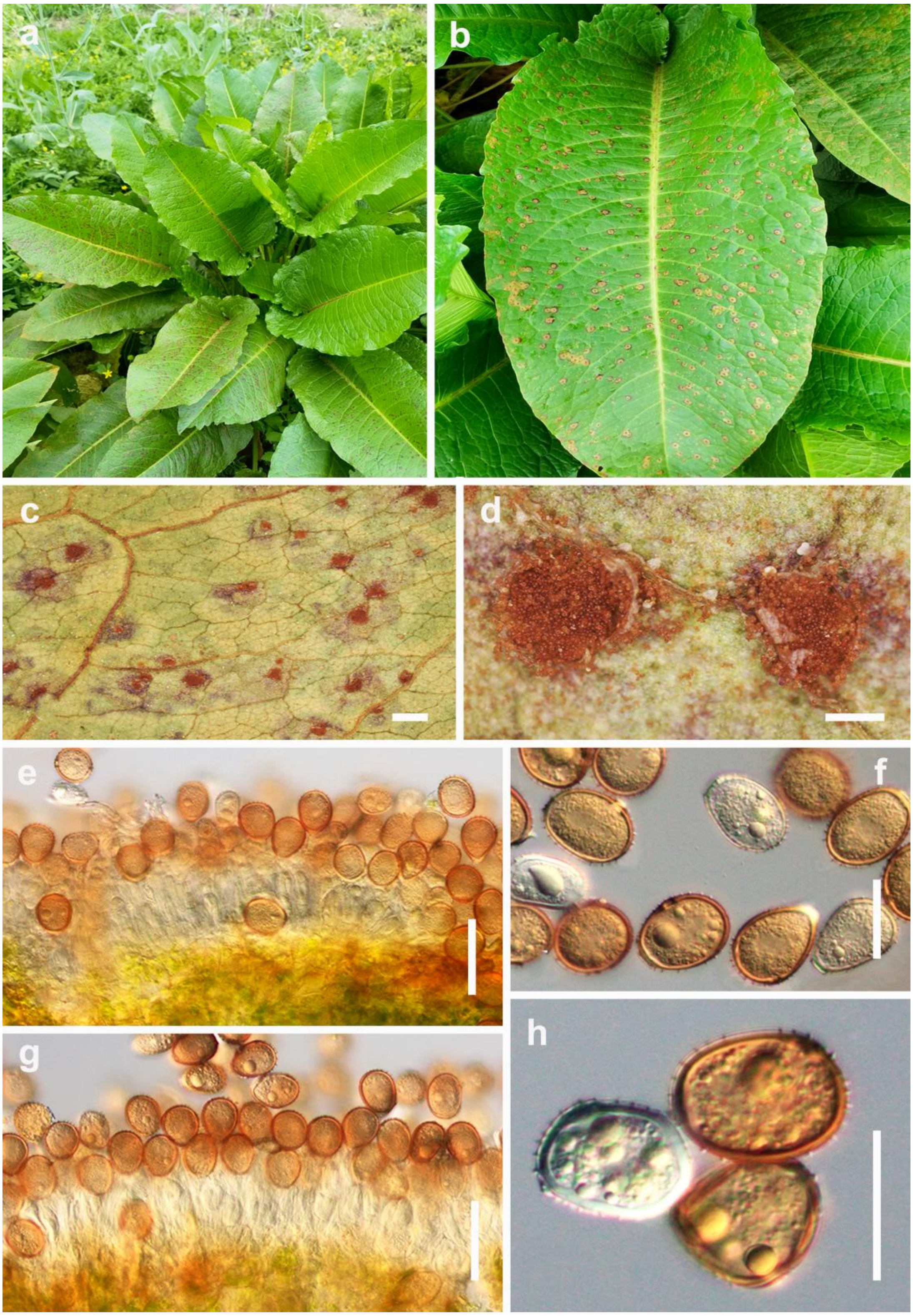

Figure 53 – *Puccinia nepalensis* (from HGUP21190) on *Rumex nepalensis*. a–d Uredinia on leaves. e–f Longitudinal section of uredinia. g–h Urediniospores. Scale bars: c = 1 mm, d = 0.5 mm, e–f = 50 µm, g–h = 25 µm.

Puccinia iridis Wallr. ex Rabenh., Deutschl. Krypt.-Fl. (Leipzig) 1: 23 (1844) Fig. 54

MycoBank number: MB234038

Description – *Aecia* and *telia* not found. *Spermogonia* produced on abaxial leaf surface, 180–240 µm diam. *Uredinia* produced on abaxial leaf surface, surrounded by host epidermis, ellipsoidal to oval, cinnamon-brown to chocolate-brown, pulverulent, 1.0–3.0 mm diam. *Urediniospores* ellipsoidal or ovoid, 25–32 × 18–29 µm ($\bar{x}$ = 28.2 × 23.9 µm, n = 30), inclusions pale to cinnamon-brown; wall 2.3–3.3 µm thick, colorless, densely and minutely echinulate.

Host – *Iris tectorum* (Iridaceae)

Material examined – CHINA, Guizhou Province, Guiyang city, 26°45'24"N, 106°65'62"W, 1003 m, 28 Jun 2021, on *Iris tectorum*, J.E. Sun, HGUP21201, HGUP21202.

Figure 54 – *Puccinia iridis* (from HGUP21201) on *Iris tectorum*. a–d Uredinia and spermogonia on leaves. e Longitudinal section of spermogonium. f Longitudinal section of uredinium. g–l Urediniospores. Scale bars: c = 5 mm, d = 1 mm, e–f = 50 µm, g–l = 25 µm.

Notes – In the phylogenetic analysis our specimens grouped with *Puccinia iridis* (ZP-R482, ZP-R1402 and ZP-R221) (Fig. 2), which were from *Iris tectorum* in China. The urediniospores from our collections are morphologically similar to those of *P. iridis* (25–32 × 18–29 µm *vs.* 25–35 × 18–27 µm) (Zhuang et al. 2005). Therefore, we identify our specimens as *P. iridis*.

Puccinia hemerocallidis Thüm., Bulletin de la Société Impériale des Naturalistes de Moscou 55 (1): 81, 1880. Fig. 55

MycoBank number: MB157213

Description – *Spermogonia*, *aecia* and *telia* not found. *Uredinia* hypophyllous, surrounded by host epidermis, ellipsoidal to oval, cinnamon-brown, pulverulent, 1.0–2.0 mm diam. *Urediniospores* ellipsoidal or ovoid, 21–29 × 17–23 µm ($\overline{x}$ = 25.4 × 19.8 µm, n = 30), inclusions pale to light yellow; wall 1.6–3.5 µm thick, colorless, densely and minutely verrucose.

Host – *Hemerocallis fulva* (Asphodelaceae)

Material examined – CHINA, Guizhou Province, Duyun city, 27°60'06"N, 107°38'92"W, 898 m, 23 Jun 2021, on *Hemerocallis fulva*, J.E. Sun, HGUP21218, HGUP21219; Tongren city, 28°16'05"N, 108°33'48"W, 780 m, 4 Sep 2021, on *H. fulva*, J.E. Sun, HGUP21220.

Notes – In the phylogenetic analysis, our specimens clustered with *P. hemerocallidis* (HMAS37736 and BRIP 53476) (Fig. 2). Our specimens agreed with the description of Zhuang et al. (2005). We, therefore, identify our collections as *P. hemerocallidis*.

Puccinia patriniae Henn., Bot. Jb. 28(3): 261 (1900) Fig. 56

MycoBank number: MB226672

Description – *Spermogonia*, *uredinia* and *telia* not found. *Aecia* produced on abaxial leaf surface, scattered, obvious boundary, roestelioid, 0.1–0.5 mm diam., 0.2–0.6 mm long, pale to yellow. *Aeciospores* ellipsoidal or oblong to irregular, 15–20 × 12–18 µm ($\overline{x}$ = 17.5 × 14.3 µm, n = 30), inclusions pale to yellow; wall 1.0–1.5 µm thick, colorless.

Host – *Patrinia scabiosifolia* (Caprifoliaceae)

Material examined – CHINA, Guizhou Province, Guiyang city, 26°51'19"N, 106°65'02"W, 1110 m, 21 Aug 2021, on *Patrinia scabiosifolia*, J.E. Sun, HGUP21221.

Notes – In the phylogenetic tree, our specimen grouped with *Puccinia patriniae* (ZP-R874, ZP-R852) (Fig. 2), collected from *Patrinia scabiosifolia*. Morphological comparisons of the two species revealed similarity in the dimension of aeciospores (Zhuang et al. 2005). Our collection is identified as *P. patriniae* based on morphological characters and phylogenetic evidence.

Puccinia plectranthi Thümen, Flora, Regensburg 58: 379 (1875) Fig. 57

MycoBank number: MB174310

Description – *Spermogonia*, *uredinia* and *telia* not found. *Aecia* covering the entire lower surface of the leaves, faint yellow to light brown, 10–20 mm diam. *Aeciospores* 23–35 × 19–30 µm ($\overline{x}$ = 28.9 × 26.6 µm, n = 30), globose or oval, yellow or golden to light brownish red; wall 1.0–1.6 µm thick, colorless, densely and minutely verrucose.

Host – *Isodon amethystoides* (Lamiaceae)

Material examined – CHINA, Guizhou Province, Guiyang city, 26°41'54"N, 106°66'79"W, 1121 m, 11 May 2021, on *Isodon amethystoides,* J.E. Sun, HGUP21234, HGUP21141.

Notes – *Puccinia plectranthi* was introduced from *Isodon* sp. by Thümen (1875). There is no nucleotide data in NCBI. Our specimens formed a distinct subclade to other species with good support (Fig. 2). *Puccinia plectranthi*, however, is only known from its telial stage (Zhuang et al. 1998), so we were unable to compare morphological characteristics. We identify our collection as *P. plectranthi*, and our specimens are an aecial stage record for *P. plectranthi*.

Puccinia panici-montani Fujik. ex Ramachar & Cummins (1965) Fig. 58

MycoBank number: MB337969

Description – *Spermogonia*, *aecia* and *telia* not found. *Uredinia* produced on abaxial leaf surface, not surrounded by host epidermis, oblong or irregular, golden spot, pulverulent, 0.1–0.5 mm diam. *Paraphyses* with evenly thickened walls, strongly curved, 32–40 × 7–10 µm. *Urediniospores* ellipsoidal or globose, 14–20 × 13–17 µm ($\overline{x}$ = 17.7 × 15 µm, n = 30), pale to light golden; wall 1.0–1.5 µm thick, colorless, densely, and minutely verrucose.

Host – *Setaria plicata* (Poaceae)

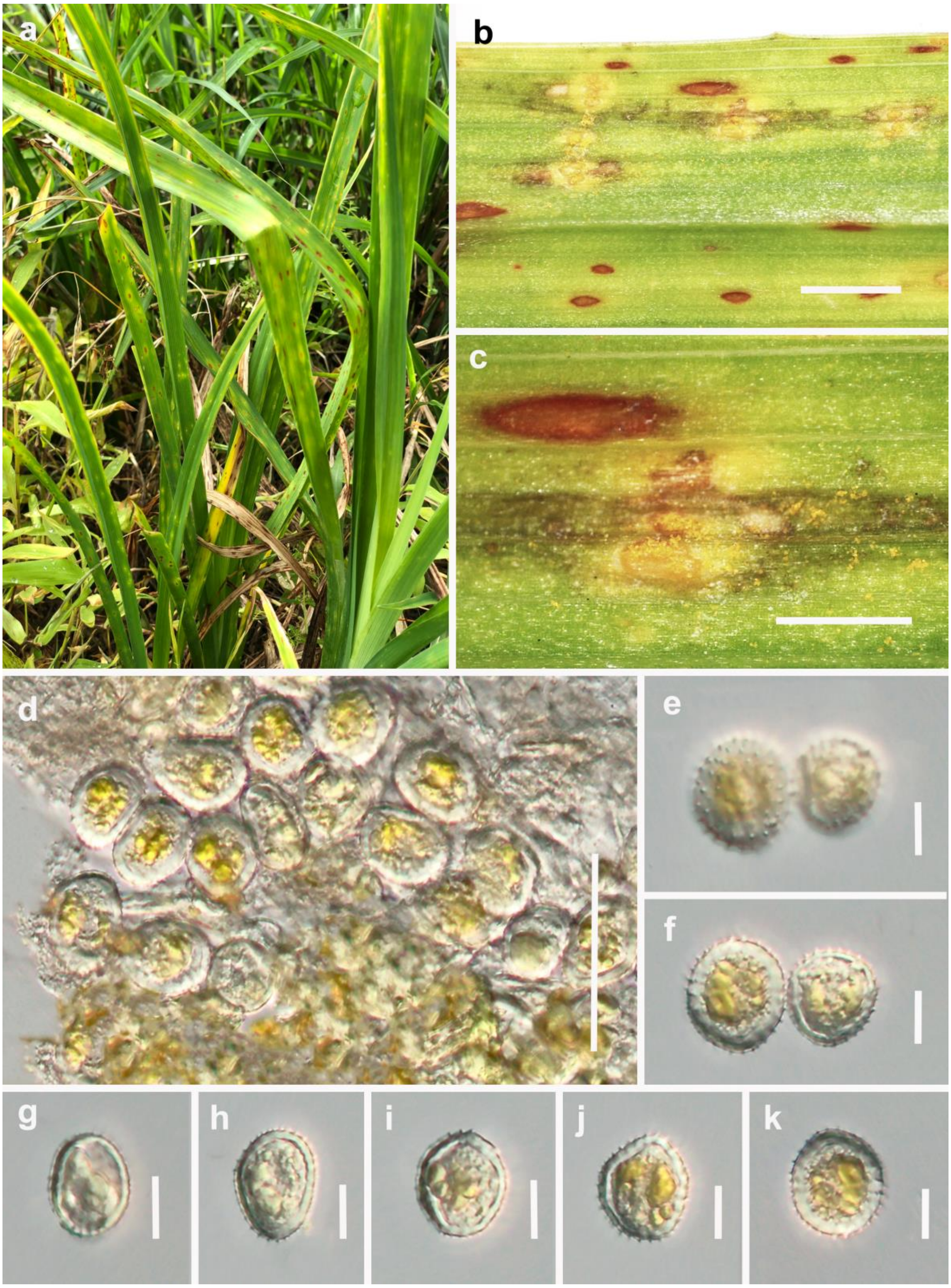

Figure 55 – *Puccinia hemerocallidis* (from HGUP21218) on *Hemerocallis fulva*. a–c Uredinia on leaves. d Longitudinal section of uredinium. e–k Urediniospores. Scale bars: b = 5 mm, c = 1 mm, d = 50 µm, e–k = 12.5 µm.

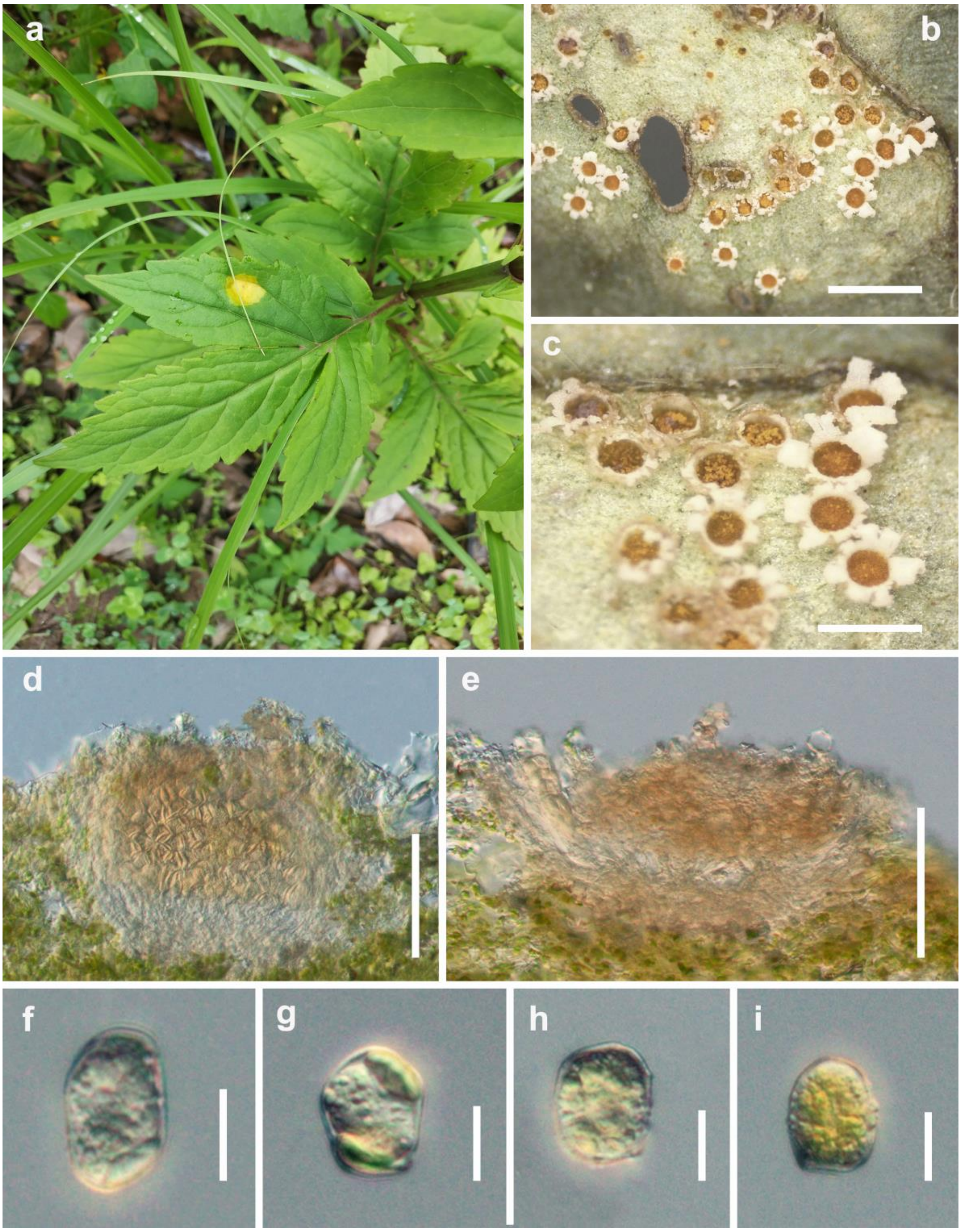

Figure 56 – *Puccinia patriniae* (from HGUP21221) on *Patrinia scabiosifolia*. a–c Aecia on leaves. d–e Longitudinal section of aecium. f–i Aeciospores. Scale bars: b = 2 mm, c = 1 mm, d–e = 50 µm, f–i = 12.5 µm.

Material examined – CHINA, Guizhou Province, Guiyang city, 26°66'59"N, 106°67'45"W, 1293 m, 21 Aug 2021, on *Setaria plicata*, J.E. Sun, HGUP21189.

Notes – *Puccinia panici-montani* was originally described on *Setaria plicata*, but unfortunately, there is no nucleotide data available in NCBI. Phylogenetic analyses show that HGUP21189 grouped in an independent clade with support ML/MP/BI: 100/94/1 (Fig. 2). The uredinial stage of *P. panici-montani* is only known in China and Japan and is very rare. The morphology of our collection is similar to *P. panici-montani* described by Zhuang et al. (1998). Thus, we identify our collection as *P. panici-montani*.

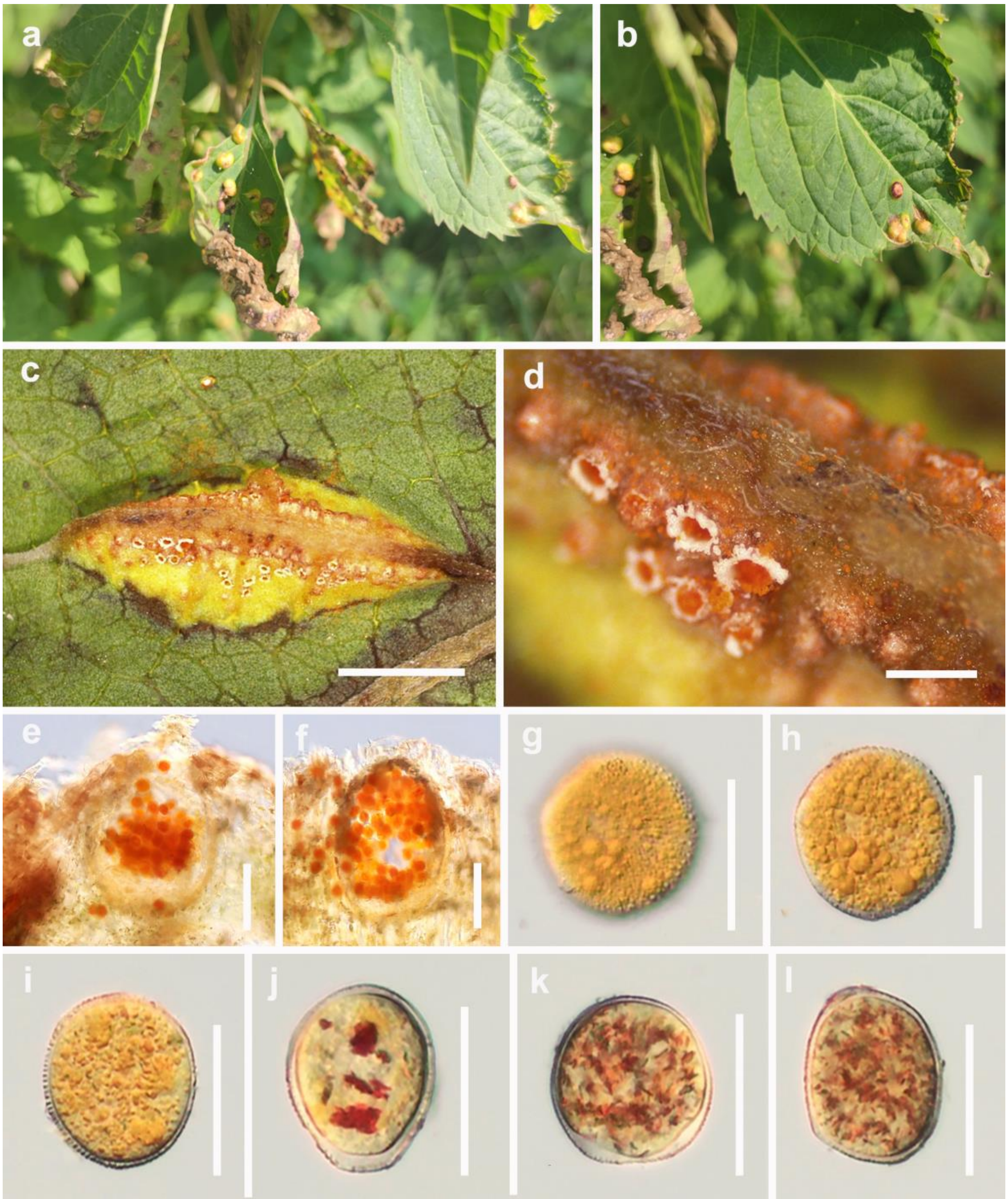

Figure 57 – *Puccinia plectranthi* (from HGUP21141) on *Isodon amethystoides*. a–d Aecia on leaves. e–f Longitudinal section of aecium. g–l Aeciospores. Scale bars: c = 5 mm, d = 1 mm, e–f = 50 µm, g–l = 25 µm.

Puccinia menthae Pers., Syn. meth. fung. (Göttingen) 1: 227 (1801) Fig. 59

MycoBank number: MB233447

Description – *Spermogonia*, *aecia* and *telia* not found. *Uredinia* hypophyllous, not surrounded by host epidermis, ellipsoidal, oval or irregular, golden, powdery, 2.0–6.0 mm diam. *Urediniospores* ellipsoidal or ovoid, 18–27 × 18–21 µm ($\bar{x}$ = 22.9 × 20.2 µm, n = 30), inclusions pale to yellow; wall 1.5–2.5 µm thick, colorless, densely and minutely echinulate.

Host – *Mentha canadensis* (Lamiaceae)

Material examined – CHINA, Guizhou Province, Guiyang city, 26°90'65"N, 106°71'12"W, 1315 m, 7 Apr 2022, on *Mentha canadensis*, Y.K. He, HGUP21277; Bijie city, 27°25′50″N, 106°14'21"W, 1193 m, 27 May 2022, on *M. canadensis*, J.E. Sun, HGUP21278.

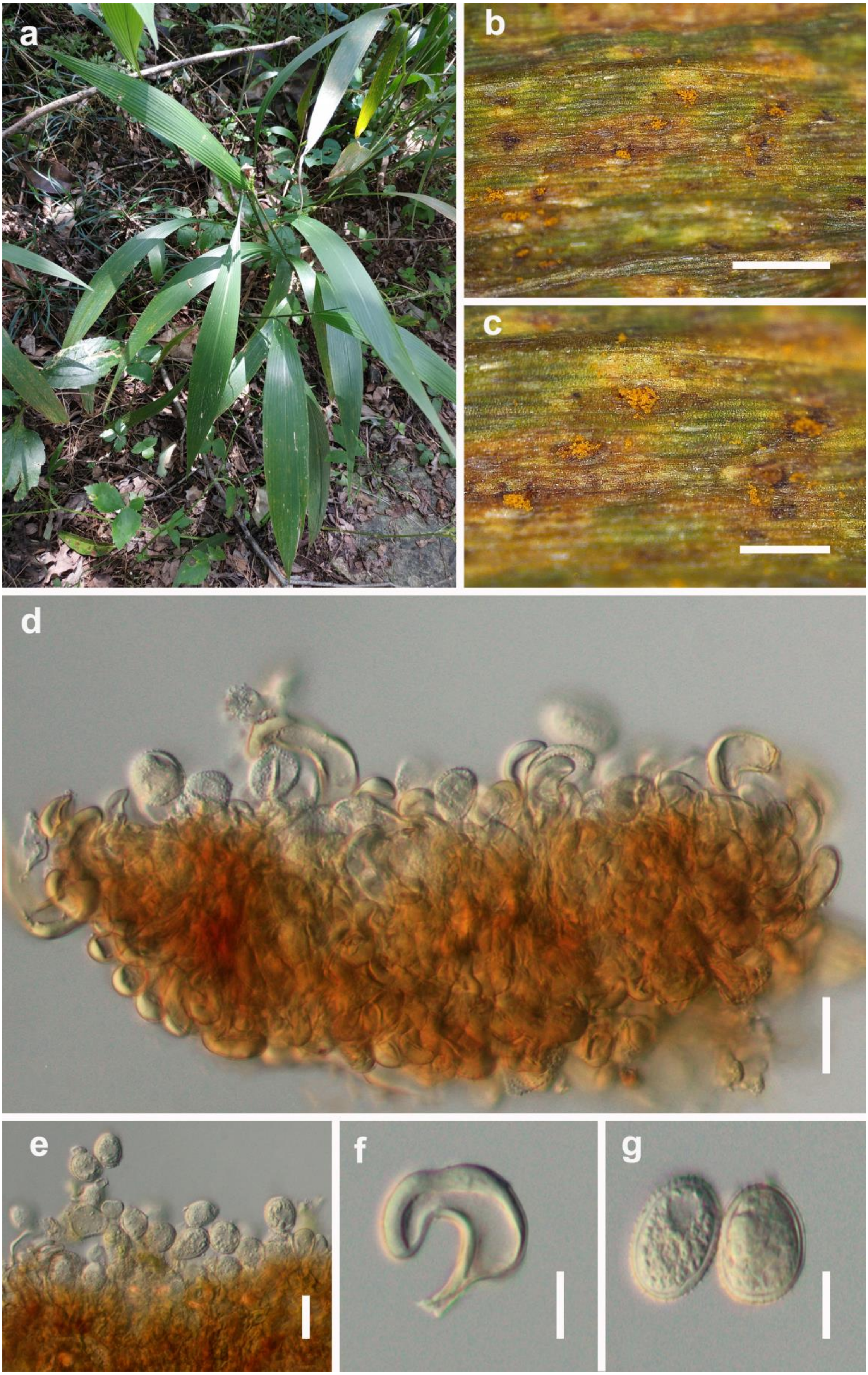

Figure 58 – *Puccinia panici-montani* (from HGUP21189) on *Setaria plicata*. a–c Uredinia on leaves. d–e Longitudinal section of uredinia. f Paraphysis. g Urediniospores. Scale bars: b = 2 mm, c = 1 mm, d–e = 50 µm, f–g = 25 µm.

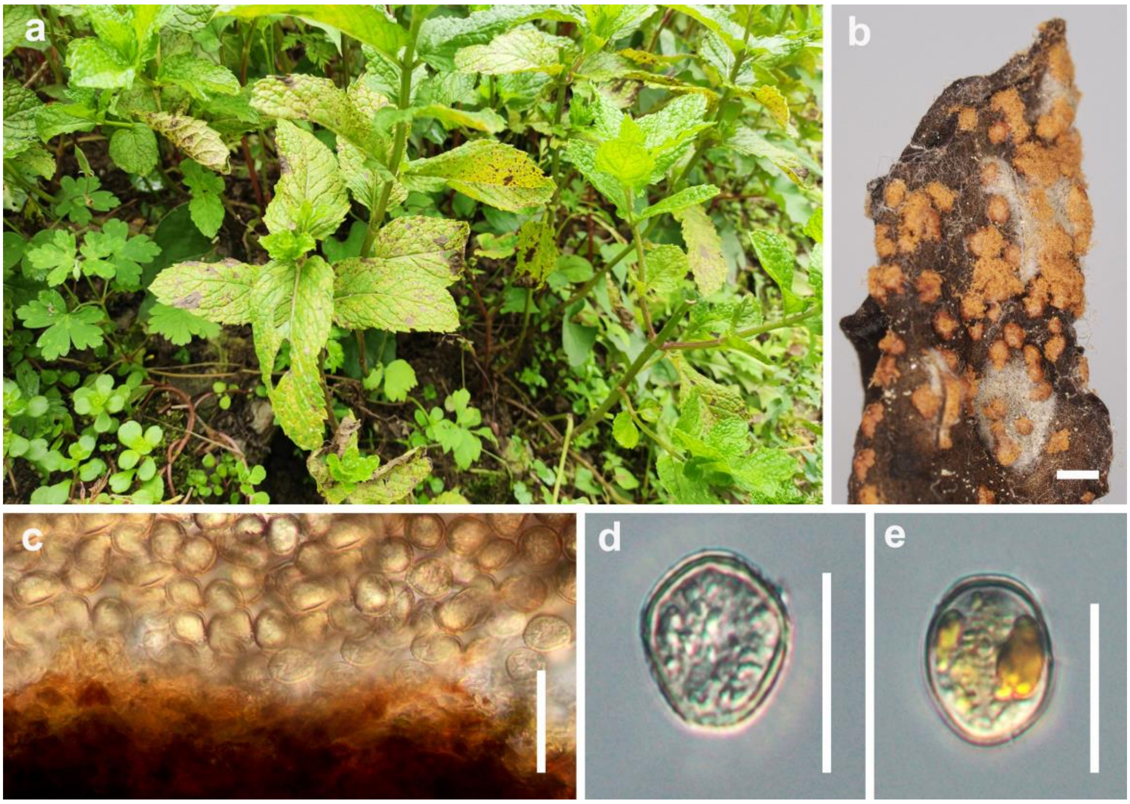

Figure 59 – *Puccinia menthae* (from HGUP212277) on *Mentha canadensis*. a–b Uredinia on leaves. c Longitudinal section of uredinium. d–e Urediniospores. Scale bars: b = 5 mm, c = 50 µm, d–e = 25 µm.

Notes – *Puccinia menthae* was often infects *Mentha canadensis* or other plants as a common rust (Zhuang et al. 1998). In this study, however, we were not obtained their nucleotide data though DNA extraction, PCR and sequencing. Therefore, only their collection information and descriptions are provided.

Phragmidiaceae Corda, Icon. fung. (Prague) 1: 6 (1837)
Phragmidium Link, Mag. Gesell. naturf. Freunde, Berlin 7: 30 (1816) [1815]

***Phragmidium rosae-kwangtungensis*e** J.E. Sun, Yong Wang bis & K.D. Hyde, sp. nov.
Fig. 60

Index Fungorum number: IF901303; Facesoffungi number: FoF15368

Etymology – The name reflects the host *Rosa kwangtungensis,* from which the type specimen was collected.

Holotype – HGUP21154

Description – *Spermogonia*, *uredinia* and *telia* unknown. *Aecia* hypophyllous, and on stems and petioles, pulverulent, yellow, scattered, nearly oval or elliptical, not surrounded by host epidermis, 1.0–6.0 mm diam. *Aeciospores*, oval or subglobose, 19–28 × 16–21 µm ($\bar{x}$ = 24.3 × 18.8 µm, n = 30), inclusions golden, to bright yellow; wall 1.9–3.1 µm thick, colorless, rough.

Host – *Rosa kwangtungensis* (Rosaceae)

Material examined – CHINA, Guizhou Province, Guiyang city, 26°44'86"N, 106°65'54"W, 1001 m, 3 Apr 2022, on *Rosa kwangtungensis*, J.E. Sun, holotype HGUP21154; Guizhou Province, Guiyang city, 26°44'86"N, 106°65'54"W, 1001 m, 3 Apr 2022, on *R. kwangtungensis*, J.E. Sun, HGUP21155.

Notes – In the phylogenetic analysis, *Phragmidium rosae-kwangtungensis*e is closely related to *P. rosae-multiflorae*, *P. longissimum* and *P. chayuensis* with 85% ML and 65% MP bootstrap support (Fig. 3). However, the aecia and aeciospores of *P. rosae-multiflorae* (Zhuang et al. 2012), *P*. *longissimum* (Yang et al. 2015) and *P*. *chayuensis* (Liu et al. 2018) are unknown. *Phragmidium rosae-kwangtungensis*e is similar to *P*. *rosae-roxburghii* with respect to aeciospores size, and differs from *P*. *rubi-coreani* by relatively large aeciospores (19–28 × 16–21 µm *vs*. 14–24 × 10–23 µm) (Sun et al. 2022).

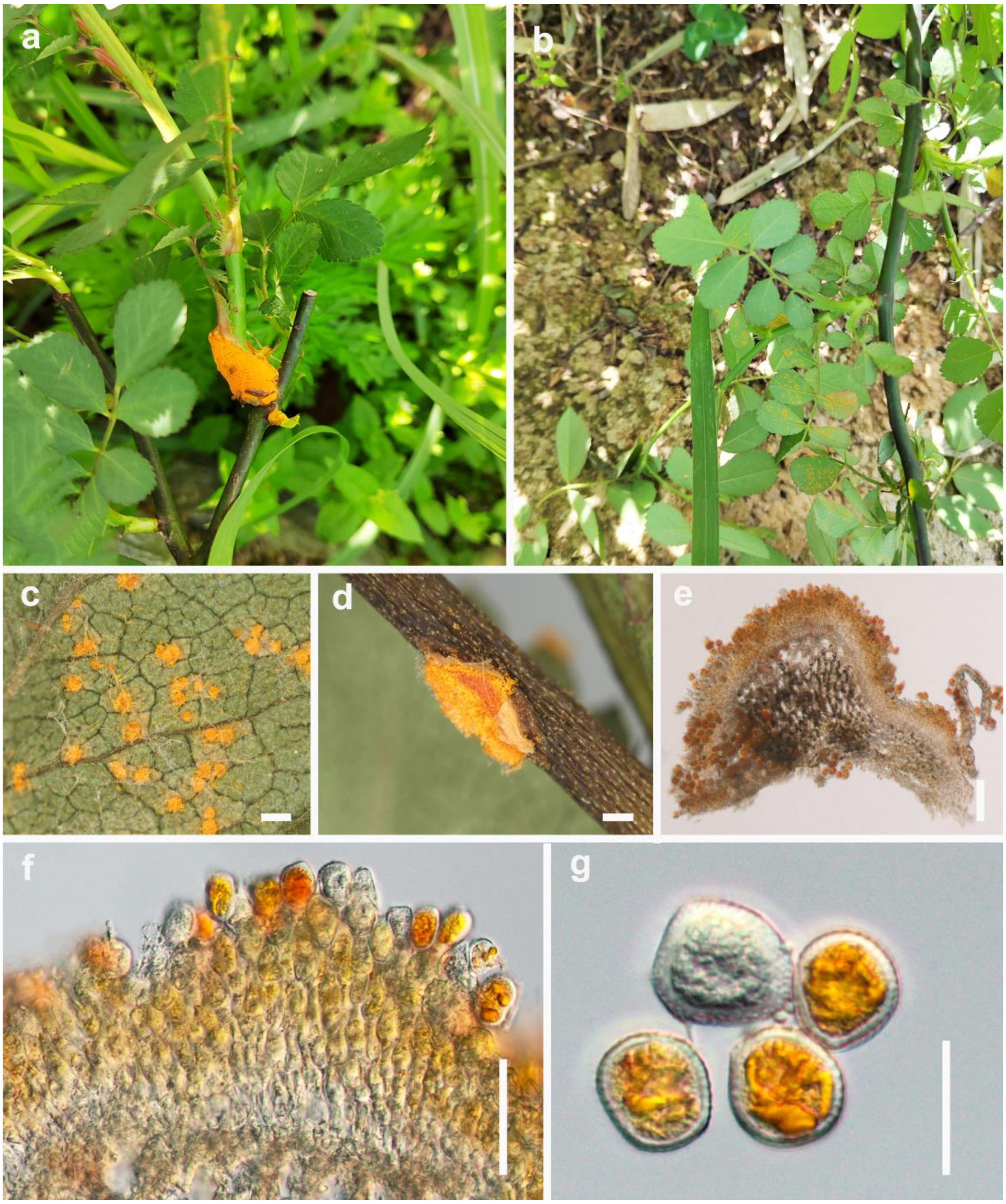

Figure 60 – *Phragmidium rosae-kwangtungensise* (from holotype HGUP21154) on *Rosa kwangtungensis*. a–d Aecia on leaves and stems. e–f Longitudinal section of aecia. g Aeciospores. Scale bars: c–d = 2 mm, e = 100 µm, f = 50 µm, g = 25 µm.

Phragmidium cymosum Q.Z. Wu, T.Z. Liu, P, Zhao & Q.R. Li, (2023) Fig. 61

MycoBank number: MB847102

Description – *Spermogonia*, *telia* unknown. *Aecia* formed on golden distinct, circular lesions on both sides of leaves, surrounded by host epidermis, scattered, flat oval to subglobose, pulverulent, 1.0–5.0 mm diam. *Aeciospores* clavate to long-ellipsoidal, or some irregular, 22–31 ×

12–19 µm ($\bar{x}$ = 26.4 × 15.7 µm, n = 30), inclusions golden, to bright yellow; wall 1.5–2.2 µm thick, colorless, irregularly elongated verrucae. *Uredinia* and *Urediniospores* please see Wu et al. (2023)

Host – *Rosa cymosa* (Rosaceae)

Material examined – CHINA, Guizhou Province, Duyun city, 25°26'81"N, 107°69'31"W, 862 m, 12 Mar 2022, on *Rosa cymosa*, J.E. Sun & W.M. Luo, HGUP21147; Guizhou Province, Duyun city, 25°26'81"N, 107°69'31"W, 862 m, 12 Mar 2022, on *R. cymosa*, J.E. Sun & W.M. Luo, HGUP21148, HGUP21149; Guiyang city, 26°45'35"N, 106°65'61"W, 1102 m, 3 Apr 2022, on *R. cymosa*, J.E. Sun, HGUP21150, HGUP21151, HGUP21153; Bijie city, 27°25'13"N, 106°14'16"W, 1190 m, 27 May 2022, on *R. cymosa*, J.E. Sun & W.M. Luo, HGUP21152.

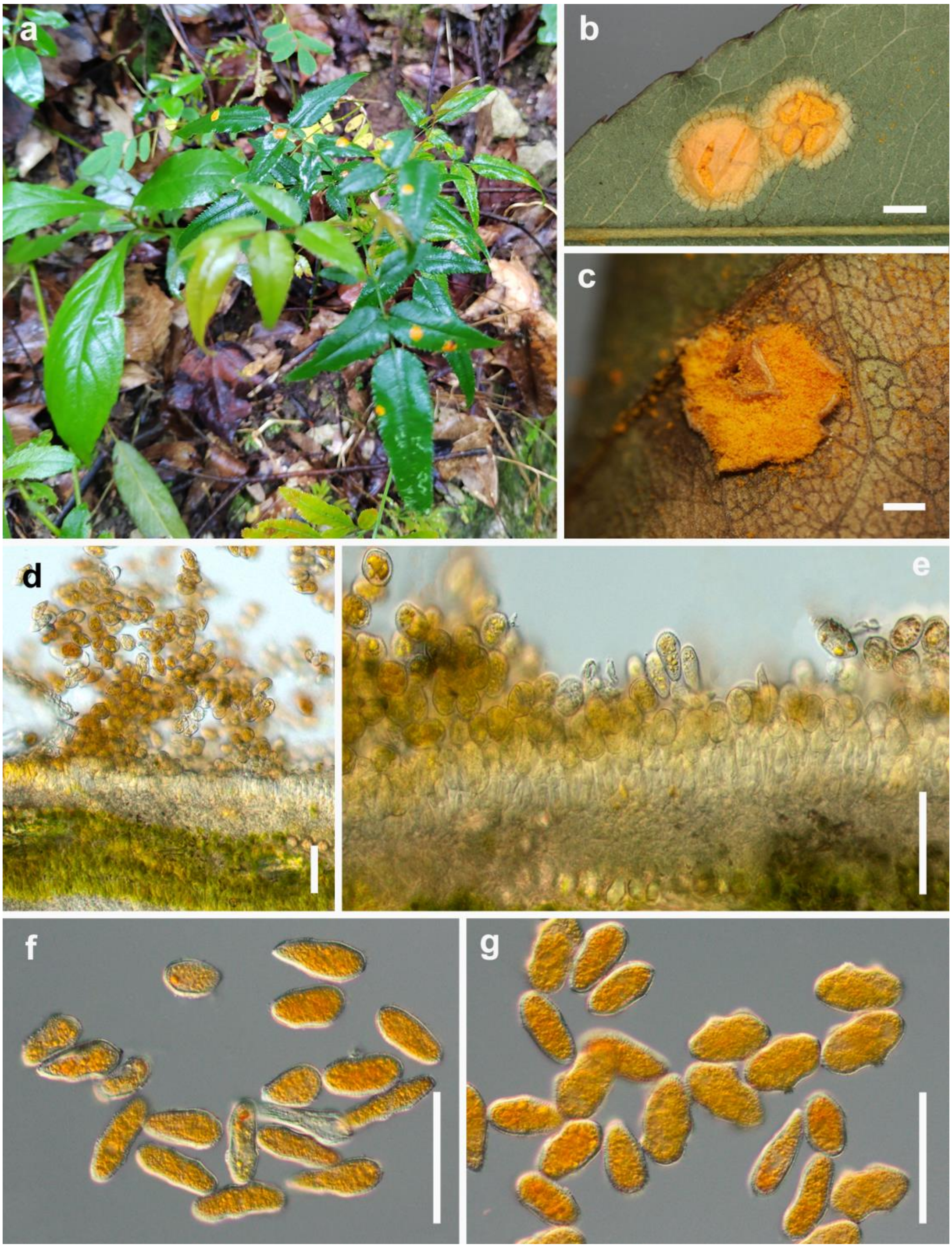

Figure 61 – *Phragmidium cymosum* (from HGUP21147) on *Rosa cymosa*. a–c Aecia on leaves. d–e Longitudinal section of aecia. f–g Aeciospores. Scale bars: b = 3 mm, c = 1 mm, d–e = 50 µm, f–g = 25 µm.

Notes – *Phragmidium cymosum* is the first species of *Phragmidium* found on *Rosa cymosa* (Wu et al. 2023). In the phylogenetic analysis, our species had a close relationship to *P. cymosum* (GMB0108) (Supplementary Fig. 1), a comparison of DNA base composition provides support that the five new specimens and *P. cymosum* are likely to be same species (7/323 in ITS and 1/579 in LSU). Based on its host and molecular phylogenetic analysis, we propose our collections as *P. cymosum*. Herein, we provided the description of aecia and aeciospores of *P. cymosum*.

Phragmidium rosae-roxburghii J.E. Sun & Yong Wang bis, MycoKeys 93: 200, 2022.
Figs 62, 63, 64

MycoBank number: MB845041

Description – *Spermogonia* and *telia* unknown. *Aecia* formed on gold, distinct, circular lesions on both sides of the leaves, stems, and petioles, although rare on abaxial leaf surface, scattered, flat oval to subcircular, pulverulent, 1.0–5.0 mm diam. *Aeciospores* oval or subglobose, 22–30 × 14–22 µm ($\bar{x}$ = 26 × 18 µm, n = 30), inclusions golden, to bright yellow; wall 1.8–3.1 µm thick, colorless, mostly with irregularly elongated verrucae on the surface. *Uredinia* abaxial, scattered to gregarious, orange or white, powdery, oval to circular, 0.1–1.0 mm diam. Marginal paraphyses in the uredinia, curved, 30–55 × 9–20 µm, colorless. *Urediniospores* generally angular, square to diamond-shaped, yellowish to orange, 20–30 × 16–21 µm (mean 25 × 19 µm, n = 30), 0.5–2.0 µm thick, colorless, regularly echinulate with stout spines.

Hosts – *Rosa roxburghii* (Rosaceae), *Rosa* sp.

Material examined – CHINA, Guizhou Province, Panzhou city, 25°89'61"N, 104°56'07"W, 750 m, 21 Mar 2021, on *Rosa roxburghii*, J.E. Sun & Y.Q. Yang, HGUP21025; Duyun city, 26°45'88"N, 106°98'42"W, 820 m, 22 Jun 2021, on *R. roxburghii*, J.E. Sun, HGUP21026; Tongren city, 28°14'09"N, 108°34'03"W, 810 m, 4 Sep 2021, on *R. roxburghii*, J.E. Sun, HGUP21027; Guiyang city, 26°44'74"N, 106°58'67"W, 960 m, 27 Mar, 2021, on *Rosa* sp., J.E. Sun, HGUP21028.

Notes – *Phragmidium rosae-roxburghii* was first reported on *Rosa roxburghii* by Sun et al. (2022). It is easy to distinguish by its unique square to diamond-shaped urediniospores, since in other *Phragmidium* species the urediniospores are oval to nearly spherical (Yun et al. 2011, Ono 2012, Zhuang et al. 2012, Yang et al. 2015, Liu et al. 2018, 2019, 2020, Ono & Wahyuno 2019). In phylogeny, this species has a close relationship to *P. warburgiana* (Fig. 3) but its urediniospores are yellowish to orange while those of *P. warburgiana* (Ono 2012).

Phragmidium rubi-coreani J.E. Sun & Yong Wang bis, MycoKeys 93: 202 (2022) Fig. 65

MycoBank number: MB845042

Description – *Spermogonia* unknown. *Aecia* golden, hypophyllous, 2.5–3.5 mm diam., subglobose to globose, pulverulent, 2.5–3.5 mm diam. *Aeciospores* subglobose, 14–24 × 10–23 µm ($\bar{x}$ = 19 × 16 µm, n = 30), bright yellow contents; wall 1.0–4.0 µm thick, colorless, echinulate. Paraphyses clavate, not or weakly incurved, 38–61 µm long, wall 2.0–2.5 µm thick. *Telia* hypophyllous, scattered, 0.3–0.5 mm diam., chocolate-brown. *Uredinia* formed on circular lesions on both sides of the leaves, pulverulent, yellow, distinct, scattered, nearly oval, surrounded by host epidermis, 0.5–1.0 mm diam. *Urediniospores* uredo-type, subglobose to oval, produced in basipetal succession, golden, or bright yellow, 19–27 × 15–25 µm ($\bar{x}$ = 23 × 20 µm, n = 30); wall 0.8–1.5 µm thick, colorless, densely and minutely echinulate. *Teliospores* ellipsoid to cylindrical, 3–5–celled, constricted at septa, bright orange, chocolate-brown to gray-brown, 29–74 × 14–37 µm ($\bar{x}$ = 50 × 25 µm, n = 30); wall 1.8–3.5 µm thick, colorless to chocolate-brown; pedicels not swollen at base, 8–34 µm long, colorless.

Host – *Rubus coreanus* (Rosaceae)

Material examined – CHINA, Guizhou Province, Guiyang city, 26°45'86"N, 106°98'77"W, 970 m, 11 Apr, 2021, on *Rubus coreanus*, J.E. Sun, HGUP21029; Guiyang city, 27°10'30"N, 106°99'91"W, 830 m, 9 Apr 2021, on *R. coreanus*, J.E. Sun, HGUP21030.

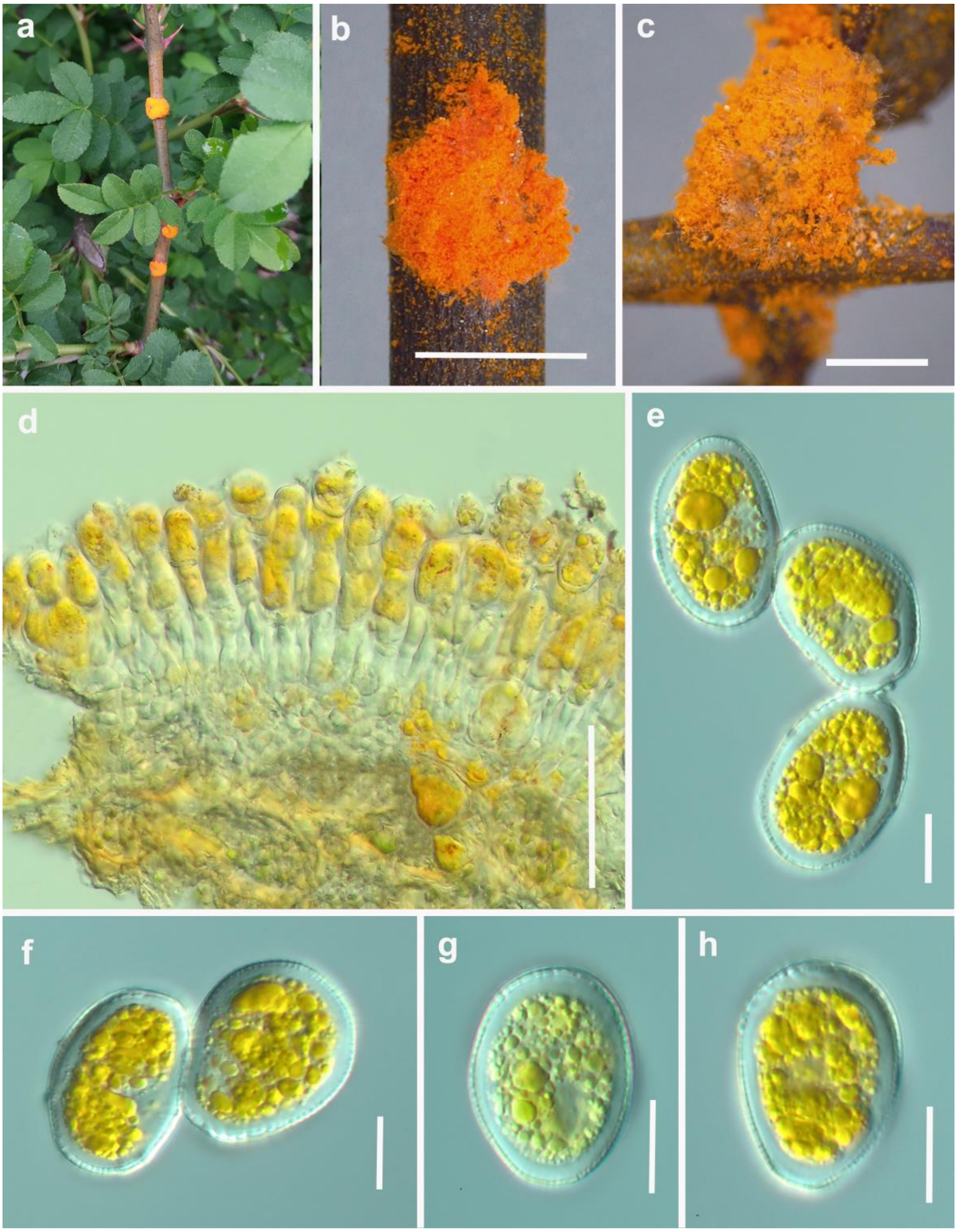

Figure 62 – *Phragmidium rosae-roxburghii* (from HGUP21025) on *Rosa roxburghii*. a–c Aecia on stems and leave. d Longitudinal section of aecium. e–h Aeciospores. Scale bars: b–c = 2 mm, d = 50 µm, e–h = 10 µm.

Notes – *Phragmidium rubi-coreani* was first reported on *Rosa roxburghii* based on phylogenetic analyses, with aeciospores, urediniospores and teliospores (Sun et al. 2022).

Phragmidium potentillae-freynianae J.E. Sun & Yong Wang bis, MycoKeys 93: 204 (2022)

Fig. 66

MycoBank number: MB845043

Description – *Spermogonia*, *aecia* and *telia* not observed. *Uredinia* hypophyllous, covering the entire lower surface of the leaves, nearly oval, pulverulent, not surrounded by host epidermis, 0.1–1.0 mm diam., on densely orange spot. *Urediniospores* *Uredo*-type, subglobose to oval, produced in basipetal succession, 19–24 × 18–24 µm ($\bar{x}$ = 21.5 × 21 µm, n = 30), yellowish, or bright-yellow; wall 0.4–1.4 µm thick, colorless, densely and minutely echinulate.

Host – *Potentilla freyniana* (Rosaceae)

Material examined – CHINA, Guizhou Province, Guiyang city, 26°44'70"N, 106°59'65"W, 801 m, 27 March, 2021, on *Potentilla freyniana*, J.E. Sun, HGUP21033; Guiyang city, 26°45'35"N, 106°65'82"W, 1021 m, 3 Apr 2022, on *P. freyniana*, J.E. Sun, HGUP21040.

Notes – In the phylogenetic tree, our specimen (HGUP21040) formed a close relationship to *Phragmidium potentillae-freynianae* with good support (100 ML/87 MP/1.00 PP) (Fig. 3). Our specimens match the description of *P. potentillae-freynianae* provided by Sun et al. (2022). We, therefore, name our collections as *P. potentillae-freynianae* based on phylogenetic and morphological analyses.

Figure 63 – *Phragmidium rosae-roxburghii* (from HGUP21026) on *Rosa roxburghii*. a–b Uredinia on leaves. c Longitudinal section of uredinium. d Paraphyses. e–i Urediniospores. Scale bars: b = 5 mm, c = 50 µm, d = 25 µm, e–i = 12.5 µm.

Phragmidium rosae-laevigatae J.E. Sun & Yong Wang bis, MycoKeys 93: 205 (2022)

Fig. 67

MycoBank number: MB845044

Description – *Spermogonia* and *aecia* not observed. *Uredinia* hypophyllous, subglobose to globose, pulverulent, yellow, 0.1–0.5 mm diam. Peripheral parahyses, hyaline, 20–31 × 10–17 µm.

Urediniospores square to diamond-shaped, oval to nearly globose, 23–35 × 16–30 µm (x̅ = 29 × 23 µm, n = 30), orange; wall 0.5–2.0 µm thick, colorless, regularly echinulate with stout spines on the surface. *Telia* scattered, compact, hypophyllous, golden, 0.1–0.5 mm diam. *Teliospores* (immature) oval, 24–60 × 8–20 µm (x̅ = 50.5 × 25.5 µm, n = 30), with apical papillae (4.0–7.0 µm high, n = 10), too immature to know how many cells, orange-yellow; pedicels swollen at the base, 15–26 µm long, colorless, detached easily; wall 0.5–2.0 µm thick.

Figure 64 – *Phragmidium rosae-roxburghii* (from HGUP21028) on *Rosa* sp. a–b Aecia on a leaf. c–d Longitudinal section of aecia. e–k Aeciospores. Scale bars: b = 2 mm, c–d = 50 µm, e–k = 12.5 µm.

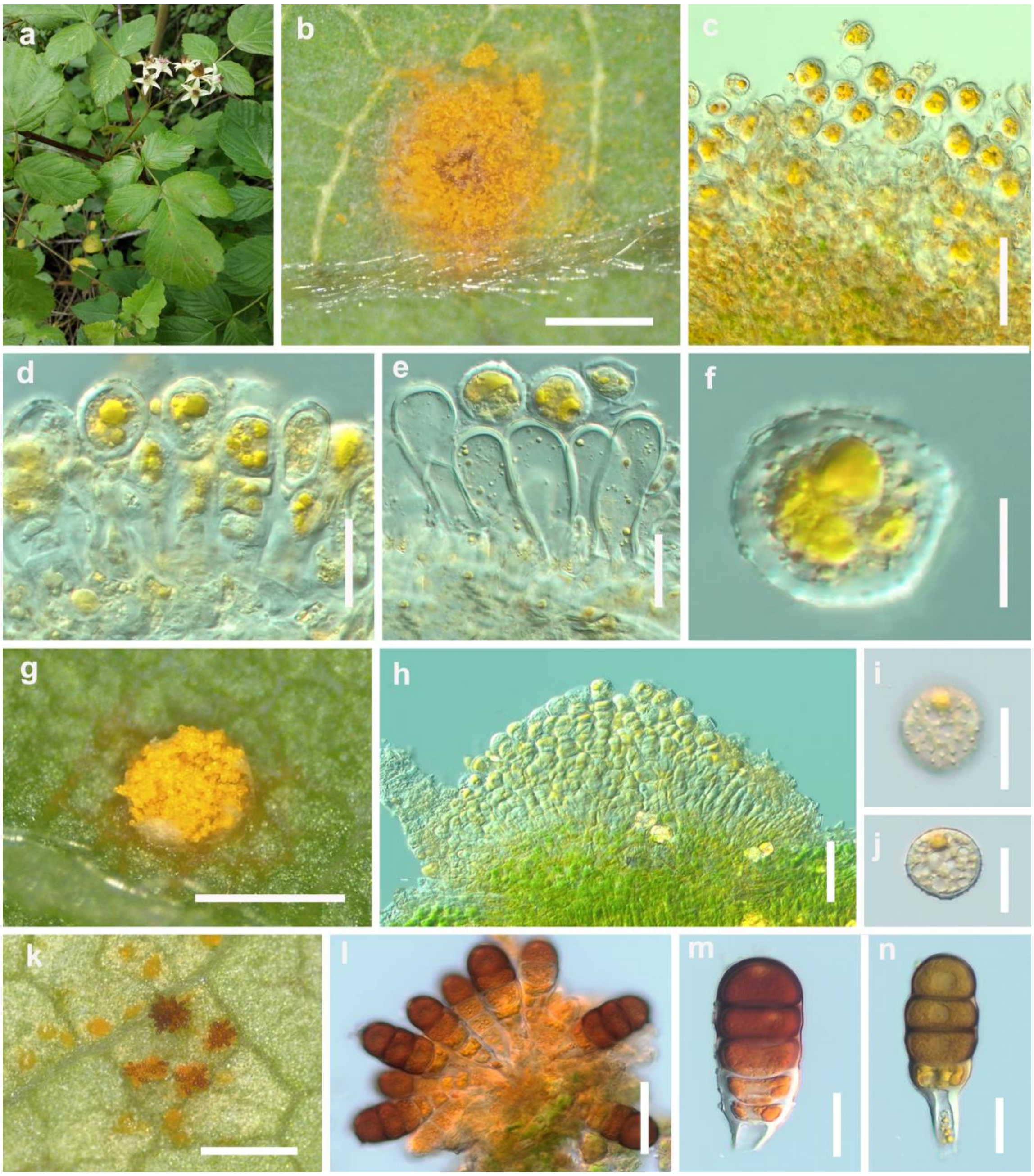

Figure 65 – *Phragmidium rubi-coreani* (from HGUP21029) on *Rubus coreanus*. a–b Uredinia on a leaf. c–d Longitudinal section of uredinium. e Paraphyses. f Urediniospore. g Aecium on a leaf. h Longitudinal section of aecium. i–j Aeciospores. k Telia on a leaf. l Longitudinal section of telium. m–n Teliospores. Scale bars: b = 2 mm, g, k = 1 mm, c–e, h, l = 50 µm, f = 10 µm, i–j, m–n = 25 µm.

Host – *Rosa laevigata* (Rosaceae)

Material examined – CHINA, Guizhou Province, Panzhou city, 25°64'56"N, 104°84'35"W, 1800 m, 19 Jul 2021, on *Rosa laevigata*, J.E. Sun, HGUP21036; Panzhou city, 25°61'81"N, 104°83'61"W, 1790 m, 19 Jul 2021, on *R. laevigata*, J.E. Sun, HGUP21037.

Notes – *Phragmidium rosae-laevigatae* was reported on *Rosa laevigata* based on phylogenetic analyses, with the urediniospores and teliospores (Sun et al. 2022).

Phragmidium duchesneae-indicae P. Zhao & L. Cai, Fungal Diversity 5:1–58 (2021)

Fig. 68

MycoBank number: MB557609

Description – *Spermogonia*, *aecia* and *telia* not observed. *Uredinia* hypophyllous, nearly oval, golden, densely bright orange-yellow, pulverulent, not surrounded by host epidermis, 0.3–1.2 mm diam., without paraphyses. *Urediniospores* produced in basipetal succession, mostly globose, 17–22 × 15–20 µm ($\bar{x}$ = 19.5 × 17.5 µm, n = 30), inclusions yellowish, or bright yellow; wall 0.7–1.8 µm thick, colorless, densely and minutely echinulate. *Telia* and *teliospores* see Zhao et al. (2021).

Host – *Duchesnea indica* (Rosaceae)

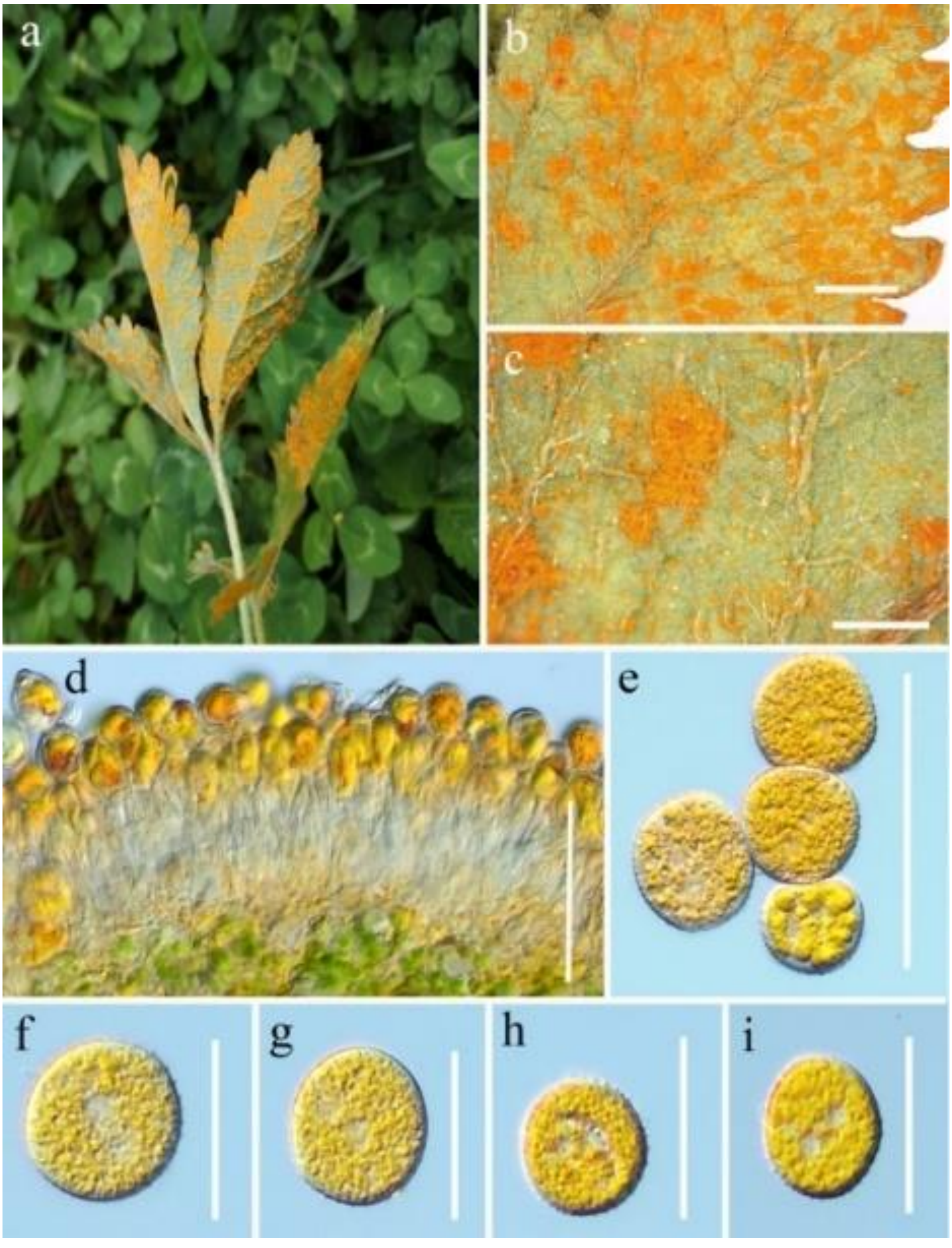

Figure 66 – *Phragmidium potentillae-freynianae* (from HGUP21033) on *Potentilla freyniana*. a–c Uredinia on leaves. d Longitudinal section of uredinium. e–i Urediniospores. Scale bars: b–c = 2 mm, d–e = 50 µm, f–i = 25 µm.

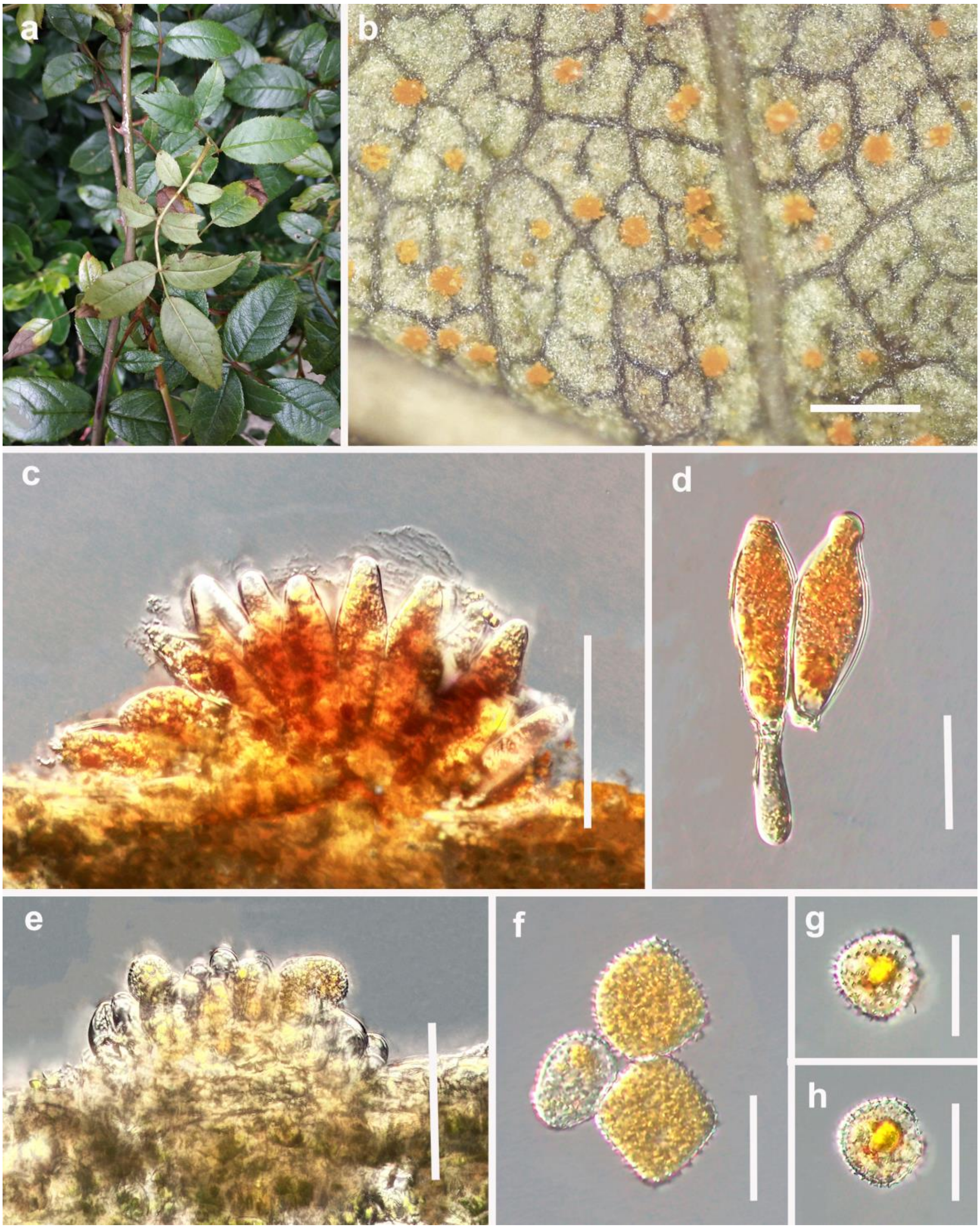

Figure 67 – *Phragmidium rosae-laevigatae* (from HGUP21036) on *Rosa laevigata*. a–b Uredinia and telia on a leaf. c Longitudinal section of telium. d Immature teliospores. e Longitudinal section of uredinium. f–h Urediniospores. Scale bars: b = 1 mm, c, e = 50 µm, d, f–h = 12.5 µm.

Material examined – CHINA, Guizhou Province, Guiyang city, 27°10'30"N, 106°99'91"W, 820 m, 9 Apr 2021, on *Duchesnea indica*, J.E. Sun, HGUP21031; Guiyang city, 27°09'26"N, 106°98'90"W, 734 m, 4 Sep 2021, on *D. indica*, J.E. Sun, HGUP21032.

Notes – *Phragmidium duchesneae-indica* was first reported on *Duchesnea indica* by Zhao et al. (2021). Our specimen had similar morphology to that described by Zhao et al. (2021). We, therefore, identified our specimens as *P. duchesneae-indicae*.

Phragmidium potentillae (Pers.) P. Karst., Bidrag till Kännedom av Finlands Naturoch Folk, 31: 49 (1879) Fig. 69

MycoBank number: MB206190

Description – *Spermogonia* and *aecia* not observed. *Uredinia* hypophyllous, pulverulent, densely bright orange, surrounded by host epidermis, 0.8–1.5 × 0.4–0.7 mm. *Urediniospores* angular to squarish, oval to nearly globose, produced in basipetal succession, 17–26 × 14–22 µm ($\bar{x}$ = 21.5 × 18 µm, n = 30), bright yellow to orange, immature urediniospores are colorless; wall 0.6–1.3 µm thick, colorless, densely, and minutely echinulate. *Telia* and *teliospores* see Liu et al. (2018).

Host – *Potentilla kleiniana* (Rosaceae)

Material examined – CHINA, Guizhou Province, Guiyang city, 27°09'26"N, 106°98'90"W, 730 m, 22 Jun 2021, on *Potentilla kleiniana*, J.E. Sun, HGUP21034.

Notes – In the phylogenetic tree (Fig. 3), our specimen clustered with *Phragmidium potentillae* (HMAS53236 and BJFCR00961). The uredinia of *P. potentillae* were described by Liu et al. (2018) as 0.2–0.8 mm diam., which is smaller than in our specimen, but the urediniospores are similar (18–25 × 15–21 µm), mostly globose and echinulate.

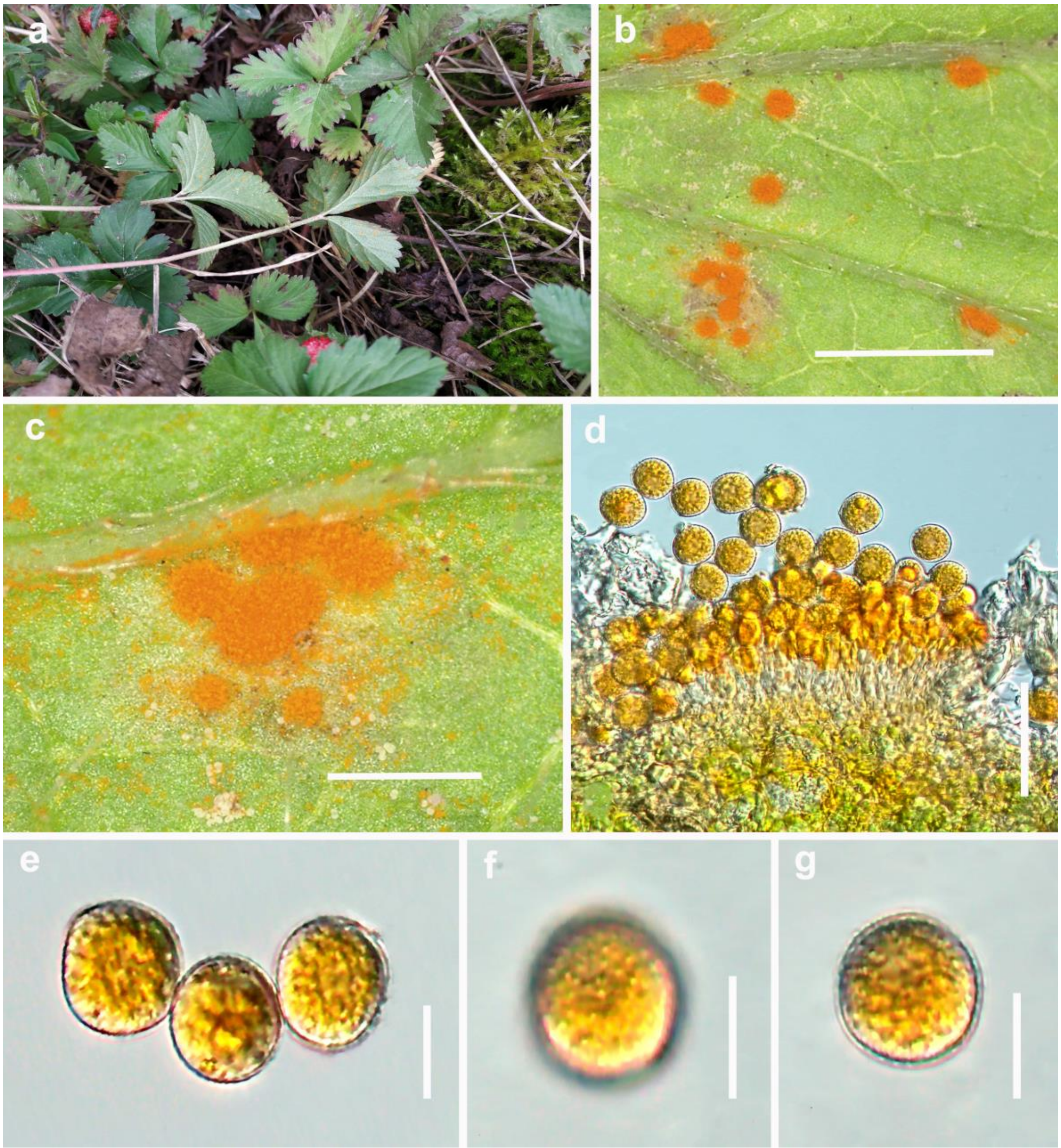

Figure 68 – *Phragmidium duchesneae-indica* (from HGUP21031) on *Duchesnea indica*. a–c Uredinia on leaves. d Longitudinal section of uredinium. e–g Urediniospores. Scale bars: b = 2 mm, c = 1 mm, d = 50 µm, e–g = 12.5 µm.

Figure 69 – *Phragmidium potentillae* (from HGUP21034) on *Potentilla kleiniana*. a–c Uredinia on leaves. d Longitudinal section of uredinium. e–j Urediniospores. Scale bars: c = 1 mm, d = 50 µm, e–j = 12.5 µm.

Phragmidium barnardii Plowr. & G. Winter, Revue Mycologique Toulouse 8 (32): 208, (1886)

Figs 70, 71

MycoBank number: MB249450

Description – *Spermogonia*, *aecia* and *telia* not observed. *Uredinia* hypophyllous, scattered to gregarious, oval to circular, orange, pulverulent, 0.1–1.0 mm diam., with hyaline and curved paraphyses, 26–39 × 10–13 µm. *Urediniospores* orange, 16–19 × 15–18 µm (mean 17.5 × 16.5 µm, n = 30), nearly globose; wall 1.3–2.2 µm thick, colorless, regularly echinulate with stout spines.

Hosts – *Rubus adenophorus* (Rosaceae), *Rubus* sp.

Material examined – CHINA, Guizhou Province, Duyun city, 27°26'05"N, 107°38'91"W, 870 m, 26 Jun 2021, on *Rubus* sp., J.E. Sun, HGUP21035, HGUP21038; Guiyang city, 26°98'30"N, 106°45'24"W, 1114 m, 25 Jun 2022, on *R. adenophorus*, J.E. Sun, HGUP21039.

Notes – *Phragmidium barnardii* was first reported on *Rubus* sp. by Winter (1886). Its DNA data was established by McTaggart et al. (2016), although without description of morphological characteristics. We confirmed specimen HGUP21035 as *P. barnardii*, through phylogenetic analyses with DNA data from McTaggart et al. (2016).

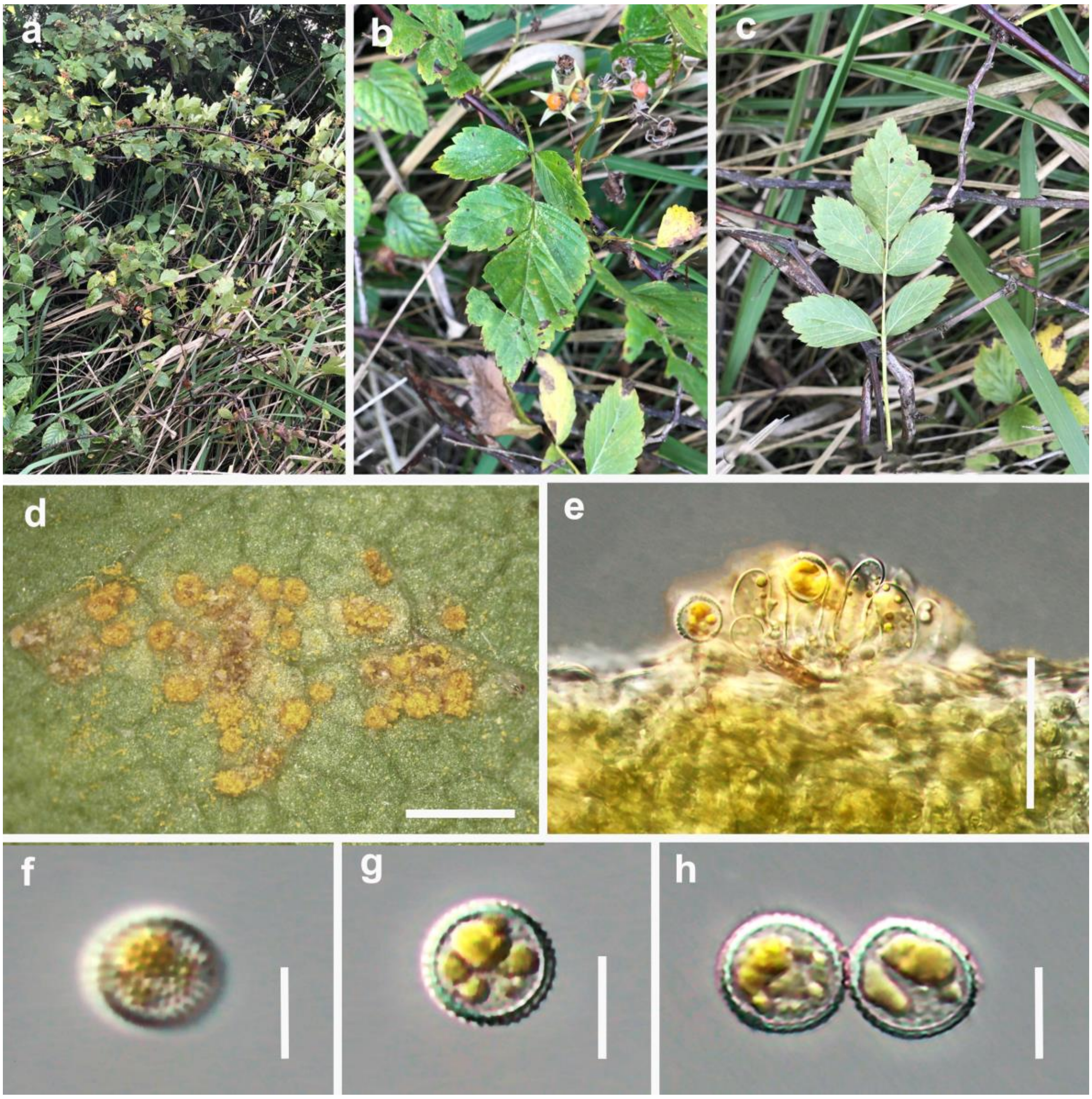

Figure 70 – *Phragmidium barnardii* (from HGUP21035) on *Rubus* sp. a–d Uredinia on leaves. e Longitudinal section of uredinium. f–h Urediniospores. Scale bars: d = 1 mm, e = 50 µm, f–h = 12.5 µm.

Phragmidium rosae-multiflorae Dietel, Hedwigia 44: 132 (1905) Fig. 72

MycoBank number: MB203481

Description – *Spermogonia*, *uredinia* and *telia* not observed. *Aecia* hypophyllous, and on stems, scattered, not surrounded by host epidermis, globose or irregular, orange, powdery, 1.0–5.0 mm diam. *Aeciospores* orange, 14–22 × 13–18 µm (mean 18.1 × 14.8 µm, n = 30), subglobose; wall 2.3–3.6 µm, colorless, smooth.

Host – *Rosa multiflora* (Rosaceae)

Material examined – CHINA, Guizhou Province, Guiyang city, 26°36'80"N, 107°16'26"W, 1235 m, 2 May 2022, on *Rosa multiflora*, J.E. Sun, HGUP21158.

Notes – our specimen (HGUP21158) and *Phragmidium rosae-multiflorae* grouped with good support (ML/MP/BI: 88%/52%/-; Fig. 3) and morphologically matched the description of Zhuang et al. (2012). We, therefore, identify our collection as *P rosae-multiflorae*.

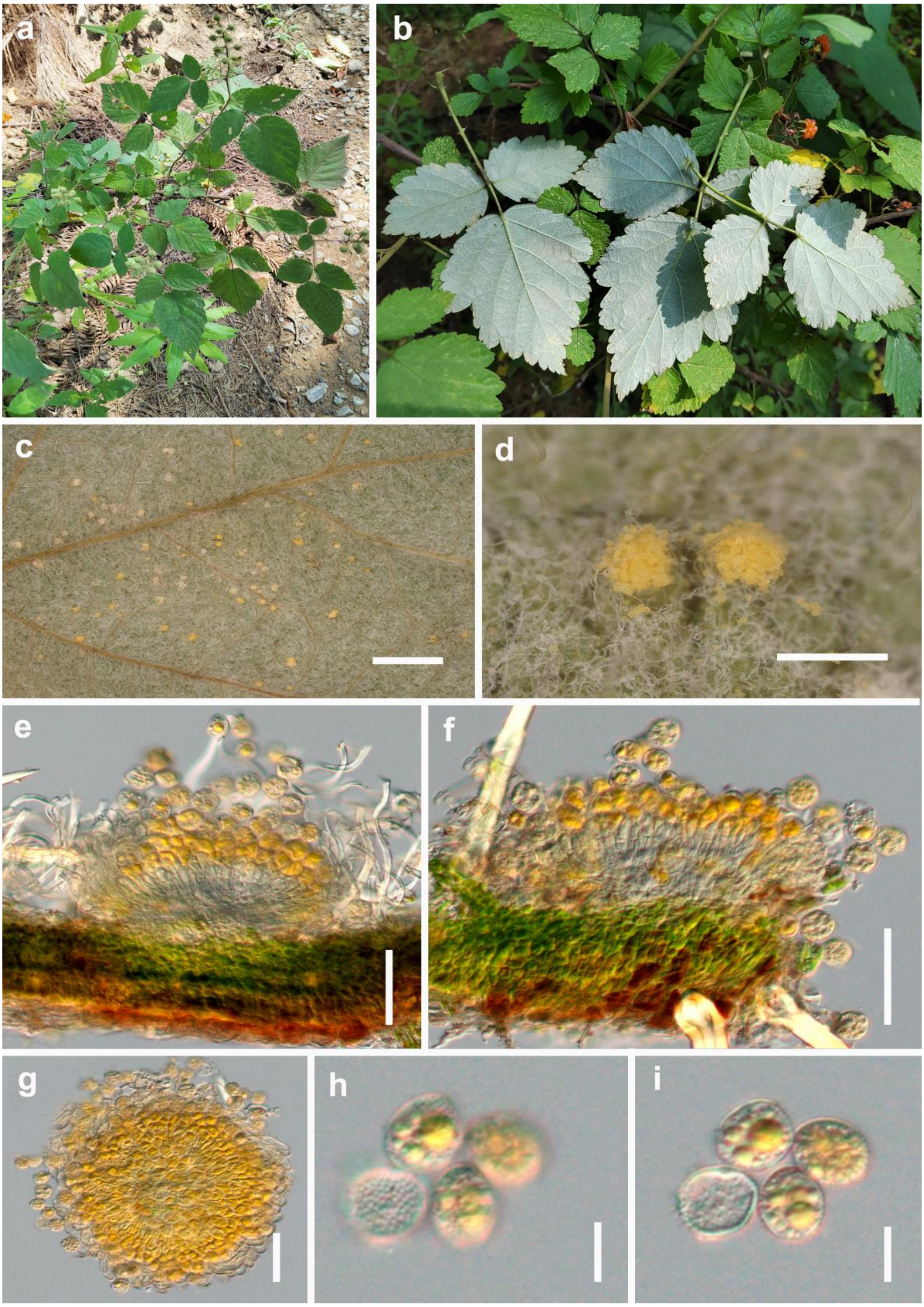

Figure 71 – *Phragmidium barnardii* (from HGUP21039) on *Rubus adenophorus*. a–d Uredinia on leaves. e–g Longitudinal section of uredinia. h–i Urediniospores. Scale bars: c = 5 mm, d = 1 mm, e–g = 50 µm, h–i = 10 µm.

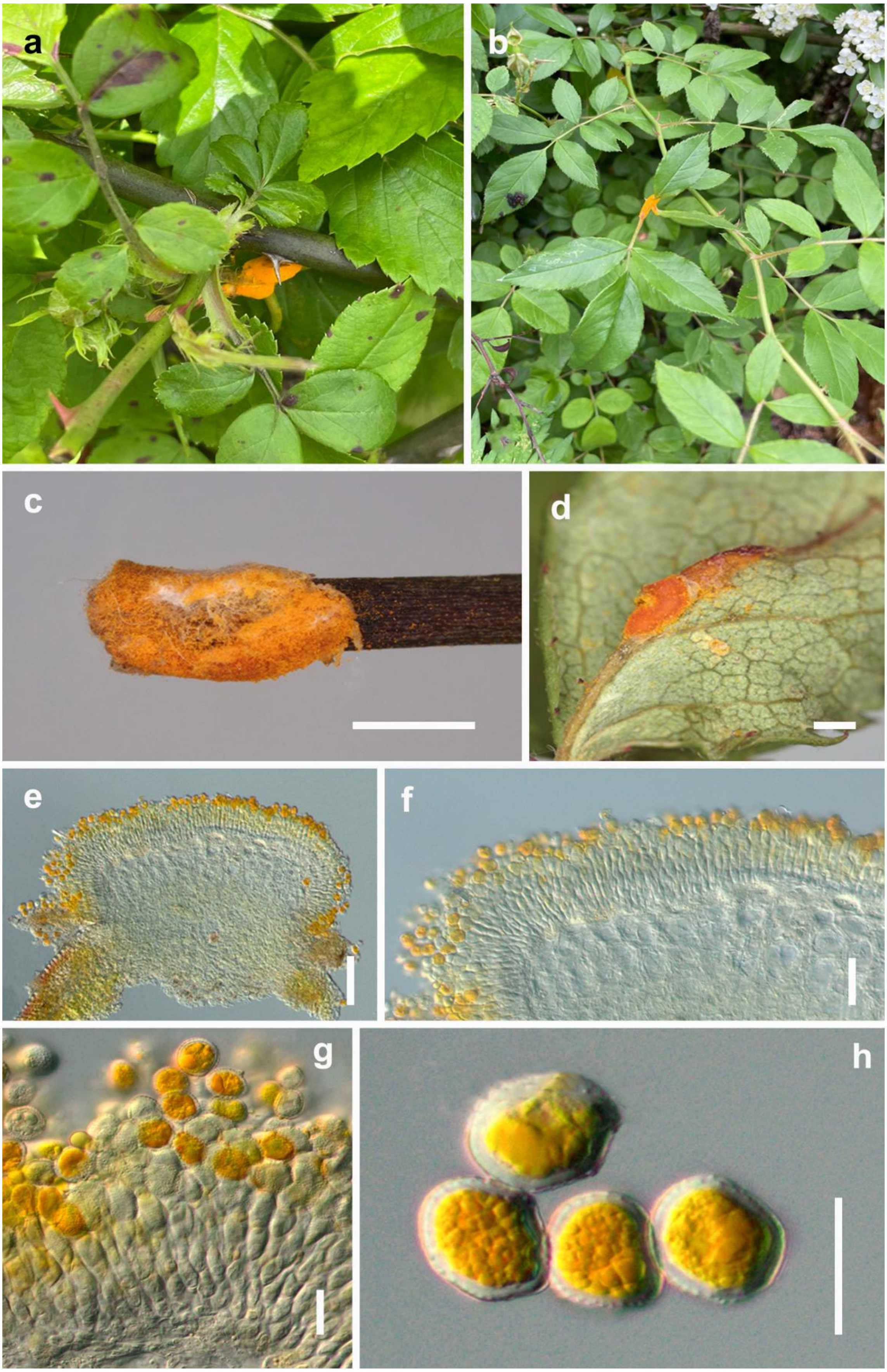

Figure 72 – *Phragmidium rosae-multiflorae* (from HGUP21158) on *Rosa multiflora*. a–d Aecia on leaves and stems. e–g Longitudinal section of aecia. h Aeciospores. Scale bars: c = 2 mm, d = 1 mm, e–g = 50 µm, h = 25 µm.

Gerwasia Racib., Bull. int. Acad. Sci. Lett. Cracovie, Cl. sci. math. nat. Sér. B, sci. nat. 3: 270 (1909)

Gerwasia rubi-setchuenensise J.E. Sun, Yong Wang bis & K.D. Hyde, sp. nov. Fig. 73

Index Fungorum number: IF901304; Facesoffungi number: FoF15369

Etymology – The name reflects the host *Rubus setchuenensis*, from which the type specimen was collected.

Holotype – HGUP21167

Description – *Spermogonia*, *aecia* and *telia* unknown. *Uredinia* hypophyllous, pulverulent, golden, scattered, irregular, surrounded by host epidermis, 0.5–1.0 mm diam. *Urediniospores* subglobose or fusiform, 18–29 × 15–22 µm ($\overline{x}$ = 24.6 × 17.9 µm, n = 30), inclusions golden or bright yellow; wall 2.1–3.2 µm thick, colorless, irregularly elongated verrucae.

Host – *Rubus setchuenensis* (Rosaceae)

Material examined – CHINA, Guizhou Province, Zunyi city, 27°66'54"N, 107°53'00"W, 827 m, 14 May 2021, on *Rubus setchuenensis*, J.E. Sun, holotype HGUP21167; Guizhou Province, Liupanshui city, 26°34'46"N, 104°48'38"W, 1850 m, 25 Sep 2021, on *R. setchuenensis*, J.E. Sun and X.Y. Zhang, HGUP21168.

Notes – *Gerwasia rubi-setchuenensise* appears to be most closely related to *G. rubi* (90 ML/94 MP; Fig. 3), which was found on *Rubus setchuenensis* in China. It is easy to distinguish from *G. rubi* by its smaller urediniospores (22–35 × 16–26 µm) (Raciborski 1909a) and *G. rubus-playfairianus* by its thinner urediniospores wall (2.1–3.2 µm *vs.* 4.0 µm) (Zhao et al. 2021). We, therefore, introduce *G. rubi-setchuenensise* as a new taxon based on phylogenetic analyses and morphological characteristics.

Gerwasia rubi-buergerii J.E. Sun, Yong Wang bis & K.D. Hyde, sp. nov. Fig. 74

Index Fungorum number: IF901305; Facesoffungi number: FoF15370

Etymology – The name reflects the host *Rubus buergeri,* from which the type specimen was collected.

Holotype – HGUP21171

Description – *Spermogonia*, *aecia* and *telia* unknown. *Uredinia* amphigenous, pulverulent, golden, scattered, irregular, surrounded by host epidermis, 0.5–3.0 mm diam. *Urediniospores* subglobose or fusiform, 25–37 × 21–27 µm ($\overline{x}$ = 30.1 × 24.7 µm, n = 30), inclusions golden; wall 2.5–3.5 µm thick, colorless, irregularly elongated verrucae.

Host – *Rubus buergeri* (Rosaceae)

Material examined – CHINA, Guizhou Province, Panzhou city, 25°89'60"N, 104°54'32"W, 803 m, 19 Jul 2021, on *Rubus buergeri*, J.E. Sun, holotype HGUP21171; Guizhou Province, Panzhou city, 25°89'60"N, 104°54'32"W, 803 m, 19 Jul 2021, on *R. buergeri*, J.E. Sun, HGUP21170; Panzhou city, 25°61'40"N, 104°82'05"W, 1862 m, 4 Aug 2022, on *R. buergeri*, J.E. Sun, HGUP21169.

Notes – In phylogeny, *Gerwasia rubi-buergerii* is closely related to *G. rubi* and *G. rubi-setchuenensise* (HGUP21167 and HGUP21168) with 85% ML and 75% MP bootstrap support (Fig. 3). *G. rubi-buergerii* is similar to *G. rubus-playfairianus* in urediniospores, although it has a slightly thinner wall (2.5–3.5 µm *vs.* 4.0 µm; Zhao et al. 2021). Therefore, we introduce *G. rubi-buergerii* as a new record in China.

Gerwasia rubi-alceifoliuse J.E. Sun, Yong Wang bis & K.D. Hyde, sp. nov. Fig. 75

Index Fungorum number: IF901306; Facesoffungi number: FoF15371

Etymology – The name reflects the host *Rubus alceifolius*, from which the type specimen was collected.

Holotype – HGUP21156

Description – *Spermogonia*, *aecia* and *telia* unknown. *Uredinia* amphigenous, pulverulent, yellow, scattered, nearly oval, not surrounded by host epidermis, 5.0–8.0 mm diam. *Urediniospores* subglobose or fusiform, 26–38 × 17–22 µm ($\bar{x}$ = 32.1 × 20.1 µm, n = 30), inclusions golden to bright yellow; wall 2.0–3.5 µm thick, colorless, irregularly elongated verrucose.

Host – *Rubus alceifolius* (Rosaceae)

Material examined – CHINA, Guizhou Province, Panzhou city, 25°89'62"N, 104°84'35"W, 877 m, 19 Jul 2021, on *Rubus alceifolius*, J.E. Sun, holotype HGUP21156; Guizhou Province, Guiyang city, 26°97'71"N, 106°45'46"W, 1151 m, 25 Jun 2022, on *R. alceifolius*, J.E. Sun, HGUP21157.

Notes – Phylogenetic analyses show that our specimens grouped a clade with good support (99 ML/99 MP/0.92 PP; Fig. 3). *Gerwasia rubi-alceifoliuse* has larger urediniospores than those of *G. rubus-playfairianus* (21–29 × 18–22 µm; Zhao et al. 2021). Thus we, identify *G. rubi-alceifoliuse* as a new species.

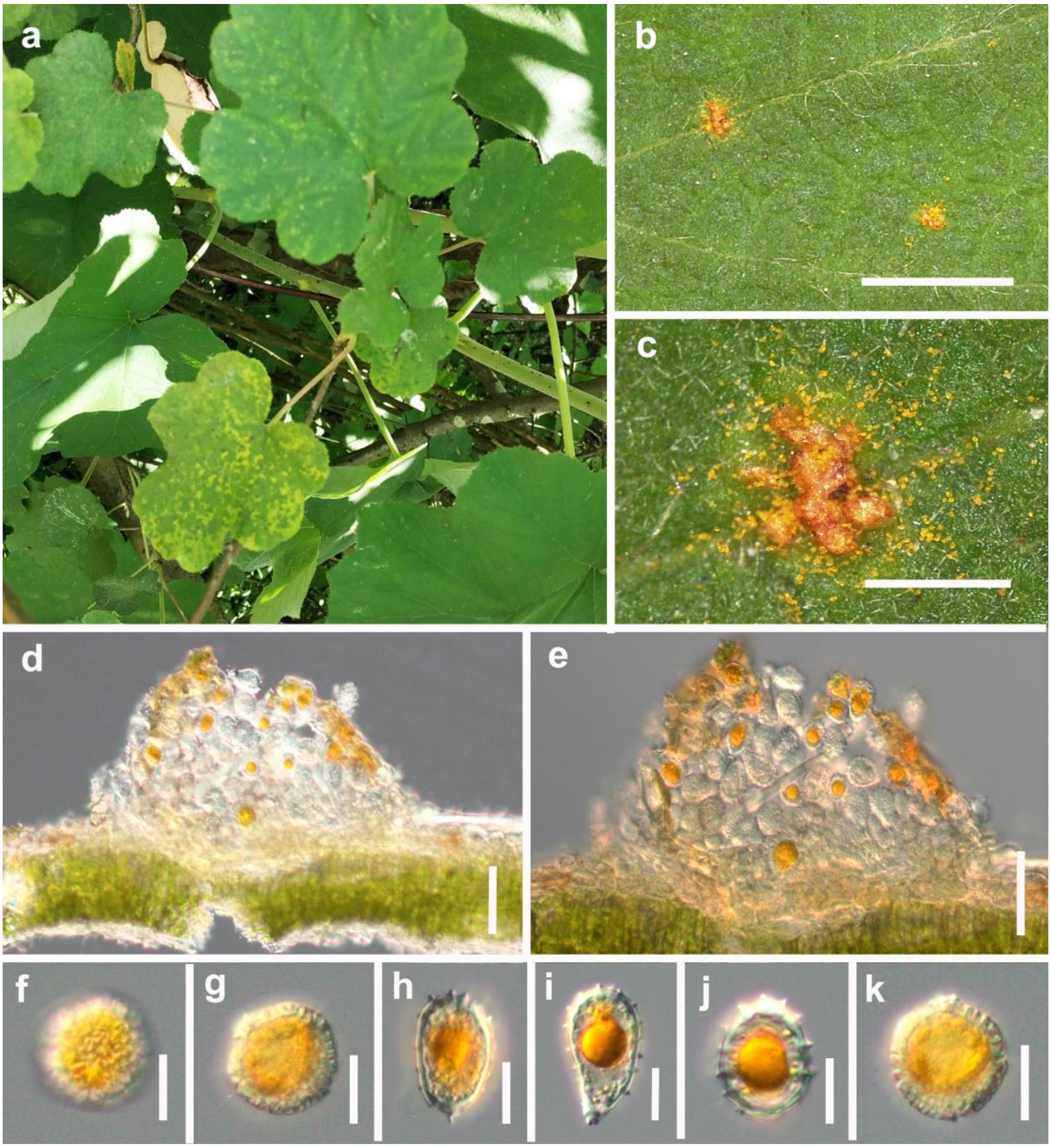

Figure 73 – *Gerwasia rubi-setchuenensise* (from holotype HGUP21167) on *Rubus setchuenensis*. a–c Uredinia on leaves. d–e Longitudinal section of uredinia. f–k Urediniospores. Scale bars: b = 5 mm, c = 1 mm, d–e = 50 µm, f–k = 12.5 µm.

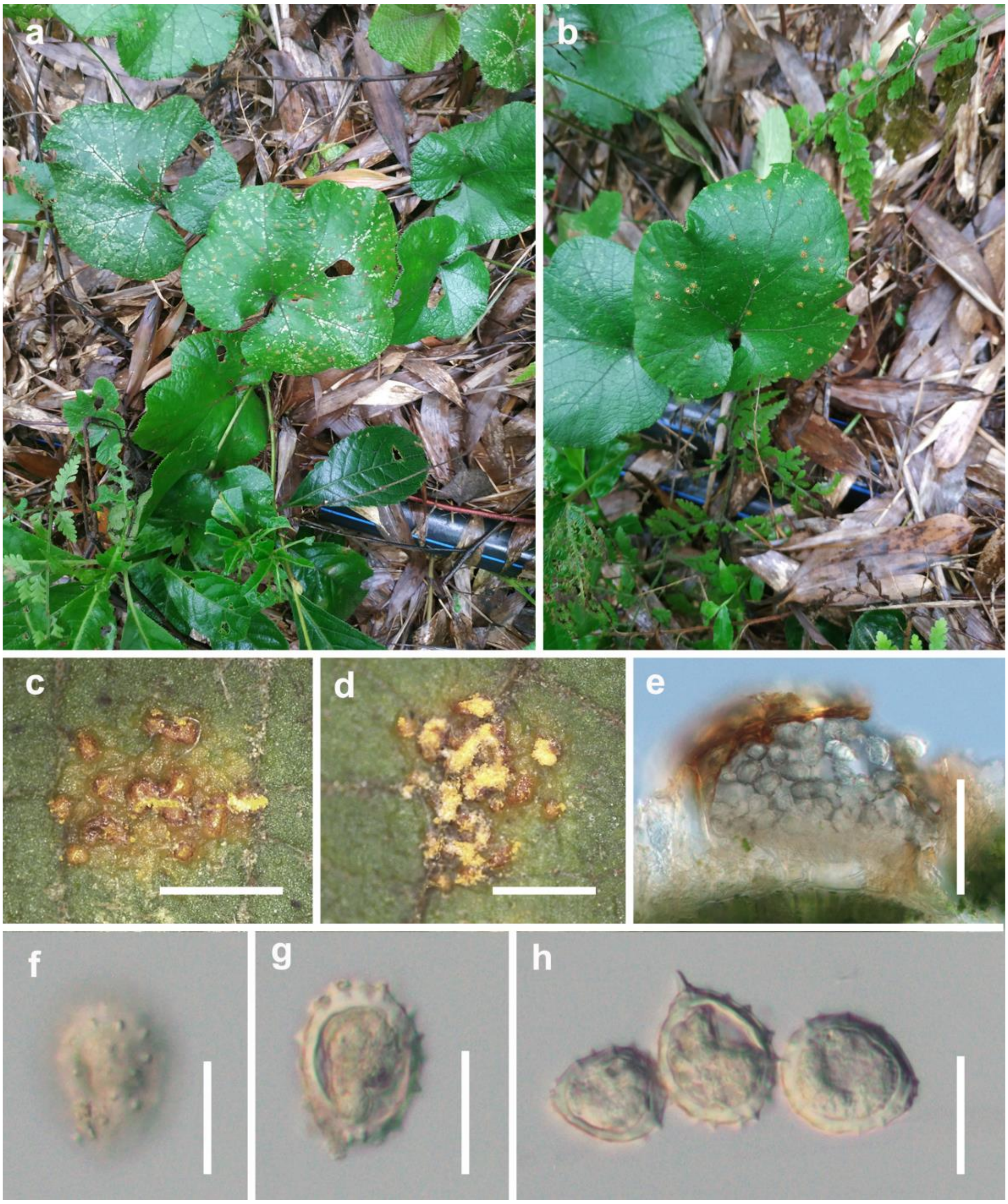

Figure 74 – *Gerwasia rubi-buergerii* (from holotype HGUP21171) on *Rubus buergeri*. a–d Uredinia on leaves. e Longitudinal section of uredinium. f–h Urediniospores. Scale bars: c–d = 2 mm, e = 50 µm, f–h = 25 µm.

Gerwasia rubi Racib., Bull. int. Acad. Sci. Lett. Cracovie, Cl. sci. math. nat. Sér. B, sci. nat. 3: 271 (1909) Fig. 76

MycoBank number: MB193888

Description – *Spermogonia*, *aecia* and *telia* not observed. *Uredinia* hypophyllous, epiphyllous and amphigenous and on stems, not surrounded by host epidermis, scattered, globose or irregular, orange, pulverulent, 0.5–1.0 mm diam. *Urediniospores* orange, 26–40 × 17–24 µm ($\bar{x}$ = 32.4 × 21.1 µm, n = 30), subglobose; wall 1.4–2.2 µm thick, colorless, regularly echinulate.

Host – *Rubus reflexus* (Rosaceae), *Rubus* sp.

Material examined – CHINA, Guizhou Province, Guiyang city, 26°36'80"N, 107°16'26"W, 1235 m, 2 May 2022, on *Rubus reflexus*, J.E. Sun, HGUP21166.

Notes – *Gerwasia rubi* was first reported on *Rubus* sp. by Raciborski (1909a). Its nucleotide data was established by McTaggart et al. (2016), although without a description of morphological characteristics. We confirmed our specimen as *G. rubi*, through phylogenetic analyses with nucleotide data from McTaggart et al. (2016).

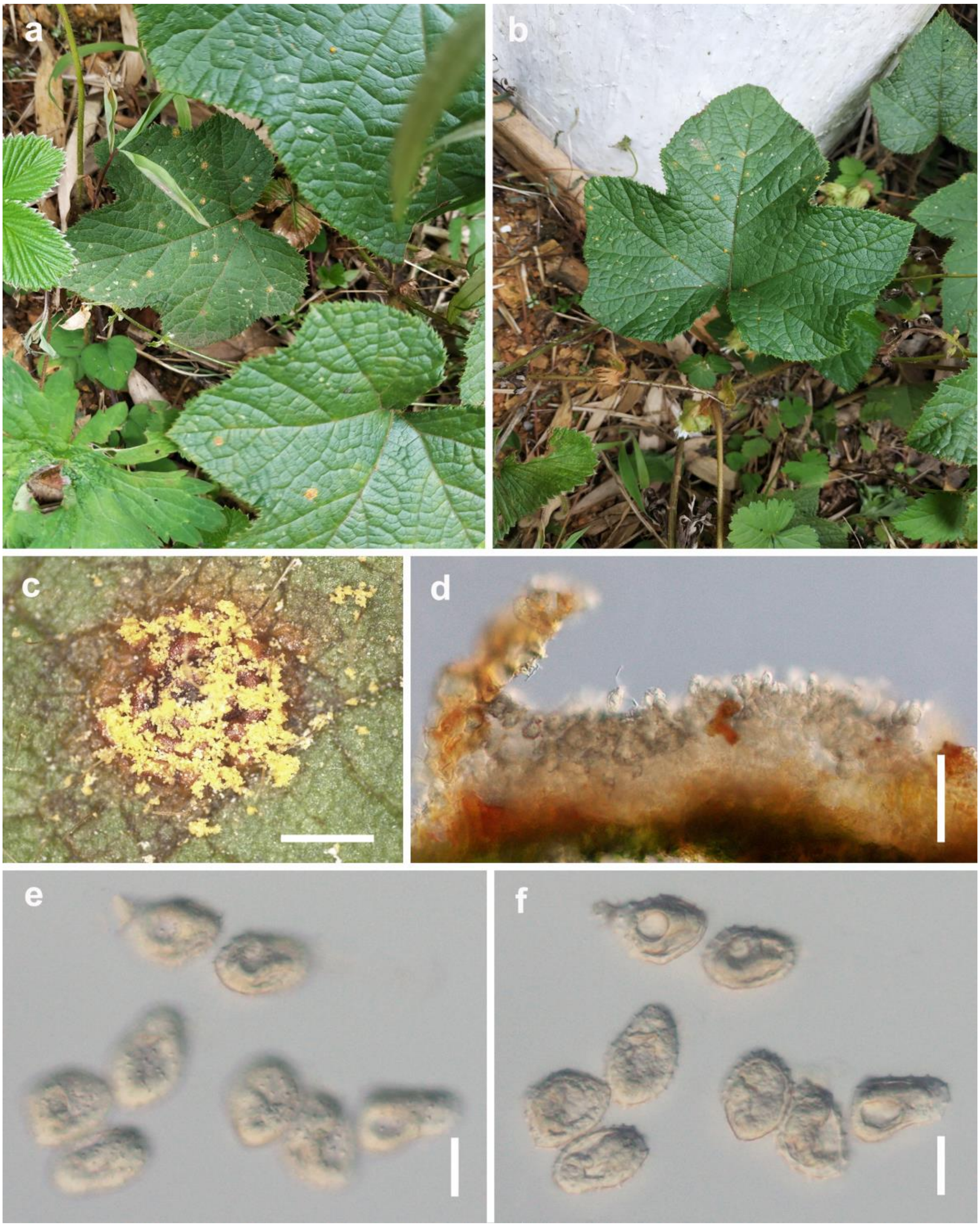

Figure 75 – *Gerwasia rubi-alceifoliuse* (from holotype HGUP21156) on *Rubus alceifolius*. a–c Uredinia on leaves. d Longitudinal section of uredinium. e–f Urediniospores. Scale bars: c = 5 mm, d = 100 µm, e–f = 25 µm.

Hamaspora Körn., Hedwigia 16: 22 (1877)

Hamaspora rubi-parkerii J.E. Sun, Yong Wang bis & K.D. Hyde, sp. nov. Fig. 77

Index Fungorum number: IF901307; Facesoffungi number: FoF15372

Etymology – The name reflects the host *Rubus parkeri*, from which the type specimen was collected.

Holotype – HGUP21162

Description – *Spermogonia*, *aecia* and *uredinia* unknown. *Telia* hypophyllous, golden, irregularly filiform, scattered, not surrounded by host epidermis, up to 3.5 cm long. *Teliospores* aggregated into fibrils, fusiform, hyaline, 4–6–-septate, 111–186 × 12–21 µm ($\bar{x}$ = 150.7 × 16.4 µm, n = 30), solid apex, 10–26 µm long; wall 1.0–2.6 µm thick, colorless, smooth. Teliospores germinated to form basidia and basidiospores, the basidiospores nearly oval, inclusions golden, 10–16 × 5–8 µm.

Host – *Rubus parkeri* (Rosaceae)

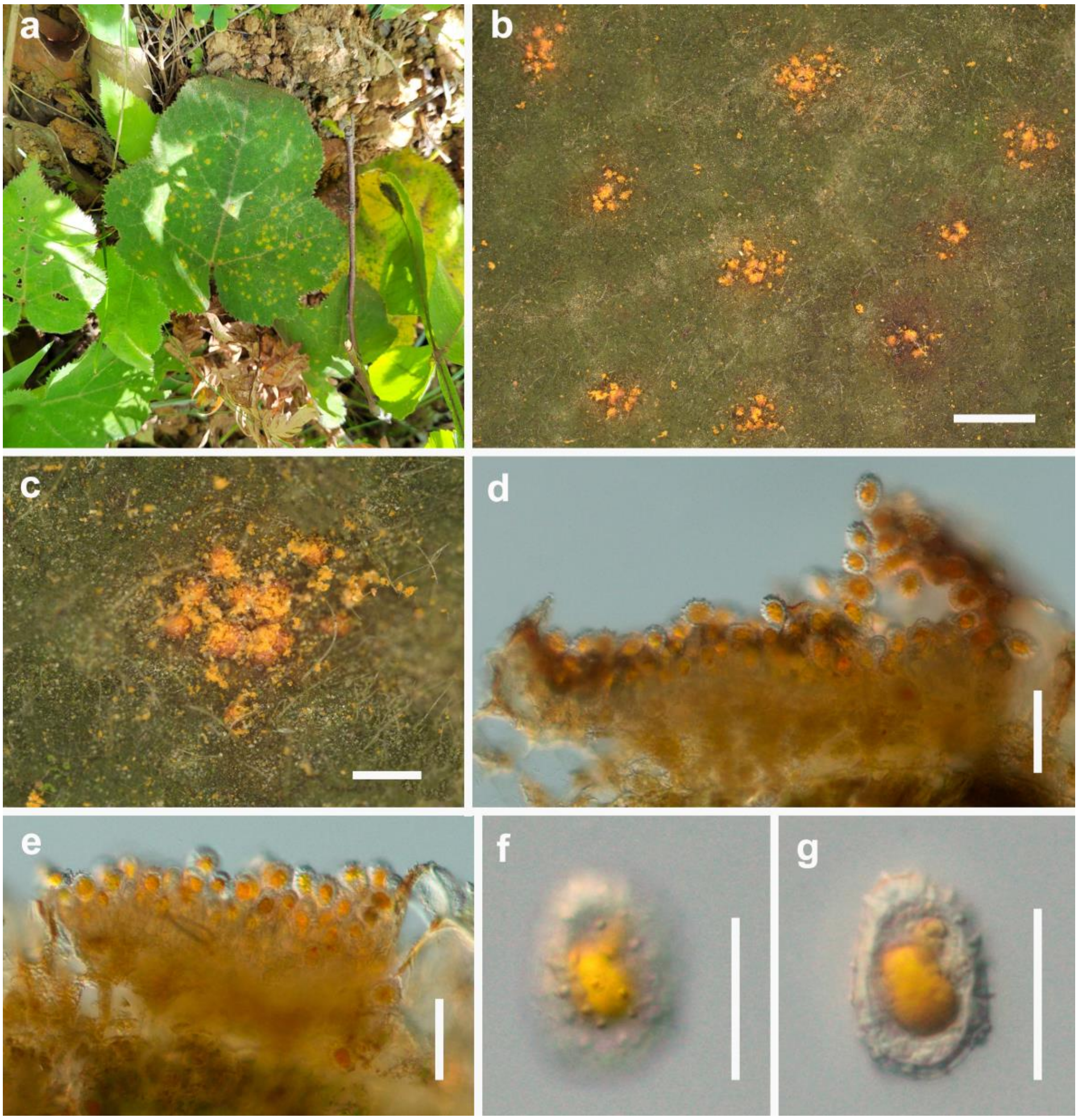

Figure 76 – *Gerwasia rubi* (from HGUP21158) on *Rubus reflexus*. a–c Uredinia on leaves. d–e Longitudinal section of uredinia. f–g Urediniospores. Scale bars: b = 2 mm, c = 0.5 mm, d–e = 50 µm, f–g = 25 µm.

Material examined – CHINA, Guizhou Province, Zunyi city, 27°66'52"N, 107°52'98"W, 863 m, 14 May 2021, on *Rubus parkeri*, J.E. Sun, holotype HGUP21162; Guizhou Province, Zunyi city, 27°67'20"N, 106°39'84"W, 1030 m, 27 May 2022, on *R. parkeri*, J.E. Sun, HGUP21159, HGUP21160; Bijie city, 27°25'14"N, 106°14'17"W, 1196 m, 27 May 2022, on *R. parkeri*, J.E. Sun, HGUP21161.

Notes – *Hamaspora rubi-parkerii* formed a small branch with high support (100 ML/99 MP/1.00 PP; Fig. 3). Our collections have teliospores with similar morphology to the holotype *H. rubus-pirifolius*. However, the solid apex of HGUP21162 is longer than in *H. rubus-pirifolius* (10–26 µm *vs*. 6–12 µm) (Zhao et al. 2021). Thus, *H. rubi-parkerii* is proposed as a new taxon.

Figure 77 – *Hamaspora rubi-parkerii* (from holotype HGUP21162) on *Rubus parkeri*. a–c Telia on leaves. d–e Longitudinal section of telium. f–g Teliospores. h–j Germinating teliospores and basidia. k–r Basidiospores. Scale bars: b–c = 5 mm, d–k = 50 µm, l–r = 12.5 µm.

Hamaspora rubi-lambertianuse J.E. Sun, Yong Wang bis & K.D. Hyde, sp. nov. Fig. 78

Index Fungorum number: IF901308; Facesoffungi number: FoF15374

Etymology – The name reflects the host *Rubus lambertianus*, from which the type specimen was collected.

Holotype – HGUP21163

Description – *Spermogonia*, *aecia* and *telia* unknown. *Uredinia* hypophyllous, pulverulent, yellowish brown, scattered, irregular, not surrounded by host epidermis, 0.5–1.5 mm diam. *Urediniospores* formed in basipetal succession, subglobose or fusiform, 18–24 × 16–20 µm ($\overline{x}$ = 21.2 × 17.9 µm, n = 30), inclusions light brown; wall 1.0–1.5 µm thick, colorless, mostly with small echinulate on the surface.

Host – *Rubus lambertianus* (Rosaceae)

Material examined – CHINA, Guizhou Province, Guiyang city, 26°44'73"N, 106°58'66"W, 899 m, 27 Mar 2021, on *Rubus lambertianus*, J.E. Sun, holotype HGUP21163; Guizhou Province, Guiyang city, 26°65'94"N, 106°67'52"W, 1320 m, 21 Aug 2021, on *R. lambertianus,* J.E. Sun, HGUP21164; Guiyang city, 26°97'71"N, 106°45'46"W, 1151 m, 25 Jun 2022, on *R. lambertianus*, J.E. Sun, HGUP21165.

Notes – Our specimens of *Hamaspora rubi-lambertianuse* were close to *H. acutissima* (BRIP:55606) in the multiple loci phylogenetic analysis (Fig. 3). *H. rubi-lambertianuse* has wider urediniospores than those of *H. rubus-pirifolius* (16–20 µm *vs.* 14–17 µm; Zhao et al. 2021). Therefore, we introduce *H. rubi-lambertianuse* as a new species.

Coleosporiaceae Dietel, in Engler & Prantl, Nat. Pflanzenfam., Teil. I (Leipzig) 1(1): 548 (1900)
Coleosporium Lév., Annales des Sciences Naturelles Botanique 8: 373 (1847)

Coleosporium septembere J.E. Sun, Yong Wang bis & K.D. Hyde, sp. nov. Fig. 79

Index Fungorum number: IF901309; Facesoffungi number: FoF15373

Etymology – The specific epithet "septembere" refers to the month, September.

Holotype – HGUP21046

Description – *Spermogonia* and *aecia* unknown. *Uredinia* and *telia* hypophyllous, surrounded by host epidermis, oblong or regular, bright brown spot, 0.5–1.0 mm diam. *Urediniospores* globose, ellipsoidal or irregular, 21–31 × 13–20 µm ($\overline{x}$ = 25.3 × 17.2 µm, n = 30), pale to golden, or yellow; wall 1.6–2.6 µm thick, colorless, densely and minutely verrucose. *Teliospores* obovoid, pale to bright-brown, 30–54 × 12–20 µm ($\overline{x}$ = 37.5 × 16.5 µm, n = 30); wall 1.0–1.9 µm thick, colorless, smooth.

Host – *Clematis florida* (Ranunculaceae)

Material examined – CHINA, Guizhou Province, Liupanshui city, 26°34'46"N, 104°48'38"W, 1840 m, 25 Sep 2021, on *Clematis florida*, X.Y. Zhang, holotype HGUP21046; Guizhou Province, Liupanshui city, 26°34'46"N, 104°48'38"W, 1840 m, 25 Sep 2021, on *C. florida*, X.Y. Zhang, HGUP21047.

Notes – There are several other species of *Coleosporium* found on *Clematis* spp. that have morphologically similar urediniospores, *Coleosporium clematidis* (18–35 × 13–23 µm; Zhuang et al. 2021), *C. clematidis-apiifoliae* (16–32 × 12–22 µm; Hiratsuka et al. 1992), *C. sichuanense* (19–30 × 15–21 µm; Zhao et al. 2021). However, the teliosporesof *C. septembere* are shorter than those of *Coleosporium clematidis* (40–125 × 15–30 µm) and *C. clematidis-apiifoliae* (40–80 × 15–25 µm) but larger than those of *C. sichuanense* (7–20 × 5–14 µm). In the phylogenetic analyses our specimens clustered in a clade with 100% ML, 70% MP and 0.99 BYPP bootstrap support (Fig. 4). Therefore, we name *C. septembere* as a new taxon.

Coleosporium julii J.E. Sun & Yong Wang bis, sp. nov. Fig. 80

Index Fungorum number: IF901310; Facesoffungi number: FoF15375

Etymology – The specific epithet "julii" refers to the month, July.

Holotype – HGUP21049

Description – *Spermogonia*, *aecia* and *telia* unknown. *Uredinia* hypophyllous, surrounded by host epidermis, oblong or irregular, golden spot, pulverulent, 0.5–1.2 mm diam. *Urediniospores* globose, ellipsoidal or regular, 15–23 × 11–16 µm (x̅ = 18.1 × 13.5 µm, n = 30), pale to golden; wall 1.1–1.7 µm thick, colorless, densely and minutely verrucose.

Host – *Smilax china* (Smilacaceae)

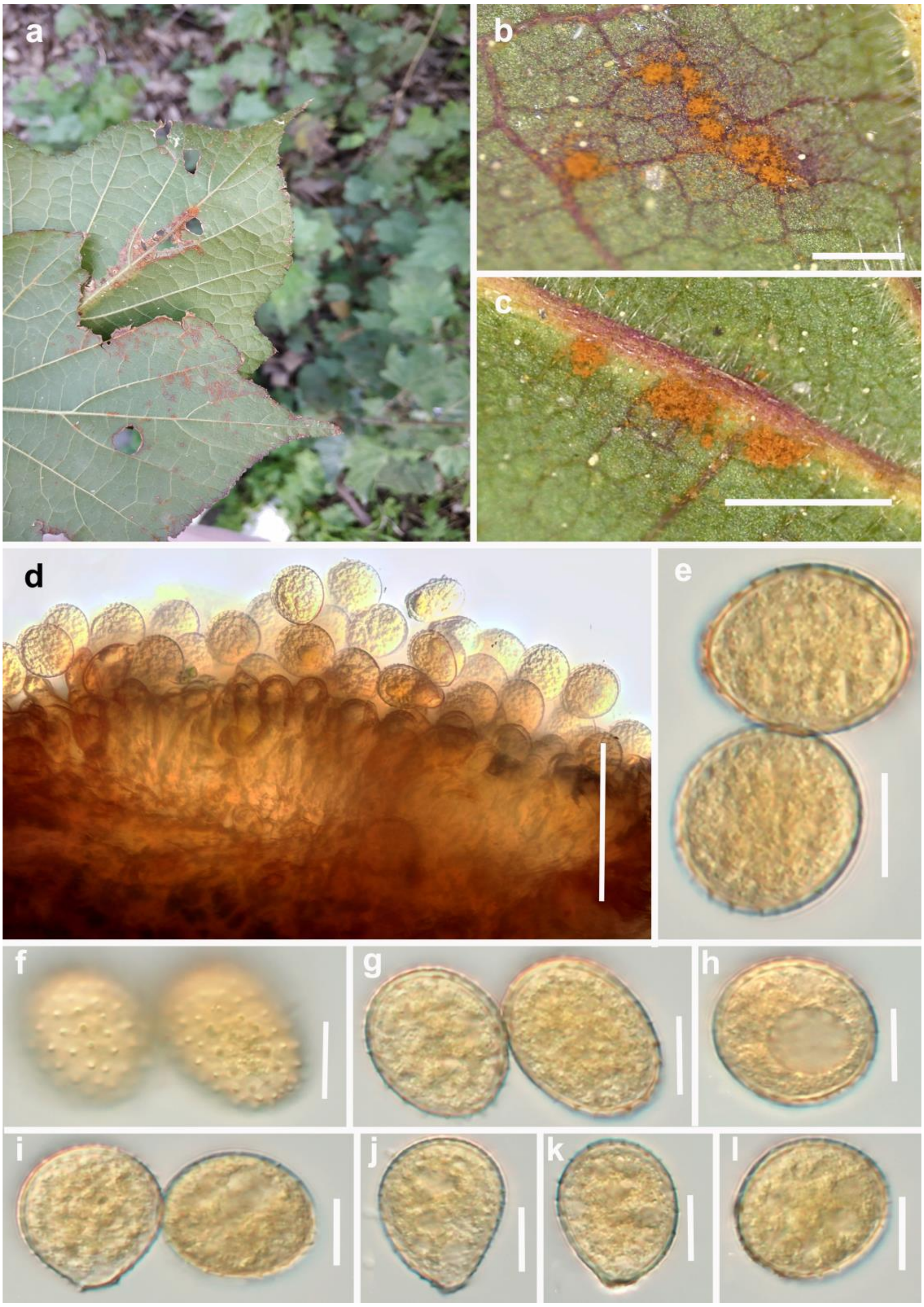

Figure 78 – *Hamaspora rubi-lambertianuse* (from holotype HGUP21163) on *Rubus lambertianus*. a–c Uredinia on leaves. d Longitudinal section of uredinium. e–l Urediniospores. Scale bars: b = 5 mm, c = 1 mm, d = 50 µm, e–l = 12.5 µm.

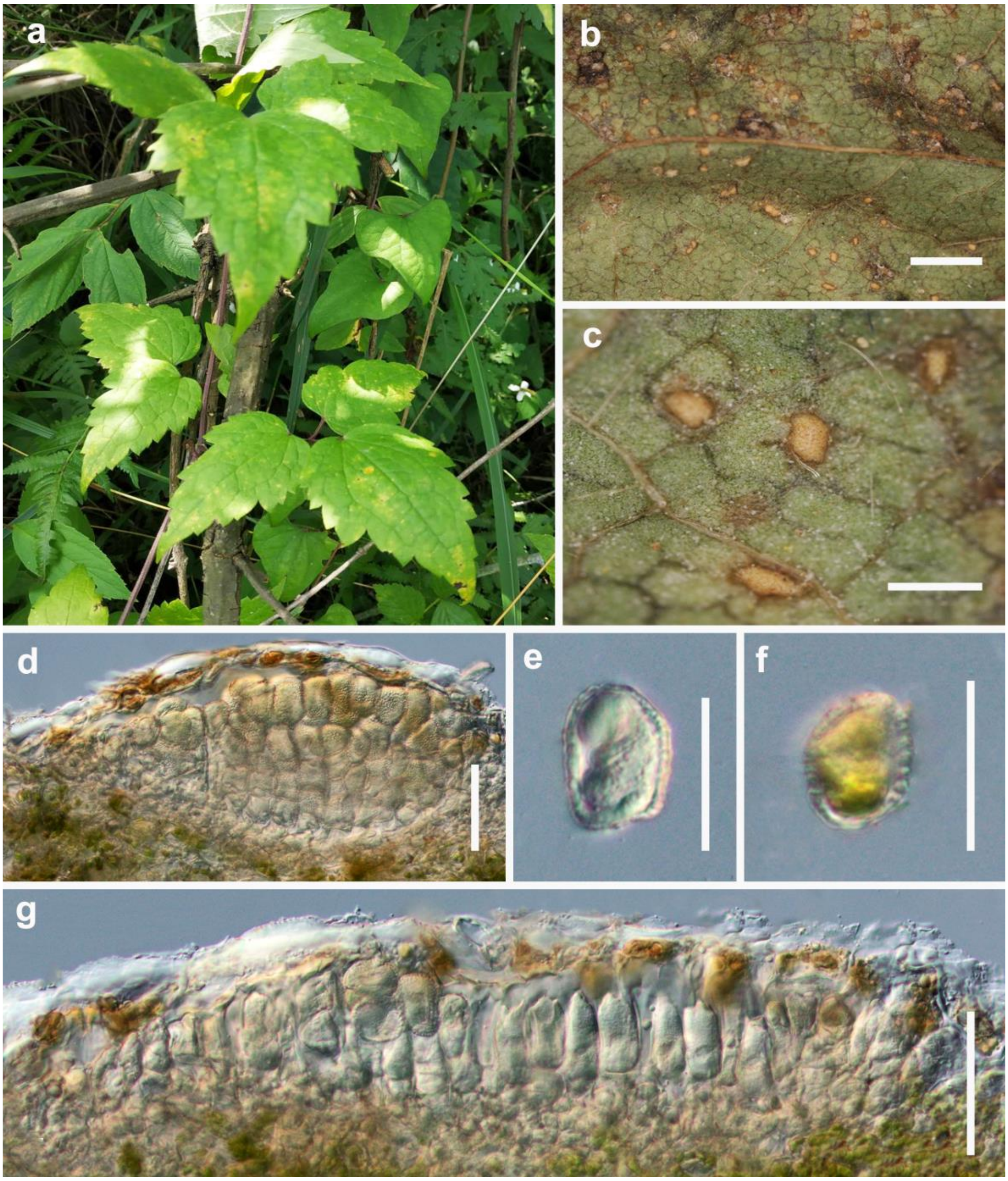

Figure 79 – *Coleosporium septembere* (from holotype HGUP21046) on *Clematis florida*. a–c Uredinia and telia on leaves. d Longitudinal section of uredinium. e–f Urediniospores. g Longitudinal section of telium and teliospores. Scale bars: b = 2 mm, c = 1 mm, d, g = 50 µm, e–f = 25 µm.

Material examined – CHINA, Guizhou Province, Liupanshui city, 26°08'26"N, 104°86'61"W, 1297 m, 15 Jul 2021, on *Smilax china*, J.E. Sun, holotype HGUP21049; Guizhou Province, Liupanshui city, 26°08'26"N, 104°86'61"W, 1297 m, 15 Jul 2021, on *S. china*, J.E. Sun, HGUP21048.

Notes – In the phylogenetic analyses, our collections formed a distant clade sister to *Coleosporium septembere* with good support (ML/MP/BI: 90/65/0.93; in Fig. 4). Our specimens have smaller urediniospores than *C. smilacis*, which also occurs in China on *Smilax* sp. (15–23 × 11–16 µm *vs.* 18–34 × 14–20 µm; Zhao et al. 2021). Hence, it is described as a new species.

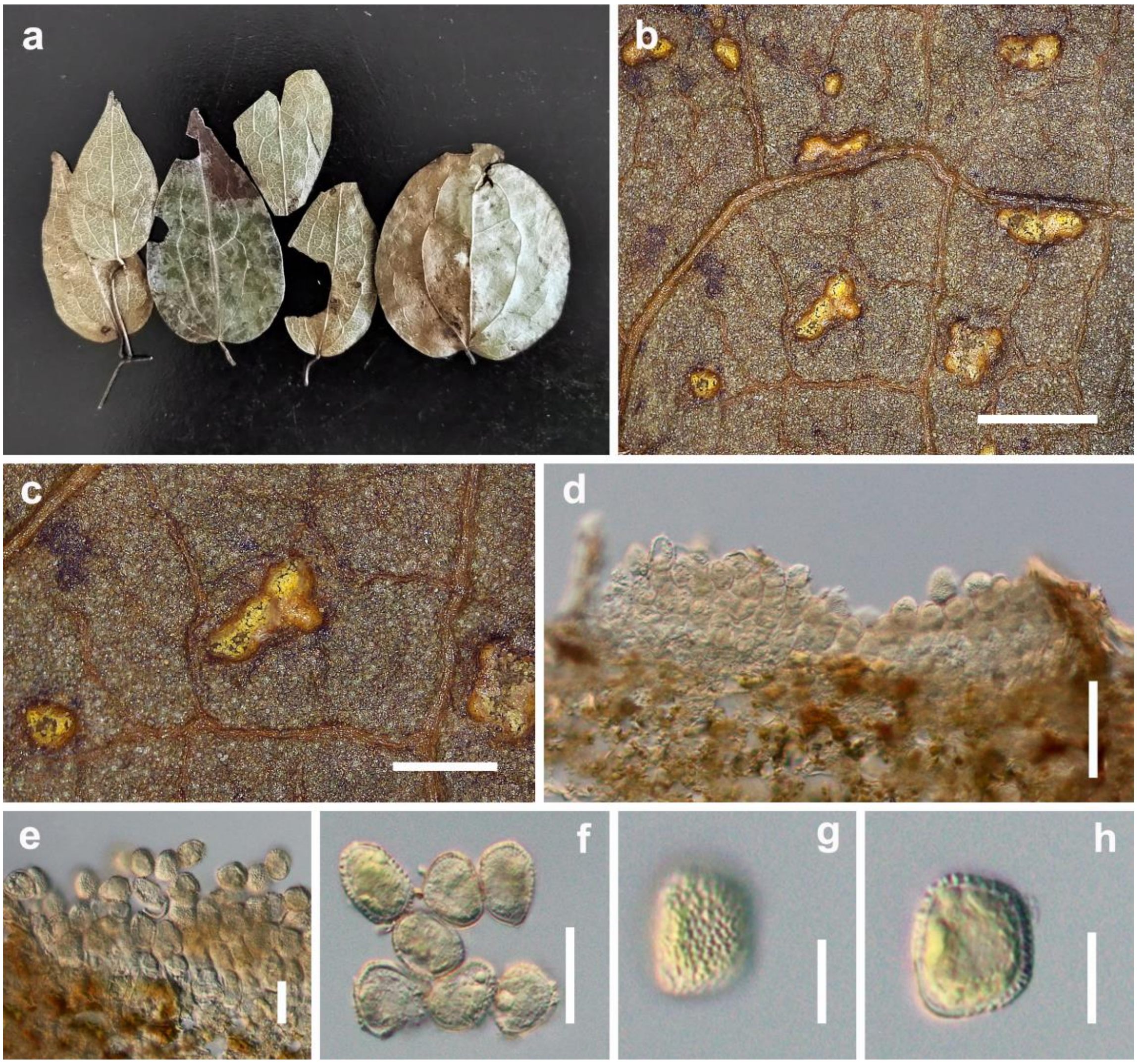

Figure 80 – *Coleosporium julii* (from holotype HGUP21049) on *Smilax china*. a–c Uredinia on leaves. d–e Longitudinal section of uredinia. f–h Urediniospores. Scale bars: b = 2 mm, c = 1 mm, d = 50 µm, e–f = 25 µm: g–h = 12.5 µm.

Coleosporium dasyandrae J.E. Sun, Yong Wang bis & K.D. Hyde, sp. nov. Fig. 81

Index Fungorum number: IF901311; Facesoffungi number: FoF15376

Etymology – The name reflects the host *Clematis dasyandra*, from which the type specimen was collected.

Holotype – HGUP21050

Description – *Spermogonia*, *aecia* and *telia* unknown. *Uredinia* hypophyllous, surrounded by host epidermis, oblong or irregular, golden spot, pulverulent, 0.5–1.5 mm diam. *Urediniospores* globose or ellipsoidal, 25–32 × 14–21 µm ($\bar{x}$ = 29 × 18.3 µm, n = 30), yellow to golden; wall 1.8–2.5 µm thick, colorless, densely, and minutely verrucose.

Host – *Clematis dasyandra* (Ranunculaceae)

Material examined – CHINA, Guizhou Province, Duyun city, 25°25'05"N, 107°71'09"W, 501 m, 12 Mar 2022, on *Clematis dasyandra*, J.E. Sun, holotype HGUP21050; Guizhou Province, Duyun city, 25°25'05"N, 107°71'09"W, 501 m, 12 Mar 2022, on *C. dasyandra*, J.E. Sun, HGUP21051, HGUP21052.

Notes – The new collections on *Clematis dasyandra* had a distant relationship to *Coleosporium geranii* (ZP-R875) and *C. pulsatillae* (KR-M-0014421 and KR-M-0021308) in the phylogenetic analysis. The urediniospores of *C. dasyandrae* are similar in size to those of *C. geranii* (18–30 × 12–20 µm; Zhuang et al. 2021) but are smaller than those of *C. pulsatillae* (20–

50 × 15–23 µm; Zhuang et al. 2021). The urediniospores of our collections are longer than those of *C. solidaginis* (25–32 µm *vs.* 15–24 µm; McTaggart and Aime 2018). Accordingly, we consider our new specimens to be a new species.

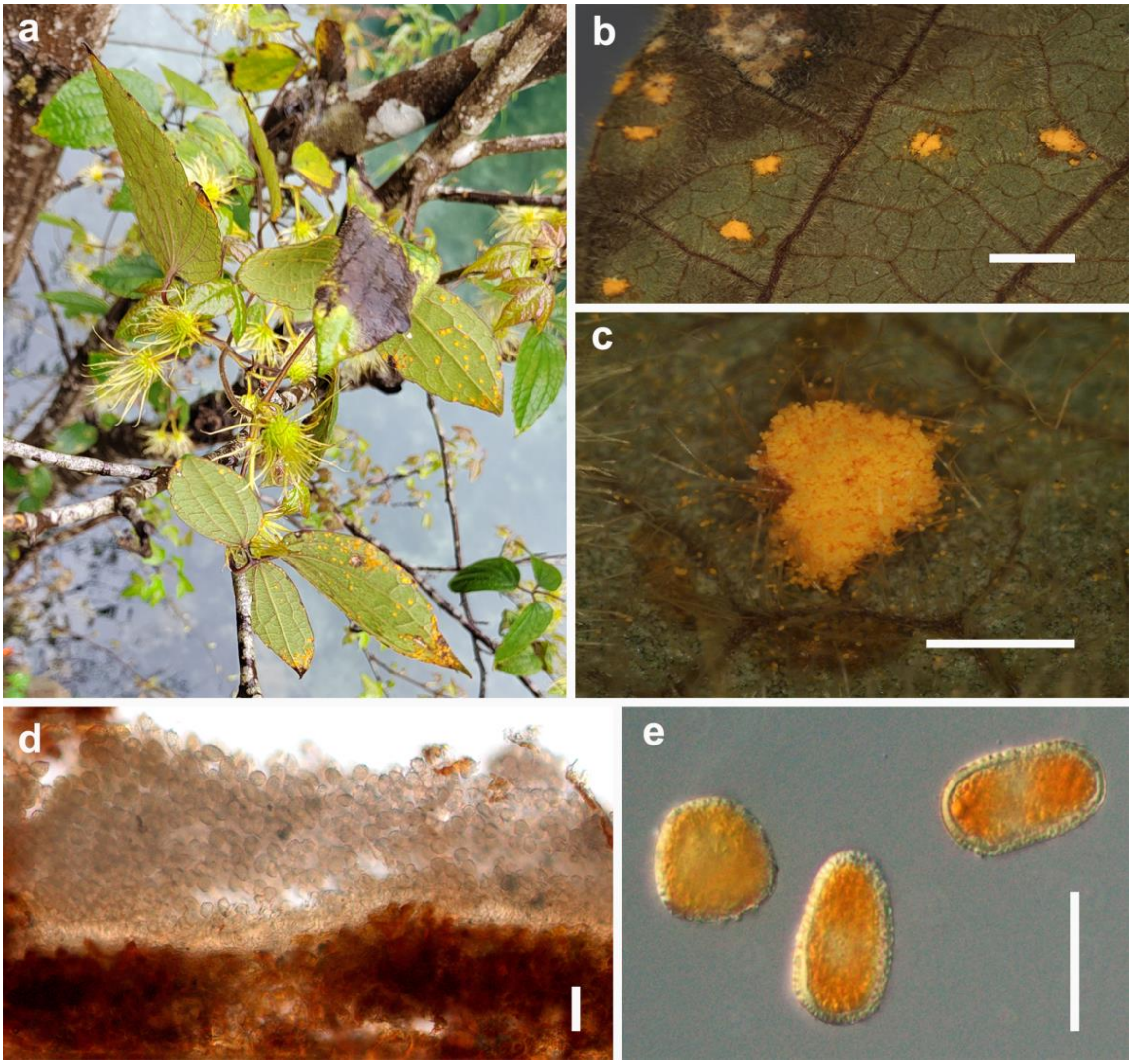

Figure 81 – *Coleosporium dasyandrae* (from holotype HGUP21050) on *Clematis dasyandra*. a–c Uredinia on leaves. d Longitudinal section of uredinium. e Urediniospores. Scale bars: b = 1 mm, c = 0.5 mm, d = 50 µm, e = 25 µm.

Coleosporium buchananianae J.E. Sun, Yong Wang bis & K.D. Hyde, sp. nov. Fig. 82

Index Fungorum number: IF901312; Facesoffungi number: FoF15377

Etymology – The name reflects the host *Clematis buchananiana*, from which the type specimen was collected.

Holotype – HGUP21053

Description – *Spermogonia*, *aecia* and *telia* unknown. *Uredinia* hypophyllous, scattered, obvious boundary, irregular, yellow, pulverulent, 0.5–1.0 mm diam. *Urediniospores* ellipsoidal or flat oval, 24–30 × 13–18 µm ($\bar{x}$ = 26.4 × 15.5 µm, n = 30), hyaline to yellow; wall 2.0–2.9 µm thick, colorless, densely and minutely verrucose.

Host – *Clematis buchananiana* (Ranunculaceae)

Material examined – CHINA, Guizhou Province, Duyun city, 26°45'88"N, 106°98'43"W, 854 m, 22 Jun 2021, on *Clematis buchananiana*, J.E. Sun, holotype HGUP21053.

Notes – In the phylogenetic analyses *Coleosporium buchananianae* formed a well-supported clade (Fig. 4). It is distinguished from *C. solidaginis* by its longer urediniospores (24–30 µm *vs.*

15–24 µm; Zhuang et al. 2021). We confirmed the specimen as a new taxon, through phylogenetic analyses and morphological characters.

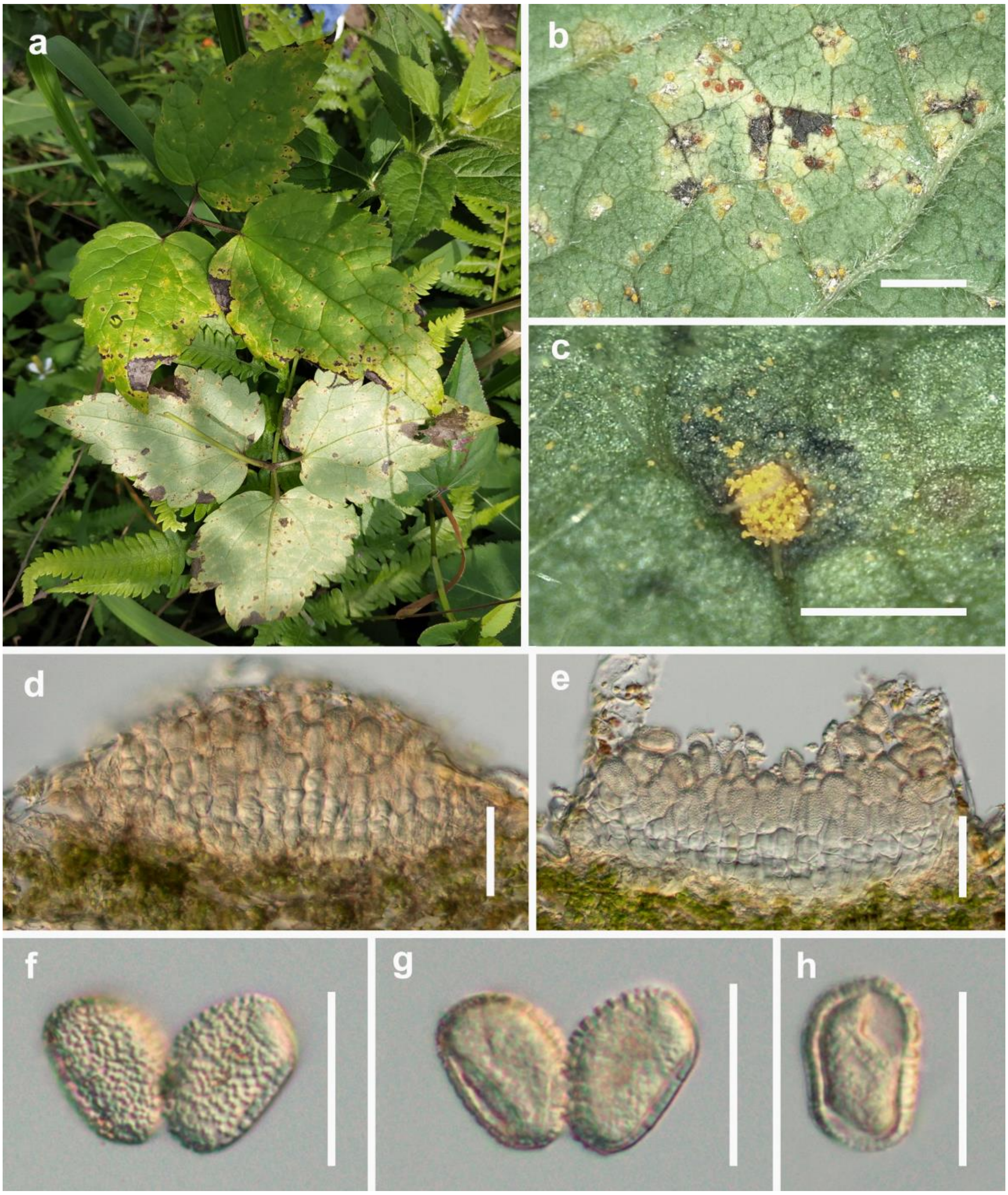

Figure 82 – *Coleosporium buchananianae* (from holotype HGUP21053) on *Clematis buchananiana*. a–c Uredinia on leaves. d–e Longitudinal section of uredinia. f–h Urediniospores. Scale bars: b = 5 mm, c = 1 mm, d–e = 50 µm, f–h = 20 µm.

Coleosporium abrotanoidesii J.E. Sun, Yong Wang bis & K.D. Hyde, sp. nov. Fig. 83

Index Fungorum number: IF901313; Facesoffungi number: FoF15378

Etymology – The name reflects the host *Carpesium abrotanoides*, from which the type specimen was collected.

Holotype – HGUP21080

Description – *Spermogonia* and *aecia* unknown. *Uredinia* hypophyllous, scattered, surrounded by host epidermis, irregular, golden spot, pulverulent, 0.5–1.0 mm diam.

Urediniospores ellipsoidal or globose, 19–27 × 14–18 µm (x̅ = 22.5 × 16.7 µm, n = 30), bright yellow to golden; wall 1.4–1.8 µm thick, colorless, densely and minutely verrucose. *Telia* produced in a crust below the epidermis, hypophyllous, irregular, bright brown, 0.5–1.0 mm diam. *Teliospores* clavate or ellipsoidal, 30–53 × 14–30 µm (x̅ = 41.5 × 22.6 µm, n = 30), golden; wall 0.8–1.2 µm thick, colorless.

Host – *Carpesium abrotanoides* (Asteraceae)

Figure 83 – *Coleosporium abrotanoidesii* (from holotype HGUP21080) on *Carpesium abrotanoides*. a–c Uredinia on leaves. d Longitudinal section of uredinium. e–f Urediniospores. g–h Telia on leaves. i Longitudinal section of telium and teliospores. j Teliospores. Scale bars: b = 5 mm, c = 1 mm, h = 2 mm, d, i = 50 µm, e–f, j = 25 µm.

Material examined – CHINA, Guizhou Province, Guiyang city, 26°65'99"N, 106°67'50"W, 1301 m, 21 Aug 2021, on *Carpesium abrotanoides,* J.E. Sun, holotype HGUP21080; Guizhou Province, Guiyang city, 26°45'99"N, 106°65'55"W, 1101 m, 15 Nov 2021, on *C. abrotanoides*, J.E. Sun, HGUP21081; Guiyang city, 26°98'30"N, 106°45'23"W, 1124 m, 25 Jun 2022, on *C. abrotanoides*, J.E. Sun, HGUP21082.

Notes – In the phylogenetic analyses our specimens formed a distinct lineage closely related to *Coleosporium eupatorii* with high support (Fig. 4). However, *C. abrotanoidesii* has shorter teliospores than *C. eupatorii* (30–53 µm *vs.* 40–80 µm; Zhuang et al. 2021). *Coleosporium carpesii*, which was also found on leaves of *Carpesium abrotanoides* in China, also has longer teliospores (50–100 µm; Zhuang et al. 2021). Therefore, we identified our collections as a new species following the suggestions for species delineation (Jeewon & Hyde 2016).

Coleosporium clematidis Barclay, Journal of the Asiatic Society of Bengal 59 (2): 89, 1890

Fig. 84

MycoBank number: MB206437

Description – *Spermogonia*, *aecia* and *telia* not found. *Uredinia* hypophyllous, scattered, obvious boundary, irregular, yellow, pulverulent, 0.5–1.0 mm diam. *Urediniospores* ellipsoidal or flat oval, 18–27 × 13–17 µm ($\overline{x}$ = 22.5 × 14.8 µm, n = 30), golden; wall 1.3–1.8 µm thick, colorless, densely and minutely verrucose.

Host – *Clematis brevicaudata* (Ranunculaceae)

Material examined – CHINA, Guizhou Province, Guiyang city, 26°65'96"N, 106°67'38"W, 1231 m, 21 Aug 2021, on *Clematis brevicaudata*, J.E. Sun, HGUP21054.

Notes – *Coleosporium clematidis* occurs on many *Clematis* species including *C apiifolia*, *C. brevicaudata*, *C. buchananiana*, *C. montana* and *C. chinensis* (Zhuang et al. 2021). Phylogenetic analyses show that our specimen grouped with *C. clematidis* (ML/MP/BI: 99/84/0.97) (Fig. 4). It has similar uredinia and urediniospore morphology to *C. clematidis* (uredinia: 0.5–1.0 mm *vs.* 0.2–1.0 mm; urediniospores: 18–27 × 13–17 µm *vs.* 18–35 × 13–23 µm; Zhuang et al. 2021). Hence, we identify our collection as *C. clematidis*.

Coleosporium asterum (Dietel) Syd. & P. Syd., Annales Mycologici 12 (2): 109 (1914)

Figs 85, 86

MycoBank number: MB119921

Description – *Spermogonia*, *aecia* and *telia* not found. *Uredinia* hypophyllous, scattered, obvious boundary, surrounded by host epidermis, globose, yellow, pulverulent, 0.5–1.0 mm diam. *Urediniospores* ellipsoidal, subglobose, some irregular, 25–31 × 15–20 µm ($\overline{x}$ = 26.3 × 17.2 µm, n = 30), yellow to golden; wall 1.6–2.1 µm thick, colorless, densely and minutely verrucose.

Hosts – *Aster ageratoides*, *Aster indicus* (Asteraceae)

Material examined – CHINA, Guizhou Province, Guiyang city, 26°65'97"N, 106°41'37"W, 1107 m, 21 Aug 2021, on *Aster ageratoides*, J.E. Sun, HGUP21059; Zunyi city, 27°76'84"N, 107°48'48"W, 864 m, 5 Oct 2022, on *A. indicus*, X.J. Chen, HGUP21062, HGUP21063; Zunyi city, 27°66'22"N, 106°65'59"W, 1124 m, 10 Jun 2022, on *A. ageratoides*, J.E. Sun, HGUP21055, HGUP21056; Guiyang city, 26°98'30"N, 106°45'24"W, 1119 m, 25 Jun 2022, on *A. ageratoides*, J.E. Sun, HGUP21060; Guiyang city, 26°45'00"N, 106°65'59"W, 1124 m, 19 Jul 2022, on *A. ageratoides*, J.E. Sun, HGUP21061; Zunyi city, 27°70'10"N, 107°70'97"W, 1010 m, 14 Aug 2022, on *A. ageratoides*, X.J. Chen, HGUP21057, HGUP21058.

Notes – The phylogenetic analysis shows that our specimens cluster with *Coleosporium asterum* (TSH:R6685, N90), *C. cacaliae* (KUS-F24178, WM 1321), *C. neocacaliae* (HMJAU8098), and *C. hedyotidis* (U896) (Fig. 4). However, our specimens match *C. asterum,* in morphology and hosts (Zhuang et al. 2021). Therefore, we name our collections as *C. asterum*.

Coleosporium bletiae Dietel, Hedwigia 37: 216, 1898. Fig. 87

MycoBank number: MB173508

Description – *Spermogonia*, *aecia* and *telia* not found. *Uredinia* hypophyllous, scattered, not surrounded by host epidermis, irregular, golden, pulverulent, 0.5–1.0 mm diam. *Urediniospores* globose, subglobose or ellipsoidal, 23–33 × 15–21 µm ($\bar{x}$ = 26.7 × 19.1 µm, n = 30), golden; wall 1.9–3.0 µm thick, colorless, densely and minutely verrucose.

Host – *Bletilla striata* (Orchidaceae)

Material examined – CHINA, Guizhou Province, Kaili city, 26°88'42"N, 108°27'42"W, 644 m, 9 Jun 2021, on *Bletilla striata*, J.E. Sun, HGUP21064, HGUP21065.

Notes – In phylogeny, our specimens grouped with *C. bletiae* (Fig. 4). Our collections have similar urediniospores to *C. bletiae* (Zhang et al. 2021). Thus, we identify the specimens as *C. bletiae*.

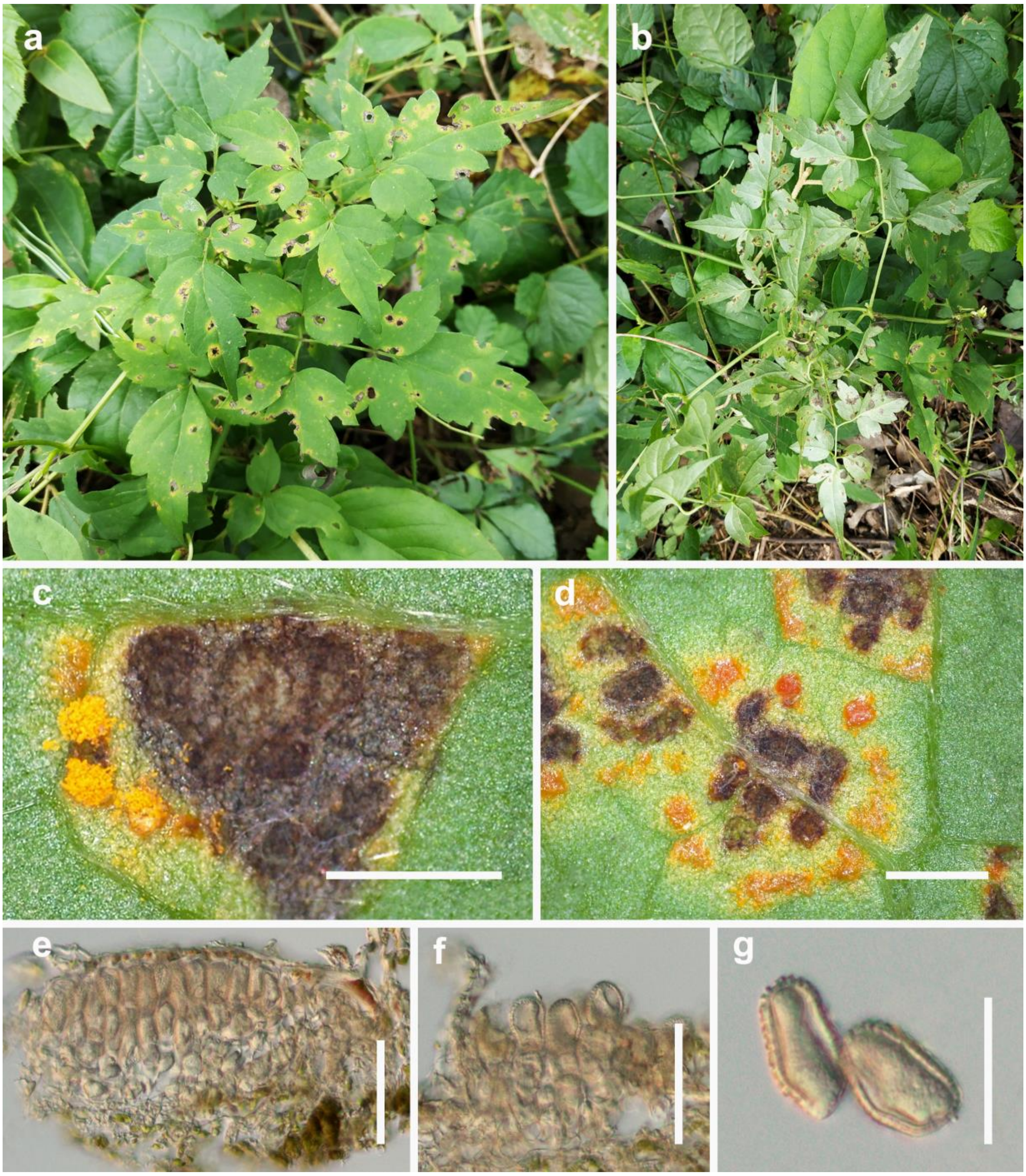

Figure 84 – *Coleosporium clematidis* (from HGUP21054) on *Clematis brevicaudata*. a–d Uredinia on leaves. e–f Longitudinal section of uredinium. g Urediniospores. Scale bars: c–d = 2 mm, e–f = 50 µm, g = 25 µm.

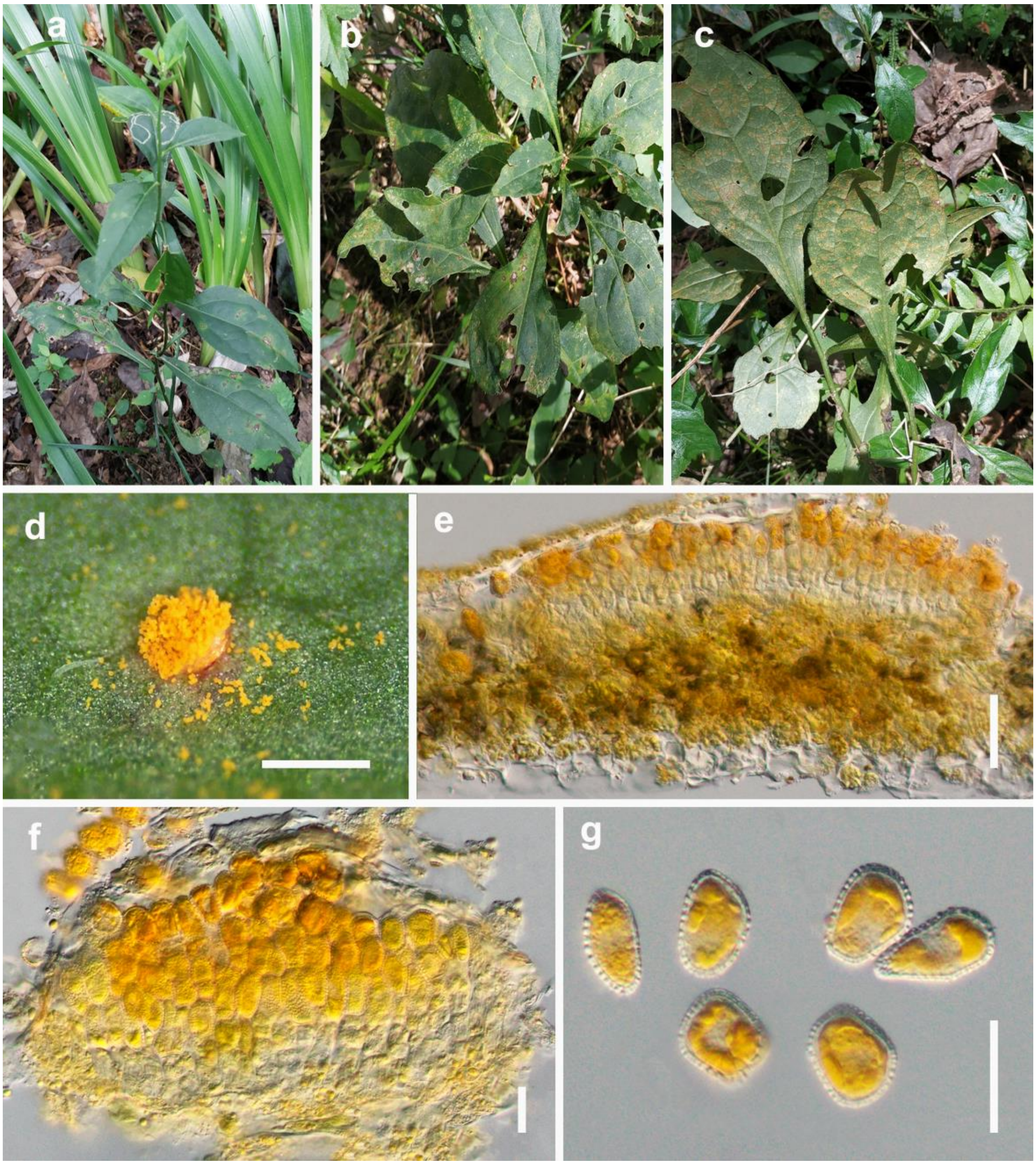

Figure 85 – *Coleosporium asterum* (from HGUP21059) on *Aster ageratoides*. a–d Uredinia on leaves. e–f Longitudinal section of uredinia. g Urediniospores. Scale bars: d = 1 mm, e = 50 μm, f–g = 20 μm.

Coleosporium zanthoxyli Dietel & P. Syd., Hedwigia 37: 217, 1898. Figs 88, 89

MycoBank number: MB223768

Description – *Spermogonia*, *aecia* and *telia* not observed. *Uredinia* hypophyllous, scattered, surrounded by host epidermis, subglobose, quadrate, or irregular, golden, pulverulent, 1.0–3.0 mm diam. *Urediniospores* subglobose, fusiform, or ellipsoidal, some irregular, 20–32 × 15–25 μm ($\bar{x}$ = 29.8 × 18.5 μm, n = 30), golden; wall 1.5–2.4 μm thick, colorless, densely and minutely verrucose.

Hosts – *Zanthoxylum armatum*, *Zanthoxylum bungeanum* (Rutaceae)

Material examined – CHINA, Guizhou Province, Zunyi city, 27°76'84"N, 107°48'48"W, 864 m, 31 May 2021, on *Zanthoxylum bungeanum*, J.E. Sun, HGUP21066, HGUP21067; Duyun city, 26°45'88"N, 106°88'42"W, 825 m, 22 Jun 2021, on *Z. armatum*, J.E. Sun, HGUP21068; Duyun city, 27°26'05"N, 107°38'91"W, 865 m, 23 Jun 2021, on *Z. bungeanum*, J.E. Sun, HGUP21071, HGUP21072; Tongren city, 28°29'08"N, 108°28'14"W, 791 m, 4 Sep 2021, on *Z. bungeanum*, J.E. Sun, HGUP21069; Tongren city, 25°61'40"N, 104°82'05"W, 1863 m, 4 Aug 2022, on

Z. bungeanum, J.E. Sun, HGUP21070; Duyun city, 25°36'81"N, 107°16'25"W, 1204 m, 1863 m, 12 May 2022, on *Z. bungeanum*, J.E. Sun, HGUP21203.

Notes – *Coleosporium zanthoxyli* is a common pathogen on Rutaceae worldwide (Dai 1979, McTaggart & Aime 2018, Zhuang et al. 2021). Eight collections clustered with *C. zanthoxyli* (KUS-F25423) in the multiple loci phylogenetic analysis (Fig. 4). The morphology of uredinia and urediniospores of our collections are similar to those of *C. zanthoxyli* (Zhuang et al. 2021). Based on both morphology and phylogenetic analyses, we identify our collections as *C. zanthoxyli*.

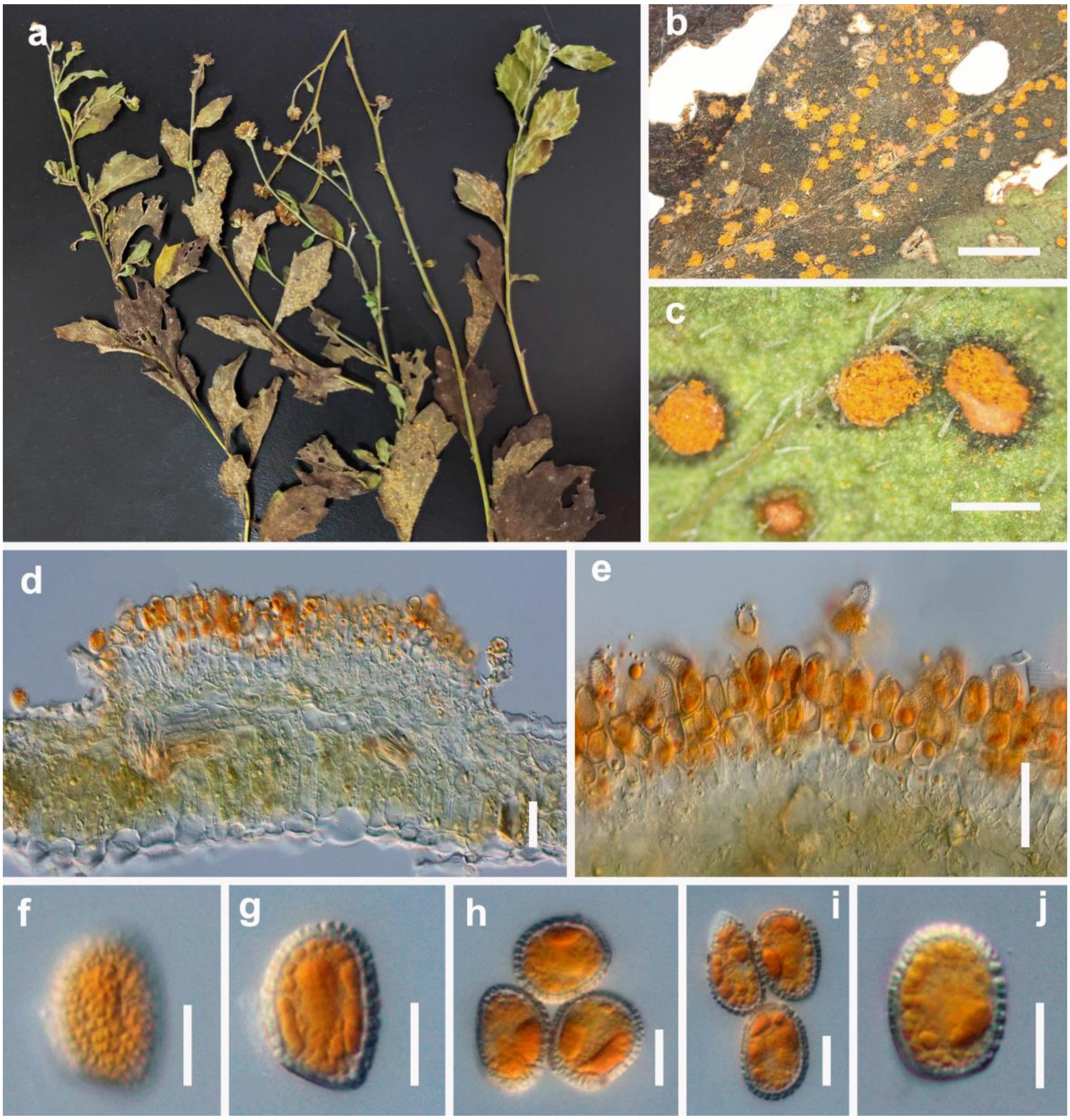

Figure 86 – *Coleosporium asterum* (from HGUP21062) on *Aster indicus*. a–c Uredinia on leaves. d–e Longitudinal section of uredinia. f–j Urediniospores. Scale bars: b = 1 mm, c = 5 mm, d–e = 50 µm, f–j = 12.5 µm.

Coleosporium phellodendri Dietel, Botanische Jahrbücher für Systematik Pflanzengeschichte und Pflanzengeographie 28 (3): 287, 1900. Fig. 90

MycoBank number: MB146812

Description – *Spermogonia*, *aecia* and *telia* not observed. *Uredinia* hypophyllous, scattered, not surrounded by host epidermis, irregular, golden, pulverulent, 0.5–1.5 mm diam. *Urediniospores* globose or ellipsoidal, golden, 22–28 × 20–24 µm ($\bar{x}$ = 25 × 22 µm, n = 30); wall 2.6–3.7 µm thick, colorless, densely and minutely verrucose.

Host – *Phellodendron amurense* (Rutaceae)

Material examined – CHINA, Guizhou Province, Xingyi city, 24°92'16"N, 105°58'29"W, 1045 m, 26 Jun 2021, on *Phellodendron amurense*, J.E. Sun, HGUP21075; Xinyi city, 24°65'23"N, 105°48'89"W, 985 m, 20 Sep 2022, on *P. amurense*, J.E. Sun, HGUP21076.

Notes – In the phylogenetic analysis our specimens formed a close lineage with *Coleosporium phellodendri* (N7, N9) (Fig. 4), which were also found on *Phellodendron amurense*. They are also similar in morphology of uredinia and urediniospores (Zhuang et al. 2021). Hence, we consider our specimens to be *C. phellodendri*.

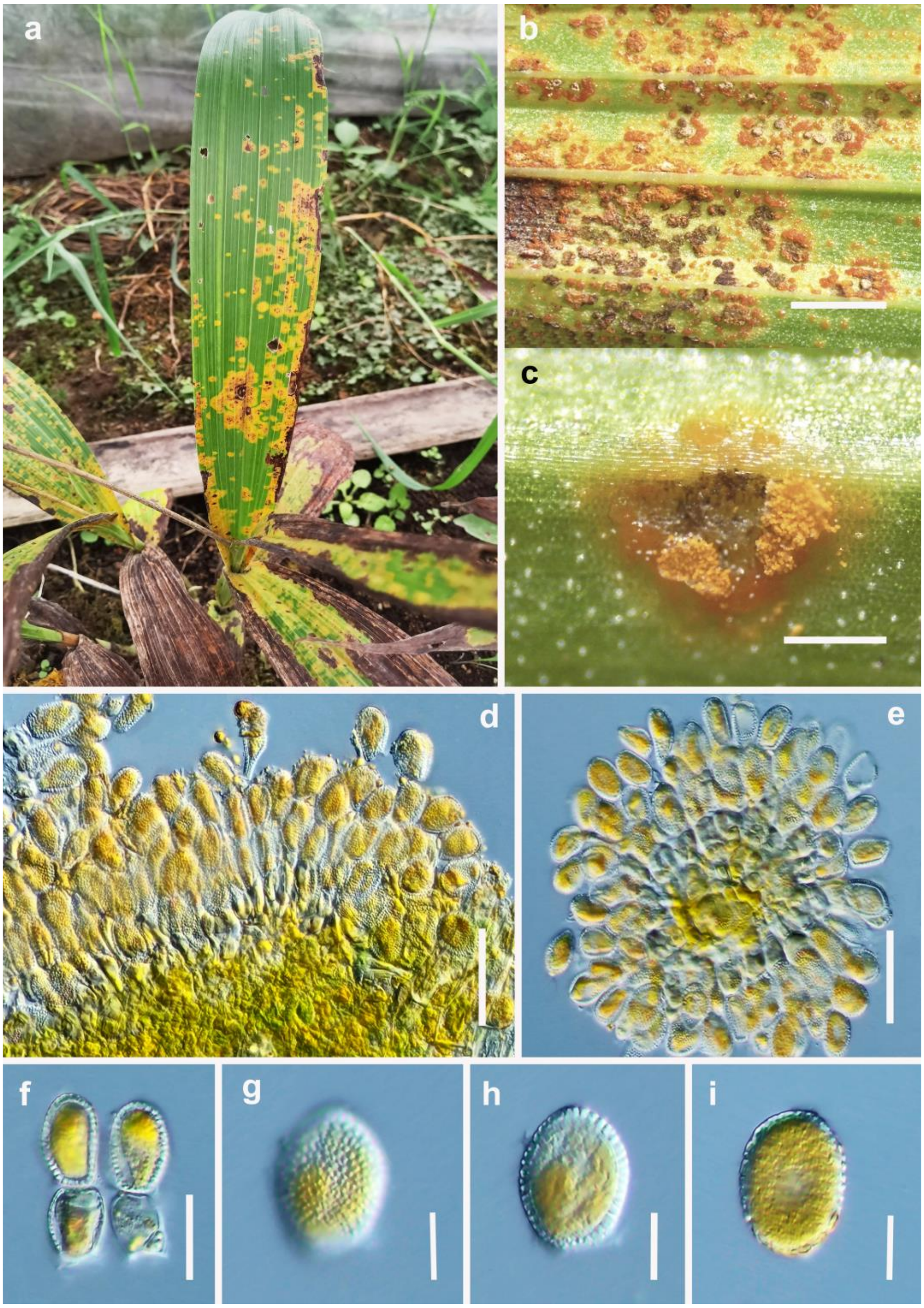

Figure 87 – *Coleosporium bletiae* (from HGUP21064) on *Bletilla striata*. a–c Uredinia on leaves. d Longitudinal section of uredinium. e–i Urediniospores. Scale bars: b = 5 mm, c = 1 mm, d–e = 50 µm, f = 25 µm, g–i = 12.5 µm.

Figure 88 – *Coleosporium zanthoxyli* (from HGUP21066) on *Zanthoxylum bungeanum*. a–c Uredinia on leaves. d Longitudinal section of uredinium. e–l Urediniospores. Scale bars: c = 1 mm, d–e = 50 µm, f–l = 25 µm.

Coleosporium perillae P. Syd., Beiblatt zur Hedwigia 38: 141, 1899. Fig. 91

MycoBank number: MB146812

Description – *Spermogonia*, *aecia* and *telia* not observed. *Uredinia* hypophyllous, scattered, not surrounded by host epidermis, ellipsoidal or irregular, golden, pulverulent, 0.5–1.0 mm diam. *Urediniospores* ellipsoidal or oval, golden, 19–25 × 15–18 µm ($\overline{x}$ = 22.5 × 16.7 µm, n = 30); wall 1.6–2.1 µm thick, colorless, densely, and minutely verrucose.

Host – *Perilla frutescens* (Lamiaceae)

Material examined – CHINA, Guizhou Province, Tongren city, 28°15'77"N, 108°33'63"W, 777 m, 4 Sep 2021, on *Perilla frutescens*, J.E. Sun, HGUP21077; Kaili city, 25°26'23"N, 108°24'04"W, 816 m, 20 Sep 2022, on *P. frutescens*, J.E. Sun, HGUP21078.

Notes – In the phylogenetic analysis, our collections had a distant relationship to *Coleosporium plectranthi* (N85 and N16) with 100% ML, 94% MP and 0.93 BYPP bootstrap support (Fig. 4). However, our specimens have a similar morphology and host to *C. perillae* as described by Zhang et al. (2021). GenBank accession numbers (ITS and LSU) for *C. perillae* have not been reported, and our identification is based only on a morphological comparison.

Coleosporium plectranthi Barclay, Descr. List Ured. Simla: 104, 1813. Fig. 92

MycoBank number: MB198075

Description – *Spermogonia*, *aecia* and *telia* not observed. *Uredinia* hypophyllous, scattered, obvious boundary, irregular, bright yellow, pulverulent, 1.0–1.5 mm diam. *Urediniospores* subglobose, ellipsoidal or oval, 15–24 × 13–17 µm ($\bar{x}$ = 18.6 × 14.9 µm, n = 30), bright yellow; wall 1.2–1.9 µm thick, colorless, densely and minutely verrucose.

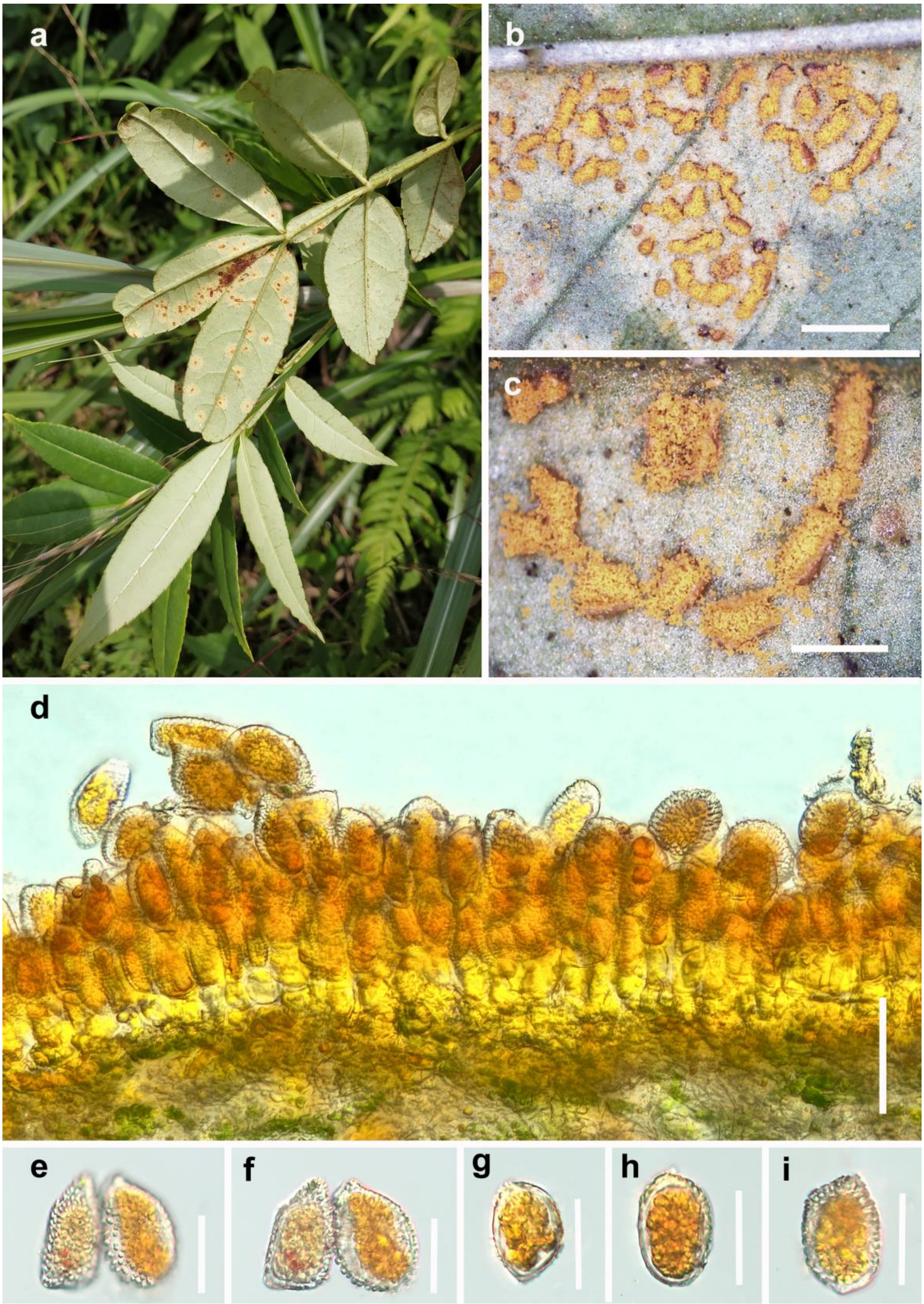

Figure 89 – *Coleosporium zanthoxyli* (from HGUP21068) on *Zanthoxylum armatum*. a–c Uredinia on leaves. d Longitudinal section of uredinium. e–i Urediniospores. Scale bars: b = 1 mm, c = 5 mm, d = 50 µm, e–i = 25 µm.

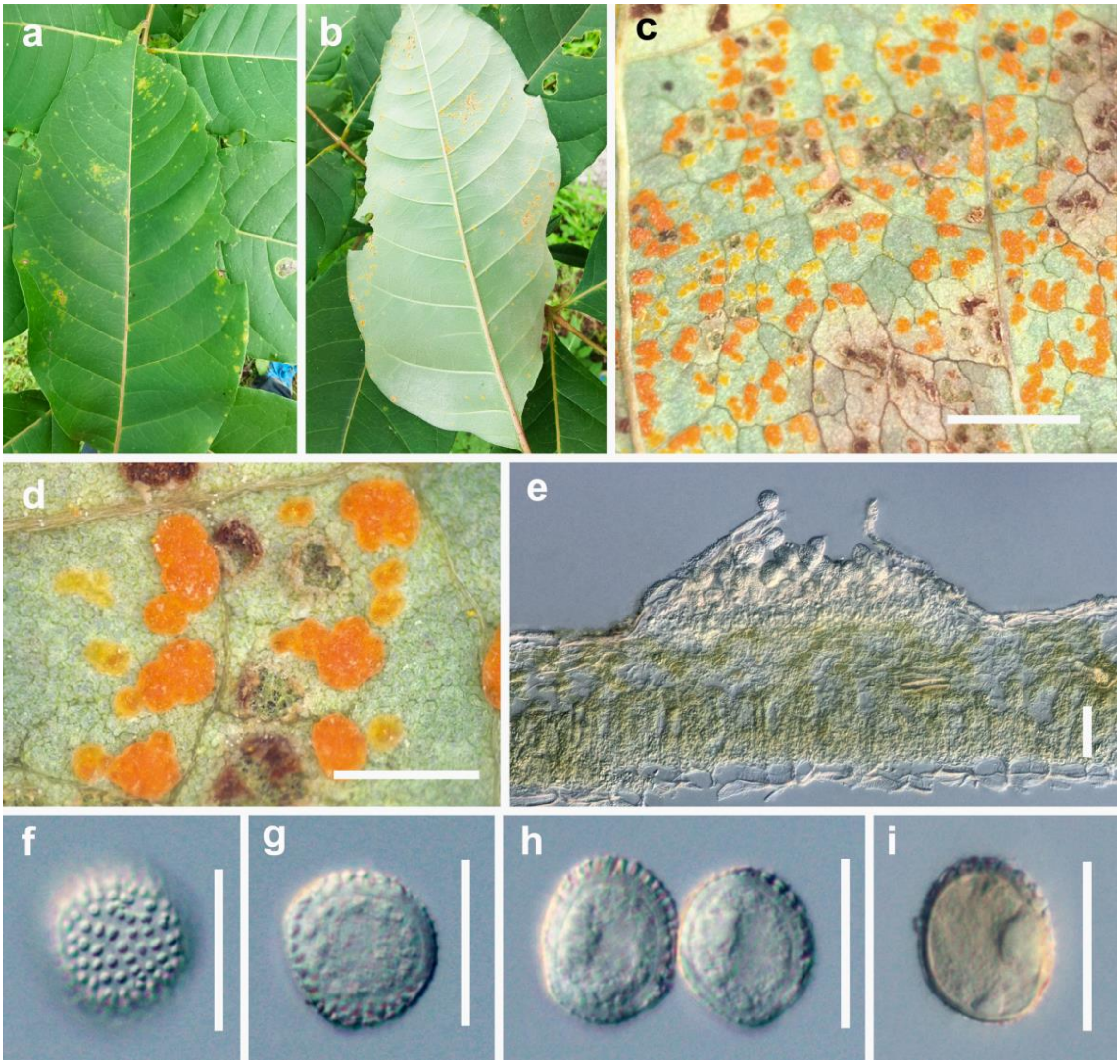

Figure 90 – *Coleosporium phellodendri* (from HGUP21075) on *Phellodendron amurense*. a–d Uredinia on leaves. e Longitudinal section of uredinium. f–i Urediniospores. Scale bars: c = 5 mm, d = 1 mm, e = 50 µm, f–i = 25 µm.

Host – *Isodon amethystoides* (Lamiaceae)

Material examined – CHINA, Guizhou Province, Guiyang city, 26°65'89"N, 106°67'51"W, 1314 m, 21 Aug 2021, on *Isodon amethystoides*, J.E. Sun, HGUP21079.

Notes – *Coleosporium plectranthi* was first reported by Barclay (1890). Phylogenetically, our collection showed a distant relationship to *C. plectranthi*, but the morphology of uredinia and urediniospores was largely similar (Zhuang et al. 2021). GenBank accession numbers (ITS and *LSU*) for *C. plectranthi* have not been reported, and our identification is based only on a morphological comparison.

Coleosporium telioevodiae L. Guo, [as 'telioeuodiae'], Fungi and Lichens of Shennongjia. Mycological and Lichenological Expedition to Shennongjia (Beijing): 112 (1989) Fig. 93

MycoBank number: MB135154

Description – *Spermogonia*, *aecia* and *telia* not found. *Uredinia* hypophyllous, scattered, obvious boundary, surrounded by host epidermis, subglobose, yellow, pulverulent, 1.0–2.5 mm diam. *Urediniospores* subglobose, ellipsoidal or oval, 25–30 × 22–28 µm ($\bar{x}$ = 27.8 × 24.6 µm, n = 30), yellow; wall 1.8–2.4 µm thick, colorless, densely and minutely verrucose.

Host – *Tetradium ruticarpum* (Rutaceae)

Material examined – CHINA, Guizhou Province, Xingyi city, 25°12'22"N, 105°26'12"W, 1236 m, 31 May 2021, on *Tetradium ruticarpum*, J.E. Sun, HGUP21073; Guiyang city, 26°97'70"N, 106°45'52"W, 1163 m, 25 Jun 2022, on *T. ruticarpum*, J.E. Sun, HGUP21074.

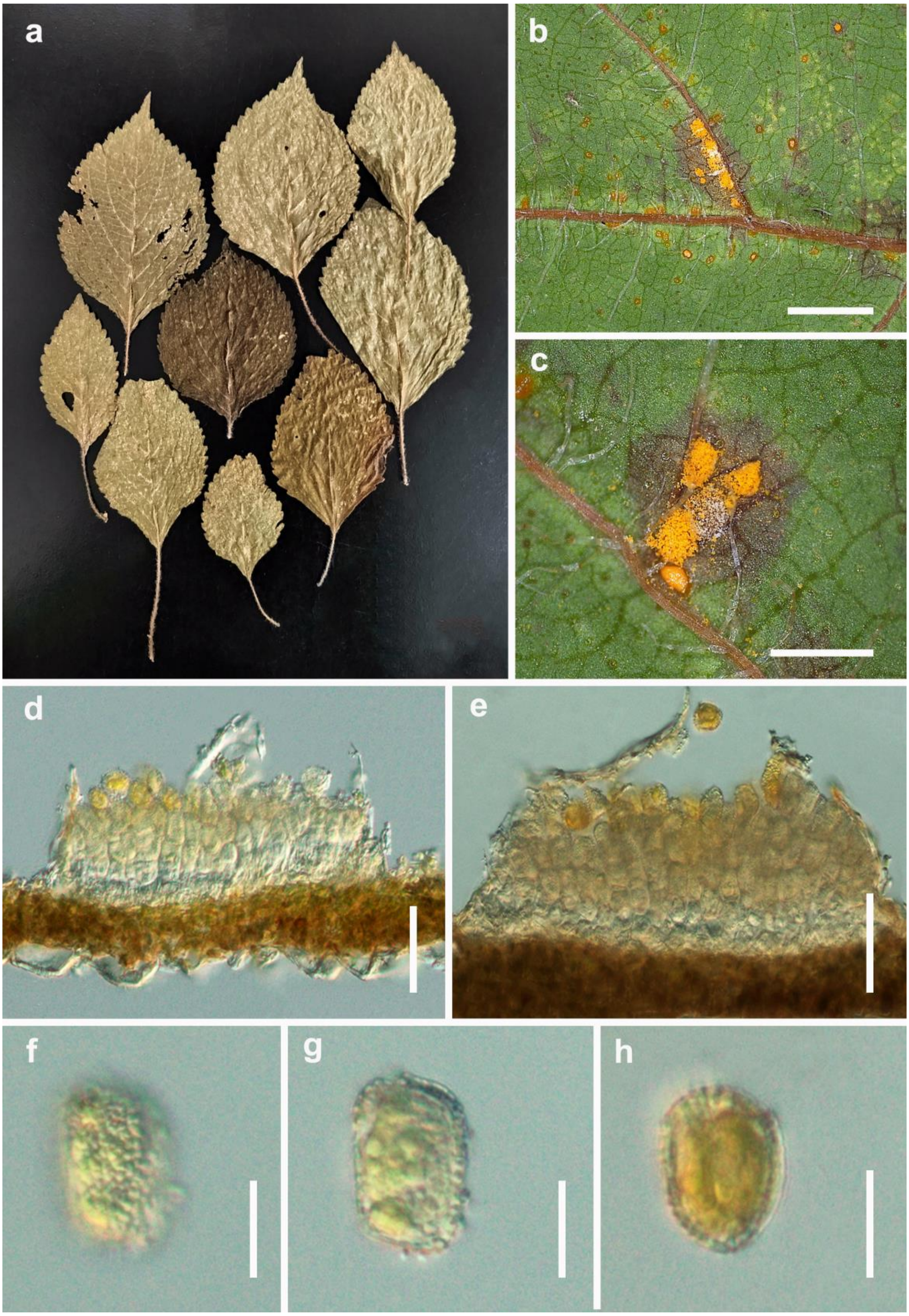

Figure 91 – *Coleosporium perillae* (from HGUP21077) on *Perilla frutescens*. a–c Uredinia on leaves. d–e Longitudinal section of uredinia. f–h Urediniospores. Scale bars: b = 5 mm, c = 1 mm, d–e = 50 µm, f–h = 12.5 µm.

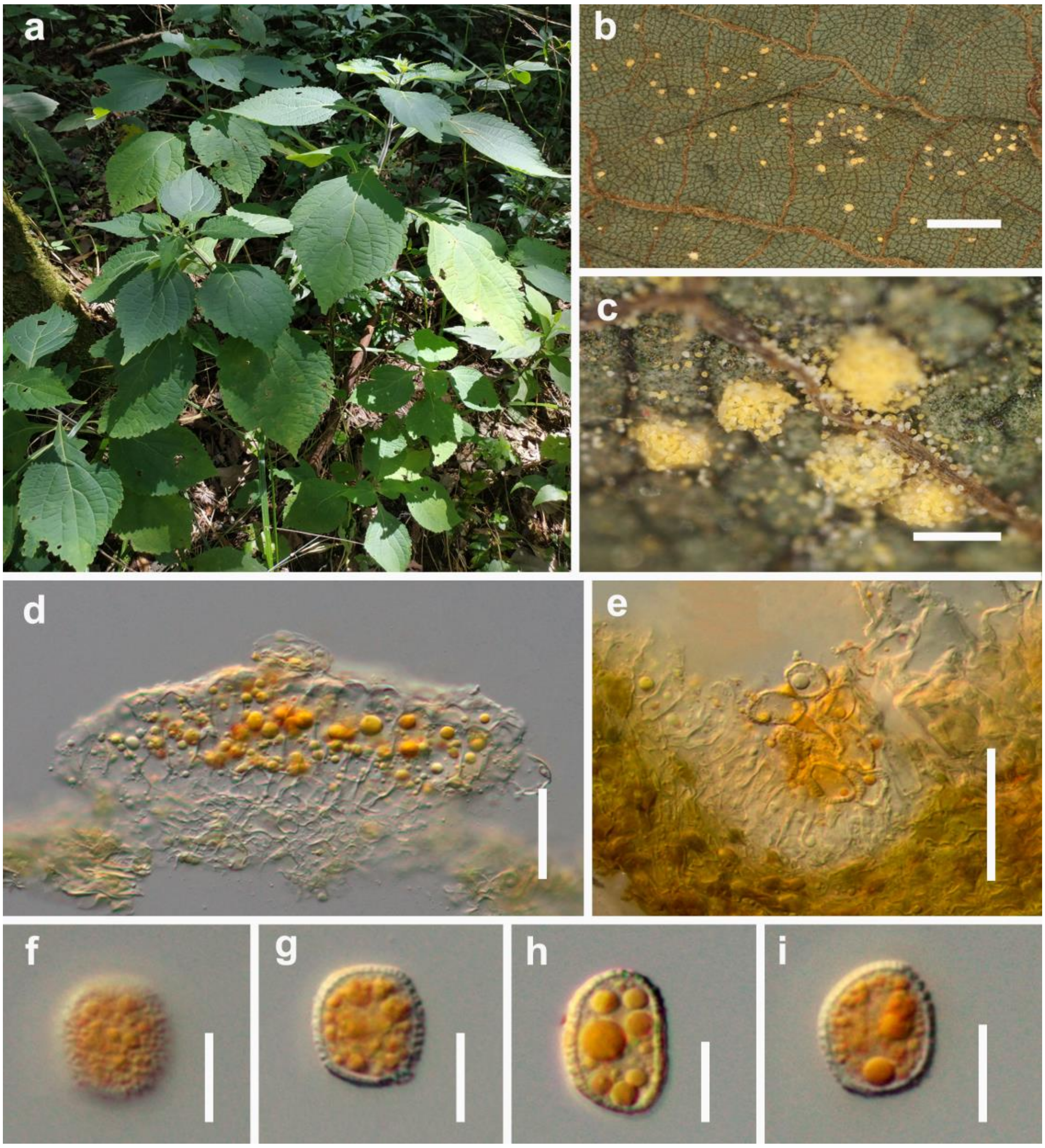

Figure 92 – *Coleosporium plectranthi* (from HGUP21079) on *Isodon amethystoides*. a–c Uredinia on leaves. d–e Longitudinal section of uredinia. f–i Urediniospores. Scale bars: b = 5 mm, c = 1 mm, d–e = 50 µm, f–i = 12.5 µm.

Notes – Our specimens were closely related to *Coleosporium telioevodiae* with good support (Fig. 4). Morphologically, our collections agree with *C. telioevodiae* in uredinia and urediniospores (Zhuang et al. 2021). Therefore, we identify this fungus as *C. telioevodiae*.

Coleosporium paederiae Dietel, Annls mycol. 7(4): 355 (1909) Fig. 94

MycoBank number: MB328582

Description – *Spermogonia*, *aecia* and *telia* not found. *Uredinia* hypophyllous, scattered, surrounded by host epidermis, boundary not obvious, irregular, orange, pulverulent, 0.5–2.0 mm diam. *Urediniospores* ellipsoidal or oval, 19–27 × 12–17 µm ($\overline{x}$ = 22.3 × 14.1 µm, n = 30), golden; wall 1.6–2.4 µm thick, colorless, densely and minutely verrucose.

Host – *Paederia foetida* (Rubiaceae)

Material examined – CHINA, Guizhou Province, Guiyang city, 26°45'20"N, 106°65'60"W, 1110 m, 6 May 2022, on *Paederia foetida*, J.E. Sun, HGUP21083; Guiyang city, 26°45'20"N, 106°65'60"W, 1110 m, 6 May 2022, on *P. foetida*, J.E. Sun, HGUP21084; Duyun city, 25°83'20"N, 107°32'59"W, 781 m, 20 Jul 2022, on *P. foetida*, J.E. Sun, HGUP21085.

Notes – In the phylogenetic tree, our specimens clustered in a clade with good support (Fig. 4). Unfortunately, there is no DNA data for *Coleosporium paederiae* in NCBI. Morphological characters of uredinia and urediniospores from our collections are similar to those of *C. paederiae* as described by Zhuang et al. (2021). Hence, based on both morphology and phylogeny, we identify our collections as *C. paederiae*.

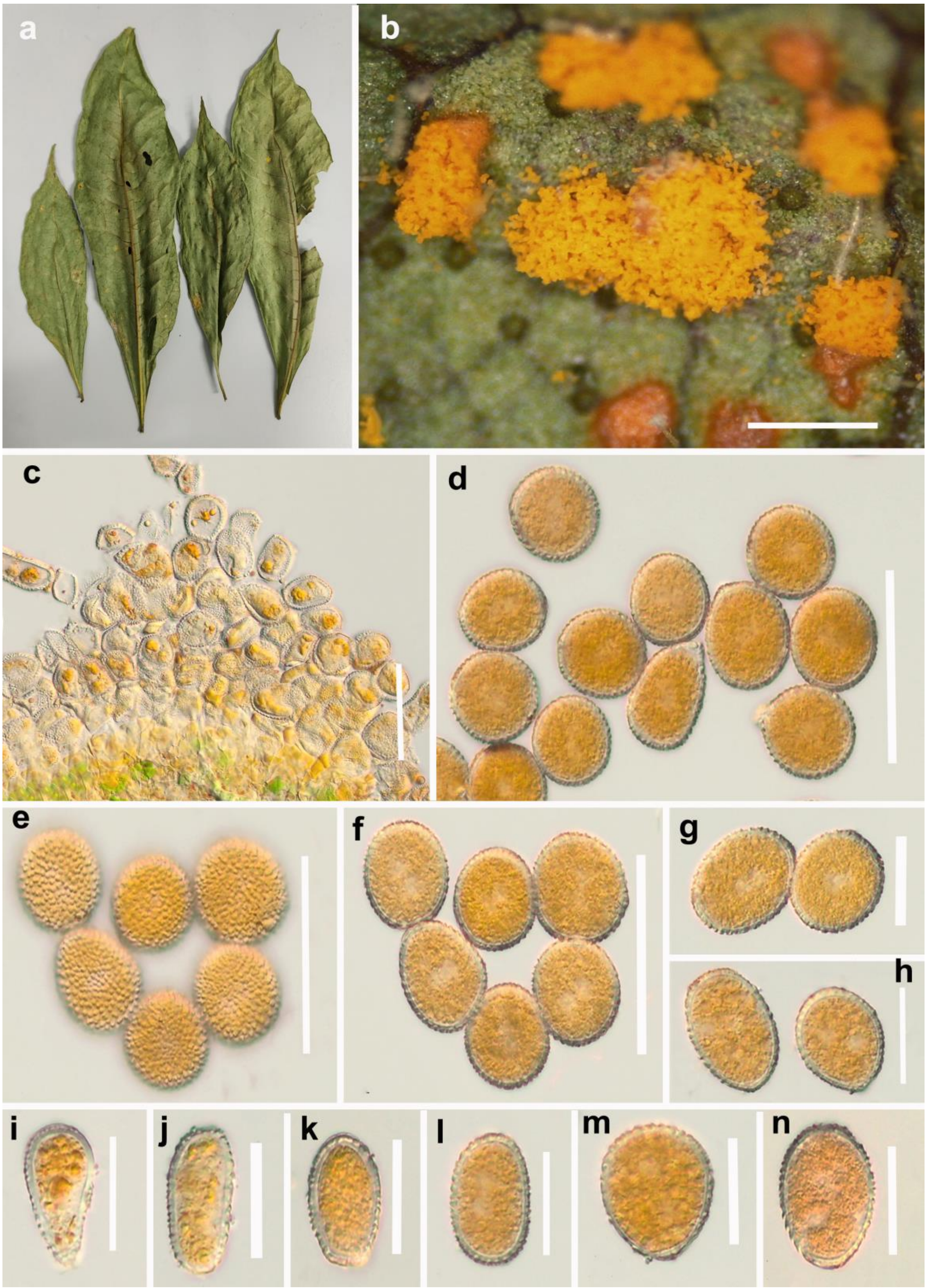

Figure 93 – *Coleosporium telioevodiae* (from HGUP21073) on *Tetradium ruticarpum*. a–b Uredinia on leaves. c Longitudinal section of uredinium. d–n Urediniospores. Scale bars: b = 1 mm, c = 50 µm, d–n = 25 µm.

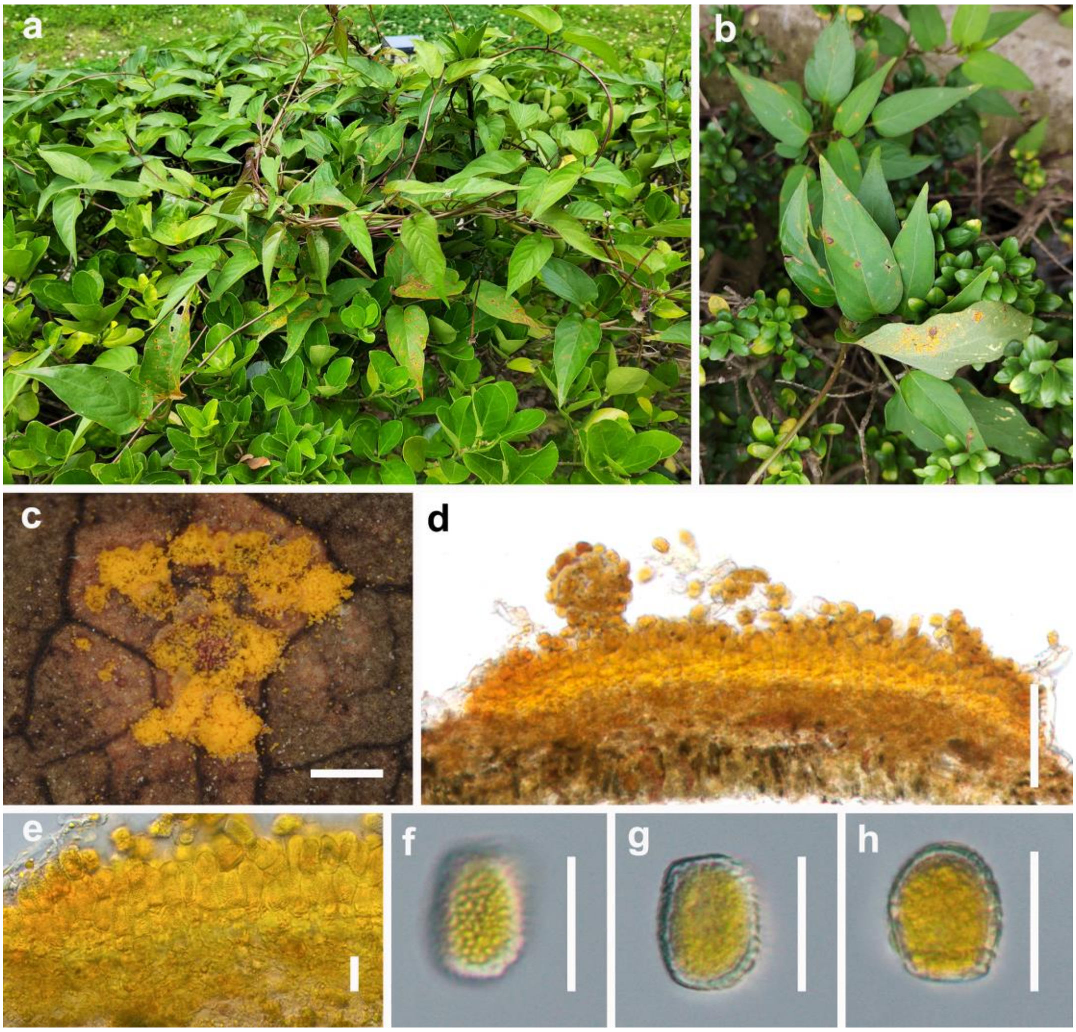

Figure 94 – *Coleosporium paederiae* (from HGUP21083) on *Paederia foetida*. a–c Uredinia on leaves. d–e Longitudinal section of uredinia. f–h Urediniospores. Scale bars: c = 0.5 mm, d = 100 µm, e = 50 µm, f–h = 20 µm.

Pucciniastraceae Gäum. ex Leppik, Annales Botanici Fennici 9 (3): 139 (1972)
Pucciniastrum G.H. Otth, Mitt. naturf. Ges. Bern 469-496: 71 (1861)

Pucciniastrum anaphalise-sinicae J.E. Sun Yong Wang bis & K.D. Hyde, sp. nov. Fig. 95

Index Fungorum number: IF901314; Facesoffungi number: FoF15379

Etymology – The name reflects the host *Anaphalis sinica*, from which the type specimen was collected.

Holotype – HGUP21108

Description – *Spermogonia*, *aecia* and *telia* not observed. *Uredinia* hypophyllous, pulverulent, yellow, distinct, scattered, nearly oval, surrounded by host epidermis, 2.0–6.0 mm diam., on densely yellowish spot. *Urediniospores* globose, ellipsoidal or obovoid, 23–28 × 14–23 µm ($\bar{x}$ = 21.2 × 17.7 µm, n = 30), bright yellow or golden; wall 1.0–1.4 µm thick, colorless, densely and minutely echinulate.

Host – *Anaphalis sinica* (Asteraceae)

Material examined – CHINA, Guizhou Province, Duyun city, 26°45'88"N, 106°98'43"W, 854 m, 22 Jun 2021, on *Anaphalis sinica*, J.E. Sun, holotype HGUP21108; Guizhou Province, Duyun city, 26°45'88"N, 106°98'43"W, 854 m, 22 Jun 2021, on *A. sinica*, J.E. Sun, HGUP21109.

Notes – The multi-locus phylogenetic analyses showed that *Pucciniastrum anaphalise-sinicae* had a close relationship to *P. circaeae* (TSH-R10187 and MCA2948), and *P. epilobii* (TSH-

R4285 and MCA2916) with good support (ML/MP/BI: 100/64/1.00; Fig. 5). *Pucciniastrum anaphalise-sinica* has larger urediniospores than those of *P. coronisporum* (17.5–22.5 × 14.0–18.5 µm; Ji et al. 2019).

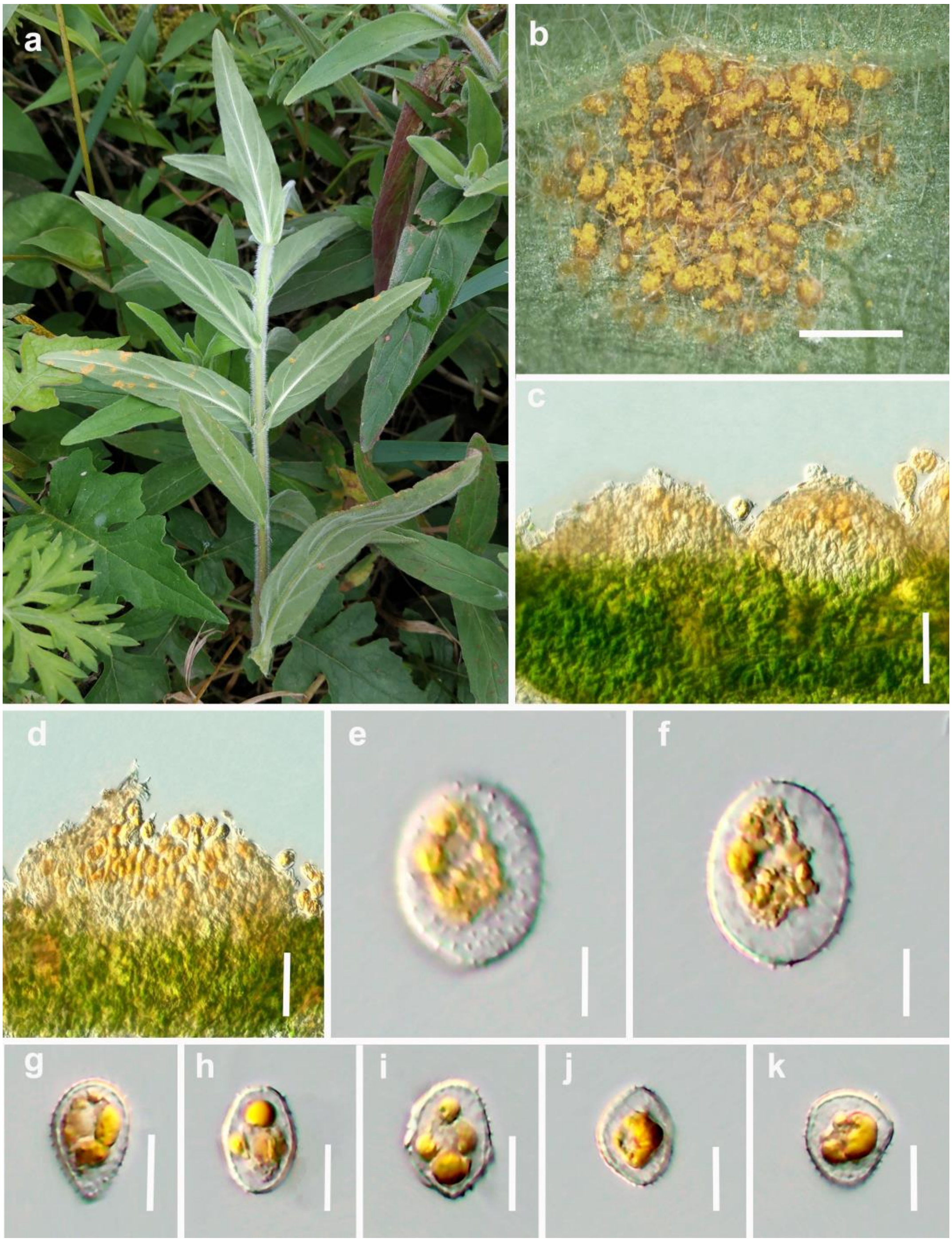

Figure 95 – *Pucciniastrum anaphalise-sinicae* (from holotype HGUP21108) on *Anaphalis sinica*. a–b Uredinia on leaves. c–d Longitudinal section of uredinia. e–k Urediniospores. Scale bars: b = 5 mm, c–d = 50 µm, e–f = 10 µm, g–k = 12.5 µm.

Pucciniastrum boehmeriae (Dietel) Syd. & P. Syd., Annales Mycologici 1 (1): 19 (1903)

Fig. 96

MycoBank number: MB231831

Description – *Spermogonia*, *aecia* and *telia* unknown. *Uredinia* hypophyllous, nearly oval, pulverulent, surrounded by host epidermis, 1.0–2.0 mm diam., on densely yellowish spot, scattered.

Urediniospores globose, ellipsoidal or obovoid, 14–24 × 10–20 µm ($\bar{x}$ = 19.1 × 14.1 µm, n = 30), pale to golden; wall 1–1.9 µm thick, colorless, irregularly, and minutely echinulate.

Host – *Boehmeria nivea* (Urticaceae)

Material examined – CHINA, Guizhou Province, Guiyang city, 26°45'28"N, 106°65'73"W, 1101 m, 21 Nov 2021, on *Boehmeria nivea*, J.E. Sun, HGUP21110; Guizhou Province, Guiyang city, 26°45'28"N, 106°65'73"W, 1101 m, 21 Nov 2021, on *B. nivea*, J.E. Sun, HGUP21111.

Notes – Our specimens are phylogenetically closely related to *P. actinidiae*, *P. boehmeriae*, *P. corni*, *P. kusanoi*, *P. styracinum* and *P. yoshinagai*, and formed a clade with good support (ML/MP/BI: 99/67/0.97; (Fig. 5). Our specimens and *P. boehmeriae* were found on *Boehmeria* spp. (Zhuang et al. 2021). The urediniospores of our specimens are similar to those of *P. boehmeriae* (16–28 × 12–18 µm; Zhuang et al. 2021). Therefore, we identify our specimens as *P. boehmeriae*.

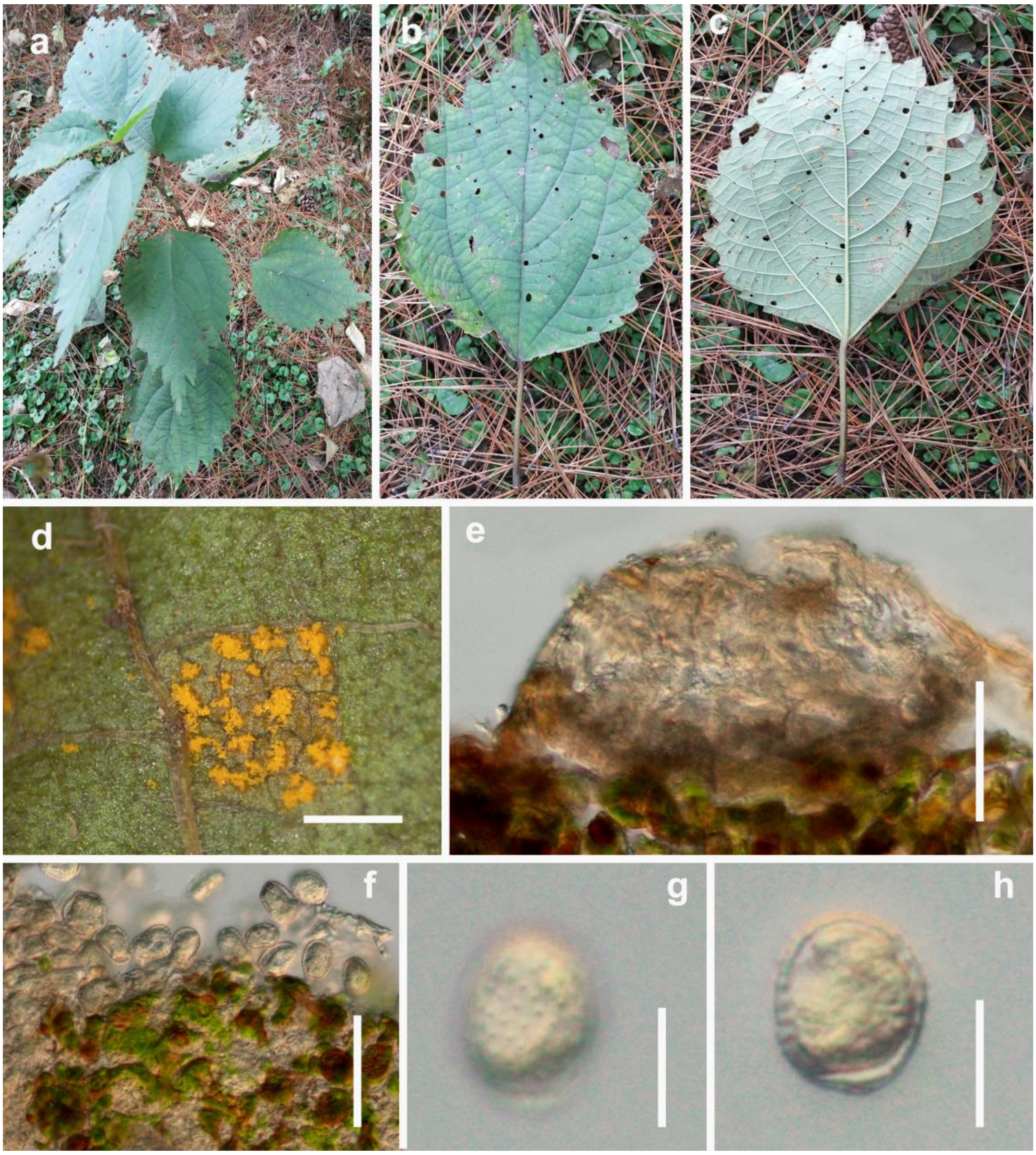

Figure 96 – *Pucciniastrum boehmeriae* (from HGUP21110) on *Boehmeria nivea*. a–d Uredinia on leaves. e–f Longitudinal section of uredinium. g–h Urediniospores. Scale bars: d = 2 mm, e–f = 50 µm, g–h = 12.5 µm.

Phakopsoraceae Cummins & Hirats. f., Illustrated genera of rust fungi: 13 (1983)
Phakopsora Dietel, Ber. dt. bot. Ges. 13: 333 (1895)

Phakopsora causonise-mollisii J.E. Sun, Yong Wang bis & K.D. Hyde, sp. nov. Fig. 97

Index Fungorum number: IF901315; Facesoffungi number: FoF15380

Etymology – The name reflects the host *Causonis mollis*, from which the type specimen was collected.

Holotype – HGUP21112

Description – *Spermogonia*, *aecia* and *telia* unknown. *Uredinia* hypophyllous, covering the entire lower surface of the leaves, nearly oval, pulverulent, not surrounded by host epidermis, 0.2–0.6 mm diam., on densely yellowish spot. *Urediniospores* globose, ellipsoidal or obovoid, 15–27 × 11–17 µm ($\bar{x}$ = 20.5 × 14 µm, n = 30), hyaline to bright yellow; wall 1–1.5 µm thick, colorless, densely and minutely echinulate.

Host – *Causonis mollis* (Vitaceae)

Material examined – CHINA, Guizhou Province, Guiyang city, 25°65'96"N, 104°67'38"W, 1230 m, 21 Aug 2021, on *Causonis mollis*, J.E. Sun & Y.R. Sun, holotype HGUP21112; Guizhou Province, Guiyang city, 25°65'96"N, 104°67'38"W, 1230 m, 21 Aug 2021, on *C. mollis,* J.E. Sun & Y.R. Sun, HGUP21113; Liupanshui city, 26°34'45"N, 104°48'35"W, 1838 m, 25 Sep 2021, on *C. mollis,* J.E. Sun, HGUP21114.

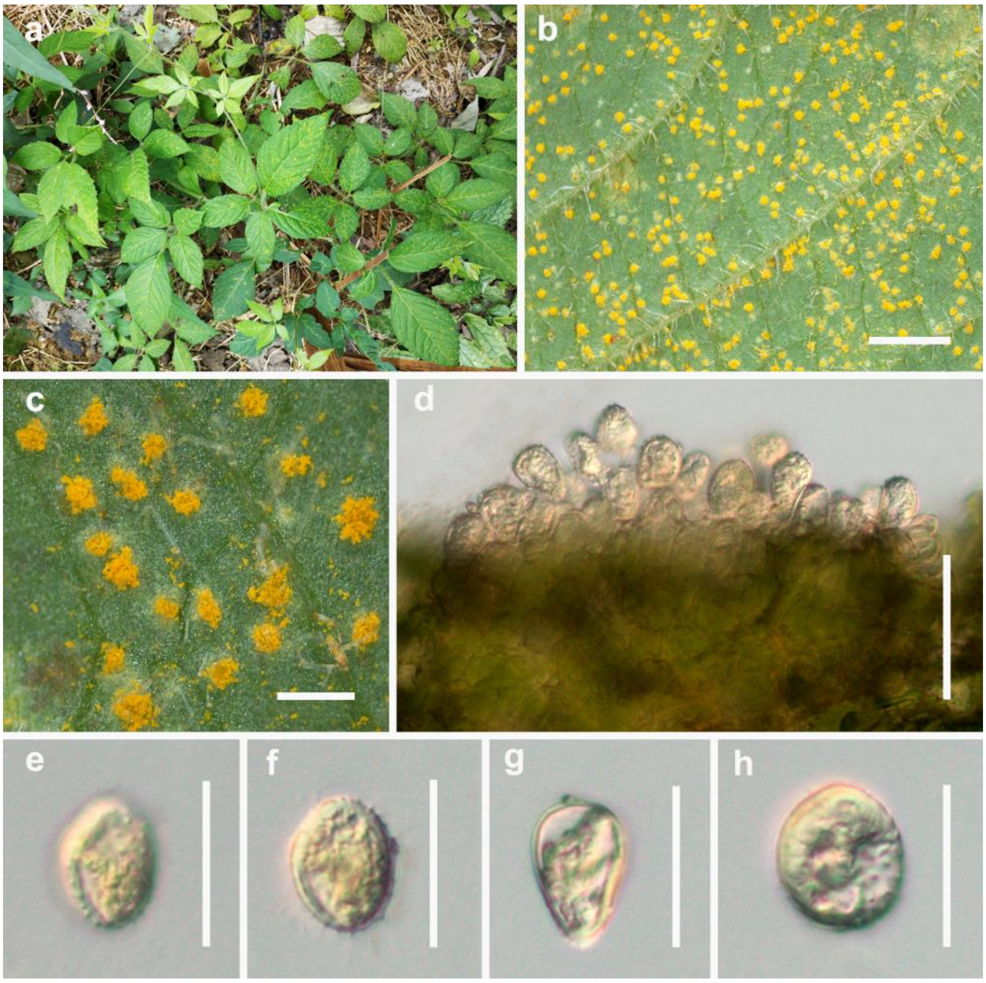

Figure 97 – *Phakopsora causonise-mollisii* (from holotype HGUP21112) on *Causonis mollis*. a–c Uredinia on leaves. d Longitudinal section of uredinium. e–h Urediniospores. Scale bars: b = 5 mm, c = 1 mm, d = 50 µm, e–h = 25 µm.

Notes – *Phakopsora causonise-mollisii* is distinguishable from *P. myrtacearum* by its slightly thinner wall of urediniospores (1–1.5 µm *vs.* 2–3 µm; Maier et al. 2016). Phylogenic analyses indicated it does not belong to any other members of *Phakopsora*. Based on both morphology and phylogenetic analyses, we propose our collections as a new species.

Phakopsora parthenocissuse-tricuspidatae J.E. Sun & Yong Wang bis, sp. nov. Fig. 98

Index Fungorum number: IF901316; Facesoffungi number: FoF15381

Etymology – Name reflects the host *Parthenocissus tricuspidata*, from which the type specimen was collected.

Holotype – HGUP21115

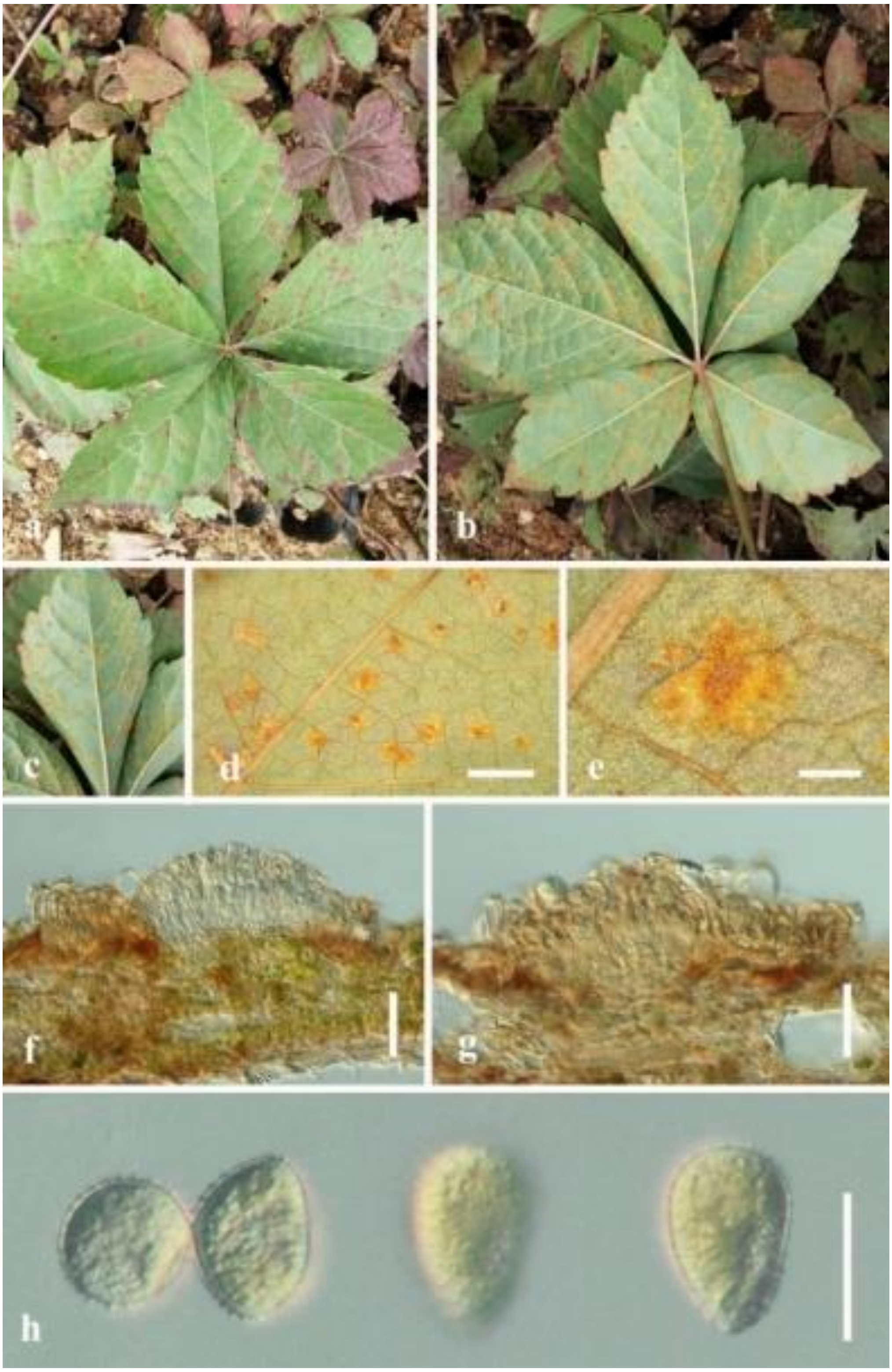

Figure 98 – *Phakopsora parthenocissuse-tricuspidatae* (from holotype HGUP21115) on *Parthenocissus tricuspidata*. a–e Uredinia on leaves. f–g Longitudinal section of uredinia. h Urediniospores. Scale bars: d = 5 mm, e = 1 mm, f–g = 50 µm, h = 25 µm.

Description – *Spermogonia*, *aecia* and *telia* not observed. *Uredinia* hypophyllous, pulverulent, yellow, distinct, scattered, nearly oval, surrounded by host epidermis, 1.0–3.0 mm diam., on densely yellowish spot. *Paraphyses* in the periphery of the uredinia, curved, 30–55 × 6–15 µm, colorless. *Urediniospores* globose, ellipsoidal or obovoid, 18–27 × 12–16 µm ($\bar{x}$ = 21.6 × 14 µm, n = 30), hyaline to bright yellow; wall 1.2–1.7 µm thick, colorless, densely and minutely echinulate.

Host – *Parthenocissus tricuspidata* (Vitaceae)

Material examined – CHINA, Yunnan Province, Dali city, 26°41'20"N, 99°65'21"W, 1894 m, 28 Oct 2021, on *Parthenocissus tricuspidata*, X.J. Chen, holotype HGUP21115; Yunnan Province: Dali city, 26°41'20"N, 99°65'21"W, 1894 m, 28 Oct 2021, on *P. tricuspidata*, X.J. Chen, HGUP21116.

Notes – *Phakopsora parthenocissuse-tricuspidatae* can be distinguished by the presence of peripheral paraphyses, and its urediniospores have a narrower wall than in *P. myrtacearum* (1.2–1.7 µm *vs.* 2–3 µm; Maier et al. 2016). Phylogenetic analyses showed that *P. parthenocissuse-tricuspidatae* is different from other *Phakopsora* species. Hence, we describe this rust fungus as a new species.

Phakopsora pachyrhizi Syd. & P. Syd., Annales Mycologici 12 (2): 108 (1914) Fig. 99

MycoBank number: MB121037

Description – *Spermogonia*, *aecia* and *telia* unobserved. *Uredinia* hypophyllous, surrounded by host epidermis, 0.1–0.3 mm diam, densely yellowish spot, powdery. *Urediniospores* globose or ellipsoidal, 16–25 × 15–24 µm ($\bar{x}$ = 21.5 × 19.5 µm, n = 30), canary-yellow to bright yellow; wall 0.8–1.2 µm thick, colorless.

Host – *Pueraria montana* var. *lobata* (Fabaceae)

Material examined – CHINA, Guizhou Province, Guiyang city, 26°44'74"N, 106°58'67"W, 976 m, 3 May 2021, on *Pueraria montana* var. *lobata*, J.E. Sun, HGUP21259, HGUP21260; Guiyang city, 25°26'72"N, 107°69'21"W, 857 m, 12 Mar 2022, on *P. montana* var. *lobata,* J.E. Sun, HGUP21261.

Notes – *Phakopsora pachyrhizi* infected many plants (Sydow & Sydow 1914), for example, *Calopogonium* spp., *Erythrina* spp., *Centrosema* spp., *Glycine* spp., *Lablab* spp., *Pachyrhizas* spp., *Phaseolus* spp., *Physostigma* spp., *Pueraria* spp., *Teramnus* spp. and *Vigna* spp. In 2006, *P. pachyrhizi* occurred on *Pueraria montana* var. *lobata* upon microscopic examination in the continental United States (Hershman et al. 2006). In morphology, our specimens are similar to *P. pachyrhizi* in urediniospores (20–28 × 18–22 µm) (Sydow & Sydow 1914). Unfortunately, we were unable to obtain their nucleotide data though DNA extraction, PCR and sequencing. Thus, we identified our collections as *P. pachyrhizi*.

Melampsoraceae Dietel, in Engler & Prantl, Nat. Pflanzenfam., Teil. I (Leipzig) 1(1): 38 (1897) [1900]

Melampsora Castagne, Observ. Uréd. 2: 18 (1843)

Melampsora babylonicae J.E. Sun, Yong Wang bis & K.D. Hyde, sp. nov. Fig. 100

Index Fungorum number: IF901317; Facesoffungi number: FoF15382

Etymology – Name reflects the host *Salix babylonica*, from which the type specimen was collected.

Holotype – HGUP21117

Description – *Spermogonia*, *aecia* and *telia* unknown. *Uredinia* hypophyllous, nearly oval, pulverulent, not surrounded by host epidermis, 0.1–0.5 mm diam, golden spot. Capitates with evenly thickened walls, 44–50 × 15–21 µm, colorless. *Urediniospores* fusiform, ellipsoidal, or clavate, 19–28 × 12–18 µm ($\bar{x}$ = 23.4 × 15.6 µm, n = 30), hyaline to pale yellow; wall 1.9–2.5 µm thick, colorless, densely and minutely verrucose.

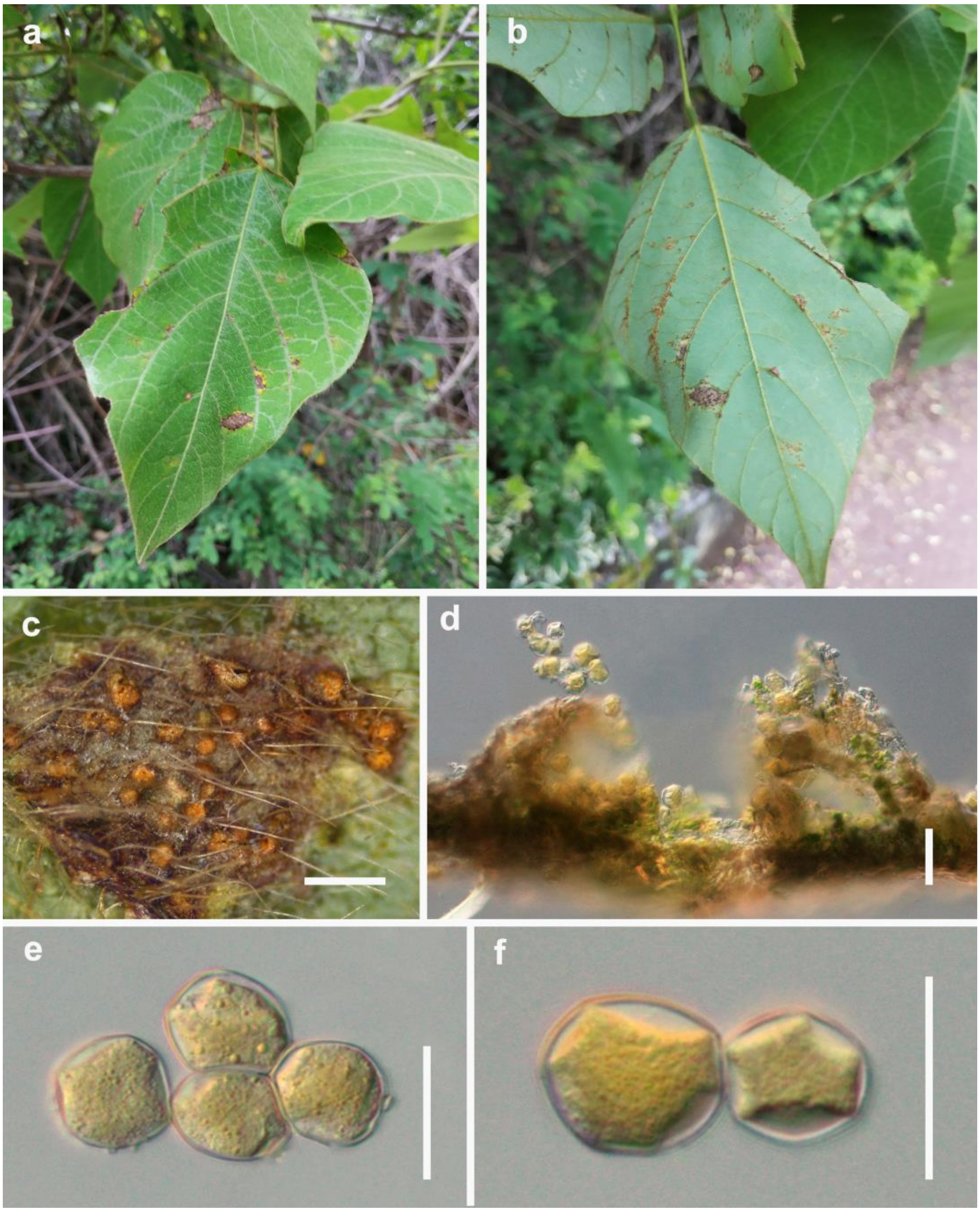

Figure 99 – *Phakopsora pachyrhizi* (from HGUP21259) on *Pueraria montana* var. *lobata*. a–c Uredinia on leaves. d Longitudinal section of uredinium. e–f Urediniospores. Scale bars: c = 1 mm, d = 50 µm, e–f = 25 µm.

Host – *Salix babylonica* (Salicaceae)

Material examined – CHINA, Guizhou Province, Longli city, 26°76'88"N, 106°68'46"W, 801 m, 22 Jun 2021, on *Salix babylonica*, J.E. Sun, holotype HGUP21117; Guizhou Province, Liupanshiui city, 25°89'63"N, 106°82'34"W, 1021 m, 19 Jul 2021, on *S. babylonica*, J.E. Sun, HGUP21118.

Notes – Many *Melampsora* spp. have been reported growing on willows (*Salix* spp.), such as *M. arctica*, *M. capraearum*, *M. coleosporioides*, *M. epiphylla*, *M. epitea*, *M. ferrinii*, *M. humilis*, *M. kamikotica*, *M. laricis-pentandrae*, *M. microsora*, *M. ribesii-purpureae*, *M. ribesii-viminalis*, *M. salicis-albae*, *M. salicis-argyraceae*, *M. salicis-bakko*, *M. salicis-cavaleriei*, *M. salicis-sinicae*, *M. salicis-viminalis*, *M. salicis-triandrae*, *M. yezoensis* (Pei et al. 2005, Zhao et al. 2014, 2015, 2017, Toom & Aime 2015). In the multi-locus phylogenetic analyses, our specimens grouped in a separated clade (Fig. 7), which was described from *Salix babylonica*. The morphology of

HGUP21117 is similar to the type of *M. salicis-albae*, except our collection has smaller urediniospores (20–36 × 11–17 *vs*. 19–28 × 12–18 µm) (Toom & Aime 2015).

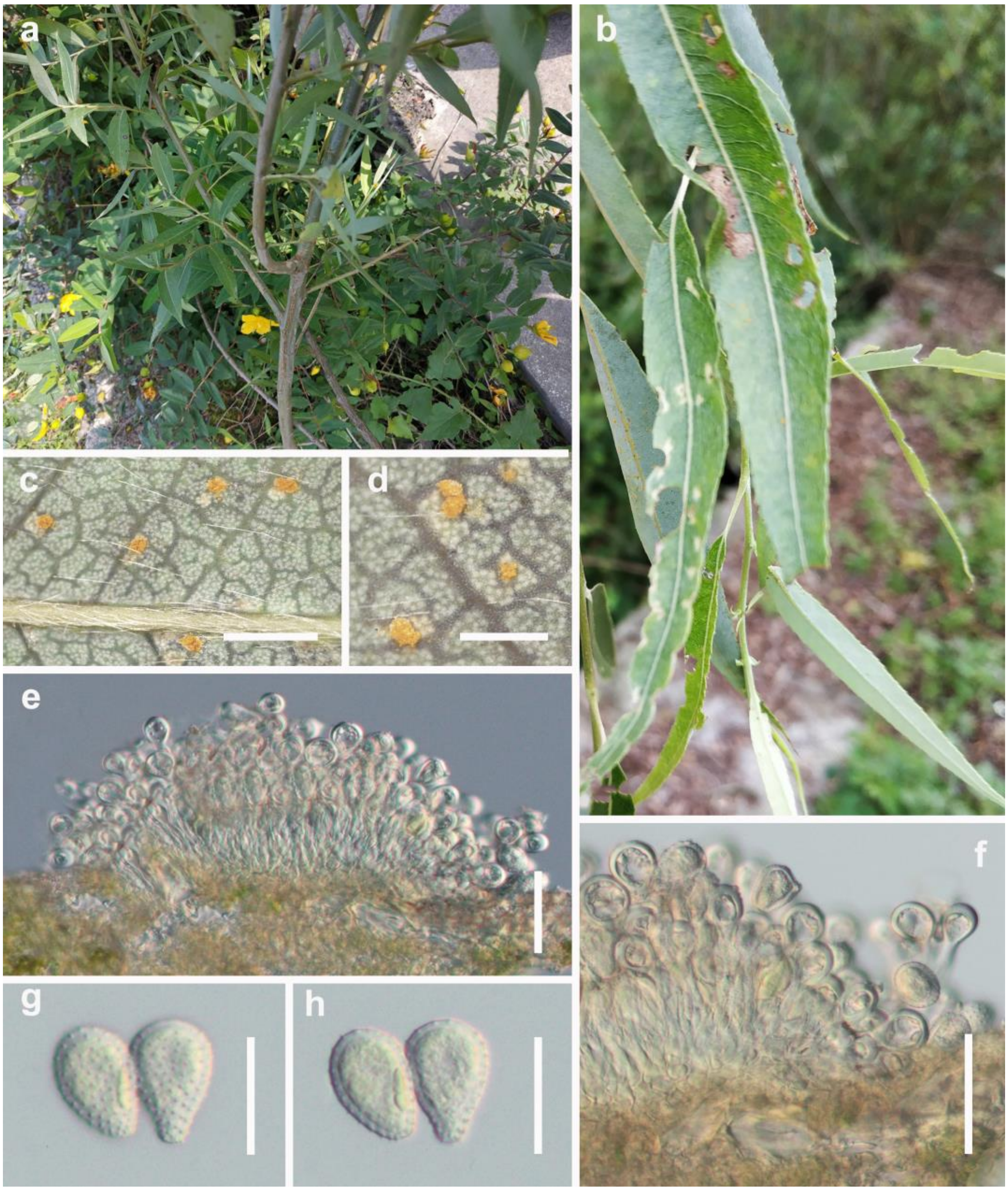

Figure 100 – *Melampsora babylonicae* (from holotype HGUP21117) on *Salix babylonica*. a–d Uredinia on leaves. e Longitudinal section of uredinium. f Capitates. g–h Urediniospores. Scale bars: c = 2 mm, d = 1 mm, e–f = 50 µm, g–h = 25 µm.

Melampsora hypericorum (DC.) J. Schröt., Jber. schles. Ges. vaterl. Kultur: 1 (1871) Fig. 101

MycoBank number: MB183385

Description – *Spermogonia*, *aecia* and *telia* unfound. *Uredinia* hypophyllous, roestelioid, nearly oval, pulverulent, semi-immersed in the host epidermis, 0.4–1.0 cm diam., large yellowish spot, scattered. *Paraphyses* 43–48 × 10–17 µm, with evenly thickened walls and an apparently thickened apex. *Urediniospores* ellipsoidal or obovoid, 13–22 × 11–16 µm ($\bar{x}$ = 17.3 × 13.4 µm, n = 30), golden; wall 1.2–1.8 µm thick, colorless, densely and minutely verrucose.

Host – *Hypericum patulum* (Hypericaceae)

Material examined – CHINA, Guizhou Province, Longli city, 26°76'88"N, 106°48'46"W, 801 m, 22 Jun 2021, on *Hypericum patulum*, J.E. Sun, HGUP21119; Liupanshui city, 26°34'46"N, 104°08'38"W, 1800 m, 25 Sep 2021, on *H. patulum*, J.E. Sun, HGUP21120; Yunnan Province: Qujing city, 19 Apr 2022, on *H. patulum,* X.J. Chen, HGUP21121.

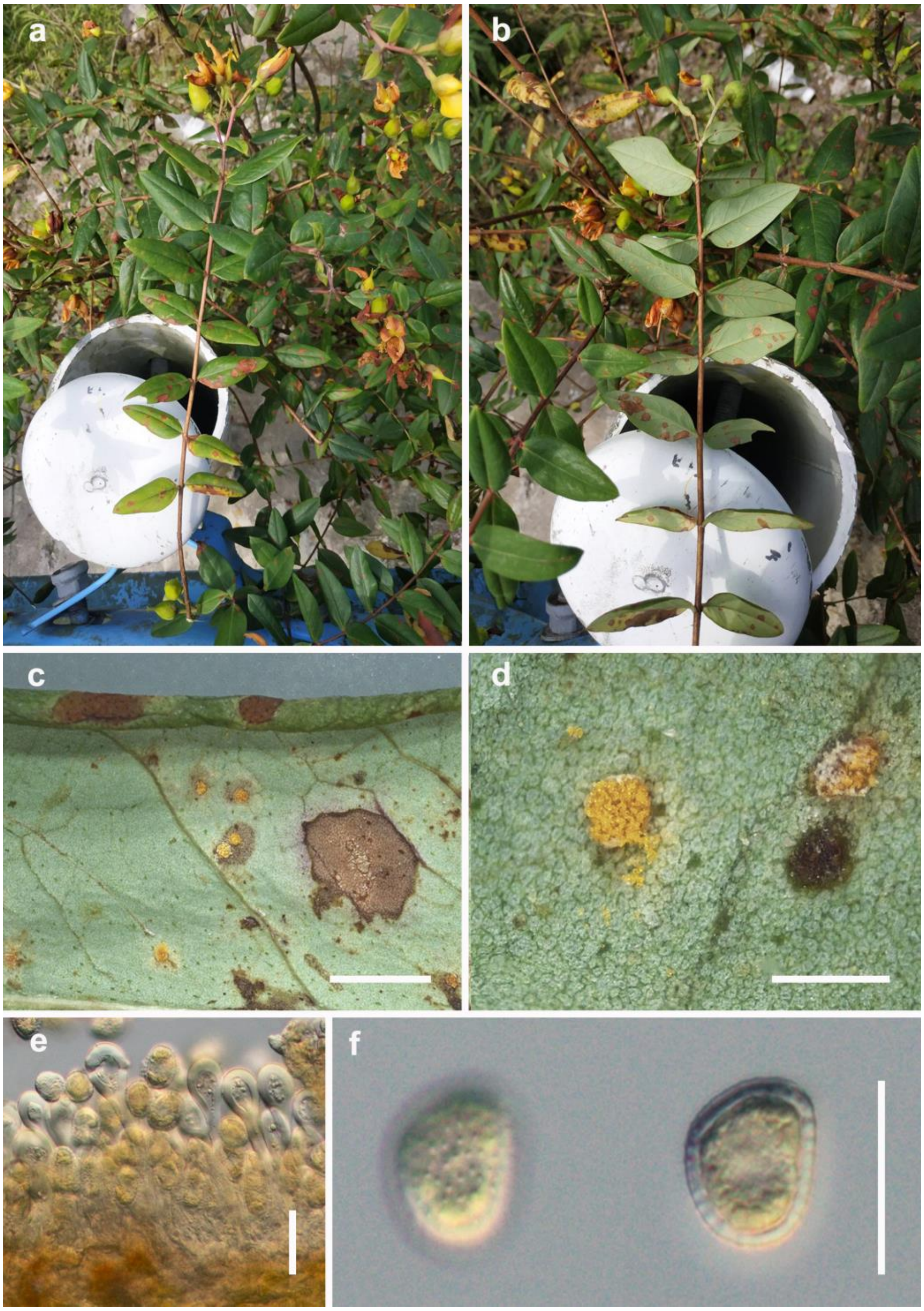

Figure 101 – *Melampsora hypericorum* (from HGUP21119) on *Hypericum patulum*. a–d Uredinia on leaves. e Longitudinal section of aecium and paraphyses. f Urediniospores. Scale bars: c = 5 mm, d = 1 mm, e = 50 µm, f = 12.5 µm.

Notes – In the multi-locus phylogenetic analyses, our specimens clustered with *Melampsora coleosporioides* HNMAP3114 (Fig. 7). However, our specimens were found on the host *Hypericum patulum*. *Melampsora hypericorum* and *M. kusanoi* was reported on the *Hypericum* sp. plants (Zhuang et al. 2012, Xu & Bai 2023). n morphology, our specimens similar to *Melampsora hypericorum* in urediniospores (Zhuang et al. 2012), and different to *M. kusanoi* (11.2–1.8 *vs.* 3.6 µm; Xu & Bai 2023) in cell wall of urediniospores.

Uredinineae incertae sedis

Nyssopsora Arthur, Résult. Sci. Congr. Bot. Wien 1905: 342 (1906)

Nyssopsora araliae-elataii J.E. Sun, Yong Wang bis & K.D. Hyde, sp. nov. Fig. 102

Index Fungorum number: IF901318; Facesoffungi number: FoF15383

Etymology – The name reflects the host *Aralia elata*, from which the type specimen was collected.

Holotype – HGUP21098

Description – *Spermogonia*, *uredinia* and *telia* not found. *Aecia* hypophyllous, nearly oval, pulverulent, semi-immersed in the host epidermis, 1.0–5.0 mm long, on a large yellowish spot, scattered. *Aeciospores* ellipsoidal or obovoid, 15–21 × 12–17 µm ($\overline{x}$ = 17.8 × 14.9 µm, n = 30), golden, or bright yellow; wall 0.6–1.3 µm thick, colorless, rugose.

Figure 102 – *Nyssopsora araliae-elataii* (from holotype HGUP21098) on *Aralia elata*. a–c Aecia on leaves. d–e Longitudinal section of aecia. f–i Aeciospores. Scale bars: b = 3 mm, c = 1 mm, d–e = 50 µm, f–i = 12.5 µm.

Host – *Aralia elata* (Araliaceae)

Material examined – CHINA, Guizhou Province, Guiyang city, 26°45'28"N, 106°65'73"W, 1112 m, 6 May 2022, on *Aralia elata*, J.E. Sun, holotype HGUP21098; Guizhou Province, Guiyang city, 26°45'28"N, 106°65'73"W, 1112 m, 6 May 2022, on *A. elata*, J.E. Sun, HGUP21099, HGUP21100.

Notes – The genus *Nyssopsora* was first described by Arthur (1906). Species of *Nyssopsora* have been described as growing often on Araliaceae and Anacardiaceae plants (Baiswar et al. 2014, De Carvalho et al. 2014). In the phylogenetic tree, our specimens clustered with *N. cedrelae*, which were collected from *Aralia elata* of Araliaceae, but kept a distant relationship with high support (Fig. 8). However, *Nyssopsora* species have mostly been reported from telial and uredinial stages without the aecial stage (Baiswar et al. 2014, De Carvalho et al. 2014, Aime & McTaggart 2021). Thus, we propose *N. araliae-elataii* as a new species, with aecial stage, based mainly on the phylogenetic analyses.

Nyssopsora koelreuteriae (Syd. & P. Syd.) Tranzschel, Zhurn. Russk. Bot. Obshch.: 129, 1925. Fig. 103

MycoBank number: MB335240

Description – *Spermogonia*, *uredinia* and *telia* not found. *Aecia* hypophyllous, nearly oval, pulverulent, semi-immersed in the host epidermis, 0.5–1.0 cm diam., on large yellowish spot. *Aeciospores* ellipsoidal or obovoid, 10–15 × 6–9 µm ($\bar{x}$ = 12.6 × 7.7 µm, n = 30), golden; wall 0.6–1.2 µm thick, colorless, rugose.

Host – *Eleutherococcus trifoliatus* (Araliaceae)

Material examined – CHINA, Guizhou Province, Zunyi city, 27°66'53"N, 107°52'98"W, 824 m, 14 May 2021, on *Eleutherococcus trifoliatus*, J.E. Sun, HGUP21103; Zunyi city, 27°66'80"N, 106°40'66"W, 1052 m, 10 Jun 2022, on *E. trifoliatus*, J.E. Sun, HGUP21104.

Notes – *Nyssopsora koelreuteriae* was first reported on *Koelreuteria paniculata* with DNA data from NCBI-BLAST database. In phylogeny, our specimens grouped with *N. koelreuteriae* (Fig. 8). Thirumalachar & Mundkur (1949) considered that *Nyssopsora* produced only uredinia and telia, but Kakishima et al. (1984) reported the aecia of *N. cedrelae* through inoculation trials. In our study, we found the aecial stage, produced on *K. paniculata*. We confirmed our specimens as *N. koelreuteriae* through phylogenetic analyses with nucleotide data from NCBI-BLAST and its aecial stage.

Nyssopsora cedrelae (Hori) Tranzschel, Zhurnal russk, bot. Obshch 129, 1925. Fig. 104

MycoBank number: MB335239

Description – *Spermogonia*, *aecia* and *telia* not found. *Uredinia* hypophyllous, roestelioid, nearly oval, pulverulent, 0.5–2.5 mm diam., yellowish spot, scattered. *Urediniospores* subglobose, 17–22 × 15–20 µm ($\bar{x}$ = 18.7 × 17.7 µm, n = 30), golden, or bright yellow; wall 2–3 µm thick, colorless, echinulate.

Host – *Toona sinensis* (Meliaceae)

Material examined – CHINA, Guizhou Province, Xingyi city, 24°92'21"N, 105°58'30"W, 1024 m, 26 Jul 2021, on *Toona sinensis*, X.J. Chen, HGUP21101, HGUP21102.

Notes – *Nyssopsora cedrelae* was first reported on *Toona sinensis* in China. Our specimens are similar to the urediniospores of *N. cedrelae* (17–22 × 15–20 µm *vs.* 15–19 × 13–17 µm; Zhuang et al. 2012). Therefore, we name the collections as *N. cedrelae*. GenBank accession numbers (ITS and *LSU*) of *N. cedrelae* are provided in this study.

Peridiopsora Kamat & Sathe, Transactions of the British Mycological Society 53: 144 (1969).

Peridiopsora mori (Barclay) K.V. Prasad, B.R.D. Yadav & Sullia, Current Science 65 (5): 426, 1993 Fig. 105

MycoBank number: MB360935

Description – *Spermogonia*, *uredinia* and *telia* not found. *Aecia*, hypophyllous, roestelioid, nearly oval, pulverulent, semi-immersed in the host epidermis, 3–6 mm diam. (width: 1–6 mm), yellowish spot, scattered. *Aeciospores* subglobose or ellipsoidal, 10–14 × 7–12 µm ($\overline{x}$ = 12.0 × 9.8 µm, n = 30), golden, or bright yellow; wall 0.6–1.2 µm thick, colorless, rugose.

Host – *Morus alba* (Moraceae)

Material examined – CHINA, Guizhou Province, Liupanshui city, 26°34'46"N, 104°48'30"W, 1840 m, 26 Sep 2021, on *Morus alba*, X.Y. Zhang, HGUP21096; Liupanshui city, 26°34'46"N, 104°48'30"W, 1840 m, 26 Sep 2021, on *M. alba*, X.Y. Zhang, HGUP21097.

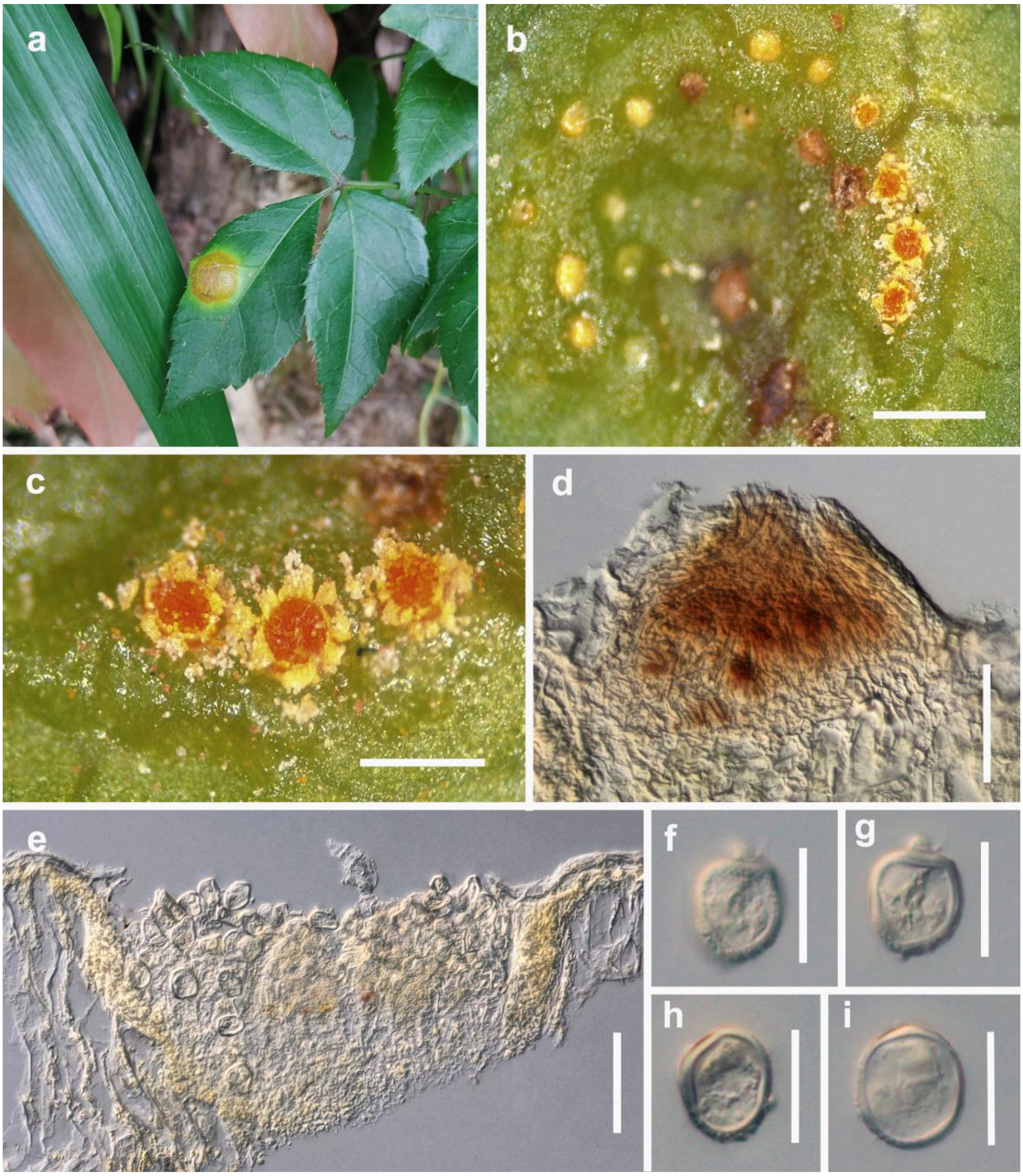

Figure 103 – *Nyssopsora koelreuteriae* (from HGUP21103) on *Eleutherococcus trifoliatus*. a–c Aecia on leaves. d–e Longitudinal section of aecia. f–i Aeciospores. Scale bars: b = 5 mm, c = 1 mm, d–e = 50 µm, e–h = 12.5 µm.

Notes – *Morus alba* is widely distributed, and is often infected by *Peridiopsora mori* (Prasad et al. 1993). GenBank accession numbers (ITS and LSU) of *Peridiopsora mori* are unpublished in NCBI, and our specimens clustered in a clade with good support (Fig. 8). Morphological characters of aecia and aeciospores from our collections are similar to *Peridiopsora mori* which was described by Prasad et al. (1993). Hence, based on both morphology and phylogeny, we identify our collections as *Peridiopsora mori*.

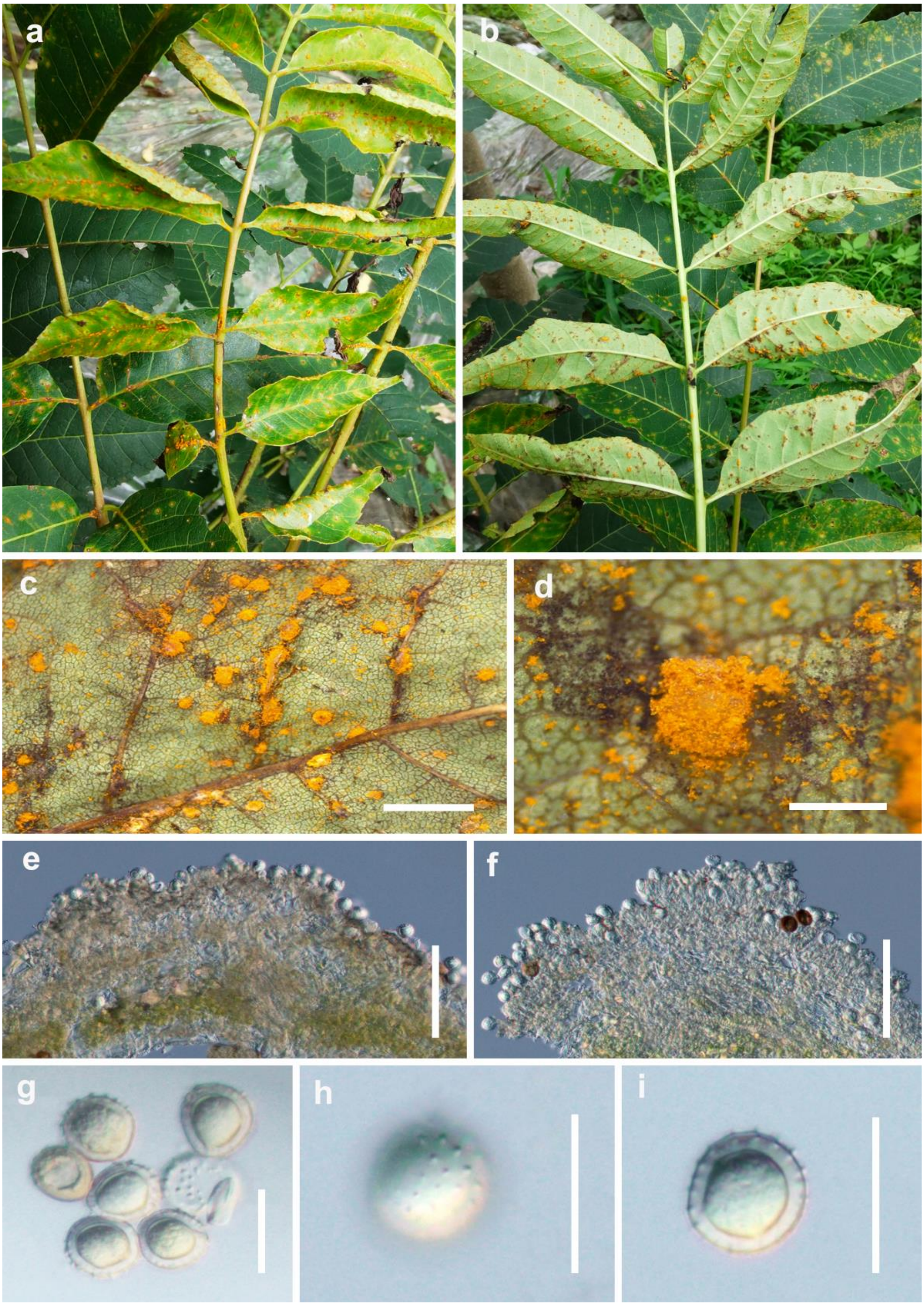

Figure 104 – *Nyssopsora cedrelae* (from HGUP21101) on *Toona sinensis*. a–d Uredinia on leaves. e–f Longitudinal section of uredinia. g–i Urediniospores. Scale bars: c = 5 mm, d = 1 mm, e–f = 50 µm, g–h = 25 µm.

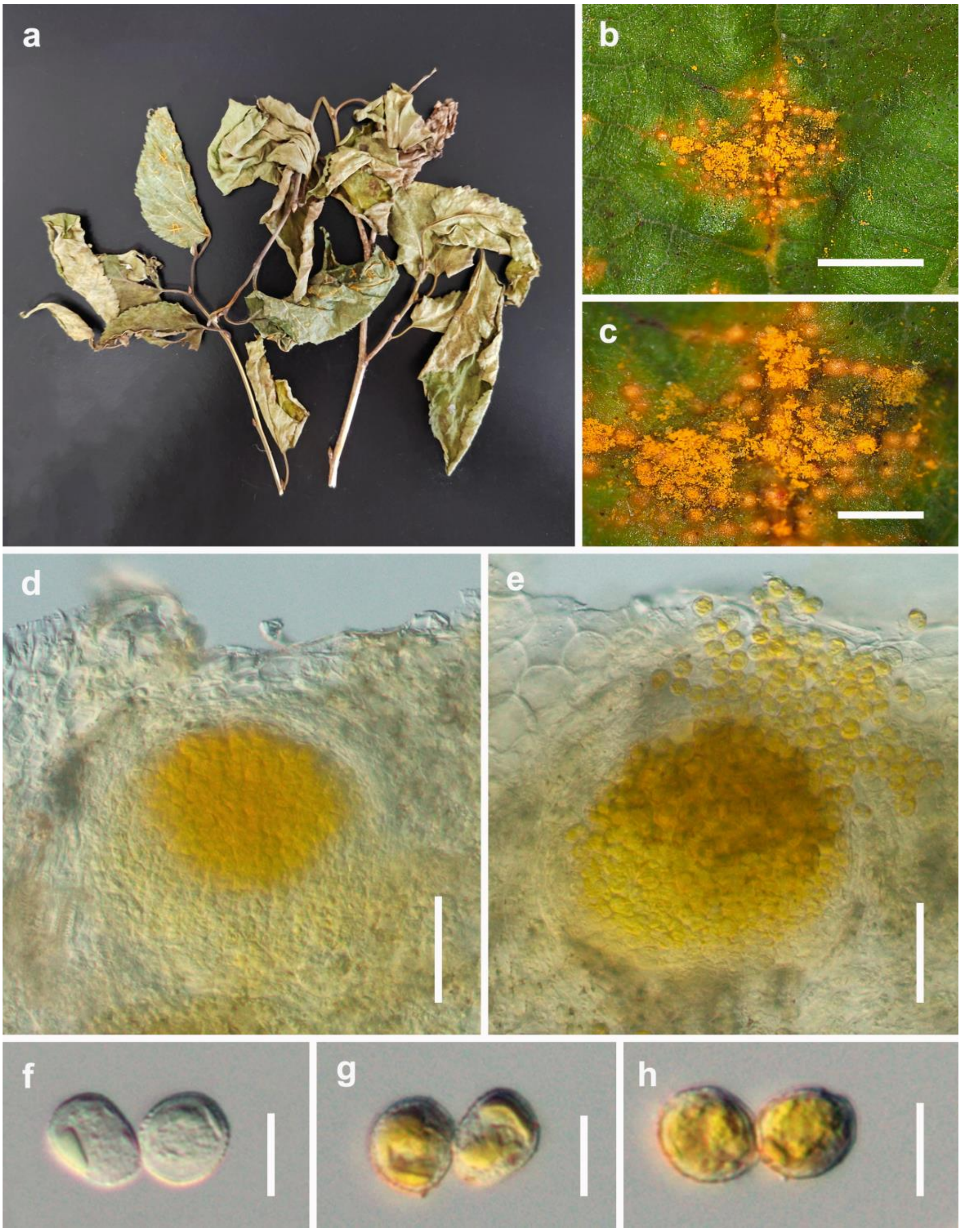

Figure 105 – *Peridiopsora mori* (from HGUP21096) on *Morus alba*. a–c Aecia on leaves. d–e Longitudinal section of aecium. f–h Aeciospores. Scale bars: b = 5 mm, c = 1 mm, d–e = 50 µm, f–h = 25 µm.

Chaconiaceae Cummins & Y. Hirats., Illustr. Gen. Rust Fungi, rev. Edn (St Paul): 14 (1983)
Mikronegeria Dietel, in Dietel & Neger, Bot. Jb. 27(1): 16 (1899) [1900]

Mikronegeria mucunae-sempervirensii J.E. Sun, Yong Wang bis & K.D. Hyde, sp. nov.
Fig. 106

Index Fungorum number: IF901319; Facesoffungi number: FoF15384

Etymology – The name reflects the host *Mucuna sempervirens*, from which the type specimen was collected.

Holotype – HGUP21043

Description – *Spermogonia*, *aecia* and *telia* not found. *Uredinia* hypophyllous, covering entire lower surface of the leaves, nearly oval, pulverulent, not surrounded by host epidermis, 1.0–3.0 mm diam., on densely golden spot. *Urediniospores* globose or ellipsoidal, 15–27 × 11–17 µm ($\bar{x}$ = 22.6 × 19.7 µm, n = 30), golden, or bright yellow; wall 1–1.4 µm thick, colorless, densely and minutely echinulate.

Host – *Mucuna sempervirens* (Fabaceae)

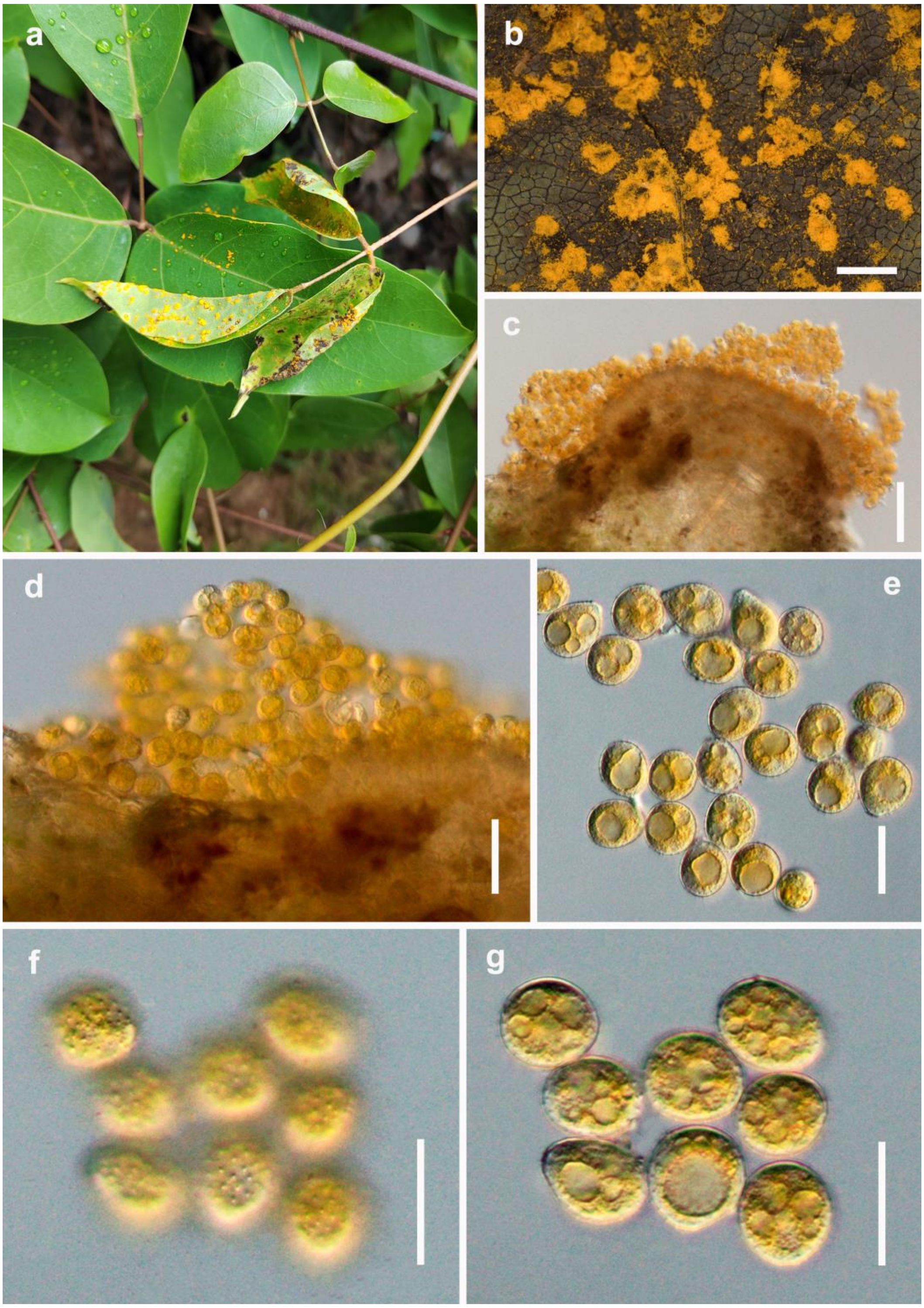

Figure 106 – *Mikronegeria mucunae-sempervirensii* (from holotype HGUP21043) on *Mucuna sempervirens*. a–b Uredinia on leaves. c–d Longitudinal section of uredinia. e–g Urediniospores. Scale bars: b = 2 mm, c = 100 µm, d = 50 µm, e–g = 25 µm.

Material examined – CHINA, Guizhou Province, Guiyang city, 26°45'02"N, 106°65'94"W, 1102 m, 20 Jul2022, on *Mucuna sempervirens*, J.E. Sun, holotype HGUP21043; Guizhou Province, Guiyang city, 26°45'02"N, 106°65'94"W, 1102 m, 20 Jul 2022, on *M. sempervirens*, J.E. Sun, HGUP21044; Guiyang city, 26°45'02"N, 106°65'94"W, 1102 m, 20 Jul 2022, on *M. sempervirens*, J.E. Sun, HGUP21045.

Notes – *Mikronegeria* was established by Dietel & Neger (1900), and has only three species (*M. alba*, *M. fagi*, *M. fuchsiae*) listed in MycoBank (https://www.mycobank.org). Our specimens are distinguished from *M. fuchsiae* by smaller urediniospores (18.6–31 × 14–24.8 µm; Crane & Peterson 2007), and phylogenic analyses indicated it does not belong to any other members of *Mikronegeria*. Based on both morphology and phylogenetic analyses, we propose our collections as a new species.

Gymnosporangiaceae Chevall., Flore Générale des Environs de Paris 1: 422 (1826)
Gymnosporangium R. Hedw. ex DC., Flore française 2: 216 (1805)

Gymnosporangium asiaticum Miyabe ex G. Yamada, Shokubutse Byorigaku (Pl. Path) Tokyo Hakubunkwan 37(9): 304 (1904) Figs 107, 108, 109

MycoBank number: MB217898

Description – *Uredinia* and *telia* not found. *Spermogonia* epiphyllous, punctate, aggregated, pale yellow to black, 180–250 µm diam. *Aecia* mainly hypophyllous and on fruit, rarely caulicolous, 2–9 mm long, peridium dehiscent at apex, no slits along the sides. *Aeciospores* 14–22 × 13–21 µm, globose, pale to yellowish brown, wall 1.1–2.4 µm thick, colorless, rugose.

Host – *Chaenomeles speciosa*, *Malus pumila*, *Pyrus bretschneideri* (Rosaceae)

Material examined – CHINA, Guizhou Province, Liupanshui city, 25°89'61"N, 104°56'07"W, 751 m, 21 Mar 2021, on *Pear*, J.E. Sun, HGUP21086; Guiyang city, 26°44'74"N, 106°56'68"W, 998 m, 3 May 2021, on *Pear*, J.E. Sun, HGUP21087, HGUP21088; Zunyi city, 27°45'25"N, 106°30'12"W, 1102 m, 3 May 2021, on *Pear*, J.E. Sun & Y.Q. Yang, HGUP21089; Guiyang city, 26°40'07"N, 106°68'62"W, 1155 m, 29 Mar 2021, on *Apple*, J.E. Sun, HGUP21093, HGUP21094; Tongren city, 28°15'81"N, 108°33'49"W, 812 m, 1 Aug 2021, on *Apple*, J.E. Sun, HGUP21095; Guiyang city, 26°41′52″N, 106°66'82"W, 1140 m, 11 May 2021, on *Chaenomeles speciosa*, J.E. Sun, HGUP21090; 26°66'31"N, 106°67'05"W, 1021 m, 24 Jun 2021, on *C. speciosa*, J.E. Sun, HGUP21091; 26°43'80"N, 106°67'73"W, 1112 m, 24 May 2021, on *C. speciosa*, J.E. Sun, HGUP21092.

Notes – *Gymnosporangium* species infect Rosaceae (Zhuang et al. 2012). In the multi-locus phylogenetic analyses, our specimens grouped with *G. asiaticum* (Fig. 10). In morphology our specimens are similar to *G. asiaticum* in spermogonia (180–250 µm *vs.* 100–200 µm), aecia (2–9 mm *vs.* 2–10 mm) and aeciospores (14–22 × 13–21 µm *vs.* 17–25 × 15–22 µm) (Zhuang et al. 2012). Thus, we identified our collections as *G. asiaticum*.

Tranzscheliaceae Aime & McTaggart, Fungal Systematics and Evolution 7: 35 (2020)
Tranzschelia Arthur, Résult. Sci. Congr. Bot. Wien 1905: 340 (1906)

Tranzschelia discolor (Fuckel) Tranzschel & M.A. Litv., Bot. Zh. SSSR 24(3): 248 (1939) Fig. 110

MycoBank number: MB251863

Description – *Spermogonia*, *telia* and *aecia* not found. *Uredinia* hypophyllous, nearly oval, pulverulent, surrounded by host epidermis, 0. 5–0.7 mm diam., small brown spot, scattered. Capitates with evenly thickened walls, 36–46 × 15–20 µm, and thickened at apex, 5.0–8.0 µm. *Urediniospores* ellipsoidal or obovoid to slightly oblong, 31–41 × 10–17 µm ($\bar{x}$ = 35.4 × 14.6 µm, n = 30), pale to brown; wall thickened at apex 1.5–2.5 µm thick, light brown, densely and minutely verrucose.

Hosts – *Prunus persica* (Rosaceae)

Material examined – CHINA, Guizhou Province, Panzhou city, 25°89'62"N, 104°84'39"W, 877 m, 19 Oct 2021, on *Prunus persica*, J.E. Sun, HGUP21105, HGUP21106; Yunnan Province: Dali city, 28 Oct 2021, on *P. persica*, J.E. Sun, HGUP21107.

Figure 107 – *Gymnosporangium asiaticum* (from HGUP21086) on *Pyrus bretschneideri*. a–b Spermogonia on leaves. c–f Longitudinal section of spermogonia. i–k Aecia on leaves.

l–m Longitudinal section of aecia. n–q Aeciospores. Scale bars: b, j–k = 5 mm, c–e, l–m = 50 µm, d = 50 µm, f, n–q = 12.5 µm.

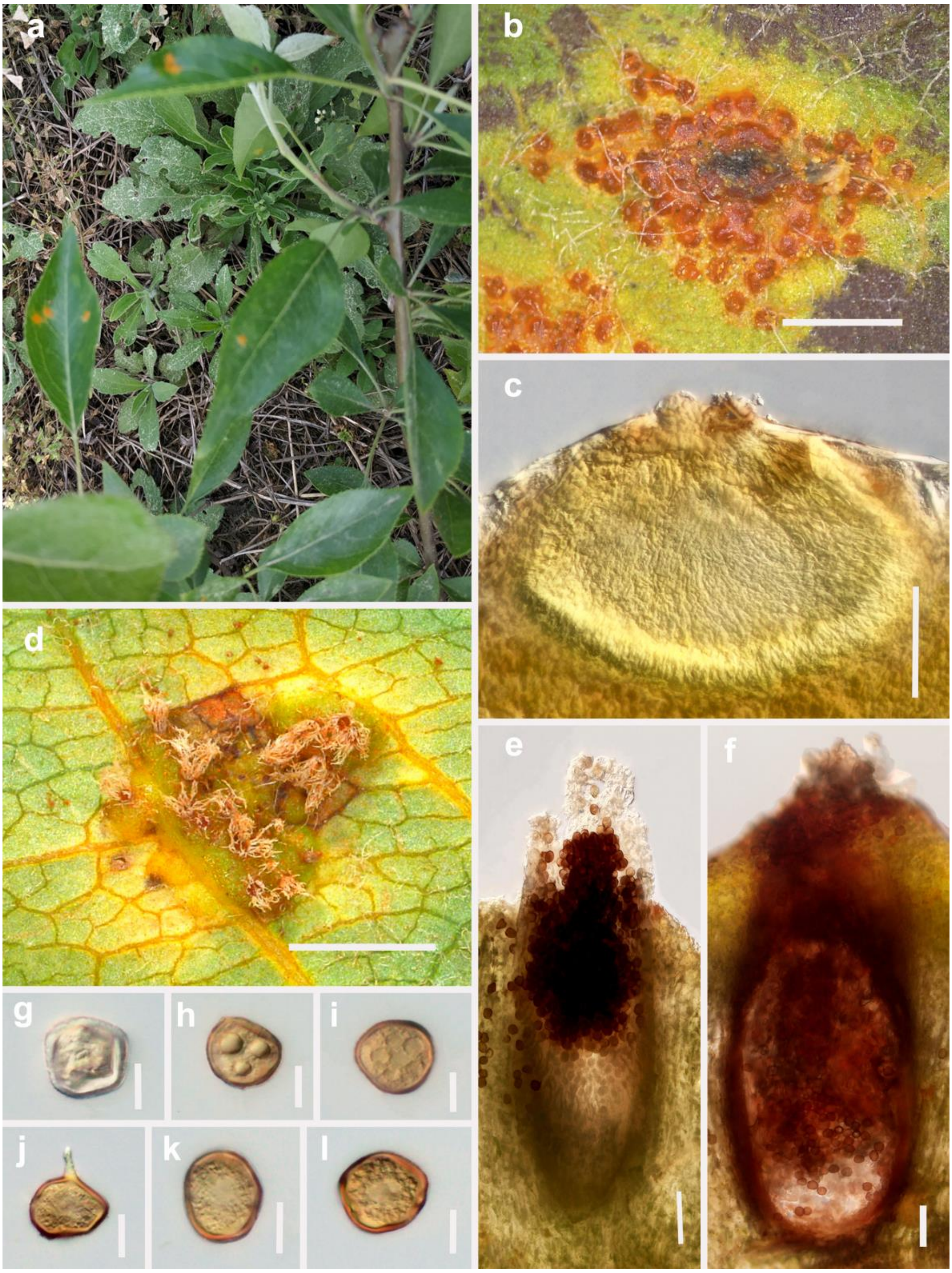

Figure 108 – *Gymnosporangium asiaticum* (from HGUP21093) on *Malus pumila*. a–b, d Spermogonia and aecia on leaves. c Longitudinal section of spermogonium. e–f Longitudinal section of aecia. g–l Aeciospores. Scale bars: b, d = 5 mm, c, e–f = 50 µm, g–l = 12.5 µm.

Notes – *Tranzschelia discolor* infects *Prunus* spp., for example, *P. persica* and *P. salician* (Zhuang et al. 2012). In the phylogenetic tree, our specimens had a close relationship with *T. discolor* (BRIP 57662, U506) with good support (Fig. 11). The urediniospores match the description of Zhuang et al. (2012). We confirmed our specimens as *T. discolor*, through phylogenetic analyses and morphology.

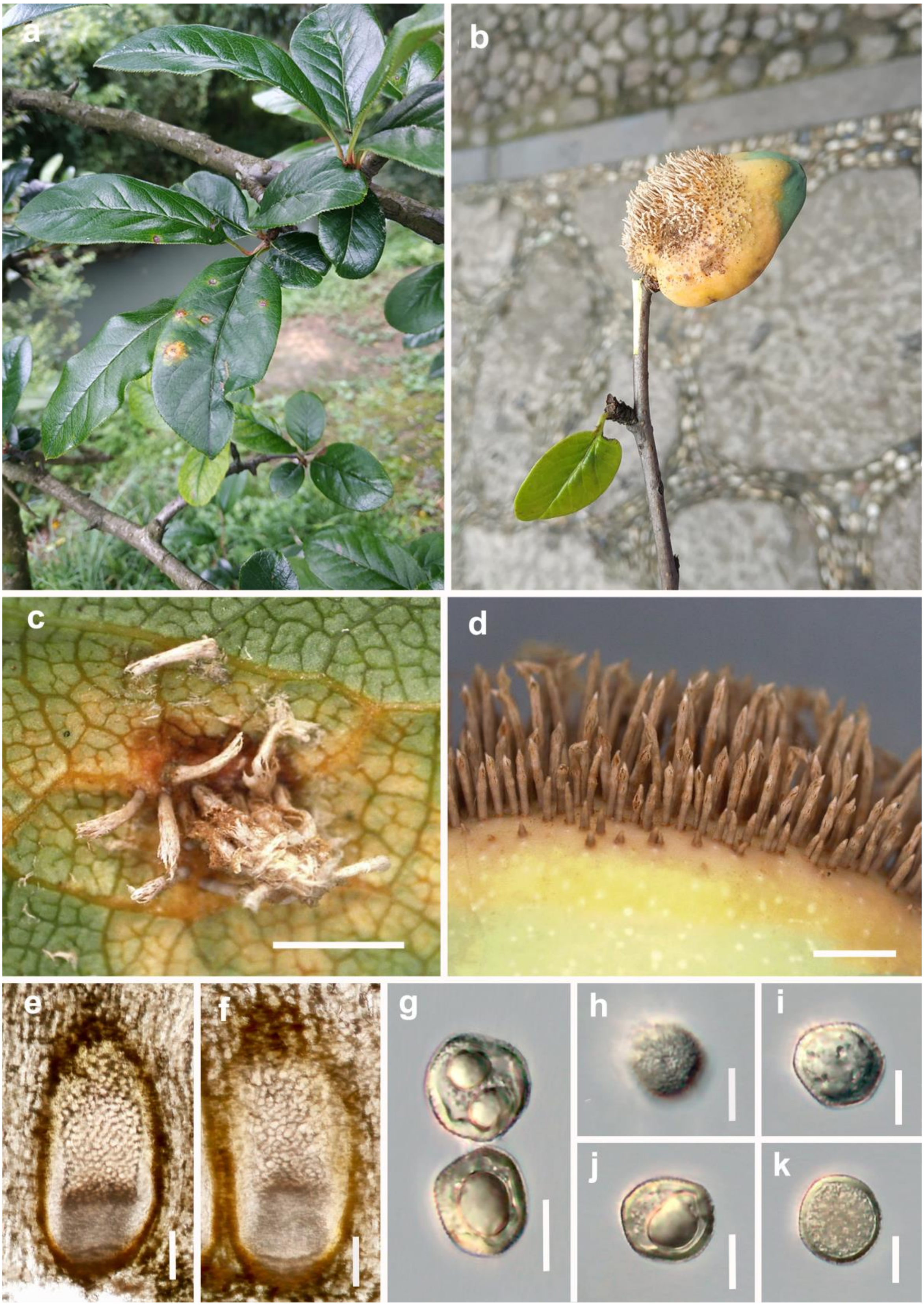

Figure 109 – *Gymnosporangium asiaticum* (from HGUP21090) on *Chaenomeles speciosa*. a, c Aecia on leaves. b, d Aecia on fruit. e–f Longitudinal section of aecia. g–k Aeciospores. Scale bars: c–d = 5 mm, e–f = 50 µm, g–k = 12.5 µm.

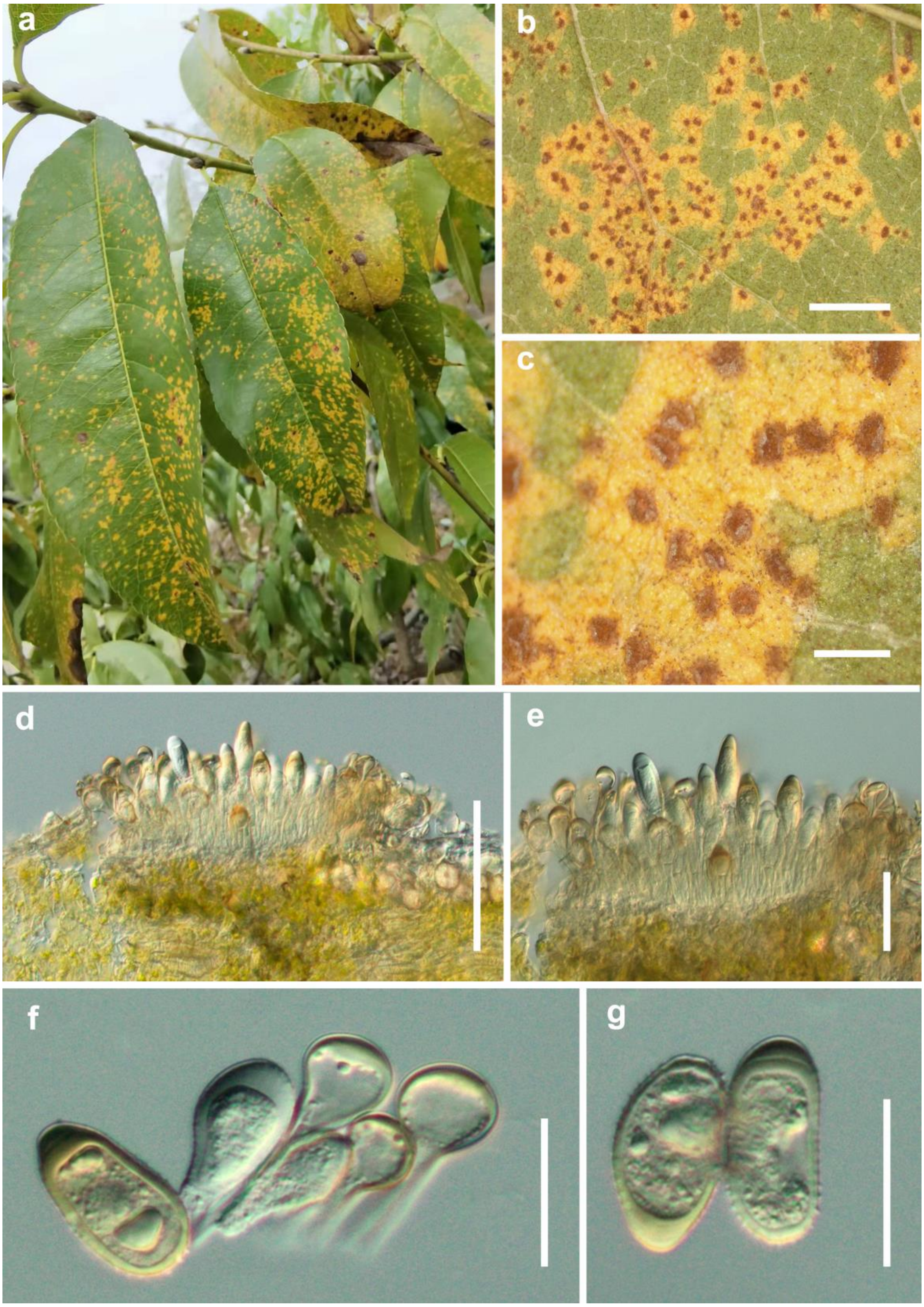

Figure 110 – *Tranzschelia discolor* (from HGUP21105) on *Prunus persica*. a–c Uredinia on leaves. d–e Longitudinal section of uredinia. f Urediniospores and capitates. g Urediniospores. Scale bars: b = 5 mm, c = 1 mm, d–e = 50 μm, f–g = 25 μm.

Pileolariaceae Cummins & Y. Hirats., Illustrated genera of rust fungi: 14 (1983)
Pileolaria Castagne, Observations sur quelques plantes acotylédonées de la famille des Urédinées et dans les sous-tribus des Nemasporées et des Aecidinées, recueillies dans le Dep. des Bouches-du-Rhône 1: 22 (1842)

Pileolaria klugkistiana (Dietel) Dietel, Annales Mycologici 19 (5-6): 301 (1921) Fig. 111

MycoBank number: MB120729

Description – *Spermogonia* and *aecia* unobserved. *Uredinia* hypophyllous, not surrounded by host epidermis, 1.0–3.0 mm diam, irregular spot, cinnamon-brown, powdery. *Urediniospores* globose or pyriform, 19–31 × 19–22 µm ($\overline{x}$ = 23.5 × 20.1 µm, n = 30), light brown to cinnamon brown, 0.8–1.8 µm thick; wall 1.2–2.1 µm thick, light brown, longitudinally striate. *Telia* hypophyllous, scattered, 1.0–3.0 mm diam., chocolate-brown, powdery. *Immature teliospores* globose to circular, or ellipsoidal, 1celled, chocolate-brown to gray-brown, 20–24 × 16–20 µm ($\overline{x}$ = 21.4 × 17.9 µm, n = 30), wall 2.2–2.8 µm thick, colorless to chocolate-brown; pedicels not swollen at the base, 20–70 µm long, colorless, rough.

Host – *Rhus chinensis* (Anacardiaceae)

Material examined – China, Guizhou Province, Duyun city, 26°01'97"N, 106°52'38"W, 805 m, 8 Aug 2022, on *Rhus chinensis*, X.J. Chen, HGUP21262, HGUP21263.

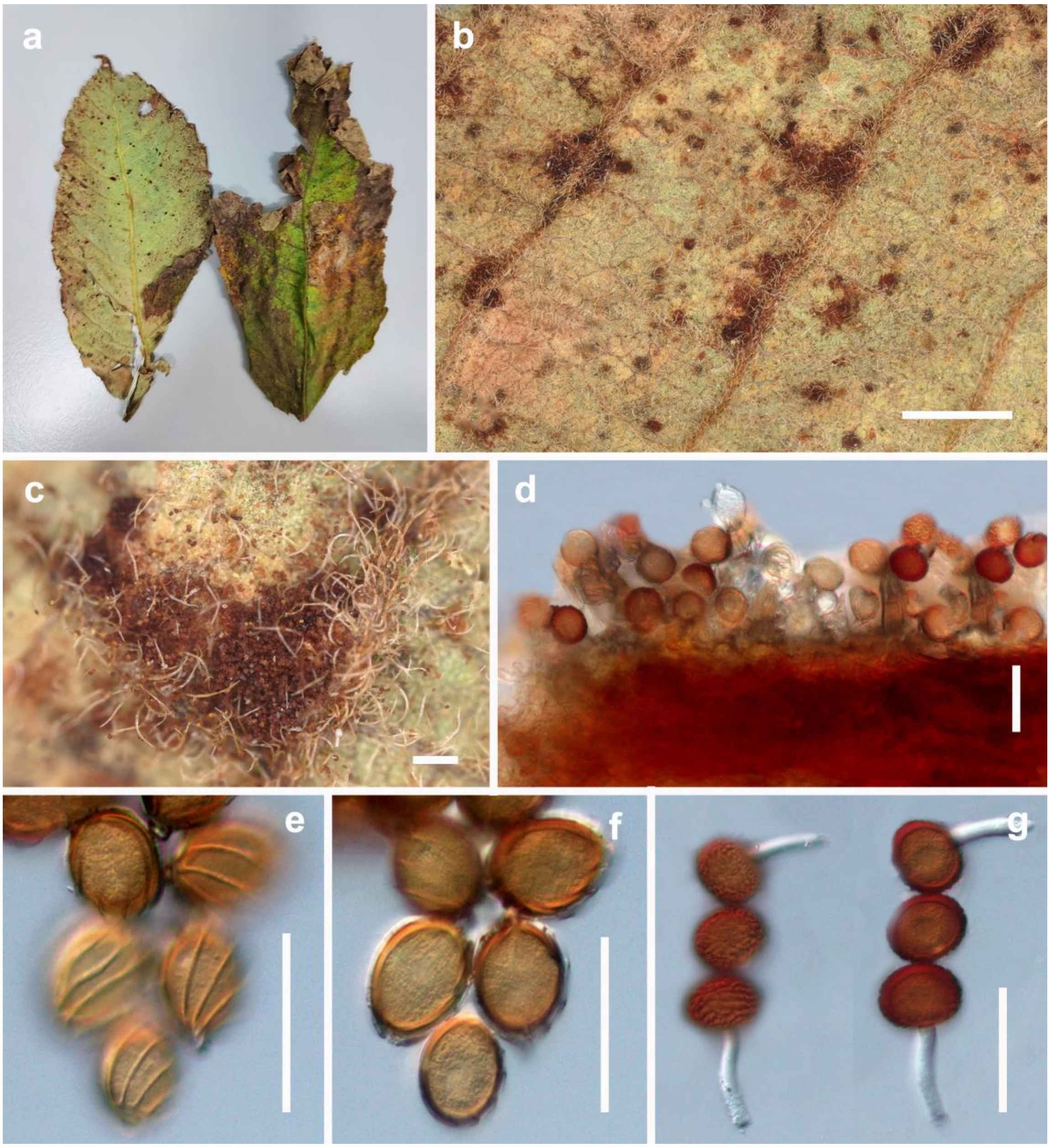

Figure 111 – *Pileolaria klugkistiana* (from HGUP21262) on *Rhus chinensis*. a–c Uredinia on leaves. d Longitudinal section of uredinium and telium. e–f Urediniospores. g Immature teliospores. Scale bars: b = 2 mm, c = 0.5 mm, d–g = 50 µm.

Notes – *Pileolaria klugkistiana* occurred on many plants, such as *Rhus chinensis*, *R. potaninii* and *Toxicodendron delavayi* (Zhuang et al. 2012). Morphologically, our collections agree with *P. klugkistian* in uredinia and urediniospores (Zhuang et al. 2012). Therefore, we identify this fungus as *P. klugkistiana*, although we were unable to obtain their nucleotide data.

Diversity of Rust Fungi

In all the rust fungi from Guizhou Province of China, the Camargo index (1/S) at the family, genus and species level was 0.090, 0.058, and 0.010, respectively. Therefore, the dominant families were Pucciniaceae (47%), Coleosporiaceae (17.2%) and Phragmidiaceae (18%). Of the fungi identified, most were specimens of *Puccinia* (33.6%), *Coleosporium* (17.2%) and *Phragmidium* (11.6%). *Puccinia* species were associated with 33 host species (78 specimens), *Coleosporium* with 14 hosts (41 specimens) and *Phragmidium* with ten hosts (26 specimens). The dominant species were *Gymnosporangium asiaticum* (4%), *Coleosporium asterum* (4%), *Coleosporium zanthoxyli* (3%) and *Phragmidium rosae-cymosaii* (3%), details as in Fig. 112. All the rust fungi were found on over 90 different hosts.

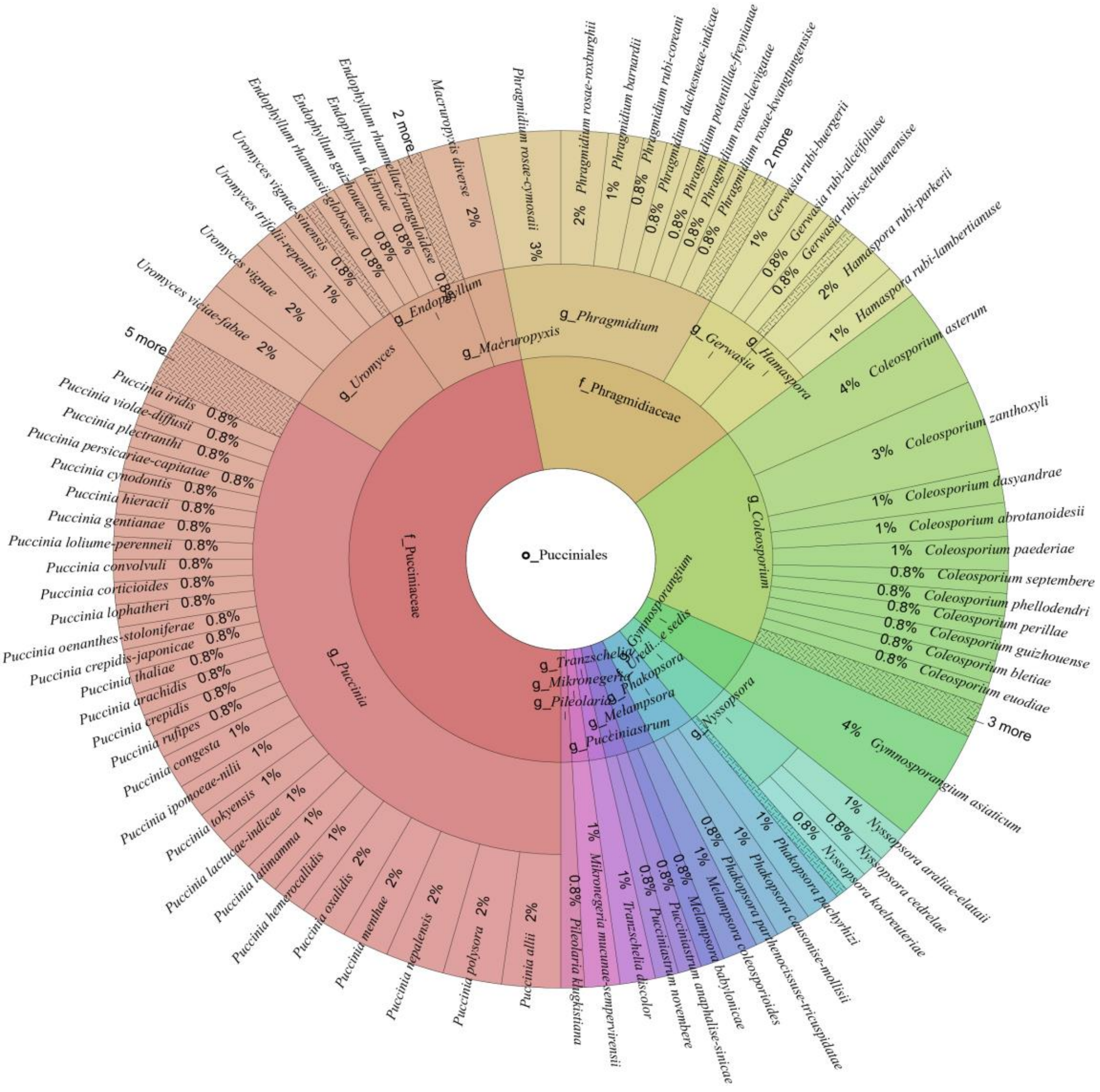

Figure 112 – Species composition of the rust fungi from Guizhou province of China. The letters before each scientific name, at the different taxonomic levels, represent the corresponding taxonomic levels: O – order, F – family, G – genus and all species.

In all the hosts of the rust fungi, the Camargo index (1/S) at the order, family, and genus levels were 0.050, 0.030, and 0.013, respectively. Therefore, the dominant order was Rosales

(26.4%); the dominant families were Rosaceae (21.9%) and Asteraceae (11.4%); of the plants, most were species of *Rubus* (9.0%) and *Rosa* (6.0%). Fabaceae (9.6%), Poaceae (9.4%), Rutaceae (4.8%), Polygonaceae (4.0%), Lamiaceae (3.6%), Rubiaceae (3.0%), Ranunculaceae (3.0%), Convolvulaceae (2.9%), Rhamnaceae (2.7%), Amaryllidaceae (2.0%), Oxalidaceae (2.0%), Apiaceae (1.9%), Araliaceae (1.9%), Liliaceae (1.9%), Vitaceae (1.9%), Clusiaceae (1.0%), Meliaceae (0.9%), Plantaginaceae (0.9%), Iridaceae (0.9%), Orchidaceae (0.9%), Gentianaceae (0.9%), Salicaceae (0.9%), Araceae (0.9%), Cannaceae (0.9%), Saxifragaceae (0.9%), Moraceae (0.9%), Urticaceae (0.9%), Anacardiaceae (0.4%), Violaceae (0.4%), Caprifoliaceae (0.4%) and Elaeagnaceae (0.4%) were infrequently associated with the rust fungi. At the same time, the proportion of fungi in each genus is clear (Fig. 113).

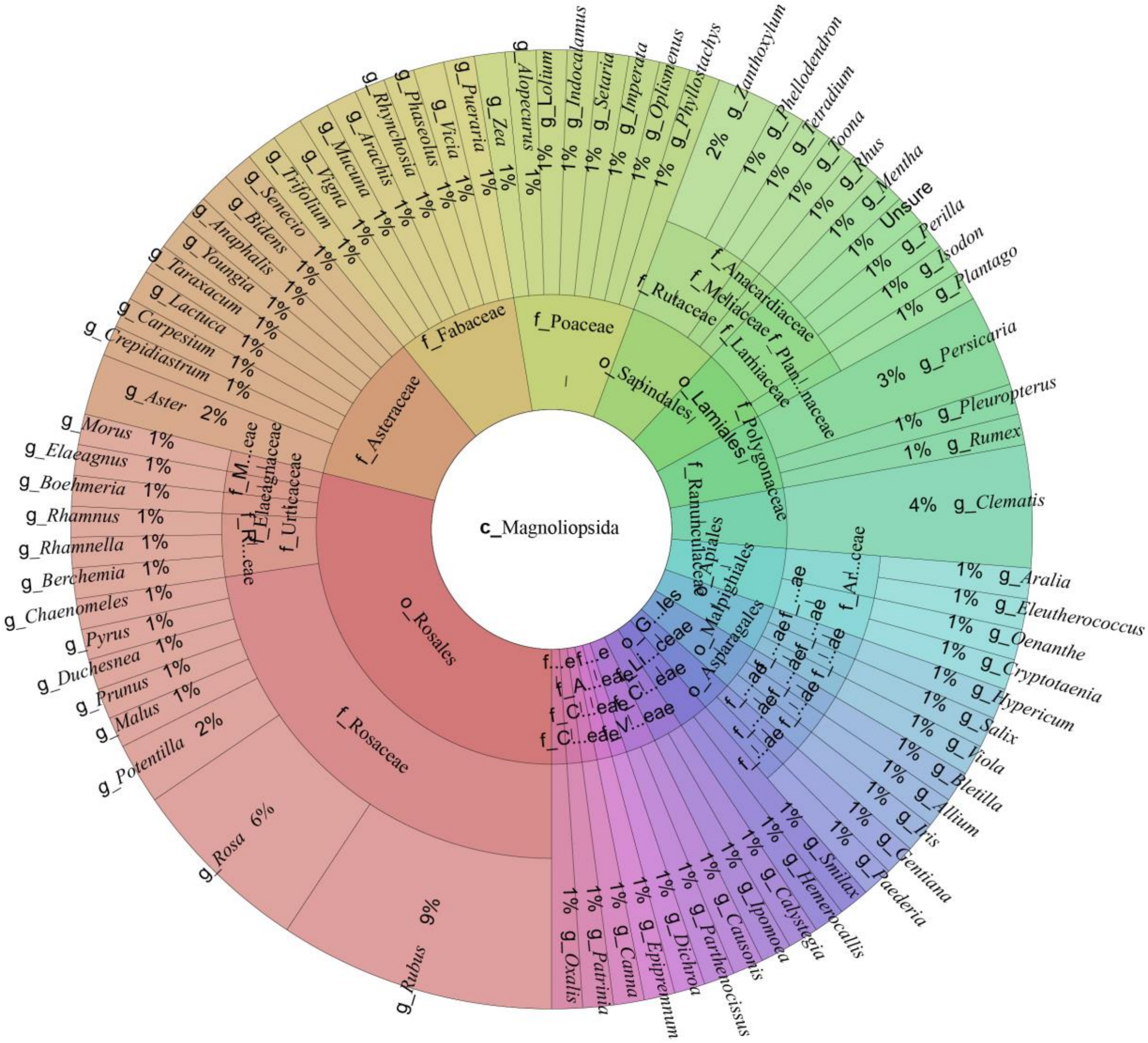

Figure 113 – Species composition of the hosts of rust fungi from Guizhou province of China. The letters before each scientific name at the different taxonomic levels represent the corresponding taxonomic levels: C – class, O – order, F – family, G – genus.

DISCUSSION

Species diversity of rust fungi

Investigation of rust fungi in China began in the middle of the 19th century when a series of monographs and papers were published. Currently, more than 1200 rust taxa have been reported (Dai 1979, Zhuang et al. 1998, 2003, 2005, 2012, 2021, Ji 2017, 2020, Zhao et al. 2021, Sun et al. 2022). In this study, over 300 plant samples with rust symptoms were collected from 33 counties in

Guizhou province in China. According to the ITS-BLAST comparison results, our specimens were allocated to seventeen genera of eleven families in Pucciniales: Pucciniaceae (*Puccinia*, *Uromyces*, *Macropyxis*, *Endophylum*), Phragmidiaceae (*Phragmidium*, *Gerwasia*, *Hamapora*), Coleosporiaceae (*Coleosporium*), Pucciniastracea (*Pucciniastram*), Phakopsoraceae (*Phakopsora*), Melampsoraceae (*Melampsora*), Uredinineae incertae sedis (*Nyssopsora*, *Peridiopsora*), Chaconiaceae (*Mikronegeria*), Gymnosporangiaceae (*Gymnosporangium*), Tranzscheliaceae (*Tranzschelia*), Pileolariaceae (*Pileolaria*). Morphological and phylogenetic analyses were employed to identify rust fungi associated with the different hosts, a total of 90 species were obtained.This study differentiated 29 novel species from twelve genera, viz. *Coleosporium* (*C. abrotanoidesii*, *C. buchananianae*, *C. dasyandrae*, *C. julii*, *C. septembere*); *Endophylum* (*E. berchemiae-floribundae*, *E. Endophyllum maiense*, *E. rhamnusii-globosae*, *E. rhamnellai-franguloidese*); *Gerwasia* (*G. rubi-alceifoliuse*, *G. rubi-buergerii*, *G. rubi-setchuenensise*); *Hamapora* (*H. rubi-lambertianuse*, *H. rubi-parkerii*); *Macropyxis* (*M. diversii*); *Melampsora* (*M. babylonicae*); *Mikronegeria* (*M. mucunae-sempervirensii*); *Nyssopsora* (*N. araliae-elataii*); *Phakopsora* (*P. causonise-mollisii*, *P. parthenocissuse-tricuspidatae*); *Phragmidium* (*P. rosae-kwangtungensise*); *Puccinia* (*P. alopecuruse*, *P. indocalamuse-latifoliusii*, *P. ipomoeae-nilii*, *P. lactucae-indicae*, *P. loliume-perenneii*, *P. persicariae-capitatae*, *P. violae-diffusii*); *Pucciniastram* (*P. anaphalise-sinicae, P. novembere*).

Pucciniales (*Basidiamycota*, *Puccinomycetes*) account for about 25% of basidiomycetes fungi, and it is one of the most abundant fungal groups (Aime & McTaggart 2021). In this study, over 300 specimens of rust pathogens were collected and identified from different hosts in total, including 17 genera of 11 families. The dominant families were Pucciniaceae (47%), Coleosporiaceae (17.2%) and Phragmidiaceae (18%); the dominant genera were *Puccinia* (33.6%), *Coleosporium* (17.2%) and *Phragmidium* (11.6%). Similar results were observed by Zhao et al. (2021) in a study of the diversity of rust fungi from natural reserves and parks in China, where the dominant families were Coleosporiaceae, Melampsoraceae, Phragmidiaceae and Pucciniaceae.

Although tremendous breakthroughs have been made in fungal species identification through molecular techniques, accurate identification remains a challenge for rust fungi related investigations, especially in Pucciniaceae. For example, specimens HGUP21172, HGUP21173 (on *Canna sativa*) formed an independent branch, not clustering with *Puccinia thaliae* (PDD:82262 and ZP-R1300) which has the same host. Thus, identification of rust fungi should be based on morphology, host specificity and phylogenetic analyses. *Rhamnus globosa* and *Rhamnella franguloides* are alternate hosts of *Puccinia coronata* (Zhuang et al. 1998), but the aecial rusts recorded in this study on these hosts did not group with *P. coronata* in the phylogenetic analyses, and also differed in morphology. It indicated that when used phylogenetic results alone, which needed more cautious. Perhaps we need to target more genes to confirm its phylogenetic placement. At present, SSU and CO3 were also used for the identification of related genera, such as *Caeoma*, *Chrysomyxa*, and *Sphaerophragmium* (Yun et al. 2011, McTaggart et al. 2016, Pscheidt & Rodriguez 2016, Liu et al. 2018, 2019, 2020, Tao et al. 2020, Zhao et al. 2021).

In addition, because no ITS and LSU sequence data were available for *Coleosporium paederiae*, *C. perillae*, *Endophyllum dichroae*, *E. elaeagni-latifoliae*, *E. paederiae*, *Puccinia cynodontis*, *Puccinia panici-montani*, *Puccinia plectranthi* and *Uromyces vignae-sinensis* (Zhuang et al. 1998, 2003, 2005, 2012), we could not compare the phylogenetic relationships between these species and our specimens which were found on the same hosts. Morphological characteristics of some species are also insufficient, especially for many of those rusts described before the mid20th century. Other species such as *Phragmidium barnardii* have not been well described, both they have been used for phylogenetic analysis (McTaggart et al. 2016). Consequently, we herein report 30 new species,1 new Chinese record and 57 known species with their molecular data and morphological characteristics (Supplementary Table 1), which present a significant contribution to the knowledge of fungal flora in China and may aid future studies and phylogenetic placement in the Pucciniales.

Table 3 Details of the specimens collected.

Rust Family-	**Genus**	**Species**	**Specimens**	**Host**	**Spore type**	**Size (µm)**	**Wall (µm)**	**Paraphyses (µm)**	**Pedicels (µm)**	**Notes**
Pucciniaceae	*Endophyllum*	*berchemiae-floribundae*	HGUP21138	*Berchemia floribunda*	Aecidioid teliospores	19–24 × 17–22	1.0–1.9			sp. new
Pucciniaceae	*Endophyllum*	*rhamnusii-globosae*	HGUP21242-HGUP21243	*Rhamnus globosa*	Aecidioid teliospores	13–18 × 10–17	1.8–2.5			sp. new
Pucciniaceae	*Endophyllum*	*rhamnellai-franguloidese*	HGUP21244-HGUP21245	*Rhamnella franguloides*	Aecidioid teliospores	12–18 × 11–14	1.2–2.0			sp. new
Pucciniaceae	*Endophyllum*	*maiense*	HGUP21246-HGUP21247	Unknown	Aecidioid teliospores	17–23 × 13–17	1.4–2.4			sp. new
Pucciniaceae	*Endophyllum*	*dichroae*	HGUP21237-HGUP21238	*Dichroa febrifuga*	Aecidioid teliospores	21–28 × 19–24	1.8–2.6			
Pucciniaceae	*Endophyllum*	*elaeagni-latifoliae*	HGUP21217	*Elaeagnus pungens*	Aecidioid teliospores	20–30 × 14–20	1.4–2.0			
Pucciniaceae	*Macruropyxis*	*diversii*	HGUP21255-HGUP21256	*Epipremnum aureum*	Aeciospores	17–22 × 14–20	0.7–1.2			sp. new
			HGUP21142-HGUP21144	*Paederia foetida*	Aeciospores	15–18 × 11–14	1.2–1.7			
Pucciniaceae	*Puccinia*	*ipomoeae-nilii*	HGUP21178-HGUP21181	*Ipomoea nil*	Urediniospores	24–30 × 19–23	1.4–2.0			sp. new
Pucciniaceae	*Puccinia*	*indocalamuse-latifoliusii*	HGUP21239	*Indocalamus latifolius*	Urediniospores	22–27 × 19–26	1.0–2.0			sp. new
Pucciniaceae	*Puccinia*	*loliume-perenneii*	HGUP21240-HGUP21241	*Lolium perenne*	Urediniospores	14–20 × 12–16	1.6–2.6			sp. new
Pucciniaceae	*Puccinia*	*alopecuruse*	HGUP21231	*Alopecurus aequalis*	Urediniospores	21–28 × 16–21	2.1–2.6			sp. new
Pucciniaceae	*Puccinia*	*lactucae-indicae*	HGUP21214-HGUP21216	*Lactuca indica*	Aeciospores	22–30 × 16–22	1.9–2.8			sp. new
					Urediniospores	19–26 × 17–22	1.3–1.6			
					Teliospores (2 celled)	28–35 × 22–29	1.9–2.7		Unsure	
Pucciniaceae	*Puccinia*	*persicariae-capitatae*	HGUP21193-HGUP21194	*Persicaria capitata*	Urediniospores	15–19 × 12–17	0.9–1.4			sp. new
					Teliospores (2 celled)	24–36 × 13–18	4.0–8.0		10–25	
Pucciniaceae	*Puccinia*	*violae-diffusii*	HGUP21204	*Viola diffusa*	Teliospores (1–2 celled)	20–27 × 13–20	1.3–2.1		8–20	sp. new
Pucciniaceae	*Puccinia*	*flaccida*	HGUP21205	*Oplismenus undulatifolius*	Urediniospores	21–26 × 19–25	1.2–2.0			

Table 3 Continued.

Rust Family-	**Genus**	**Species**	**Specimens**	**Host**	**Spore type**	**Size (µm)**	**Wall (µm)**	**Paraphyses (µm)**	**Pedicels (µm)**	**Notes**
Pucciniaceae	*Puccinia*	*phyllostachydis*	HGUP21174-HGUP21175	*Phyllostachys nuda*	Urediniospores	26–35 × 24–29	2.4–3.4	40–80 × 15–30		
Pucciniaceae	*Puccinia*	*thaliae*	HGUP21172-HGUP21173	*Canna indica*	Urediniospores	24–38 × 18–24	2.2–3.2			
Pucciniaceae	*Puccinia*	*rufipes*	HGUP21176-HGUP21177	*Imperata cylindrica*	Urediniospores	25–36 × 18–27	1.4–2.4	50–65 × 14–23		
Pucciniaceae	*Puccinia*	*convolvuli*	HGUP21182-HGUP21183	*Calystegia hederacea*	Aeciospores	17–25 × 14–20	1.3–2.1			
Pucciniaceae	*Puccinia*	*oenanthes-stoloniferae*	HGUP21184-HGUP21185	*Oenanthe javanica*	Urediniospores	19–27 × 15–22	1.7–2.2			
Pucciniaceae	*Puccinia*	*allii*	HGUP21225-HGUP21229	*Allium sativum*	Urediniospores	25–35 × 17–23	2.2–2.8			
					Teliospores	35–75 × 15–25	1.2–2.8		Unsure	
Pucciniaceae	*Puccinia*	*oxalidis*	HGUP21232-HGUP21233; HGUP21235-HGUP21236	*Oxalis corniculate*	Urediniospores	19–26 × 18–25	1.0–1.6			
Pucciniaceae	*Puccinia*	*corticioides*	HGUP21139-HGUP21140	*Bamboo*	Urediniospores	16–25 × 14–20	1.6–2.3			
Pucciniaceae	*Puccinia*	*polysora*	HGUP21248-HGUP21252	*Zea mays*	Urediniospores	21–30 × 21–25	1.7–3.1			
Pucciniaceae	*Puccinia*	*cynodontis*	HGUP21253-HGUP21254	*Plantago asiatica*	Aeciospores	20–26 × 19–25	1.3–2.1			
Pucciniaceae	*Puccinia*	*hieracii*	HGUP21208-HGUP21209	*Taraxacum mongolicum*	Urediniospores	23–31 × 19–25	1.7–3.1			
Pucciniaceae	*Puccinia*	*crepidis-japonicae*	HGUP21210-HGUP21211	*Youngia japonica*	Urediniospores	17–23 × 15–20	1.2–2.0			
Pucciniaceae	*Puccinia*	*crepidis*	HGUP21212-HGUP21213	*Crepidiastrum sonchifolium*	Urediniospores	20–25 × 16–23	1.4–2.3			
Pucciniaceae	*Puccinia*	*arachidis*	HGUP21199-HGUP21200	*Arachis hypogaea*	Urediniospores	21–30 × 17–23	1.5–2.2			
Pucciniaceae	*Puccinia*	*senecionis*	HGUP21198	*Asteraceae*	Aeciospores	17–22 × 15–19	0.8–1.3			
Pucciniaceae	*Puccinia*	*tokyensis*	HGUP21195-HGUP21197	*Cryptotaenia japonica*	Urediniospores	20–26 × 16–23	1.4–2.3			
Pucciniaceae	*Puccinia*	*latimamma*	HGUP21186-HGUP21188	*Pleuropterus multiflorus*	Urediniospores	20–28 × 17–22	1.0–1.6			

Table 3 Continued.

Rust Family-	Genus	Species	Specimens	Host	Spore type	Size (μm)	Wall (μm)	Paraphyses (μm)	Pedicels (μm)	Notes
Pucciniaceae	*Puccinia*	*gentianae*	HGUP21206-HGUP21207	*Gentiana macrophylla*	Urediniospores	24–30 × 23–28	1.7–2.4			
					Teliospores (2 celled)	34–41 × 23–30	2.3–3.3		Unsure	
Pucciniaceae	*Puccinia*	*congesta*	HGUP21222-HGUP21224	*Persicaria posumbu*, host of Polygonaceae	Teliospores (1–2 celled)	35–45 × 15–21	1.8–2.7		50–110	
Pucciniaceae	*Puccinia*	*nepalensis*	HGUP21181; HGUP21230; HGUP21190-HGUP21192	*Rumex nepalensis*	Urediniospores	25–34 × 22–29	1.4–2.6			
Pucciniaceae	*Puccinia*	*iridis*	HGUP21201-HGUP21202	*Iris tectorum*	Spermogonia	180–240				
					Urediniospores	25–32 × 18–29	2.3–3.3			
Pucciniaceae	*Puccinia*	*hemerocallidis*	HGUP21218-HGUP21220	*Hemerocallis fulva*	Urediniospores	21–29 × 17–23	1.6–3.5			
Pucciniaceae	*Puccinia*	*patriniae*	HGUP21221	*Patrinia scabiosifolia*	Aeciospores	15–20 × 12–18	1.0–1.5			
Pucciniaceae	*Puccinia*	*plectranthi*	HGUP21234, HGUP21141	*Isodon amethystoides*	Aeciospores	23–35 × 19–30	1.0–1.6			
Pucciniaceae	*Puccinia*	*panici-montani*	HGUP21189	*Setaria plicata*	Urediniospores	14–20 × 13–17	1.0–1.5	32–40 × 7–10		
Pucciniaceae	*Puccinia*	*menthae*	HGUP21277-HGUP21278	*Mentha canadensis*	Urediniospores	18–27 × 18–21	1.5–2.5			
Pucciniaceae	*Uromyces*	*viciae-fabae*	HGUP21122-HGUP21126	*Vicia faba*	Urediniospores	26–38 × 19–31	1.4–3.1			
					Teliospores	30–43 × 16–27	0.5–2.1		18–57	
Pucciniaceae	*Uromyces*	*trifolii-repentis*	HGUP21127-HGUP21129	*Trifolium repens*	Urediniospores	22–27 × 19–26	1.0–1.9			
					Teliospores	23–28 × 17–23	1.4–2.5		19–39	
Pucciniaceae	*Uromyces*	*vignae*	HGUP21131-HGUP21134	*Phaseolus vulgaris*	Urediniospores	22–27 × 19–26	1.0–1.9			
					Teliospores	27–35 × 22–28	1.7–3.4		19–39	

Table 3 Continued.

Rust Family-	Genus	Species	Specimens	Host	Spore type	Size (µm)	Wall (µm)	Paraphyses (µm)	Pedicels (µm)	Notes
Pucciniaceae	*Uromyces*	*vignae-sinensis*	HGUP21135-HGUP21136	*Vigna unguiculata*	Urediniospores	21–27 × 17–23	1.0–2.0			
					Teliospores	25–33 × 21–27	1.5–2.7		17–35	
Pucciniaceae	*Uromyces*	*bidenticola*	HGUP21037	*Bidens pilosa*	Urediniospores	21–28 × 17–22	1.5–2.2			
Phragmidiaceae	*Gerwasia*	*rubi-setchuenensise*	HGUP21167-HGUP21168	*Rubus setchuenensis*	Urediniospores	18–29 × 15–22	2.1–3.2			sp. new
Phragmidiaceae	*Gerwasia*	*rubi-buergerii*	HGUP21169-HGUP21171	*Rubus buergeri*	Urediniospores	25–37 × 21–27	2.5–3.5			sp. new
Phragmidiaceae	*Gerwasia*	*rubi-alceifoliuse*	HGUP21156-HGUP21157	*Rubus alceifolius*	Urediniospores	26–38 × 17–22	2.0–3.5			sp. new
Phragmidiaceae	*Gerwasia*	*rubi*	HGUP21166	*Rubus reflexus*	Urediniospores	26–40 × 17–24	1.4–2.2			
Phragmidiaceae	*Hamaspora*	*rubi-parkerii*	HGUP21159-HGUP21162	*Rubus parkeri*	Teliospores (4–6 celled)	111–186 × 12–21	1.0–2.6		solid apex 10–26	sp. new
					Basidiospores	10–16 × 5–8				
Phragmidiaceae	*Hamaspora*	*rubi-lambertianuse*	HGUP21163-HGUP21165	*Rubus lambertianus*	Urediniospores	18–24 × 15–20	1.0–1.5			sp. new
Phragmidiaceae	*Phragmidium*	*cymosum*	HGUP21147-HGUP21152	*Rosa cymosa*	Aeciospores	22–31 × 12–19	1.5–2.2			
Phragmidiaceae	*Phragmidium*	*rosae-kwangtungensise*	HGUP21154-HGUP21155	*Rosa kwangtungensis*	Aeciospores	19–28 × 16–21	1.9–3.1			sp. new
Phragmidiaceae	*Phragmidium*	*rosae-roxburghii*	HGUP21025-HGUP21028	*Rosa roxburghii*, *Rosa* sp.	Aeciospores	22–30 × 14–22	1.8–3.1			
					Urediniospores	20–30 × 16–21	0.5–2.0	30–55 × 9–20		
Phragmidiaceae	*Phragmidium*	*rubi-coreani*	HGUP21029-HGUP21030	*Rubus coreanus*	Aeciospores	14–24 × 10–23	1.0–4.0	38–61 long		
					Teliospores (3–5 celled)	29–74 × 14–37	1.8–3.5		8–34	
					Urediniospores	19–27 × 15–25	0.8–1.5			
Phragmidiaceae	*Phragmidium*	*potentillae-freynianae*	HGUP21033-HGUP21040	*Potentilla freyniana*	Urediniospores	19–24 × 18–24	0.4–1.4			
Phragmidiaceae	*Phragmidium*	*rosae-laevigatae*	HGUP21036-HGUP21037	*Rosa laevigata*	Urediniospores	23–35 × 16–30	0.5–2.0	20–31 × 10–17		

Table 3 Continued.

Rust Family-	**Genus**	**Species**	**Specimens**	**Host**	**Spore type**	**Size (µm)**	**Wall (µm)**	**Paraphyses (µm)**	**Pedicels (µm)**	**Notes**
					Teliospores (immature)	24–60 × 8–20	0.5–2.0		15–26	
Phragmidiaceae	*Phragmidium*	*duchesneae-indicae*	HGUP21031-HGUP21032	*Duchesnea indica*	Urediniospores	17–22 × 15–20	0.7–1.8			
Phragmidiaceae	*Phragmidium*	*potentillae*	HGUP21034	*Potentilla kleiniana*	Urediniospores	17–26 × 14–22	0.6–1.3			
Phragmidiaceae	*Phragmidium*	*barnardii*	HGUP21035, HGUP21038-39	*Rubus* sp., *Rubus adenophorus*	Urediniospores	16–19 × 15–18	1.3–2.2			
Phragmidiaceae	*Phragmidium*	*rosae-multiflorae*	HGUP21158	*Rosa multiflora*	Aeciospores	14–22 × 13–18	2.3–3.6			
Coleosporiaceae	*Coleosporium*	*septembere*	HGUP21046-HGUP21047	*Clematis florida*	Urediniospores	21–31 × 13–20	1.6–2.6			sp. new
					Teliospores	30–54 × 12–20	1.0–1.9			
Coleosporiaceae	*Coleosporium*	*julii*	HGUP21048-HGUP21049	*Smilax china*	Urediniospores	15–23 × 11–16	1.1–1.7			sp. new
Coleosporiaceae	*Coleosporium*	*dasyandrae*	HGUP21050-HGUP21052	*Clematis dasyandra*	Urediniospores	25–32 × 14–21	1.8–2.5			sp. new
Coleosporiaceae	*Coleosporium*	*abrotanoidesii*	HGUP21080-HGUP21082	*Carpesium abrotanoides*	Urediniospores	19–27 × 14–18	1.4–1.8			sp. new
					Teliospores	30–53 × 14–30	0.8–1.2			
Coleosporiaceae	*Coleosporium*	*buchananianae*	HGUP21053	*Clematis buchananiana*	Urediniospores	24–30 × 13–18	2.0–2.9			sp. new
Coleosporiaceae	*Coleosporium*	*clematidis*	HGUP21054	*Clematis brevicaudata*	Urediniospores	18–27 × 13–17	1.3–1.8			
Coleosporiaceae	*Coleosporium*	*asterum*	HGUP21055-HGUP21063	*Aster ageratoides*, *A. indicus*	Urediniospores	25–31 × 15–20	1.6–2.1			
Coleosporiaceae	*Coleosporium*	*bletiae*	HGUP21064-HGUP21065	*Bletilla striata*	Urediniospores	23–33 × 15–21	1.9–3.0			
Coleosporiaceae	*Coleosporium*	*zanthoxyli*	HGUP21066-HGUP21072, HGUP21203	*Zanthoxylum bungeanum*, *Z. armatum*	Urediniospores	20–32 × 15–25	1.5–2.4			
Coleosporiaceae	*Coleosporium*	*phellodendri*	HGUP21075-HGUP21076	*Phellodendron amurense*	Urediniospores	22–28 × 20–24	2.6–3.7			
Coleosporiaceae	*Coleosporium*	*perillae*	HGUP21077-HGUP21078	*Perilla frutescens*	Urediniospores	19–25 × 15–18	1.6–2.1			

Table 3 Continued.

Rust Family-	**Genus**	**Species**	**Specimens**	**Host**	**Spore type**	**Size (µm)**	**Wall (µm)**	**Paraphyses (µm)**	**Pedicels (µm)**	**Notes**
Coleosporiaceae	*Coleosporium*	*plectranthi*	HGUP21079	*Isodon amethystoides*	Urediniospores	15–24 × 13–17	1.2–1.9			
Coleosporiaceae	*Coleosporium*	*euodiae*	HGUP21073-HGUP21074	*Tetradium ruticarpum*	Urediniospores	25–30 × 22–28	1.8–2.4			
Coleosporiaceae	*Coleosporium*	*paederiae*	HGUP21083-HGUP21085	*Paederia foetida*	Urediniospores	19–27 × 12–17	1.6–2.4			
Chaconiaceae	*Mikronegeria*	*mucunae-sempervirensii*	HGUP21043-HGUP21045	*Mucuna sempervirens*	Urediniospores	15–27 × 11–17	1–1.4			sp. new
Gymnosporangiaceae	*Gymnosporangium*	*asiaticum*	HGUP21086-HGUP21095	*Pyrus* sp., *Malus* sp., *Chaenomeles speciosa*	Spermogonia	180–250				
					Aeciospores	14–22 × 13–21	1.1–2.4			
Melampsoraceae	*Melampsora*	*babylonicae*	HGUP21117-HGUP21118	*Salix babylonica*	Urediniospores	19–28 × 12–18	1.9–2.5	44–50 × 15–21		sp. new
Melampsoraceae	*Melampsora*	*hypericorum*	HGUP21119-HGUP21121	*Hypericum patulum*	Urediniospores	13–22 × 11–16	1.2–1.8	43–48 × 10–17		
Phakopsoraceae	*Phakopsora*	*causonise-mollisii*	HGUP21112-HGUP21114	*Causonis mollis*	Urediniospores	15–27 × 11–17	1–1.5			sp. new
Phakopsoraceae	*Phakopsora*	*parthenocissuse-tricuspidatae*	HGUP21115-HGUP21116	*Parthenocissus tricuspidata*	Urediniospores	18–27 × 12–16	1.2–1.7	30–55 × 6–15		sp. new
Pucciniastraceae	*Pucciniastrum*	*anaphalise-sinicae*	HGUP21108-HGUP21109	*Anaphalis sinica*	Urediniospores	23–28 × 14–23	1.0–1.4			sp. new
Pucciniastraceae	*Pucciniastrum*	*novembere*	HGUP21110-HGUP21111	*Boehmeria nivea*	Urediniospores	14–24 × 10–20	1–1.9			sp. new
Tranzscheliaceae	*Tranzschelia*	*discolor*	HGUP21105-HGUP21107	*Prunus persica*	Urediniospores	31–41 × 10–17	1.5–2.5	36–46 × 15–20		
Uredinineae incertae sedis	*Nyssopsora*	*araliae-elataii*	HGUP21098-HGUP21100	*Aralia elata*	Aeciospores	15–21 × 12–17	0.6–1.3			sp. new
Uredinineae incertae sedis	*Nyssopsora*	*koelreuteriae*	HGUP21103-HGUP21104	*Eleutherococcus trifoliatus*	Aeciospores	10–15 × 6–9	0.6–1.2			
Uredinineae incertae sedis	*Nyssopsora*	*cedrelae*	HGUP21101-HGUP21102	*Toona sinensis*	Urediniospores	17–22 × 15–20	2–3			
Uredinineae incertae sedis	*Peridiopsora*	*mori*	HGUP21096-HGUP21097	*Morus alba*	Aeciospores	10–14 × 7–12	0.6–1.2			
Pileolariaceae	*Pileolaria*	*klugkistiana*	HGUP21262-HGUP21263	*Rhus chinensis*	Urediniospores	19–31 × 19–22 µm	1.2–2.1			
					Immature teliospores	20–24 × 16–20 µm	2.2–2.8		20–70	

Distribution of rust pathogenic fungi

Over 300 plant samples with typical rust symptoms were collected from 33 counties in nine cities of Guizhou Province, including Guiyang, Zunyi, Duyun, Tongren, Liupanshui, Bijie, Kaili, Anshun, and Xingyi (Fig. 114). Guiyang and Duyun, Guizhou Province We collected more samples in Guiyang and Duyun, Guizhou Province, followed by Zunyi and Liupanshui. We speculated it may be related to geography and climate. We found that three genera, *Puccinia*, *Phragmidium* and *Coleosporium*, are distributed in multiple places. These probably indicate the abundant species and stronger environmental adaptability of *Puccinia* spp., *Phragmidium* spp. and *Coleosporium* spp.

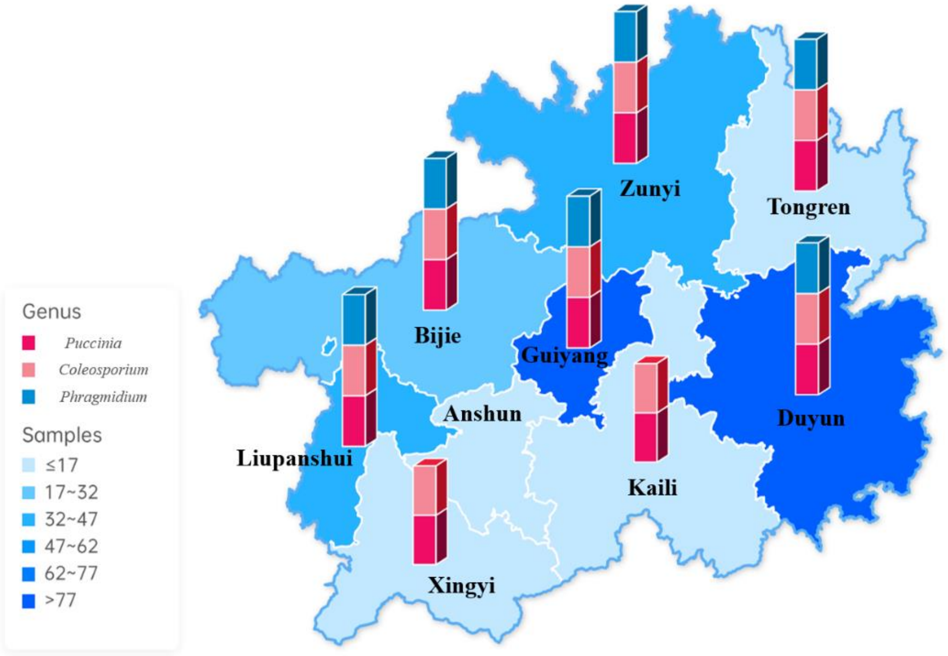

Figure 114 – Distribution of collecting sites.

Hosts diversity of rust fungi

Almost all families of plants, from ferns, gymnosperms to angiosperms are hosts of rust fungi (Kolmer et al. 2009, Fernandez et al. 2013). In this study, rust samples came from 99 host plants in 33 families, mainly angiosperms. The dominant host plant order was Rosales (26.4%); the dominant families were Rosaceae (21.9%) and Asteraceae (11.4%), Fabaceae (9.6%), Poaceae (9.4%), Rutaceae (4.8%), Polygonaceae (4.0%), Lamiaceae (3.6%); the dominant genera were *Rubus* (9.0%) and *Rosa* (6.0%). These findings are consistent with the fact that rust species have a wide range of hosts (Aime et al. 2018, Aime & McTaggart 2021, Zhao et al. 2021). Wang et al. (2015) reported that there were more than 35000 species of higher plants in 454 families, 3818 genera in China. It is estimated that 1000 to 9000 of them may support rust diseases (Zhao et al. 2021). Xiong & Cao (2017) recorded 10134 species of higher plants in 353 families and 2131 genera in Guizhou Province. According to the number of rust species in given area may equate to about 5–25% of plant species (Hennen & McCain 1993). These probably indicate the host universality (about 506–2533 host plants) of rust fungi in Guizhou Province of China.

Despite rust fungi often being quite host specific, some host plants were infected by more than one genus/species of rust while some genera/species of rust were found in different hosts. In the present study, *Puccinia*, *Phragmidium* and *Coleosporium*, were found to have the most species. *Puccinia* species were found on 18 families, Poaceae, Fabaceae, Asteraceae, Polygonaceae, Apiaceae, Lamiaceae, Plantaginaceae, Violaceae, Iridaceae, Amaryllidaceae, Liliaceae, Convolvulaceae, Gentianaceae, Araceae, Oxalidaceae, Caprifoliaceae, Cannaceae and Saxifragaceae (Table 3) in this study. *Phragmidium* species often caused severe rust diseases in

Rosaceae plants (*Rosa*, *Rubus*, *Potentilla*, *Sanguisorba*, *Duchesnea* and *Acaena*) (Cummins & Hiratsuka 2003, Maier et al. 2003, Yun et al. 2011, Pscheidt & Rodriguez 2016, Liu et al. 2018, 2019, 2020). Most species of *Coleosporium* are heteroecious, causing rust disease in *Pinus* spp., also damaging other woody and herbaceous plants, comprising Lamiaceae, Compositae, Orchidaceae, Ranunculaceae, Rubiaceae or other plants (Dai 1979, You et al. 2010, Zhuang et al. 2012, 2021, McTaggart & Aime 2018, Song 2019, Zhao et al. 2021). These details can be found in Table 3.

Relationship between rust fungi and their hosts

Rust host plant specificity is widely accepted (Cummins & Hiratsuka 2003, Zhuang et al. 1998, 2003, 2005, 2012, 2021, Zhao et al. 2014, 2021), and identification of the host often provides assistances for identification of the rust fungi.

Nevertheless, in order to adapt to the environment, rust pathogens or other parasitic organisms mutate or recombine so that they can infect new hosts. This adaptation is called “host jumping”, a term proposed by Hart (1988), as being the driving force for the diversity of rust fungi. Aime (2006) reported that the phylogenetic relationship among rust fungi at the family level was related to their hosts. McTaggart et al. (2016) also believed that host transfer determined the diversity of rust fungi. According to the host coordination analysis, Aime et al. (2018) proposed that the host relationship of the rust life cycle could better reflect the relationship between the rust fungi. Accordingly, we also found that there were rust taxa belonging to different genera but in the same hosts (Zhuang et al. 2021, Sun et al. 2022), and one rust species was able to parasitize different plants (Liu et al. 2018). For example, *Coleosporium asterum* can be found on two different plants (*Aster indicus* and *A. ageratoides*), and *Phragmidium potentilla* can be found on over twenty plants (*Potentilla anglica*, *P. chinensia*, *P. chinensis* var. *lineariloba*, *P. chrysantha*, *P. conferta*, *P. griffithii*, *P. kleiniana*, *P. longifolia*, *P. multicaulis*, *P. multifida*, *P. nivea*, *P. pensylvanica*, *P. potaninii*, *P. recta*, *P. reptans*, *P. sericea*, *P. simulatrix*, *P. supine*, *P. tabernaemontani*, *P. verticillaris*, *P. virgate*) (Kakishima et al. 1986, Yun et al. 2011, Khouader et al. 2012, Zhuang et al. 2012, Liu et al. 2018). Alternatively, *Puccinia plectranthi* and *Coleosporium plectranthi* with different stages can parasitize the same host plant, *Isodon amethystoides*. *Erysiphe* powdery mildew fungi also exhibit a similar phenomenon. For example, *Erysiphe betulina* can be found on three different plants (*Betula platyphylla*, *B. ermanii* and *B. grossa*) (Takamatsu et al. 2015, Liu et al. 2017), or *E. cruciferarura* and *E. arabidis* can infect the Brassicaceae plants (Chen & Zheng 1984).

Aime et al. (2018) suggested that coevolution could be responsible for the patterns seen between rust fungi and their hosts. Up to now, however, the reaction mechanism of rust species to realize large-scale jump among diverse host plants is not clear. Based on previous study, we believe that the development of genomics will gradually reveal the interaction between rust fungi and their hosts.

ACKNOWLEDGEMENTS

This research is supported by the following projects: National Natural Science Foundation of China (No. 31972222), Program of Introducing Talents of Discipline to Universities of China (111 Program, D20023), Talent project of Guizhou Science and Technology Cooperation Platform ([2017]5788-5, [2019]5641, [2019]13), Guizhou Science, Technology Department of International Cooperation Base project ([2018]5806), the project of Guizhou Provincial Education Department ([2020]001), and Guizhou Science and Technology Innovation Talent Team Project ([2020]5001). Yu LF would like to thank Yunnan Province Science and Technology Talent and Platform Plan Construction Project (2018DH011); Science and Technology Plan of Yunnan Provincial Department of Science and Technology – Local University Joint Special Project (202001BA070001-187); Central Guiding Local Science and Technology Development Fund Project (202207AB11007); Lincang Science and Technology Innovation Team (202204AC100001-TD01).

REFERENCES

Aime MC. 2006 – Toward resolving family–level relationships in rust fungi (Uredinales). Mycoscience 47, 112–122.

Aime MC, McTaggart AR. 2021 – A higher–rank classification for rust fungi, with notes on genera. Fungal Systematics and Evolution 7, 21–47.

Aime MC, Bell CD, Wilson AW. 2018 – Deconstructing the evolutionary complexity between rust fungi (Pucciniales) and their plant hosts. Studies in Mycology 89, 143–152.

Arthur JC. 1906 – Eine auf die Struktur und Entwicklungsgeschichte begründete Klassifikation der Uredineen. Resultats Scientifiques du Congres International de Botanique Vienne 1905, 331–348.

Baiswar P, Ngachan SV, Chandra S. 2014 – Identification of *Nyssopsora thwaitesii* on *Schefflera* in northeast India. Australasian Plant Disease Notes 9, 124.

Barclay A. 1890 – A descriptive list of the Uredineae occuring in the neighbourhood of Simla (Western Himalya). Pt. III. Journal of the Asiatic Society of Bengal 59(2, no. 2), 75–112.

Beenken L, Zoller S, Berndt R. 2012 – Rust fungi on Annonaceae II: the genus *Dasyspora* Berk. & M.A. Curtis. Mycologia 104, 659–681.

Berndt R. 2009 – New species of rust fungi (Uredinales) from South Africa and observations about already known species. Mycological Progress 8, 99–114.

Camargo JA. 1992 – Can dominance influence stability in competitive interactions? Oikos 64, 605–609.

Carbone I, Kohn LM. 1999 – A method for designing primer sets for speciation studies in filamentous ascomycetes. Mycologia 91, 553–556.

Carnegie AJ, Lidbetter JR, Walker J, Horwood MA et al. 2010 – *Uredo rangelii*, a taxon in the guava rust complex, newly recorded on Myrtaceae in Australia. Australasian Plant Pathology 39, 463–466.

Castagne L. 1842 – Observations sur quelques plantes acotylédonées de la famille des Urédinées et dans les sous–tribus des Nemasporées et des Aecidinées, recueillies dans le Dep. des Bouches–du–Rhône 1, 1–35.

Chen GQ, Zheng RY. 1984 – Taxonomic study on the genus *Erysiphe* of China IV.A new species on Cruciferae. Mycosystema 1, 1–4.

Chen YY, Dissanayake AJ, Liu ZY, Liu JK. 2020 – Additions to karst fungi 4: *Botryosphaeria* spp. associated with woody hosts in Guizhou province, China including *B. guttulata* sp. nov. Phytotaxa 454, 186–202.

Chu RT, Dou ZP, He W, Zhang Y. 2021 – Two novel species of *Botryosphaeria* causing stem canker of blueberries from China. Mycosystema 40, 473–486.

Crane PE, Peterson RS. 2007 – *Mikronegeria fuchsiae* sp. nov., a rust fungus on *Fuchsia* and *Phyllocladus* in New Zealand. New Zealand Journal of Botany 45(4), 707–713.

Cummins GB. 1971 – The rust fungi of cereals, grasses and bamboos. New York: Springer–Verlag.

Cummins GB, Hiratsuka Y. 2003 – Illustrated genera of rust fungi. 3 rd Edn., American Phytopathological Society Press 222–223.

Dai FL. 1979 – China fungus confluence. Science Press, Beijing, China 1527.

De Carvalho JAA, Hennen JF. 2009 – *Maravalia perae,* a new species of rust fungus on *Pera* from Brazil. Mycologia 101(2), 239–242.

De Carvalho JAA, Rios EE, Piepenbring M. 2014 – A new species of *Nyssopsora* (Pucciniales) from Panama. Nova Hedwigia 99, 1–2, 65–70.

Dean R, Van Kan JA, Pretorius ZA, Hammond–Kosack KE et al. 2012 – The top 10 fungal pathogens in molecular plant pathology. Molecular Plant Pathology 13, 414–430.

Dietel P. 1890 – Uredineen aus dem Himalaya. Hedwigia 29, 259–270.

Dietel P. 1895 – Einige neue exotische Pilze. Hedwigia 34, 291–292.

Dietel P, Neger FW. 1900 – Uredinaceae chilenses III. Botanische Jahrbücher für Systematik Pflanzengeschichte und Pflanzengeographie 27, 1–16.

Ebinghaus M, Wingfield MJ, Begerow D, Maier W. 2020 – The genus *Ravenelia* (Pucciniales) in South Africa. Mycological Progress 19, 59–290.

Fernandez D, Talhinhas P, Duplessis S. 2013 – Rust fungi: achievements and future challenges on genomics and host–parasite interactions. Fungal Diversity 11, 316–341.

Gardner ED, Hodges SC. 1989 – The rust fungi (Uredinales) of Hawaii. Pacific Science 43, 41–56.

Hall T, Biosciences I, Carlsbad C. 2011 – BioEdit: an important software for molecular biology. GERF Bulletin Biosciences 2(1), 60−61.

Harkness HW, Cooke MC. 1878 – Californian fungi. Grevillea 7(41), 1–4.

Hart JA. 1988 – Rust fungi and host plant coevolution: do primitive hosts harbor primitive parasites? Cladistics 4, 339–366.

He F, Kakishima M, Sato S. 1990 – Annual sporulation cycle of the bamboo culm rust, *Stereostratum corticioides* on *Pleioblastus simonii* in Tsukuba, Japan. Reports of the Tottori Mycological Institute (Japan) 28, 43–249.

Hennen JF, McCain JW. 1993 – New species and records of Uredinales from the neotropics. Mycologia 85, 970–986.

Hershman DE, Bachi PR, Harmon CL, Harmon PF et al. 2006 – First Report of Soybean Rust caused by *Phakopsora pachyrhizi* on Kudzu (*Pueraria montana* var. *lobata*) in Kentucky. The American Phytopathological Society 96 (6).

Hiratsuka N, Sato S, Katsuya K, Kakishima M et al. 1992 – The rust flora of Japan. Tsukuba Shuppankai, Tsukuba 1–1205.

Hopple JS. 1994 – Phylogenetic investigations in the genus *Coprinus* based on morphological and molecular characters. PhD Thesis, Duke University, North Carolina, USA.

Jayasiri SC, Hyde KD, Ariyawansa HA, Bhat J et al. 2015 – The Faces of Fungi database: fungal names linked with morphology, phylogeny and human impacts. Fungal Diversity 74(1), 3–18.

Jeewon R, Hyde KD. 2016 – Establishing species boundaries and new taxa among fungi: recommendations to resolve taxonomic ambiguities. Mycosphere 7, 1669–1677.

Ji JX, Li Z, Wang Q, Li Y et al. 2017 – Life cycle of *Aecidium klugkistianum* on *Ligustrum* and its new combination, *Puccinia klugkistiana*. Mycoscience 58, 307–311

Ji JX, Li Z, Li Y, Kakishima M. 2019 – Two new species of *Pucciniastrum* producing dimorphic sori and spores from northeast of China. Mycological Progress 18, 529–540.

Ji JX, Li Z, Li Y, Kakishima M. 2020 – Life cycle and taxonomy of *Chrysomyxa succinea* in China and phylogenetic positions of *Caeoma* species on Rhododendron. Forest Pathology 50, e12585

Kakishima M, Sato T, Sato S. 1984 – Notes on two rust fungi, *Pileolaria klugkistiana* and *Nyssopsora cedrelae*. Transactions Mycology Society Japan 25, 355–359.

Kakishima M, Yamaoka Y, Sato S. 1986 – Rust fungi (Uredinales) collected from the Tsukuba botanical garden (i). Annals Tsukuba Botanical Garden 4, 43–59.

Kakishima M, Ji JX, Kasuya T. 2018 – *Puccinia neovelutina* nom. nov., a replaced name for *Aecidium elaeagni* and its new aecial host from Japan. Phytotaxa 336(2), 197–200.

Kalyaanamoorthy S, Minh BQ, Wong TKF, von Haeseler A et al. 2017 – ModelFinder: fast model selection for accurate phylogenetic estimates. Nature Methods 14, 587–589.

Katoh K, Rozewicki J, Yamada KD. 2019 – MAFFT online service: multiple sequence alignment, interactive sequence choice and visualization. Briefings in Bioinformatics 20, 1160–1166.

Katumoto K. 1968 – Notes on the bambusicolous rust fungi with special reference to Japanese species. Bulletin of the Faculty of Agriculture, Yamaguchi University 19, 1135–1158.

Kern FD. 1973 – A revised taxonomic account of *Gymnosporangium*. University Park, Pennsylvania: Pennsylvania State University Press 1–124.

Khouader M, Bammi J, Benkirane R, Ouazzani A et al. 2012 – Bibliographic inventory of Uredinales of Morocco. Journal of Animal and Plant Sciences 1, 1873–1911.

Kolmer JA, Ordonez ME, Groth JV. 2009 – The rust fungi. In: Encyclopedia of life sciences. John Wiley & Sons, Ltd: Chichester.

Kusari P, Kusari S, Spiteller M, Kayser O. 2013 – *Endophytic* fungi harbored in *Cannabis sativa* L.: diversity and potential as biocontrol agents against host plant–specific phytopathogens. Fungal Diversity 60, 137–151.

Larsson A. 2014 – AliView: a fast and lightweight alignment viewer and editor for large datasets. Bioinformatics 30, 3276–3278.

Li GQ, Liu FF, Li JQ, Liu QL et al. 2018 – Botryosphaeriaceae from *Eucalyptus* plantations and adjacent plants in China. Persoonia 40, 63–95.

Li GQ, Slippers B, Wingfield MJ, Chen SF. 2020 – Variation in Botryosphaeriaceae from Eucalyptus plantations in Yunnan Province in southwestern China across a climatic gradient. IMA Fungus 11, 22.

Liu TZ, Wen J, Tian HM, Yang XP. 2017 – Four new records of the powdery mildews in Inner Mongolia. Journal of fungal research 15(02).

Liu Y, Cao B, Tao SQ, Tian GM et al. 2018 – *Phragmidium* species parasitizing species of Rosaceae in Tibet, China, with descriptions of three new species. Mycological Progress 17(8), 967–988.

Liu Y, Ono Y, Kakishima M, Gaforov Y et al. 2019 – Taxonomy and phylogenetic position of *Phragmidium altaicum*, a newly described rust fungus on *Rosa*, based on molecular and morphological data. Phytotaxa 423(3), 187–194.

Liu Y, Liang YM, Ono Y. 2020 – Taxonomic revision of species of *Kuehneola* and *Phragmidium* on *Rosa*, including two new species from China. Mycologia 112(4), 742–752.

Magnus P. 1899 – Über die bei verwandten Arten auftretenden modifikationen der charaktere von Uredineengattungen. Berichte der Deutschen Botanischen Gesellschaft 17, 178–184.

Maier W, Begerow D, Weiss M, Oberwinkler F. 2003 – Phylogeny of the rust fungi: an approach using nuclear large subunit ribosomal DNA sequences. Canadian Journal of Botany 81, 12–23.

Maier W, McTaggart AR, Roux J, Wingfield MJ. 2016 – *Phakopsora myrtacearum* sp. nov., a newly described rust (Pucciniales) on eucalypts in eastern and southern Africa. Plant Pathology 65, 189–195.

Martin LA, Lloyd Evans D, Castlebury LA, Sifundza JT et al. 2017 – *Macruropyxis fulva* sp. nov., a new rust (Pucciniales) infecting sugarcane in southern Africa. Australasian Plant Pathology 46, 63–74.

McTaggart AR, Shivas RG, Nest MA, Roux J et al. 2016 – Host jumps shaped the diversity of extant rust fungi (Pucciniales). The New Phytologist 209(3), 1149–1158.

McTaggart AR, Aime MC. 2018 – The species of *Coleosporium* (Pucciniales) on *Solidago* in North America. Fungal Biology 122(8), 800–809.

Nguyen LT, Schmidt HA, Von Haeseler A, Minh BQ. 2015 – IQ–TREE: a fast and effective stochastic algorithm for estimating maximum–likelihood phylogenies. Molecular Biology and Evolution 32, 268–274.

Okane I, Ando Y, Yamaoka Y, Akib M et al. 2020 – First report of heteroecism in *Stereostratum corticioides*, the causal agent of bamboo culm rust. Mycoscience 61(4), 172–178.

Ono Y. 2012 – *Kuehneola warburgiana* comb. nov. (Phragmidiaceae, Pucciniales), causing witches'brooms on *Rosa bracteata*. Mycotaxon 121(1), 207–213.

Ono Y, Wahyuno D. 2019 – *Phragmidium satoanum*, a new rust pathogen of *Rosa hirtula* in Japan. Mycoscience 60, 237–245.

Pedley KF. 2009 – PCR–based assays for the detection of *Puccinia horiana* on chrysanthemums. Plant Disease 93(12), 1252–1258.

Pei MH, Bayon C, Ruiz C. 2005 – Phylogenetic relationships in some *Melampsora* rusts on Salicaceae assessed using rDNA sequence information. Mycological Research 109 (4), 401–409.

Prasad KV, Yadav BRD, Sullia SB. 1993 – Taxonomic status of rust on mulberry in India. Current Science 65(5), 424–426.

Pscheidt JW, Rodriguez TG. 2016 – Diseases of rose. In: McGovern R, Elmer W (Eds) Handbook of florists' crops diseases. Handbook of Plant Disease Management 1–29.

Raciborski M. 1909a – Über einige javanische Uredineae (Moose). Bulletin International de l'Academie des Sciences de Cracovie Classe des Sciences Mathematiques et Naturelles 3, 266–280.

Raciborski M. 1909b – Parasitische und epiphytische Pilze Javas. Bulletin International de l'Academie des Sciences de Cracovie Classe des Sciences Mathematiques et Naturelles 3, 346–394.

Rehner SA, Buckley E. 2005 – A Beauveria phylogeny inferred from nuclear ITS and EF1–alpha sequences: evidence for cryptic diversification and links to *Cordyceps* teleomorphs. Mycologia 97, 84–98.

Ronquist F, Teslenko M, Mark VD, Ayres P et al. 2012 – MrBayes 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. Systematic Biology 61, 539–542.

Roux J, Greyling I, Coutinho TA, Verleur M. 2013 – The myrtle rust pathogen, *Puccinia psidii*, discovered in Africa. IMA Fungus 4, 155–159.

Scholler M, Abbasi M, Friedrich F. 2014 – *Tranzschelia* in the Americas revisited: two new species and notes on the *Tranzschelia thalictri* complex. Mycologia 106(3), 448–455.

Senanayake IC, Rathnayake AR, Marasinghe DS, Calabon MS et al. 2020 – Morphological approaches in studying fungi: collection, examination, isolation, sporulation and preservation. Mycosphere: Journal of Fungal Biology 11(1), 2678–2754.

Song LS. 2019 – Studies on pathogen identification and disease control of major fungal diseases on *Bletilla striata*. Guizhou University, Guizhou, China.

Sun JE, Zhang Q, Luo WM, Yang YQ et al. 2022 – Four new *Phragmidium* (Phragmidiaceae, Pucciniomycetes) species from Rosaceae plants in Guizhou Province of China. MycoKeys 93, 193–213.

Swofford DL. 2002 – PAUP*: Phylogenetic analysis using parsimony (and other methods), version 4.0 b10. MA: Sinauer Associates. Sunderland, UK.

Sydow H, Sydow P. 1914 – Beitrag zur Kenntnis der parasitischen Pilze der Insel Formosa. Annales Mycologici 12(2), 105–112.

Takamatsu S, Ito Arakawa H, Shiroya Y, Kiss L et al. 2015 – First comprehensive phylogenetic analysis of the genus *Erysiphe* (Erysiphales, Erysiphace) II: the *Uncinula* lineage. Mycologia 107(5), 903–914.

Tao SQ, Cao B, Kakishima M, Liang YM. 2020 – Species diversity, taxonomy, and phylogeny of *Gymnosporangium* in China. Mycologia 179–272.

Thirumalachar MJ, Mundkur BB. 1949 – Genera of rusts II. Indian Phytopathology 2(2):1–52.

Thümen F. 1875 – Fungi Austro – Africani. Flora (Regensburg) 58, 378–380.

Toome M, Aime MC. 2015 – Reassessment of rust fungi on weeping willows in the Americans and description of *Melampsora ferrinii* sp. nov. Plant Pathology 64, 216–224.

Trifinopoulos J, Nguyen LT, von Haeseler A, Minh BQ. 2016 – W-IQ-TREE: a fast-online phylogenetic tool for maximum likelihood analysis. Nucleic Acids Research 44, 232–235.

Vaidya G, Lohman DJ, Meier R. 2011 – SequenceMatrix: Concatenation software for the fast assembly of multi–gene datasets with character set and codon information. Cladistics 27, 171–180.

Van der Auwera G, Chapelle S, De Wächter R. 1994 – Structure of the large ribosomal subunit RNA of *Phytophthora megasperma* and phylogeny of the oomycetes. FEBS Letters 338, 133–136.

Vilgalys R, Hester M. 1990 – Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several *Cryptococcus* species. Journal of Bacteriology 172, 4238–4246.

Vu D, Groenewald M, Vries MD, Stielow B et al. 2019 – Large–scale generation and analysis of filamentous fungal DNA barcodes boosts coverage for kingdom fungi and reveals thresholds for fungal species and higher taxon delimitation. Studies in Mycology 92, 135–154.

Wahyuno D, Kakishima M, Ono Y. 2001 – Morphological analyses of urediniospores and teliospores in seven *Phragmidium* species parasitic on ornamental roses. Mycoscience 42(6), 519–533.

Wang LS, Jia Y, Zhang XC, Qin HN. 2015 – Overview of higher plant diversity in China. Biodiversity 23, 217–224.

Wei SX. 1988 – A taxonomic study of the genus *Phragmidium* of China. Junwu Xuebao 1, 179–210.

Wilson AW, Aime MC. 2014 – The rose rust fungus, *Phragmidium tuberculatum*, is widespread in the Americas: First reports from California, Oregon, Massachusetts, and Honduras. Plant Disease 98(11), 1581.

Winter G. 1886 – Fungi australienses. Revue Mycologique Toulouse 8, 207–213.

Wood AR, Crous PW. 2005 – Morphological and molecular characterization of *Endophyllum* species on perennial asteraceous plants in South Africa. Mycological Research 109(4), 387–400.

Wu QZ, He MH, Liu TZ, Hu HM et al. 2023 – Rust Fungi on medicinal plants in Guizhou province with descriptions of three new species. Journal of fungi 9, 953.

Xiong YX, Cao W. 2017 – Review of researches on plant taxonomy in Guizhou. Journal of Mountain Agriculture and Biology 36(1), 1–11.

Xu Q, Bai L. 2023 – Occurrence of Leaf Rust on *Hypericum przewalskii* caused by *Melampsora kusanoi* in China. Plant Disease.

Yang T, Chang W, Cao B, Tian CM et al. 2015 – Two new *Phragmidium* species identified on *Rosa* plants native to China. Phytotaxa 217, 182–190.

You CJ, Liang YM, Li J, Tian CM. 2010 – A new rust species of *Coleosporium* on *Ligularia fischeri* from China. Mycotaxon 111, 233–239.

Yun HY, Minnis AM, Kim YH, Castlebury LA et al. 2011 – The rust genus *Frommeëlla* revisited: A later synonym of *Phragmidium* after all. Mycologia 103(6), 1451–1463.

Zhang D, Gao F, Jakovlić I, Zou H et al. 2020 – PhyloSuite: an integrated and scalable desktop platform for streamlined molecular sequence data management and evolutionary phylogenetics studies. Molecular ecology resources 20(1), 348–355.

Zhang H, Wei TP, Li LZ, Luo MY et al. 2021 – Multigene Phylogeny, Diversity and antimicrobial potential of endophytic Sordariomycetes from *Rosa roxburghii*. Frontiers in Microbiology 12, 755–919.

Zhao P, Tian CM, Yao YJ, Wang Q et al. 2014 – *Melampsora salicis–sinicae* (Melam *Rosa roxburghii* psoraceae, Pucciniales), a new rust fungus found on willows in China. Mycoscience 55, 390–399.

Zhao P, Wang QH, Tian CM, Kakishima M. 2015 – Integrating a numerical taxonomic method and molecular phylogeny for ppecies delimitation of *Melampsora* Species (Melampsoraceae, Pucciniales) on willows in China. PLoS ONE 10(12), e0144883.

Zhao P, Kakishima M, Wang Q, Cai L. 2017 – Resolving the *Melampsora epitea* complex. Mycologia 109(3), 391–407.

Zhao P, Zhang ZF, Hu DM, Tsui KM et al. 2021 – Contribution to rust flora in China I, tremendous diversity from natural reserves and parks. Fungal Diversity 5, 1–58.

Zhuang JY, Wei SX, Wang YC. 1998 – Flora Fungorum Sinicorum. Vol 10. Uredinales (I). Science Press, Beijing, China.

Zhuang JY, Wei SX, Wang YC. 2003 – Flora Fungorum Sinicorum. Vol 19. Uredinales (II). Science Press, Beijing, China.

Zhuang JY, Wei SX, Wang YC. 2005 – Flora Fungorum Sinicorum. Vol 25. Uredinales (III). Science Press, Beijing, China.

Zhuang JY, Wei SX, Wang YC. 2012 – Flora fungorum Sinicorum. Vol. 41. Uredinales IV. Science Press, Beijing, China.

Zhuang JY, Wei SX, Wang YC. 2021 – Flora Fungorum Sinicorum. Vol 62. Uredinales (V). Science Press, Beijing, China.

Supplementary materials

Supplementary Table 1 Hosts of the rust fungi.

Family	Host	Specimens	Genus of rust fungi
Rosaceae	*Rubus parvifolius*	HGUP21035, HGUP21038	*Phragmidium*
Rosaceae	*Ru. adenophorus*	HGUP21039	*Phragmidium*
Rosaceae	*Ru. coreanus*	HGUP21029-HGUP21030	*Phragmidium*
Rosaceae	*Ru. alceifolius*	HGUP21156-HGUP21157	*Gerwasia*
Rosaceae	*Ru. setchuenensis*	HGUP21167-HGUP21168	*Gerwasia*
Rosaceae	*Ru. buergeri*	HGUP21169-HGUP21171	*Gerwasia*
Rosaceae	*Ru. reflexus*	HGUP21166	*Gerwasia*
Rosaceae	*Ru. lambertianus*	HGUP21163-HGUP21165	*Hamaspora*
Rosaceae	*Ru. parkeri*	HGUP21159-HGUP21162	*Hamaspora*
Rosaceae	*Ro. roxburghii*	HGUP21025-HGUP21027	*Phragmidium*
Rosaceae	*Rosa* sp.	HGUP21028	*Phragmidium*
Rosaceae	*Ro. multiflora*	HGUP21158	*Phragmidium*
Rosaceae	*Ro. kwangtungensis*	HGUP21154-HGUP21155	*Phragmidium*
Rosaceae	*Ro. laevigata*	HGUP21036-HGUP21037	*Phragmidium*
Rosaceae	*Ro. cymosa*	HGUP21147-HGUP21153	*Phragmidium*
Rosaceae	*Potentilla freyniana*	HGUP21033, HGUP21040	*Phragmidium*
Rosaceae	*P. kleiniana*	HGUP21034	*Phragmidium*
Rosaceae	*Duchesnea indica*	HGUP21031- HGUP21032	*Phragmidium*
Rosaceae	*Chaenomeles speciosa*	HGUP21090-HGUP21092	*Gymnosporangium*
Rosaceae	Pear	HGUP21086-HGUP21089	*Gymnosporangium*
Rosaceae	*Malus pumila*	HGUP21093-HGUP21095	*Gymnosporangium*
Rosaceae	*Prunus persica*	HGUP21105-HGUP21107	*Tranzschelia*
Rhamnaceae	*Berchemia floribunda*	HGUP21137-HGUP21138	*Endophyllum*
Rhamnaceae	*Rhamnus globosa*	HGUP21242-HGUP21243	*Endophyllum*
Rhamnaceae	*Rhamnella franguloides*	HGUP21244-HGUP21245	*Endophyllum*
Moraceae	*Morus alba*	HGUP21096-HGUP21097	*Peridiopsora*
Urticaceae	*Boehmeria nivea*	HGUP21110-HGUP21111	*Pucciniastrum*
Elaeagnaceae	*Elaeagnus pungens*	HGUP21217	*Endophyllum*
Asteraceae	*Youngia japonica*	HGUP21210-HGUP21211	*Puccinia*
Asteraceae	*Taraxacum mongolicum*	HGUP21208-HGUP21209	*Puccinia*
Asteraceae	*Lactuca indica*	HGUP21214-HGUP21216	*Puccinia*
Asteraceae	*Crepidiastrum sonchifolium*	HGUP21212-HGUP21213	*Puccinia*
Asteraceae	*Senecio scandens*	HGUP21198	*Puccinia*
Asteraceae	*Carpesium abrotanoides*	HGUP21080-HGUP21082	*Coleosporium*
Asteraceae	*Aster ageratoides*	HGUP21055-HGUP21061	*Coleosporium*
Asteraceae	*A. indicus*	HGUP21062-HGUP21063	*Coleosporium*
Asteraceae	*Bidens pilosa*	HGUP21037	*Uromyces*
Asteraceae	*Anaphalis sinica*	HGUP21108-HGUP21109	*Pucciniastrum*
Poaceae	*Alopecurus aequalis*	HGUP21231	*Puccinia*
Poaceae	*Zea mays*	HGUP21248-HGUP21252	*Puccinia*
Poaceae	*Lolium perenne*	HGUP21240-HGUP21241	*Puccinia*
Poaceae	*Setaria plicata*	HGUP21189	*Puccinia*
Poaceae	*Imperata cylindrica*	HGUP21176-HGUP21177	*Puccinia*
Poaceae	*Indocalamus latifolius*	HGUP21239	*Puccinia*
Poaceae	*Oplismenus undulatifolius*	HGUP21205	*Puccinia*
Fabaceae	*Vicia faba*	HGUP21122-HGUP21126	*Uromyces*
Fabaceae	*Phaseolus vulgaris*	HGUP21130-HGUP21134	*Uromyces*
Fabaceae	*Vigna unguiculata*	HGUP21135-HGUP21136	*Uromyces*
Fabaceae	*Trifolium repens*	HGUP21127-HGUP21129	*Uromyces*
Fabaceae	*Arachis hypogaea*	HGUP21199-HGUP21200	*Puccinia*

Supplementary Table 1 Continued.

Family	Host	Specimens	Genus of rust fungi
Fabaceae	*Mucuna sempervirens*	HGUP21043-HGUP21045	*Mikronegeria*
Fabaceae	*Pueraria montana* var. *lobata*	HGUP21259-HGUP21261	–
Fabaceae	*Rhynchosia volubilis*	HGUP21257-HGUP21258	–
Rutaceae	*Tetradium ruticarpum*	HGUP21073-HGUP21074	*Coleosporium*
Rutaceae	*Zanthoxylum bungeanum*	HGUP21066-HGUP21067, HGUP21069-HGUP21072, HGUP210203	*Coleosporium*
Rutaceae	*Z. armatum*	HGUP21068	*Coleosporium*
Rutaceae	*Phellodendron amurense*	HGUP21075-HGUP21076	*Coleosporium*
Meliaceae	*Toona sinensis*	HGUP21101-HGUP21102	*Nyssopsora*
Anacardiaceae	*Rhus chinensis*	HGUP21262-HGUP21263	–
Polygonaceae	*Pleuropterus multiflorus*	HGUP21186-HGUP21188	*Puccinia*
Polygonaceae	*Rumex nepalensis*	HGUP21190-HGUP21192, HGUP21181, HGUP21270	*Puccinia*
Polygonaceae	*Persicaria posumbu*	HGUP21222-HGUP21223	*Puccinia*
Polygonaceae	*P. capitata*	HGUP21193-HGUP21194	*Puccinia*
Polygonaceae	Unknown	HGUP21224	*Puccinia*
Apiaceae	*Cryptotaenia japonica*	HGUP21195-HGUP21197	*Puccinia*
Apiaceae	*Oenanthe javanica*	HGUP21184-HGUP21185	*Puccinia*
Araliaceae	*Aralia elata*	HGUP21098-HGUP21100	*Nyssopsora*
Araliaceae	*Eleutherococcus \trifoliatus*	HGUP21103-HGUP21104	*Nyssopsora*
Ranunculaceae	*Clematis buchananiana*	HGUP21053	*Coleosporium*
Ranunculaceae	*C. florida*	HGUP21046-HGUP21047	*Coleosporium*
Ranunculaceae	*C. brevicaudata*	HGUP21054	*Coleosporium*
Ranunculaceae	*C. dasyandra*	HGUP21050-HGUP21052	*Coleosporium*
Lamiaceae	*Isodon amethystoides*	HGUP21079, HGUP21234, HGUP21141	*Coleosporium*, *Puccinia*
Lamiaceae	*Perilla frutescens*	HGUP21077-HGUP21078	*Coleosporium*
Lamiaceae	*Mentha canadensis*	HGUP21277-HGUP21278	*Puccinia*
Lamiaceae	Unknown	HGUP21145-HGUP21146	–
Plantaginaceae	*Plantago asiatica*	HGUP21253-HGUP21254	*Puccinia*
Salicaceae	*Salix babylonica*	HGUP21117-HGUP21118	*Melampsora*
Violaceae	*Viola diffusa*	HGUP21204	*Puccinia*
Iridaceae	*Iris tectorum*	HGUP21201-HGUP21202	*Puccinia*
Orchidaceae	*Bletilla striata*	HGUP21064-HGUP21065	*Coleosporium*
Amaryllidaceae	*Allium sativum*	HGUP21225-HGUP21229	*Puccinia*
Liliaceae	*Hemerocallis fulva*	HGUP21218-HGUP21220	*Puccinia*
Liliaceae	*Smilax china*	HGUP21048-HGUP21049	*Coleosporium*
Vitaceae	*Causonis mollis*	HGUP21112-HGUP21114	*Phakopsora*
Vitaceae	*Parthenocissus tricuspidata*	HGUP21115-HGUP21116	*Phakopsora*
Convolvulaceae	*Calystegia hederacea*	HGUP21182-HGUP21183	*Puccinia*
Convolvulaceae	*Ipomoea nil*	HGUP21178-HGUP21180	*Puccinia*
Rubiaceae	*Paederia foetida*	HGUP21142-HGUP21144; HGUP21083-HGUP21085	*Macruropyxis*, *Puccinia*
Gentianaceae	*Gentiana macrophylla*	HGUP21206-HGUP21207	*Puccinia*
Araceae	*Epipremnum aureum*	HGUP21255-HGUP21256	*Macruropyxis*
Oxalidaceae	*Oxalis corniculata*	HGUP21232-HGUP21233, HGUP21235-HGUP21236	*Puccinia*
Caprifoliaceae	*Patrinia scabiosifolia*	HGUP21221	*Puccinia*
Cannaceae	*Canna indica*	HGUP21172-HGUP21173	*Puccinia*
Saxifragaceae	*Dichroa febrifuga*	HGUP21237-HGUP21238	*Puccinia*
–	Unknown	HGUP21246-HGUP21247	*Endophyllum*

Supplementary Table 2 Specimens and GenBank accession numbers of rust isolates used to construct phylogenetic tree of Pucciniaceae. The newly generated specimens are indicated in bold.

Species	**Voucher specimens**	**Host**	**Country**	**GenBank No.**	
				ITS	**LSU**
Endophyllum berchemiae-floribundae	**HGUP21138**	***Berchemia floribunda***	**China**	**OR470071**	**OR528381**
E. dichroae	**HGUP21237**	***Dichroa febrifuga***	**China**	**OR470069**	**–**
E. dichroae	**HGUP21238**	***Dichroa febrifuga***	**China**	**OR470070**	**–**
E. dimorphothecae	PREM 57919	Perennial asteraceous plants	South Africa	AY652759	–
E. dimorphothecae	PREM 57918	Perennial asteraceous plants	South Africa	AY652758	–
E. elaeagni-latifoliae	**HGUP21217**	***Elaeagnus pungens***	**China**	**OR470077**	**–**
Endophyllum elytropappi	PREM 57917	Perennial asteraceous plants	South Africa	AY652761	–
E. elytropappi	PREM 57915	Perennial asteraceous plants	South Africa	AY652760	–
E. maiense	**HGUP21246**	**Unknown**	**China**	**OR470072**	**OR528382**
E. maiense	**HGUP21247**	**Unknown**	**China**	**OR470073**	**OR528383**
E. osteospermi	PREM 57902	Perennial asteraceous plants	South Africa	AY652757	–
E. osteospermi	PREM 57898	Perennial asteraceous plants	South Africa	AY652756	–
E. osteospermi	PREM 57893	Perennial asteraceous plants	South Africa	AY652755	–
E. osteospermi	PREM 57888	Perennial asteraceous plants	South Africa	AY652754	–
E. osteospermi	PREM 57887	Perennial asteraceous plants	South Africa	AY652753	–
E. osteospermi	PREM 57895	Perennial asteraceous plants	South Africa	AY652752	–
E. osteospermi	PREM 57893.2	Perennial asteraceous plants	South Africa	AY652751	–
E. osteospermi	PREM 57893.1	Perennial asteraceous plants	South Africa	AY652750	–
E. rhamnellae-franguloidese	**HGUP21244**	***Rhamnella franguloides***	**China**	**OR470078**	**OR528387**
E. rhamnellae-franguloidese	**HGUP21245**	***Rhamnella franguloides***	**China**	**OR470079**	**OR528388**
E. rhamnusii-globosae	**HGUP21242**	***Rhamnus globosa***	**China**	**OR470080**	**OR528389**
E. rhamnusii-globosae	**HGUP21243**	***Rhamnus globosa***	**China**	**OR470081**	**OR528390**
Macruropyxis diversii	**HGUP21142**	***Paederia foetida***	**China**	**OR470075**	**OR528385**
M. diversii	**HGUP21143**	***Paederia foetida***	**China**	**OR470076**	**OR528386**
M. diversii	**HGUP21144**	***Paederia foetida***	**China**	**OR470074**	**OR528384**
M. diversii	**HGUP21255**	***Epipremnum aureum***	**China**	**OR470082**	**OR528391**
M. diversii	**HGUP21256**	***Epipremnum aureum***	**China**	**OR470083**	**OR528392**
M. fraxini	ZT Myc 56551	*Fraxinus platypoda*	Japan	KP858144	KP858145
M. fulva	Rust_isolate_P7	*Saccharum* hybrid cultivar N41	South Africa	JX036026	–
M. fulva	Rust_isolate_M9	*Saccharum* hybrid cultivar N41	South Africa	JX036027	–
Uromyces betae	BPI 910289	*Beta* sp.	–	–	KY764187
U. bidenticola	BRIP 57564	*Bidens pilosa*	Australia	–	KX999897
U. bidenticola	**HGUP21037**	***Bidens Pilosa***	**China**	**–**	**OR528401**
U. chenopodii-fruticosi	K(M)107793	*Suaeda maritima*	United Kingdom	–	MT053261
U. euphorbiae-corniculati	F561	*Lotus corniculatus*	–	AF180164	–
U. euphorbiae-corniculati	F425	–	–	AF180158	–

Supplementary Table 2 Continued.

Species	Voucher specimens	Host	Country	GenBank No.	
				ITS	LSU
U. galegae	BPI 863535	*Galega officinalis*	Turkey	DQ250133	–
U. geranii	BRIP 60100	*Geranium potentilloides*	Australia	–	KX999898
U. hawksworthii	UB:22875	*Passovia ovata*	Brazil	KR821138	KR821140
U. hawksworthii	UB:22382	*Passovia ovata*	Brazil	KR821137	KR821139
U. orientalis	BRIP 60934	*Indigofera linifolia*	Australia	KX999899	–
U. pisi	E272	*Euphorbia cyparissias*	–	AF180191	–
U. pisi	F427	*Lathyrus pratensis*	–	AF180159	–
U. pisi-sativi	BRIP 60151	*Genista monspessulana*	Australia	–	KX999900
U. poae	TUB 14998	*Ranunculus ficaria*	–	–	DQ917744
U. punctatus	F555	*Euphorbia cyparissias*	–	AF180163	–
U. punctatus	F421	*Astragalus glycyphyllos*	–	AF180156	–
U. rebeccae	FDWSRU 15-022	*Suaeda californica*	USA	–	MN386999
U. salsolae	BRIP 57696	*Kali australe*	Australia	–	KX999901
U. scutellatus	E270	*Euphorbia cyparissias*	–	AF180199	–
U. scutellatus	E269	*Euphorbia cyparissias*	–	AF180198	–
U. striatus	BRIP 61228	*Melilotus indicus*	Australia	—	KX999903
U. striatus	F430	*Medicago lupulina*	–	AF180160	–
U. striatus	F456	*Trifolium arvense*	–	AF180161	–
U. striolatus	E405	*Euphorbia cyparissias*	–	AF180201	–
U. tenuicutis	BRIP 60012	*Sporobolus africanus*	Australia	–	KX999904
U. trifolii	–	–	Colombia	–	GU936634
U. trifolii-repentis	BRIP 57653	*Trifolium repens*	Australia	–	KX999905
U. trifolii-repentis	**HGUP21127**	***Trifolium repens***	**China**	**OR470087**	**–**
U. trifolii-repentis	**HGUP21128**	***Trifolium repens***	**China**	**OR470086**	**OR528396**
U. trifolii-repentis	**HGUP21129**	***Trifolium repens***	**China**	**OR470088**	**OR528397**
U. viciae-fabae	BRIP:59246	*Vicia faba*	Australia	–	KM249865
U. viciae-fabae	**HGUP21122**	***Vicia faba***	**China**	**OR470084**	**OR528393**
U. viciae-fabae	**HGUP21123**	***Vicia faba***	**China**	**OR461539**	**OR528395**
U. viciae-fabae	**HGUP21124**	***Vicia faba***	**China**	**OR470085**	**OR528394**
U. viciae-fabae	**HGUP21125**	***Vicia faba***	**China**	**OR461540**	**–**
U. viciae-fabae	**HGUP21126**	***Vicia faba***	**China**	**OR461541**	**–**
U. vignae	BRIP 60213	*Vigna marina*	Australia	–	KX999906
U. vignae	**HGUP21130**	***Phaseolus vulgaris***	**China**	**OR470089**	**OR528398**
U. vignae	**HGUP21131**	***Phaseolus vulgaris***	**China**	**OR470090**	**OR528399**
U. vignae	**HGUP21132**	***Phaseolus vulgaris***	**China**	**OR470091**	**–**
U. vignae	**HGUP21133**	***Phaseolus vulgaris***	**China**	**OR470092**	**OR528400**
U. vignae	**HGUP21134**	***Phaseolus vulgaris***	**China**	**OR470093**	**–**
U. vignae-siensis	**HGUP21135**	***Vigna unguiculata***	**China**	**OR470094**	**OR528402**
U. vignae-siensis	**HGUP21136**	***Vigna unguiculata***	**China**	**OR470095**	**OR528403**
Melampsora epiphylla	TSH-R3884	*Willows*	China	KF780787	KF780670
M. epiphylla	CJ01/2/01	*Salix viminalis*	China	AY652947	AY444792

Supplementary Table 3 Specimens and GenBank accession numbers of rust isolates used to construct phylogenetic tree of *Puccinia*. The newly generated specimens are indicated in bold.

Species	Voucher specimens	Host	Country	GenBank No.	
				ITS	LSU
Puccinia acroptili	BPI 863523	Asteraceae	Turkey	JN204187	–
P. allii	HSZ 1992	*Allium sativum*	USA	JX402206	–
P. allii	BRIP:59595	*Allium sativum*	Australia	KM249849	–
P. allii	HMJAU8954	*Allium tuberosum*	China	OK489434	OK489426

Supplementary Table 3 Continued.

Species	**Voucher specimens**	**Host**	**Country**	**GenBank No.**	
				ITS	**LSU**
P. allii	**HGUP21225**	***Allium sativum***	**China**	**OR470016**	**–**
P. allii	**HGUP21226**	***Allium sativum***	**China**	**OR470017**	**–**
P. allii	**HGUP21227**	***Allium sativum***	**China**	**OR470018**	**–**
P. allii	**HGUP21228**	***Allium sativum***	**China**	**OR470019**	**–**
P. allii	**HGUP21229**	***Allium sativum***	**China**	**OR470020**	**–**
P. alopecuruse	**HGUP21231**	***Alopecurus aequalis***	**China**	**OR470021**	**OR548173**
P. amari	BPI 089009	*Panicum amarum*	USA	KX190837	KX190915
P. amari	BPI 893097	*Panicum* sp.	USA	KX190839	KX190917
P. arachidis	**HGUP21199**	***Arachis hypogaea***	**China**	**OR470004**	**OR548167**
P. arachidis	**HGUP21200**	***Arachis hypogaea***	**China**	**OR470005**	**OR548168**
P. arenariae	TUB 14961	*Dianthus barbatus*	–	–	DQ917731
P. arenariae	BPI 893275	*Sagina subulata*	–	KY798385	–
P. artemisiae-keiskeanae	TSH-R4183	*Artemisia keiskeana*	Japan	AB188133	AB190893
P. artemisiae-keiskeanae	TSH-R4184	*Artemisia keiskeana*	Japan	AB188200	AB190894
P. atra	DAOM:108870	*Setaria grisebachii*	Mexico	KX190841	–
P. atra	BPI 893214	*Mirabilis longiflora*	Mexico	KX190842	–
P. arundinariae	ZP-R1349	–	China	–	MK518688
P. brachypodii	DAOM:240993	*Poa annua*	China	HQ012447	–
P. brachypodii	BRIP 59466	*Poa annua*	Australia	–	KX999868
P. calcitrapae var. *bardanae*	BJFC-R00624	*Arctium tomentosum*	China	KP240635	KP240633
P. calcitrapae var. *centaureae*	U-209	*Centaurea calcitrapa*	Turkey	JN204183	–
P. carduorum	U-218	*Carduus nutans*	Turkey	JN204184	–
P. cardui-pycnocephali	ZP-R207	–	China	MK518962	MK518657
P. caricis	NYS-F-53826	–	China	MK518857	MK518514
P. caricis	NYS-F-2537	–	China	MK518851	MK518508
P. carucus	ZP-R1034	–	China	–	MK518751
P. carucus	ZP-R411	–	China	MK518818	MK518458
P. carucus	ZP-R458	–	China	MK519043	MK518459
P. chrysanthemi	CA1	Asteraceae	–	EU816926	–
P. cnici-oleracei	DAOM:88895	*Cirsium heterophyllum*	United Kingdom	MW009550	–
P. convolvuli	ZP-R352	–	China	–	MK518646
P. convolvuli	ZP-R1388	–	China	MK518981	MK518679
P. convolvuli	**HGUP21182**	***Calystegia hederacea***	**China**	**OR469994**	**–**
P. convolvuli	**HGUP21183**	***Calystegia hederacea***	**China**	**OR469995**	**–**
P. coronata var. *coronata*	BP89353	*Frangula alnus*	Hungary	HM131313	–
P. coronata var. *coronata*	B 70 0006597	*Frangula alnus*	Hungary	HM131312	–
P. coronata var. *coronata*	BP 89076	*Calamagrostis epigejos*	Hungary	HM057141	–
P. coronata	BPI 718354	*Bromus erectus*	Germany	HM131345	–
P. coronata	PUR N1057	*Helictotrichon virescens*	Nepal	HM131339	–
P. coronata	**HGUP21222**	***Persicaria posumbu***	**China**	**OR469984**	**OR548154**
P. coronata	**HGUP21223**	***Persicaria posumbu***	**China**	**OR469985**	**OR548155**
P. coronata	**HGUP21224**	***Persicaria posumbu***	**China**	**OR469986**	**–**
P. corticioides	TSH:R9960	*Yuichi Yamaoka*	Japan	LC514363	LC514363
P. corticioides	ZP-R1001	–	China	MK519023	MK518727
P. corticioides	ZP-R1002	–	China	MK518988	MK518687
P. corticioides	**HGUP21139**	***Bamboo***	**China**	**OR470035**	**–**
P. corticioides	**HGUP21140**	***Bamboo***	**China**	**OR470036**	**–**
P. crepidis	**HGUP21212**	***Crepidiastrum sonchifolium***	**China**	**OR470014**	**OR548171**

Supplementary Table 3 Continued.

Species	Voucher specimens	Host	Country	GenBank No.	
				ITS	LSU
P. crepidis	**HGUP21213**	***Crepidiastrum sonchifolium***	**China**	**OR470015**	**OR548172**
P. crepidis-japonicae	BPI 910311	*Youngia japonica*	–	KY798395	–
P. crepidis-japonicae	**HGUP21210**	***Youngia japonica***	**China**	**OR470012**	**–**
P. crepidis-japonicae	**HGUP21211**	***Youngia japonica***	**China**	**OR470013**	**–**
P. cumminsii	DAOM:114238	*Panicum* sp.	USA	KX190847	–
P. cumminsii	DAOM:114237	*Panicum* sp.	USA	KX190846	–
P. cynodontis	**HGUP21253**	***Plantago asiatica***	**China**	**OR469992**	**–**
P. cynodontis	**HGUP21254**	***Plantago asiatica***	**China**	**OR469993**	**–**
P. cyperi	ZP-R452	–	China	MK519010	MK518713
P. digitata	DAOM:36609	*Endotropis crocea* subsp. *Ilicifolia*	USA	KF661256	–
P. digitata	BPI 085602	*Endotropis crocea* subsp. *Ilicifolia*	–	KX036376	–
P. dimidipes	BPI195034	*Lycium* sp.	–	MH144395	–
P. dioicae	ZP-R873	–	–	MK518963	MK518658
P. elaeagni	ZP-R297	–	China	MK518919	MK518595
P. emaculata	BPI 064483	*Panicum capillare*	USA	KX190860	KX190926
P. emaculata	DAOM:JD927	*Panicum* sp.	Canada	KX190851	–
P. erianthi	ZP-R240	–	China	–	MK518485
P. esclavensis	BPI 048988	*Zuloagaea bulbosa*	USA	KX190861	KX190927
P. esclavensis	BPI 893096	*Mirabilis melantrich*	Mexico	KX190866	KX190928
P. gentianae	**HGUP21206**	***Gentiana macrophylla***	**China**	**OR470008**	**–**
P. gentianae	**HGUP21207**	***Gentiana macrophylla***	**China**	**OR470009**	**–**
P. geitonoplesii	BRIP 55679	*Geitonoplesium cymosum*	Australia	KM249860	–
P. gilgiana	BRIP 57723	*Lechenaultia linarioides*	Australia	KF690673	KF690690
P. globosipes	PUR 63265	*Lycium exsertum*	–	MH144386	–
P. globosipes	PUR 69701	*Lycium andersonii*	–	MH144387	–
P. graminis	–	*Agropyron repens*	China	AF468044	–
P. haemodori	BRIP 57777	*Conostylis candicans*	Australia	KF690676	KF690694
P. hemerocallidis	HMAS37736	–	China	MK518894	–
P. hemerocallidis	HMAS56424	–	China	MK518900	MK518573
P. hemerocallidis	HMAS66841	–	China	MK518904	MK518576
P. hemerocallidis	BRIP 53476	Liliaceae	Australia	KM249855	–
P. hemerocallidis	**HGUP21218**	***Hemerocallis fulva***	**China**	**OR470037**	**OR548190**
P. hemerocallidis	**HGUP21219**	***Hemerocallis fulva***	**China**	**OR470038**	**OR548191**
P. hemerocallidis	**HGUP21220**	***Hemerocallis fulva***	**China**	**OR470039**	**OR548192**
P. hieracii	ZP-R501	–	China	MK518930	MK518610
P. hieracii	**HGUP21208**	***Taraxacum mongolicum***	**China**	**OR470010**	**–**
P. hieracii	**HGUP21209**	***Taraxacum mongolicum***	**China**	**OR470011**	**–**
P. hordei	PUR F17397	*Bromus oxyodon*	Afghanistan	HQ012452	–
P. indocalamuse-latifoliusii	**HGUP21239**	***Indocalamus latifolius***	**China**	**OR469987**	**OR548156**
P. infra-aequatorialis	ZP-R802	–	China	MK518949	MK518641
P. infra-aequatorialis	HMAS52872	–	China	MK518899	MK518572
P. ipomoeae-nilii	**HGUP21178**	***Ipomoea nil***	**China**	**OR469974**	**OR548148**
P. ipomoeae-nilii	**HGUP21179**	***Ipomoea nil***	**China**	**OR469975**	**OR548149**
P. ipomoeae-nilii	**HGUP21180**	***Ipomoea nil***	**China**	**OR469976**	**OR548150**
P. iridis	ZP-R221	–	China	–	MK518532

Supplementary Table 3 Continued.

Species	Voucher specimens	Host	Country	GenBank No.	
				ITS	LSU
P. iridis	ZP-R1402	–	China	MK518998	MK518703
P. iridis	ZP-R482	–	China	MK518880	MK518553
P. iridis	**HGUP21201**	***Iris tectorum***	**China**	**OR470006**	**OR548169**
P. iridis	**HGUP21202**	***Iris tectorum***	**China**	**OR470007**	**OR548170**
P. jaceae	CUP-448	–	China	MK518842	MK518498
P. jaceae	FDWSRU 14-004	*Centaurea solstitialis*	USA	KU127238	–
P. kuehnii	Q124MD25	*Saccharum officinarum*	Australia	GU564419	–
P. kuehnii	BPI 879137	*Saccharum* sp.	El Salvador	GQ283007	–
P. kusanoi	TNM F0029955	*Yushania niitakayamensis*	China	KX610657	–
P. kusanoi	TNM F0029314	*Deutzia pulchra*	China	KU309318	–
P. lactucae-indicae	**HGUP21214**	***Lactuca indica***	**China**	**OR469981**	**OR548151**
P. lactucae-indicae	**HGUP21215**	***Lactuca indica***	**China**	**OR469982**	**OR548152**
P. lactucae-indicae	**HGUP21216**	***Lactuca indica***	**China**	**OR469983**	**OR548153**
P. lagenophorae	BRIP 57563	*Emilia sonchifolia*	Australia	KF690677	KF690696
P. lapsanae	U-886	*Lapsana* sp.	Oman	–	HQ412649
P. lapsanae	PDD:98713	*Lapsana communis*	New Zealand	KX985747	–
P. lapsanae	ZP-R105	–	China	MK518940	MK518626
P. latimamma	ZP-R387	–	China	MK518876	MK518546
P. latimamma	ZP-R1398	–	China	MK518986	MK518685
P. latimamma	**HGUP21186**	***Pleuropterus multiflorus***	**China**	**OR469998**	**OR548161**
P. latimamma	**HGUP21187**	***Pleuropterus multiflorus***	**China**	**OR469999**	**OR548162**
P. latimamma	**HGUP21188**	***Pleuropterus multiflorus***	**China**	**OR470000**	**OR548163**
P. loliume-perenneii	**HGUP21240**	***Lolium perenne***	**China**	**OR469970**	**OR548144**
P. loliume-perenneii	**HGUP21241**	***Lolium perenne***	**China**	**OR469971**	**OR548145**
P. magnusiana	HMJAU8451	–	China	MW406952	MW397079
P. malvacearum	PDD:101511	*Malva* sp.	New Zealand	KX985756	–
P. menthae	PDD 99229	*Mentha spicata*	–	KJ716344	–
P. menthae	BPI 871110	*Cunila origanoides*	USA	DQ354513	–
P. miscanthi	HMJAU8643	–	China	MW406956	MW397083
P. miscanthi	ZP-R333	–	China	MK518815	MK518455
P. miscanthi	ZP-R122	–	China	–	MK518623
P. mixta	BRIP 61576	*Allium schoenoprasum*	Germany	KU296893	–
P. nakanishikii	BPI 910261	*Cymbopogon citratus*	–	KY764147	–
P. nakanishikii	BPI 879283	*Cymbopogon citratus*	USA	–	GU058002
P. nepalensis	BA65	*Rumex nepalensis*	Pakistan	KU886228	–
P. nepalensis	BA66	*Rumex nepalensis*	Pakistan	–	KX014746
P. nepalensis	**HGUP21181**	***Rumex nepalensis***	**China**	**–**	**OR548185**
P. nepalensis	**HGUP21190**	***Rumex nepalensis***	**China**	**–**	**OR548187**
P. nepalensis	**HGUP21191**	***Rumex nepalensis***	**China**	**–**	**OR548188**
P. nepalensis	**HGUP21192**	***Rumex nepalensis***	**China**	**–**	**OR548184**
P. nepalensis	**HGUP21230**	***Rumex nepalensis***	**China**	**–**	**OR548186**
P. novopanici	CUP 068152	*Panicum virgatum*	USA	–	MH704493
P. novopanici	BPI 747673	*Panicum virgatum*	USA	NR_148109	–
P. novopanici	BPI 089011	*Panicum amarum*	USA	KX190883	KX190942
P. oenanthes-stoloniferae	**HGUP21184**	***Oenanthe javanica***	**China**	**OR469996**	**–**
P. oenanthes-stoloniferae	**HGUP21185**	***Oenanthe javanica***	**China**	**OR469996**	**–**

Supplementary Table 3 Continued.

Species	Voucher specimens	Host	Country	GenBank No.	
				ITS	LSU
P. osoyoosensis	ZP-R465	–	China	MK518927	MK518607
P. osoyoosensis	DAOM:139216	*Schoenoplectus americanus*	Canada	MW009486	–
P. oxalidis	MCA3567	*Oxalis* sp.	USA	–	MG907250
P. oxalidis	RO1	*Oxalis debilis*	India	MZ442316	MZ425499
P. oxalidis	**HGUP21232**	***Oxalis corniculata***	**China**	**OR470023**	**OR548176**
P. oxalidis	**HGUP21233**	***Oxalis corniculata***	**China**	**OR470024**	**OR548177**
P. oxalidis	**HGUP21235**	***Oxalis corniculata***	**China**	**OR470025**	**–**
P. oxalidis	**HGUP21236**	***Oxalis corniculata***	**China**	**–**	**–**
P. oxyriae	ZP-R115	–	China	MK518865	–
P. oxyriae	ZP-R1363	–	China	MK518973	MK518669
P. pammelii	DAOM 695781	*Panicum virgatum*	USA	KX190895	KX190949
P. pampeana	PUR 87662	*Capsicum* sp.	–	MH144396	–
P. panici-montani	**HGUP21189**	***Setaria plicata***	**China**	**–**	**OR548189**
P. paradoxopoda	Berndt 5814	*Lycium* sp.	–	MH144390	–
P. paradoxopoda	S-F233802	*Grabowskia obtusa*	–	MH144391	–
P. pascua	DAOM 114286	*Panicum virgatum*	USA	KX190905	–
P. patriniae	ZP-R852	–	China	MK518889	MK518758
P. patriniae	ZP-R874	–	China	MK518966	MK518663
P. patriniae	**HGUP21221**	***Patrinia scabiosifolia***	**China**	**OR470031**	**–**
P. penicillariae	UFS15	*Solanum melongena*	South Africa	MZ057697	–
P. peradeniyae	BPI 089014	*Panicum repens*	USA	KX190906	–
P. persicariae-capitatae	**HGUP21193**	***Persicaria capitata***	**China**	**OR469977**	**–**
P. persicariae-capitatae	**HGUP21194**	***Persicaria capitata***	**China**	**OR469978**	**–**
P. persisten	IRAN 11511 F	*Thalictrum minus*	–	AY956561	–
P. persistens subsp. *triticina*	IRAN 8274 F	*Aegilops taushii*	Iran	AY956549	–
P. phyllostachydis	HMAS80647	–	China	–	MK51876
P. phyllostachydis	HMAS12370	–	China	–	MK518561
P. phyllostachydis	**HGUP21174**	***Phyllostachys nuda***	**China**	**OR469990**	**OR548159**
P. phyllostachydis	**HGUP21174**	***Phyllostachys nuda***	**China**	**OR469991**	**OR548160**
P. plectranthi	**HGUP21141**	***Isodon amethystoides***	**China**	**OR470033**	**OR548183**
P. plectranthi	**HGUP21234**	***Isodon amethystoides***	**China**	**OR470034**	**OR548182**
P. poae-nemoralis	HMJAU8596	–	China	MW404812	MW404972
P. poae-nemoralis	HMJAU8597	–	China	MW404811	MW404971
P. polysora	HSZ1879	*Zea mays*	–	HQ189433	–
P. polysora	U1781	*Zea mays*	USA	–	OL468037
P. polysora	**HGUP21248**	***Zea mays***	**China**	**OR470027**	**OR548178**
P. polysora	**HGUP21249**	***Zea mays***	**China**	**OR470028**	**OR548179**
P. polysora	**HGUP21250**	***Zea mays***	**China**	**OR470029**	**–**
P. polysora	**HGUP21251**	***Zea mays***	**China**	**OR470030**	**OR548180**
P. polysora	**HGUP21252**	***Zea mays***	**China**	**OR470026**	**–**
P. polygoni-amphibii	ZP-R716	–	China	MK519001	MK518706
P. porri	BRIP 61579	Liliaceae	United Kingdom	KU296902	–
P. punctiformis	ZP-R103	–	China	MK518864	MK518528
P. punctiformis	ZP-R219	–	China	–	MK518798
P. purpurea	TNM F0029759	*Sorghum bicolor*	China	KY964765	–
P. purpurea	ZP-R286	–	China	MK518917	MK518592
P. recondita	IRAN 11486 F	*Cerinthe minor*	–	AY956562	–
P. rufipes	**HGUP21176**	***Imperata cylindrica***	**China**	**OR469972**	**OR548146**
P. rufipes	**HGUP21177**	***Imperata cylindrica***	**China**	**OR469973**	**OR548147**
P. senecionis	**HGUP21198**	***Senecio scandens***	**China**	**OR470032**	**OR548181**
P. setariae	BPI 188745	*Setaria parviflora*	Mexico	KX190907	–

Supplementary Table 3 Continued.

Species	**Voucher specimens**	**Host**	**Country**	**GenBank No.**	
				ITS	**LSU**
P. setariae	DAOM 116092	*Setaria parviflora*	Mexico	KX190908	KX190908
P. scirpi	BRIP 61027	*Nymphoides indica*	Australia	KX999892	–
P. smilacis	BPI 871784	*Smilax rotundifolia*	USA	DQ354533	–
P. similis	BPI<USA-MD>:863644	*Artemisia cana*	USA	–	GU168943
P. similis	ZP-R705	–	China	–	MK518525
P. spegazzinii	R189	*Mikania micrantha*	Colombia	–	EU851150
P. spegazzinii	R160	*Mikania micrantha*	Colombia	–	EU851148
P. striiformis	HSZ1834	Poaceae	–	GQ457306	GQ457306
P. stylidii	BRIP 60107	*Stylidium armeria*	Australia	KJ622216	KJ622215
P. striiformis	BPI 195217	*Hordeum comosum*	Argentina	HM057136	–
P. striiformis	PUR 61492	*Triticum aestivum*	USA	HM057132	–
P. symphoricarpi	BPI 879286	*Symphoricarpos albus*	USA	–	GU058006
P. thaliae	PDD:82262	*Canna indica*	Palau	–	JX206995
P. thaliae	ZP-R1300	–	China	MK518968	MK518666
P. thaliae	**HGUP21172**	***Canna indica***	**China**	**OR469988**	**OR548157**
P. thaliae	**HGUP21173**	***Canna indica***	**China**	**OR469989**	**OR548158**
P. tokyensis	ZP-R447	–	China	MK518991	MK518693
P. tokyensis	ZP-R406	–	China	MK518990	MK518691
P. tokyensis	ZP-R339	–	China	–	MK518689
P. tokyensis	**HGUP21195**	***Cryptotaenia japonica***	**China**	**OR470001**	**OR548164**
P. tokyensis	**HGUP21196**	***Cryptotaenia japonica***	**China**	**OR470003**	**OR548166**
P. tokyensis	**HGUP21197**	***Cryptotaenia japonica***	**China**	**OR470002**	**OR548165**
P. tumidipes	PUR N8357	*Lycium pallidum*	–	MH144389	–
P. tumidipes	PUR N5423	*Lycium barbarum*	–	MH144388	–
P. tumidipes	PUR 8370	*Lycium halimifolium*	–	MH144397	–
P. turgida	NA224	*Lycium* sp.	–	MH144383	–
P. ursiniae	BRIP 57993	*Ursinia anthemoides*	Australia	KF690684	KF690705
P. violae	BPI 842321	*Viola cucullata*	USA	DQ354509	–
P. violae	ZP-R1180	–	China	MK518850	MK518507
P. violae-diffusii	**HGUP21204**	***Viola diffusa***	**China**	**OR469979**	**–**
P. violae-diffusii	**HGUP21205**	***Viola diffusa***	**China**	**OR469980**	**–**
P. virgaureae	TUB 14995	*Solidago virgaurea*	–	–	DQ917709
P. virgaureae	ZP-R281	–	China	MK518873	MK518539
Melampsora epiphylla	TSH-R3884	*Willows*	China	KF780787	–
M. epiphylla	CJ01/2/01	*Salix viminalis*	China	AY652947	–

Supplementary Table 4 Specimens and GenBank accession numbers of rust isolates used to construct phylogenetic tree of Phragmidiaceae. The newly generated specimens are indicated in bold.

Species	**Voucher specimens**	**Host**	**Country**	**GenBank No.**	
				ITS	**LSU**
Gerwasia rubi	BRIP:58369	*Rubus* sp.	South Africa	–	KT199397
Ge. rubi	**HGUP21166**	***Rubus reflexus***	**China**	**OR470051**	**–**
G. rubi-alceifoliuse	**HGUP21156**	***Rubus alceifolius***	**China**	**OR470049**	**–**
G. rubi-alceifoliuse	**HGUP21157**	***Rubus alceifolius***	**China**	**OR470050**	**–**
Ge. rubi-buergerii	**HGUP21169**	***Rubus buergeri***	**China**	**OR470046**	**–**
Ge. rubi-buergerii	**HGUP21170**	***Rubus buergeri***	**China**	**OR470048**	**OR528542**
Ge. rubi-buergerii	**HGUP21171**	***Rubus buergeri***	**China**	**OR470047**	**OR528541**
Ge. rubi-setchuenensise	**HGUP21167**	***Rubus setchuenensis***	**China**	**OR470044**	**–**
Ge. rubi-setchuenensise	**HGUP21168**	***Rubus setchuenensis***	**China**	**OR470045**	**OR528540**
Ge. pittieriana	BPI 843556	*Rubus* sp.	USA	KY764065	–

Supplementary Table 4 Continued.

Species	Voucher specimens	Host	Country	GenBank No.	
				ITS	LSU
Gymnoconia peckiana	BPI 879271	*Rubus* sp.	USA	GU058010	GU058010
Gy. peckiana	BPI:747600	*Rubus allegheniensis*	USA	JF907677	JF907677
Gy. peckiana	AFTOL-ID 1630	*Rubus* sp.	USA	DQ521421	DQ521421
Hamaspora acutissima	BRIP:55606	*Rubus moluccanus*	Australia	–	KT199398
H. longissima	BPI 871506	*Rubus ludwigii*	–	–	MW049262
H. rubi-lambertianuse	**HGUP21163**	***Rubus lambertianus***	**China**	**OR470052**	**–**
H. rubi-lambertianuse	**HGUP21164**	***Rubus lambertianus***	**China**	**OR470053**	**OR528547**
H. rubi-lambertianuse	**HGUP21165**	***Rubus lambertianus***	**China**	**OR470054**	**OR528546**
H. rubi-parkerii	**HGUP21159**	***Rubus parkeri***	**China**	**OR470055**	**OR528543**
H. rubi-parkerii	**HGUP21160**	***Rubus parkeri***	**China**	**OR470056**	**OR528545**
H. rubi-parkerii	**HGUP21161**	***Rubus parkeri***	**China**	**OR470057**	**OR528544**
H. rubi-parkerii	**HGUP21162**	***Rubus parkeri***	**China**	**OR470058**	**–**
Kuehneola malvicola	BPI 893271	*Hibiscus* sp.	USA	KY798357	KY798357
K. japonica	BPI 910185	*Rosa* sp.	USA	KY764067	–
K. uredinis	AFTOL-ID 987	–	USA	DQ911604	AY745696
K. uredinis	R216	*Rubus fruticosus*	Belgium	EU014068	–
K. uredinis	BPI 879274	*Rubus* sp.	USA	GU058013	–
Phragmidium sp.	HMAS41561	*Rosa multiflora*	China	MN264717	MN264735
P. altaicum	BJFCR03246	–	–	MH285384	MH285380
P. altaicum	BJFCR03217^{T}	–	–	MH285383	MH285379
P. andersoni	HMAS-53231^{T}	*Potentilla fruticosa*	China	–	MG669120
P. barclayi	HMAS-67281	*Rubus austrotibetanus*	China	–	MG669117
P. barnardii	BRIP 56945	*Rubus* sp.	South Africa	–	KT199402
P. barnardii	**HGUP21035**	***Rubus parvifolius***	**China**	**OL684828**	**OL684839**
P. barnardii	**HGUP21038**	***Rubus*** **sp.**	**China**	**OR470041**	**–**
P. barnardii	**HGUP21039**	***Rubus adenophorus***	**China**	**OR470042**	**OR528549**
P. butleri	HMAS-67841	*Rosa macrophylla*	China	–	MG669118
P. chayuensis	BJFC-R02532^{T}	*Rosa duplicata*	China	–	MG669112
P. chayuensis	BJFC-R03014^{T}	*Rosa duplicata*	China	–	MG669113
P. cibanum	**BJFCR02528**^{T}	***Rubus niveus***	**China**	**MH128370**	**MG669110**
P. cibanum	**BJFCR03012**^{T}	***Rubus niveus***	**China**	**MH128371**	**MG669111**
P. duchesneae-indica	**HGUP21031**	***Duchesnea indica***	**China**	**OL684824**	**OL684835**
P. duchesneae-indica	**HGUP21032**	***Duchesnea indica***	**China**	**OL684825**	**OL684836**
P. fragariae	WM 1317	*Potentilla steriliz*	Europe	–	AF426217
P. fructigenum	HMUT100472	*Rosa glomerata*	China	–	KU059168
P. fusiforme	T-10	*Rosa pendulina*	Switzerland	–	AJ715522
P. griseum	BJFCR03451	*Rubus crataegifoliu*	China	MN264713	MN264731
P. griseum	HMAS56906	*Rubus crataegifoliu*	China	–	MG669115
P. handelii	BJFC-R01030	*Rosa webbiana*	China	–	KP407631
P. handelii	BJFC-R01421	*Rosa webbiana*	China	–	KP407628
P. ivesiae	BPI-877968	*Potentilla gracilis*	USA	–	JF907673
P. ivesiae	BPI-863637	*Potentilla gracilis*	USA	–	JF907672
P. japonicum	HMAS41585	*Rosa laevigata*	China	MN264716	MN264734
P. japonicum	IBAR8174	*Rosa luciae*	Japan	MN882389	MN848143
P. jiangxiense	BJFCR03452	*Rosa laevigata*	China	MN264714	MN264732
P. jiangxiense	BJFCR03453^{T}	*Rosa laevigata*	China	MN264715	MN264733
P. leucoaecium	BJFCR02116	*Rosa* sp.	China	MN264718	MN264736
P. leucoaecium	BJFCR02118^{T}	*Rosa* sp.	China	MN264719	MN264737
P. longissima	BJFC-R00338	*Rosa lichiangensis*	China	–	KP407633
P. longissima	BJFC-R00360	*Rosa lichiangensis*	China	–	KP407634
P. mexicanum	BPI 843961	*Potentilla indica*	USA	JF907660	JF907660
P. mexicanum	BPI 843829	*Potentilla indica*	USA	JF907659	JF907659
P. montivagum	HMAS67176	*Rosa davurica*	China	–	KU059173
P. montivagum	FO 47828	*Rosa* cf. *woodsii*	–	–	AF426213

Supplementary Table 4 Continued.

Species	Voucher specimens	Host	Country	GenBank No.	
				ITS	LSU
P. *mucronatum*	RUBO	*Rosa* sp.	Germany	–	KU059171
P. *mucronatum*	TUB 012090	*Rosa corymbifera*	Germany	–	AJ715520
P. *octoloculare*	HMAS-140416	*Rubus biflorus*	China	–	MG669119
P. *potentillae*	HMAS-53236	*Potentilla virgata*	China	–	MG669114
P. *potentillae*	BJFCR 00961	*Potentilla chinensis*	China	MN264720	MN264738
P. _potentillae_	**HGUP21034**	**_Potentilla kleiniana_**	**China**	**OL684827**	**OL684838**
P. *potentillae-canadensis*	BPI:877885	*Potentilla canadensis*	USA	–	JF907668
P. *potentillae-canadensis*	BPI:877886	*Potentilla* sp.	USA	–	JF907667
P. _potentillae-freynianae_	**HGUP21033**^{T}	**_Potentilla freyniana_**	**China**	**OL684826**	**OL684837**
P. _potentillae-freynianae_	**HGUP21040**	**_Potentilla freyniana_**	**China**	**OR470043**	–
P. *punjabense*	BA65A^{T}	*Rosa brunonii*	Pakistan	–	KX358854
P. *punjabense*	BA65B	*Rosa brunonii*	Pakistan	–	KX358855
P. _rosae-cymosaii_	**HGUP21147**	**_Rosa cymosa_**	**China**	**OR470062**	**OR528551**
P. _rosae-cymosaii_	**HGUP21148**	**_Rosa cymosa_**	**China**	**OR470063**	**OR528552**
P. _rosae-cymosaii_	**HGUP21149**	**_Rosa cymosa_**	**China**	**OR470064**	**OR528553**
P. _rosae-cymosaii_	**HGUP21150**	**_Rosa cymosa_**	**China**	**–**	**–**
P. _rosae-cymosaii_	**HGUP21151**	**_Rosa cymosa_**	**China**	**–**	–
P. _rosae-cymosaii_	**HGUP21152**	**_Rosa cymosa_**	**China**	**OR470065**	–
P. _rosae-cymosaii_	**HGUP21153**	**_Rosa cymosa_**	**China**	**–**	–
P. _rosae-kwangtungensis_e	**HGUP21154**	**_Rosa kwangtungensis_**	**China**	**OR470067**	–
P. _rosae-kwangtungensis_e	**HGUP21155**	**_Rosa kwangtungensis_**	**China**	**OR470068**	–
P. _rosae-laevigatae_	**HGUP21036**^{T}	**_Rosa laevigata_**	**China**	**OL684829**	**OL684840**
P. _rosae-laevigatae_	**HGUP21037**	**_Rosa laevigata_**	**China**	**OL684830**	**OL684841**
P. *rosae-multiflorae*	BJFCR 03454	*Rosa multiflora*	China	MN264721	MN264739
P. _rosae-multiflorae_	**HGUP21158**	**_Rosa multiflora_**	**China**	**OR470059**	**OR528548**
P. _rosae-roxburghii_	**HGUP21025**^{T}	**_Rosa roxburghii_**	**China**	**OL684818**	**OL684831**
P. _rosae-roxburghii_	**HGUP21026**	**_Rosa roxburghii_**	**China**	**OL684819**	**OL684832**
P. _rosae-roxburghii_	**HGUP21027**	**_Rosa roxburghii_**	**China**	**OL684820**	**–**
P. _rosae-roxburghii_	**HGUP21028**	**_Rosa_ sp.**	**China**	**OL684821**	**OL678103**
P. *rosae-rugosae*	BJFCR 03455	*Rosa rugosa*	China	MN264722	MN264740
P. *rosae-rugosae*	BJFCR 03456	*Rosa rugosa*	China	MN264723	MN264741
P. _rubi-corean_	**HGUP21029**^{T}	**_Rubus coreanus_**	**China**	**OL684822**	**OL684833**
P. _rubi-corean_	**HGUP21030**	**_Rubus coreanus_**	**China**	**OL684823**	**OL684834**
P. *rubi-idaei*	WM 1024	*Rubus idaeus*	Europe	–	AF426215
P. *rubi-idaei*	BRIP 59372	*Rubus idaeus*	Australia	–	MW147044
P. *rubi-oldhami*	HMAS-64306	*Rubus pungens*	China	–	MG669116
P. *sanguisorbae*	BPI 872232	*Sanguisorba minor*	USA	–	JF907674
P. *sanguisorbae*	ML 957	*Sanguisorba minor*	Europe	–	AF426216
P. *tormentillae*	BPI 843392	*Potentilla canadensis*	USA	DQ354553	DQ354553
P. *tormentillae*	BPI:877888	*Potentilla simplex*	USA	–	JF907669
P. *tuberculatum*	BPI877978	*Rosa* sp.	USA	–	KJ841919
P. *tuberculatum*	BPI843677	*Rosa* sp.	Argentina	–	KJ841921
P. *violaceum*	BPI 871510	*Rubus* sp.	USA	DQ142910	DQ142910
P. *violaceum*	BJFCR03457	*Rubus* sp.	New Zealand	MN264724	MN264742
P. *warburgianum*	BJFCR03458	*Rosa bracteata*	Japan	MN264726	MN264744
P. *warburgianum*	BJFCR03459	*Rosa bracteata*	Japan	MN264727	MN264745
P. *zangdongii*	BJFCR02447^{T}	*Rosa tibetica*	China	MH128372	MG669108
P. *zangdongii*	BJFCR03013^{T}	*Rosa tibetica*	China	MH128373	MG669109
P. *zhouquensis*	BJFCR01516^{T}	*Rosa omeiensis*	China	MN264728	MN264746
P. *zhouquensis*	BJFCR01529^{T}	*Rosa omeiensis*	China	MN264729	MN264747
Trachyspora intrusa	BPI 84328	*Alchemilla vulgaris*	USA	DQ354550	–
T. intrusa	WM 1019	*Alchemilla vulgaris*	Germany	–	AF426220
Melampsora epiphylla	TSH-R3884	*Willows*	China	KF780787	–
M. epiphylla	CJ01/2/01	*Salix viminalis*	China	AY652947	–

Supplementary Table 5 Specimens and GenBank accession numbers of rust isolates used to construct phylogenetic tree of Coleosporiaceae. The newly generated specimens are indicated in bold.

Species	Voucher specimens	Host	Country	GenBank No.	
				ITS	LSU
Coleosporium asterum	TSH:R6685	*Aster microcephalus* var. *ovatus*	Japan	LC333799	LC333799
C. asterum	N90	*Aster ageratoides*	Japan	KX386013	KX386045
C. asterum	BPI 879270	*Solidago* sp.	USA	GU058009	GU058009
C. asterum	**HGUP21055**	***Aster ageratoides***	**China**	**OR470515**	**–**
C. asterum	**HGUP21056**	***Aster ageratoides***	**China**	**OR470516**	**–**
C. asterum	**HGUP21057**	***Aster ageratoides***	**China**	**OR470519**	**–**
C. asterum	**HGUP21058**	***Aster ageratoides***	**China**	**OR470518**	**–**
C. asterum	**HGUP21059**	***Aster ageratoides***	**China**	**OR470513**	**OR462090**
C. asterum	**HGUP21060**	***Aster ageratoides***	**China**	**OR470517**	**OR462091**
C. asterum	**HGUP21061**	***Aster ageratoides***	**China**	**OR470514**	**–**
C. asterum	**HGUP21062**	***Aster indicus***	**China**	**OR470528**	**–**
C. asterum	**HGUP21063**	***Aster indicus***	**China**	**OR470529**	**–**
C. bletiae	N87	*Bletilla striata*	Japan	KX386006	KX386038
C. bletiae	BSC1	*Bletilla striata*	China	MN108161	MN108162
C. bletiae	**HGUP21064**	***Bletilla striata***	**China**	**OR470494**	**OR462077**
C. bletiae	**HGUP21065**	***Bletilla striata***	**China**	**OR470495**	**OR462078**
C. buchananianae	**HGUP21053**	***Clematis buchananiana***	**China**	**OR470523**	**–**
C. cacaliae	KUS-F24178	*Syneilesis palmata*	–	–	JF273971
C. cacaliae	WM 1321	*Adenostyles glabra*	Germany	–	AF426243
C. cacaliae	ZT_Myc_58004	*Adenostyles alliariae*	Switzerland	KY810462	KY810462
C. campanulae	ZT_Myc_58002	*Campanula latifolia*	Switzerland	KY810467	–
C. campanulae	ZT_Myc_57999	*Campanula rotundifolia*	Switzerland	KY810466	–
C. abrotanoidesii	**HGUP21080**	***Carpesium abrotanoides***	**China**	**OR470521**	**–**
C. abrotanoidesii	**HGUP21081**	***Carpesium abrotanoides***	**China**	**OR470522**	**OR462093**
C. abrotanoidesii	**HGUP21082**	***Carpesium abrotanoides***	**China**	**OR470520**	**OR462092**
C. cimicifugatum	HMBF-95Y8	*Cimicifuga* sp.	China	KP017559	KP017559
C. cimicifugatum	HMBF-95Y7	*Cimicifuga* sp.	China	KP017558	KP017558
C. clematidis	N79	*Clematis* sp.	Japan	KX386010	KX386042
C. clematidis	N81	*Clematis* sp.	Japan	KX386007	KX386039
C. clematidis	**HGUP21054**	***Clematis brevicaudata***	**China**	**OR470524**	**OR462095**
C. clematidis-apiifoliae	TSH:R6521	*Clematis apiifolia*	Japan	LC333796	LC333796
C. dasyandrae	**HGUP21050**	***Clematis dasyandra***	**China**	**OR470510**	**OR462089**
C. dasyandrae	**HGUP21051**	***Clematis dasyandra***	**China**	**OR470511**	**–**
C. dasyandrae	**HGUP21052**	***Clematis dasyandra***	**China**	**OR470512**	**–**
C. delicatulum	BPI 871737	*Symphyotrichum novae-angliae*	USA	MF769638	MF769638
C. delicatulum	U347	*Euthamia graminifolia*	USA	MG907221	MG907221
C. euodiae	HMAS:41515	*Tetradium glabrifolium*	China	MG561465	–
C. euodiae	HMBF-11	*Tetradium glabrifolium*	China	KP017557	KP017567
C. euodiae	**HGUP21073**	***Tetradium ruticarpum***	**China**	**OR470525**	**OR462096**
C. euodiae	**HGUP21074**	***Tetradium ruticarpum***	**China**	**OR470526**	**–**

Supplementary Table 5 Continued.

Species	Voucher specimens	Host	Country	GenBank No.	
				ITS	LSU
C. eupatorii	MCA 4471	*Eupatorium formosanum*	China	–	MF769674
C. eupatorii	MCA 4470	*Eupatorium formosanum*	China	–	MF769673
C. geranii	ZP-R875	–	China	MK518969	MK518667
C. hedyotidis	U896	*Rubiaceae Kadua*	South Africa	–	MG907222
C. ipomoeae	U365	*Ipomoea* sp.	USA	MF769642	MF769642
C. ipomoeae	JRH 485	*Distimake quinquefolius*	Puerto Rico	MF769644	MF769644
C. inulae	ZT_Myc_57996	*Inula salicina*	Switzerland	KY810470	KY810470
C. inulae	KR-M-0024891	*Inula hirta*	Germany	KY783689	KY783689
C. jonesii	BPI 910183	*Ribes* sp.	USA	–	KY764062
C. julii	**HGUP21048**	***Smilax china***	**China**	**OR470508**	**OR462087**
C. julii	**HGUP21049**	***Smilax china***	**China**	**OR470493**	**–**
C. lycopodis	TSH:R6560	*Adenophora triphylla* var. *japonica*	Japan	LC333800	LC333800
C. montanum	WU:43601	*Symphyotrichum novae-angliae*	Austria	MW284589	MW284589
C. montanum	BPI 877858	*Solidago* sp.	USA	MF769635	MF769635
C. neocacaliae	HMJAU8098	–	China	–	KX344990
C. paederiae	**HGUP21083**	***Paederia foetida***	**China**	**OR470506**	**–**
C. paederiae	**HGUP21084**	***Paederia foetida***	**China**	**OR470507**	**–**
C. paederiae	**HGUP21085**	***Paederia foetida***	**China**	**OR470509**	**OR462088**
C. pedicularidis	HMBF-74454	*Pedicularis* sp.	China	KP017554	KP017564
C. perillae	**HGUP21077**	***Perilla frutescens***	**China**	**OR470531**	**–**
C. perillae	**HGUP21078**	***Perilla frutescens***	**China**	**OR470532**	**–**
C. petasitidis	ZT_Myc_58000	*Petasites hybridus*	Switzerland	KY810471	KY810471
C. phellodendri	N9	*Phellodendron amurense*	Japan	KX386016	KX386048
C. phellodendri	N7	*Phellodendron amurense*	Japan	KX386015	KX386047
C. phellodendri	**HGUP21075**	***Phellodendron amurense***	**China**	**OR470504**	**OR462085**
C. phellodendri	**HGUP21076**	***Phellodendron amurense***	**China**	**OR470505**	**OR462086**
C. phlomidis	HMAS-76121	*Phlomis umbrosa*	China	KP017553	KP017563
C. plectranthi	N85	*Phellodendron amurense*	Japan	KX386011	KX386043
C. plectranthi	N16	*Phellodendron amurense*	Japan	KX386009	KX386041
C. plectranthi	**HGUP21079**	***Isodon amethystoides***	**China**	**OR470527**	**OR462097**
C. plumeriae	BPI 880744	*Plumeria* sp.	–	KY764063	KY764063
C. plumeriae	BPI 843715	*Plumeria rubra*	Nigeria	MF769646	MF769646
C. pulsatillae	KR-M-0014421	*Pulsatilla vulgaris*	Germany	KY783666	KY783666
C. pulsatillae	KR-M-0021308	*Pulsatilla vulgaris*	Germany	KY783671	KY783671
C. saussureae	HMJAU8179	–	China	–	KX344989
C. saussureae	HMJAU8161	–	China	–	KX344988
C. senecionis	PDD 98309	*Senecio* sp.	New Zealand	KJ716348	–
C. septembere	**HGUP21046**	***Clematis florida***	**China**	**OR470496**	**OR462079**
C. septembere	**HGUP21047**	***Clematis florida***	**China**	**OR470497**	**OR462080**
C. solidaginis	U389	*Solidago* sp.	USA	MF769652	MF769652

Supplementary Table 5 Continued.

Species	Voucher specimens	Host	Country	GenBank No.	
				ITS	LSU
C. solidaginis	U430	*Solidago* sp.	USA	MF769649	MF769649
C. telioevodiae	BJFC:QL15	*Euodia* sp.	China	MG561473	MG561473
C. telioevodiae	BJFC:QL14	*Euodia* sp.	China	MG561472	MG561472
C. tussilaginis	PDD:93250	*Brachyglottis huntii*	New Zealand	KX985766	KX985766
C. verbesinae	JRH151	*Verbesina* sp.	Costa Rica	–	MG907229
C. vernoniae	RB 772265	–	–	MK296504	MK296504
C. vernoniae	RB 772200	–	–	MK296503	MK296503
C. zanthoxyli	KUS-F25423	*Zanthoxylum planispinum*	China	MH465096	MH460678
C. zanthoxyli	**HGUP21066**	***Zanthoxylum bungeanum***	**China**	**OR470501**	**OR462083**
C. zanthoxyli	**HGUP21067**	***Zanthoxylum bungeanum***	**China**	**OR470499**	**–**
C. zanthoxyli	**HGUP21068**	***Zanthoxylum armatum***	**China**	**OR470498**	**OR462081**
C. zanthoxyli	**HGUP21069**	***Zanthoxylum bungeanum***	**China**	**OR470530**	**OR462098**
C. zanthoxyli	**HGUP21070**	***Zanthoxylum bungeanum***	**China**	**OR470500**	**OR462082**
C. zanthoxyli	**HGUP21071**	***Zanthoxylum bungeanum***	**China**	**OR470502**	**OR462084**
C. zanthoxyli	**HGUP21072**	***Zanthoxylum bungeanum***	**China**	**OR470503**	**–**
C. zanthoxyli	**HGUP21203**	***Zanthoxylum bungeanum***	**China**	**OR470533**	**–**
Chrysomyxa arctostaphyli	503CHA_PCG_NO1	–	Canada	GU049496	GU049543
C. arctostaphyli	1301CHA_ARU_KE	–	Canada	GU049494	GU049542
C. arctostaphyli	1299CHA_PCE_WY	–	Canada	GU049492	GU049541
C. diebuensis	BJFC:R00556	–	–	KX225393	MW898417
C. diebuensis	BJFC-R00524	*Picea asperata*	China	MK770378	MK874640
C. zhuoniensis	BJFC:R00521	–	–	KX225396	MZ444061
Cronartium flaccidum	HMAS:89231	*Paeonia lactiflora*	China	MK193822	MK208289
C. orientale	HMAS:242642	*Quercus aquifolioides*	China	MK193821	MK208290
Diaphanopellis purpurea	BJFC-R02299	–	China	KX225401	MW063518
D. purpurea	BJFC-R02623	*Rhododendron* sp.	China	MK770364	MK874624
D. purpurea	BJFC-R02302	*Picea purpurea*	China	MK770363	MK874623
Quasipucciniastrum agrimoniae	HMAS:248095	*Agrimonia pilosa*	China	MK193852	MK208281
Q. agrimoniae	HMAS:248096	*Agrimonia pilosa*	China	MK193854	–
Q. agrimoniae	HMAS:248097	*Agrimonia pilosa*	China	MK193853	–
Rossmanomyces pyrolae	356	*Pyrola media*	–	MF926524	–
Thekopsora rubiae	HMJAU8574	–	China	MG787115	MG787140
T. symphyti	HeRB 4732	*Symphytum officinale*	–	–	AF426230
Melampsora epiphylla	TSH-R3884	*Willows*	China	KF780787	–
M. epiphylla	CJ01/2/01	*Salix viminalis*	China	AY652947	–

Supplementary Table 6 Specimens and GenBank accession numbers of rust isolates used to construct phylogenetic tree of Pucciniastraceae. The newly generated specimens are indicated in bold.

Species	**Voucher specimens**	**Host**	**Country**	**GenBank No.**	
				ITS	**LSU**
Calyptospora goeppertianum	TDB1497	–	–	–	AF522180
Coleopuccinia sinensis	BJFC-R02506	–	China	MF802288	MF802285
Co. sinensis	BJFC-R02364	–	China	MF802287	MF802284
Melampsoridium alni	H 7019539	*Alnus mandshurica*	Finland	KF031557	KF031534
M. betulinum	PDD 64927	*Betula pendula*	New Zealand	KF031563	KF031548
M. betulinum	PDD 77196	*Betula nana*	Austria	KF031562	KF031549
M. hiratsukanum	421	*Alnus rhombifolia*	USA	KC313888	KC313888
M. hiratsukanum	H 6035362	*Alnus incana*	Finland	KF031553	KF031536
Melampsorella caryophyllacearum	WM 1092	*Abies alba*	–	–	AF426232
M. caryophyllacearum	PUR 82	*Cerastium* sp.	USA	–	MG907233
Hyalopsora aspidiotus	PUR N4641	*Gymnocarpium dryopteris*	–	–	MW049264
H. nodispora	BPI 893261	*Adiantum capillus-veneris*	–	KY798372	KY798372
Pucciniastrum actinidiae	TSH-R4267 = IBA7716	*Actinidia rufa*	Japan	AB221447	AB221404
P. anaphalise-sinicae	**HGUP21108**	***Anaphalis sinica***	**China**	**OR462142**	**–**
P. anaphalise-sinicae	**HGUP21109**	***Anaphalis sinica***	**China**	**OR462143**	**–**
P. boehmeriae	TSH-R4253 = IBA8481	*Boehmeria platanifolia*	Japan	AB221451	AB221391
P. boehmeriae	**HGUP21110**	***Boehmeria nivea***	**China**	**OR462144**	**–**
P. boehmeriae	**HGUP21111**	***Boehmeria nivea***	**China**	**OR462145**	**–**
P. corni	TSH-R4273 = IBA7671	*Cornus kuosa*	Japan	AB221436	AB221408
P. coryli	TSH-R4237 = IBA8641	*Corylus sieboldiana*	Japan	AB221419	AB221381
P. circaeae	TSH-R10187	*Circaea erubescens*	Japan	AB221456	AB221387
P. circaeae	MCA2948	*Circaea alpina*	USA	–	MG907238
P. epilobii	MCA2916	Onagraceae	USA	–	MG907239
P. epilobii	TSH-R4285 = IBA2253	*Epilobium cephalostigma*	Japan	–	AB221386
P. fagi	TSH-R4245 = IBA8447	*Fagus crenata*	Japan	AB221423	AB221377
P. guttatum	WM 1203	*Galium odoratum*	–	–	AF426231
P. guttatum	AM2	*Galium* sp.	Pakistan	–	KX254357
P. hikosanense	HMAS 249354-2	*Acerpictum* subsp. *Mono*	China	MW543709	MW541916
P. hydrangeae	BPI 893293	*Hydrangea* sp.	–	–	KY798378
P. hydrangeae	MCA2837	*Hydrangea* sp.	USA	–	MG907240
P. hydrangeae-petiolaris	TSH-R4264 = IBA7881	*Hydrangea petiolaris*	Japan	AB221439	AB221385
P. kusanoi	TSH-R21252	*Clethra barbinervis*	Japan	AB221430	AB221401
P. minimum	BRIP52832	*Vaccinium corymbosum*	Australia	–	KC763342
P. minimum	MCA2988	*Vaccinium* sp.	USA	MG907243	–
P. miyabeanum	TSH-R4281 = IBA8721	*Viburnum furcatum*	Japan	AB221442	AB221394
H. polypodii	PDD 71999	*Deparia petersenii*	New Zealand	–	KJ698627
H. polypodii	FO 47825	*Cystopteris fragilis*	–	–	AF426229

Supplementary Table 6 Continued.

Species	Voucher specimens	Host	Country	GenBank No.	
				ITS	LSU
P. styracinum	TSH-R1527	*Styrax japonica*	Japan	AB221433	AB221417
P. tiliae	TSH-R4295 = IBA7878	*Tilia japonica*	Japan	AB221454	AB221415
P. yoshinagai	TSH-R4270 = IBA8404	*Stewartia monadelpha*	Japan	AB221435	AB221410
Uredinopsis filicina	–	*Phegopteris connectilis*	–	–	AF426237
U. filicina	KR-M-0050313	*Phegopteris connectilis*	European	MH908489	MK302215
U. osmundae	U1188	*Athyrium* sp.	USA	–	MG907244
U. osmundae	U856	*Osmunda* sp.	USA	–	MG907245
U. pteridis	BRIP 60091	*Pteridium esculentum*	Australia	–	KM249869
Gymnosporangium annulatum	BJFC-R01456	*Cotoneaster* sp.	China	MH178662	MH184510
G. pleoporum	BJFC-R02952	*Juniperus przewalskii*	China	MH178658	MH184506

Supplementary Table 7 pecimens and GenBank accession numbers of rust isolates used to construct phylogenetic tree of Phakopsoraceae. The newly generated specimens are indicated in bold.

Species	Voucher specimens	Host	Country	GenBank No.	
				ITS	LSU
Cerotelium fici	BRIP:58068	*Ficus* sp.	Australia	–	KP753385
C. fici	UACH-107	*Ficus carica*	Mexico	–	MF580676
Kweilingia divina	BPI 872335	*Bambusa domestica*	USA	–	EF192212
K. divina	BPI 871105	*Bambusa* sp.	Costa Rica	–	DQ354554
K. divina	MCA3493	*Poaceae bamboo*	Borneo	–	MG907215
Nothoravenelia japonica	HMJAU8599	–	China	–	MK296510
N. japonica	HMJAU8597	–	China	MK296533	MK296508
N. japonica	HMJAU8598	–	China	MK296532	MK296509
N. japonica	HMJAU8600	–	China	–	MK296511
Phakopsora causonise-mollisii	**HGUP21112**	***Causonis mollis***	**China**	**OR462111**	**OR462116**
P. causonise-mollisii	**HGUP21113**	***Causonis mollis***	**China**	**OR462112**	**OR462117**
P. causonise-mollisii	**HGUP21114**	***Causonis mollis***	**China**	**OR462113**	**OR462118**
P. coca	BPI 910190	*Erythroxylum coca*	United States Ports	KY764072	–
P. cingens	BRIP:55628	*Bridelia tomentosa*	Australia	–	KP729474
P. cherimoliae	85	*Annona cherimola*	–	KF528011	–
P. cherimoliae	30	*Annona cherimola x squamosa*	–	KF528012	–
P. crucis-filii	80	*Annona paludosa*	–	KF528013	–
P. crucis-filii	61	*Annona squamosa*	–	KF528017	–
P. gossypii	BPI 910191	*Gossypium* sp.	–	–	KY764073
P. jatrophicola	BPI 910195	*Jatropha curcas*	United States Ports	–	KY764079
P. jatrophicola	BPI 910196	*Jatropha gossypiifolia*	United States Ports	KY764075	–
P. meibomiae	R188	*Aeschynomene* sp.	Colombia	–	EU851164
P. meibomiae	LP24	*Soybean*	USA	GQ146467	–
P. myrtacearum	PREM 61155	*Eucalyptus grandis*	Kenya	NR_132913	NG_060142
P. nishidana	U_9	*Fiscus* sp.	USA	MH790113	–
P. nishidana	BPI 910197	*Fiscus carica*	United States Ports	–	KY764080

Supplementary Table 7 Continued.

Species	Voucher specimens	Host	Country	GenBank No.	
				ITS	LSU
P. pachyrhizi	BPI 871755	*Glycine max*	Zimbabwe	DQ354537	DQ354537
P. pachyrhizi	HMAS70143	–	China	–	MK518484
P. pachyrhizi	ZP-R283	–	China	–	MK518591
P. parthenocissuse-tricuspidatae	**HGUP21115**	***Parthenocissus tricuspidata***	**China**	**OR462114**	**–**
P. parthenocissuse-tricuspidatae	**HGUP21116**	***Parthenocissus tricuspidata***	**China**	**OR462115**	**–**
P. phyllanthi	83	*Phyllanthus acidus*	–	KF528025	–
P. phyllanthi	BPI 843632	*Phyllanthus acidus*	United States Ports	–	KY764084
P. pistila	26	*Annona sericea*	–	KF528026	–
P. pistila	42	*Annona sericea*	–	KF528027	–
P. tecta	MCA_2965	*Commelina* sp.	USA	MH790109	–
P. tecta	JRH_476	*Commelina* sp.	USA	MH790108	–
Gymnosporangium asiaticum	TNM F0027941	*Juniperus chinensis*	China	KP308392	–
G. clavariiforme	RSP05-32	–	–	KJ720164	–

Supplementary Table 8 Specimens and GenBank accession numbers of rust isolates used to construct phylogenetic tree of Melampsoraceae. The newly generated specimens are indicated in bold.

Species	Voucher specimens	Host	Country	GenBank No.	
				ITS	LSU
Ceropsora weirii	916CHW-PCG-SG8	–	Canada	–	FJ666465
C. weirii	545CHW-PC-ON31	–	Canada	–	FJ666458
Melampsora abietis-canadensis	1399MEA-POG-USA	*Populus grandidentata*	USA	JN881733	JN934918
M. aecidioides	664ME-POA-BC45.1	*White* and *aspen poplars*	Canada	EU808021	FJ666510
M. albertensis	BPI 0021209	–	USA	JX416848	JX416843
M. allii-populina	1260MEAP-POC-HU	*Populus canadensis*	Hungary	JN881728	JN934902
M. apocyni	LYR3	*Apocynum venetum*	China	KR296802	KR296803
M. arctica	HMAS52919	*Salix iliensis*	China	KX386083	KX386112
M. babylonicae	**HGUP21117**	***Salix babylonica***	**China**	**OR462100**	**OR462105**
M. babylonicae	**HGUP21118**	***Salix babylonica***	**China**	**OR462101**	**OR462106**
M. capraearum	NYS-F-003819	*Salix caprea*	Germany	KU550034	KU550033
M. coleosporioides	HNMAP3114	*Willows*	China	KF780755	KF780638
M. coleosporioides	**HGUP21119**	***Hypericum patulum***	**China**	**OR462103**	**OR462108**
M. coleosporioides	**HGUP21120**	***Hypericum patulum***	**China**	**OR462102**	**OR462107**
M. coleosporioides	**HGUP21121**	***Hypericum patulum***	**China**	**OR462104**	**OR462109**
M. epitea	TNS-F-121034	*Salix viminalis*	Germany	KX386070	KX386097
M. epiphylla	TSH-R3884	*Willows*	China	KF780787	KF780670
M. epiphylla	CJ01/2/01	*Salix viminalis*	China	AY652947	AY444792
M. euphorbiae	AFTOL-ID 1400	–	Syria	DQ911599	AF426195
M. ferrinii	SAG 21943	*Salix* sp.	China	KY053852	KY053853
M. humilis	TSH-R7550	*Willows*	China	KF780812	KF780695
M. iranica	HMAAC4055	*Willows*	China	MK372158	MK372191
M. kamikotica	HNMAP3186	*Willows*	China	KF780760	KF780643
M. laricis-miyabeana	TSH-R18314	*Salix reinii*	Japan	KX386071	KX386098
M. laricis-pentandrae	HNMAP3201	*Willows*	China	KF780801	KF780684

Supplementary Table 8 Continued.

Species	Voucher specimens	Host	Country	GenBank No.	
				ITS	LSU
M. larici-populina	HMAS 247977	*Populus simonii*	China	MK028583	MK064524
M. larici-tremulae	PFH04-5	*Populus tremula*	France	JN881744	JN934956
M. magnusiana	1426MEG-CJ-DSD.1	*Chelidonium majus*	Germany	GQ479845	JN934927
M. medusae f. sp. *deltoidis*	98D10	*Populus x euramericana*	South Africa	GQ479307	JN934962
M. medusae f. sp. *tremuloidis*	1028ME-LAL-LJ.1	*Larix laricina*	Canada	GQ479883	–
M. microsora	HH-53150	*Willows*	China	KF780834	KF780717
M. microspora	1407MEMI-PON-IRQ	*Populus nigra*	Iraq	JN881737	JN934931
M. nujiangensis	1423MEN-POY-CHI	*Populus yunnanensis*	China	JN881739	JN934933
M. occidentalis	1452MO-PTC-USA	*Populus trichocarpa*	USA	JN881740	JN934934
M. pakistanica	BA13c	*Euphorbia helioscopia*	Pakistan	KX237555	KX237556
M. pinitorqua	97MP10.1	*White* and *aspen poplars*	France	EU808035	–
M. populnea	AAH00-1	*Populus alba*	–	AY444772	AY444786
M. pruinosae	1343MEPR-POR-CHI.1	*Populus diversifolia*	China	GQ479899	JN934938
M. pulcherrima	08ZK2	*Mercurialis annua*	Italy	GQ479321	JN934940
M. pulcherrima	08ZK4	*Mercurialis annua*	Italy	GQ479320	JN934941
M. ribesii-purpureae	PURP897-1	*Salix purpurea*	–	AY444770	AY444791
M. ribesii-viminalis	HNMAP1698	*Salix viminalis*	China	KX386069	KX386096
M. rostrupii	PFH08-3	*Populus alba*	France	JN881752	JN934981
M. salicis-albae	NWC-06210	*Willows*	China	KF780757	KF780640
M. salicis-argyraceae	HMAS 52894	*Willows*	China	KF780733	KF780616
M. salicis-bakko	TSH-R3879	*Willows*	China	KC631854	KC685611
M. salicis-cavaleriei	HMAAC4043	*Willows*	China	MK277296	MK277301
M. salicis-futurae	TSH-R9620	*Willows*	China	KC631860	KC685617
M. salicis-sinicae	HNMAP1710	*Willows*	China	KC631839	KC685596
M. salicis-viminalis	HMAS 38658	*Willows*	China	KF780732	KF780615
M. salicis-triandrae	HNMAP3181	*Willows*	China	KF780829	KF780712
M. yezoensis	TSH-R7335	*Willows*	China	KF780833	KF780730
Melampsora sp.	HMAS 62584	*Willows*	China	KF780766	KF780649
Chrysomyxa empetri	287CHE_EMN_SA1	–	–	GU049434	GU049526
C. monesis	1309CHM_MOU_GR	–	–	GU049476	GU049547

Supplementary Table 9 Specimens and GenBank accession numbers of rust isolates used to construct phylogenetic tree of Uredinineae incertae sedis. The newly generated specimens are indicated in bold.

Species	Voucher specimens	Host	Country	GenBank No.	
				ITS	LSU
Aecidium kalanchoe	BPI 843633 holotype	*Kalanchoe blossfeldiana*	USA	–	AY463163
Ae. ranunculi-insignis	PDD:101515	*Ranunculus insignis*	New Zealand	KX985751	KX985751
Ae. otagense	PDD:102314	*Clematis forsteri*	New Zealand	KX985741	KX985741

Supplementary Table 9 Continued.

Species	Voucher specimens	Host	Country	GenBank No.	
				ITS	**LSU**
Ae. otagense	PDD:104485	*Clematis paniculata*	New Zealand	KX985737	KX985737
Ae. myopori	PDD:93248	*Myoporum laetum*	New Zealand	KX985769	KX985769
Ae. brachycomes	DAR 77060	*Brachyscome spathulata*	South Africa	EF635896	EF635896
Ae. deightonii	PC 0096724	*Xylopia aethiopica*	–	KM217351	–
Ae. deightonii	PC 0096730	*Xylopia aethiopica*	–	KM217350	–
Aecidium sp.	HMUT 5668	*Zygophyllum fabago*	China	MW280145	MW280141
Aecidium sp.	HMUT 8003	*Z. fabago*	China	MW280144	MW280140
Aecidium sp.	PUR 43011	*Annona spraguei*	–	KF528007	KF528007
Aecidium sp.	IBA-9682	*Meliosma tenuis*	Japan	AB354813	AB354770
Allodus podophylli	U803	*Podophyllum peltatum*	USA	JQ423260	JQ423260
Al. podophylli	U273	*Podophyllum peltatum*	USA	JQ423259	JQ423259
Al. podophylli	U272	*Podophyllum peltatum*	USA	JQ423258	JQ423258
Al. podophylli	BPI 842277	*P. peltatum*	USA	DQ354543	DQ354543
Caeoma rhododendri-capitati	BJFC-R00549	*Rhododendron* sp.	China	–	MK874649
Ca. rhododendri-capitati	BJFC-R02433	*Rhododendron* sp.	China	MW900429	MW898420
Ca. dumeticola	BJFC-R02707	*Rhododendron micranthum*	China	MK770387	MK874651
Ca. dumeticola	BJFC-R02706	*Rhododendron micranthum*	China	MK770386	MK874650
Coleopuccinia sinensis	BJFC-R02506	–	China	MF802288	MF802285
Co. sinensis	BJFC-R02364	–	China	MF802287	MF802284
Co. sinensis	BJFC-R02358	–	China	MF802286	MF802283
Peridiopsora mori	**HGUP21096**	***Morus alba***	**China**	**OR463894**	**OR462152**
P. mori	**HGUP21097**	***Morus alba***	**China**	**OR463895**	**OR462153**
Nyssopsora araliae-elataii	**HGUP21098**	***Aralia elata***	**China**	**OR463891**	**OR462149**
N. araliae-elataii	**HGUP21099**	***Aralia elata***	**China**	**OR463892**	**OR462150**
N. araliae-elataii	**HGUP21100**	***Aralia elata***	**China**	**OR463893**	**OR462151**
N. cedrelae	**HGUP21101**	***Toona sinensis***	**China**	**OR463896**	**OR462154**
N. cedrelae	**HGUP21102**	***Toona sinensis***	**China**	**OR463897**	**OR462155**
N. koelreuteriae	BBSW-1	–	China	KT750965	–
N. koelreuteriae	**HGUP21103**	***Eleutherococcus trifoliatus***	**China**	**OR463890**	**OR462148**
N. koelreuteriae	**HGUP21104**	***Eleutherococcus trifoliatus***	**China**	**OR463889**	**OR462147**
N. thwaitesii	AMH:9528	*Schefflera wallichiana*	India	KF550283	–
N. echinata	KR0012164	*Meum athamanticum*	–	–	MW049272
Gymnosporangium annulatum	BJFC-R01456	*Cotoneaster* sp.	China	MH178662	MH184510
G. pleoporum	BJFC-R02952	*Juniperus przewalskii*	China	MH178658	MH184506

Supplementary Table 10 Specimens and GenBank accession numbers of rust isolates used to construct phylogenetic tree of Chaconiaceae. The newly generated specimens are indicated in bold.

Species	Voucher specimens	Host	Country	GenBank No.		
				ITS	**LSU**	**SSU**
Achrotelium sp. 1	HMAS45350	–	China	MK519025	MK518729	MK488273
A. ichnocarpi	BRIP:55634	*Ichnocarpus frutescens*	Australia	–	KT199393	KT199381

Supplementary Table 10 Continued.

Species	**Voucher specimens**	**Host**	**Country**	**GenBank No.**		
				ITS	**LSU**	**SSU**
Blastospora smilacis	PUR N270	*Smilax sieboldii*	Japan	–	DQ354568	DQ354567
B. smilacis	US01	*Prunus mume*	South Korea	LC198778	LC198776	–
Caeoma torreyae	ECS553	–	–	–	–	AY123284
Ca. torreyae	DV29.1	–	–	–	AF522183	–
Cystopsora notelaeae	BRIP:58325	*Notelaea microcarpa*	Australia	–	KT199396	KT199384
Hemileia aff. *wrightiae*	BRIP 57470	*Wrightia pubescens*	Philippines	–	KT199400	KT199386
H. vastatrix	BPI 843642	*Coffea arabica*	Mexico	–	DQ354566	DQ354565
H. vastatrix	Hvas231-246	–	–	DQ022191	KT199399	–
Maravalia cryptostegiae	BRIP:56898	*Cryptostegia grandiflora*	Australia	–	KT199401	KT199387
Ma. guianensis	R164	*Coussarea* sp.	Colombia	–	EU851143	–
Mikronegeria fuchsiae	PDD 101517	*Phyllocladus trichomanoides*	New Zealand	KJ716350	–	KJ746826
Mi. fuchsiae	PDD:94465	*Fuchsia excorticata*	New Zealand	KX985771	–	–
Mi. fuchsiae	PDD:101516	*Phyllocladus trichomanoides*	New Zealand	KX985772	–	–
Mi. fuchsiae	PDD:97448	*Fuchsia excorticata*	New Zealand	KX985773	–	–
Mi. mucunae-sempervirensii	**HGUP21043**	***Mucuna sempervirens***	**China**	**OR470591**	**OR470594**	–
Mi. mucunae-sempervirensii	**HGUP21044**	***Mucuna sempervirens***	**China**	**OR470592**	**OR470595**	–
Mi. mucunae-sempervirensii	**HGUP21045**	***Mucuna sempervirens***	**China**	**OR470590**	**OR470593**	–
Ochropsora ariae	KR-M-43444	–	–	KX228772	KX228777	–
O. ariae	KR-M-42604	–	–	KX228773	KX228778	–
O. ariae	HeRB 4153	*Anemone nemorosa*	–	–	AF426221	–
O. ariae	FO 47848	*Aruncus dioicus*	–	–	AF426222	–
Olivea scitula	BPI 871108	*Vitex doniana*	Zambia	–	DQ354541	DQ354540
Zaghouania phillyreae	ZP-R222	*Osmanthus fragrans*	China	–	MK518799	MK488101
Septobasidium apiculatum	DUKE:DAH (064)	–	–	DQ241442	DQ241475	–

Supplementary Table 11 Specimens and GenBank accession numbers of rust fungi used to construct phylogenetic tree of Gymnosporangiaceae. The newly generated specimens are indicated in bold.

Species	**Voucher specimens**	**Host**	**Country**	**GenBank No.**		
				ITS	**LSU**	**TEF1**
Gymnosporangium amelanchieris	20141009	*Amelanchier ovalis*	Spain	KP261040	KP261041	–
G. amelanchieris	20140331-1	*Juniperus oxycedrus*	Spain	KM486547	KM486546	–
G. annulatum	BJFC-R01456	*Cotoneaster* sp.	China	MH178662	MH184510	MH202934
G. annulatum	BJFC-R01502	*Cotoneaster* sp.	China	MH178663	MH184511	MH202935

Supplementary Table 11 Continued.

Species	Voucher specimens	Host	Country	GenBank No.		
				ITS	LSU	TEF1
G. asiaticum	BJFC-R01918	*Juniperus chinensis*	China	MH178615	MH184463	MH202885
G. asiaticum	BJFC-R03131	*Pyrus* sp.	China	MH178619	MH184467	MH202889
G. asiaticum	BJFC-R02870	*Juniperus chinensis*	China	MH178617	MH184465	MH202887
G. asiaticum	BJFC-R02849	*Juniperus chinensis*	China	MH178616	MH184464	MH202886
G. asiaticum	BJFC-R03100	*Chaenomeles speciosa*	China	MH178618	MH184466	MH202888
G. asiaticum	**HGUP21086**	**Pear**	**China**	**OR462046**	**OR462061**	**–**
G. asiaticum	**HGUP21087**	**Pear**	**China**	**OR462048**	**OR462063**	**–**
G. asiaticum	**HGUP21088**	**Pear**	**China**	**OR462049**	**OR462064**	**–**
G. asiaticum	**HGUP21089**	**Pear**	**China**	**OR462047**	**OR462062**	**–**
G. asiaticum	**HGUP21090**	**Pear**	**China**	**OR462050**	**OR462065**	**–**
G. asiaticum	**HGUP21091**	**Pear**	**China**	**OR462051**	**OR462066**	**–**
G. asiaticum	**HGUP21092**	**Pear**	**China**	**OR462052**	**OR462067**	**–**
G. asiaticum	**HGUP21093**	**Pear**	**China**	**OR462053**	**OR462068**	**–**
G. asiaticum	**HGUP21094**	**Pear**	**China**	**OR462054**	**OR462069**	**–**
G. asiaticum	**HGUP21095**	**Pear**	**China**	**OR462055**	**OR462070**	–
G. atlanticum	20150227-M1	*Juniperus phoenicea* subsp. *Turbinata*	Spain	KT160250	KT160254	KT160255
G. atlanticum	20150227-M2	*Juniperus phoenicea* subsp. *Turbinata*	Spain	KT160251	KT160253	KT160256
G. clavariiforme	20120515	*Juniperus communis*	Spain	KP261048	KP261049	–
G. clavariiforme	20150417-M1	*Juniperus communis*	Spain	KT160260	–	KT160263
G. confusum	BJFC-R03203	*Crataegus altaica*	China	MH178623	MH184471	MH202893
G. confusum	BJFC-R03160	*Crataegus* sp.	China	MH178620	MH184468	MH202890
G. confusum	BJFC-R03191	*Crataegus* sp.	China	MH178622	MH184470	MH202892
G. confusum	BJFC-R03164	*Crataegus* sp.	China	MH178621	MH184469	MH202891
G. confusum	20150227-M14&M15	*Juniperus phoenicea* subsp. *Turbinata*	Spain	KT160257	KT160261	–
G. corniforme	TNM F0028733	*Juniperus formosana*	Taiwan	KY964738	–	–
G. corniforme	TNM F0028734	*Juniperus formosana*	Taiwan	KY964739	–	–
G. cornutum	BJFC-R03201	*Sorbus* sp.	China	MH178625	MH184473	MH202895
G. cornutum	BJFC-R03196	*Sorbus* sp.	China	MH178624	MH184472	MH202894
G. distortum	BJFC-R02539	*Cotoneaster* sp.	China	MH178627	MH184475	MH202897
G. distortum	BJFC-R02544	*Cotoneaster* sp.	China	MH178629	MH184477	MH202899
G. distortum	BJFC-R02515	*Cotoneaster* sp.	China	MH178626	MH184474	MH202896

Supplementary Table 11 Continued.

Species	Voucher specimens	Host	Country	GenBank No.		
				ITS	LSU	TEF1
G. distortum	BJFC-R02542	*Cotoneaster* sp.	China	MH178628	MH184476	MH202898
G. echinulatum	BJFC-R01476	*Sorbus koehneana*	China	MH178630	MH184478	MH202900
G. echinulatum	BJFC-R01526	*Sorbus koehneana*	China	MH178631	MH184479	MH202901
G. fusisporum	BJFC-R02958	*Juniperus sabina*	China	MH178636	MH184484	MH202906
G. fusisporum	BJFC-R02036	*Cotoneaster* sp.	China	MH178633	MH184481	MH202903
G. fusisporum	BJFC-R02037	*Cotoneaster* sp.	China	MH178634	MH184482	MH202904
G. fusisporum	BJFC-R02597	*Juniperus sabina*	China	MH178635	MH184483	MH202905
G. fusisporum	BJFC-R02015	*Cotoneaster* sp.	China	MH178632	MH184480	MH202902
G. globosum	DAOM 234634	*Juniperus scopulorum*	Canada	HQ317506	–	–
G. gracile	20140529-1a	*Cydonia oblonga*	Spain	KM486543	KM486545	KM486541
G. gracile	20140326-1	*Juniperus oxycedrus*	Spain	KM486542	KM486544	KM486540
G. huanglongense	BJFC-R01984^{T}	*Juniperus przewalskii*	China	NR_154077	NG_060670	MH202908
G. huanglongense	BJFC-R01966	*Juniperus przewalskii*	China	MH178637	MH184485	MH202907
G. huanglongense	BJFC-R02956	*Juniperus przewalskii*	China	MH178638	MH184486	MH202909
G. japonicum	BJFC-R02607	*Juniperus chinensis*	China	MH178640	MH184488	MH202911
G. japonicum	BJFC-R01930	*Juniperus chinensis*	China	MH178639	MH184487	MH202910
G. juniperi-virginianae	TNM F0029763	*Malus domestica*	USA	KY964761	–	–
G. lianhuaense	BJFC-R03115	*Crataegus* sp.	China	MH178643	MH18449	MH202914
G. lianhuaense	BJFC-R02240	*Crataegus* sp.	China	MH178641	MH184489	MH202912
G. lianhuaense	BJFC-R02959^{T}	*Juniperus chinensis*	China	MH178642	MH184490	MH202913
G. nanwutaianum	BJFC-R02198	*Cotoneaster* sp.	China	MH178646	MH184494	MH202917
G. nanwutaianum	BJFC-R02177	*Cotoneaster* sp.	China	MH178644	MH184492	MH202915
G. nanwutaianum	BJFC-R02180	*Cotoneaster* sp.	China	MH178645	MH184493	MH202916
G. nelsonii	NYBG 193254	*Juniperus* sp.	USA	KU288663	KU342740	–
G. nelsonii	NYBG 193243	*Juniperus* sp.	USA	KU288653	KU342739	–
G. niitakayamense	TNM F0027945	*Photinia niitakayamensis*	China	KP308396	MH184498	MH202922
G. niitakayamense	TNM F0027944	*Photinia niitakayamensis*	China	KP308395	–	–
G. nidus-avis	NYBG 237080	*Juniperus* sp.	Canada	KU288700	KU342757	–

Supplementary Table 11 Continued.

Species	Voucher specimens	Host	Country	GenBank No.		
				ITS	**LSU**	**TEF1**
G. nidus-avis	NYBG 237094	*Juniperus* sp.	USA	KU288686	KU342755	–
G. pleoporum	BJFC-R02952^{T}	*Juniperus przewalskii*	China	MH178658	MH184506	MH202930
G. pleoporum	BJFC-R02953	*Juniperus przewalskii*	China	MH178659	MH184507	MH202931
G. przewalskii	BJFC-R02061	*Sorbus tianschanica*	China	MH178648	MH184496	MH202920
G. przewalskii	BJFC-R01859^{T}	*Juniperus przewalskii*	China	NR_154073	NG_060667	MH202919
G. przewalskii	BJFC-R01509	*Sorbus koehneana*	China	MH178647	MH184495	MH202918
G. sabinae	BPI 893287	*Pyrus calleryana*	USA	KU593568	–	–
G. sabinae	TNM F0030475	*Pyrus communis*	Bulgaria	KY964762	–	–
G. sikangense	BJFC-R02453	*Cotoneaster* sp.	China	MH178649	MH184497	MH202921
G. sikangense	BJFC-R02455	*Cotoneaster* sp..	China	MH178650	MH184498	MH202922
G. tremelloides	CUP 56165	*Malus* sp.	USA	KU288675	KU342748	–
G. tsingchenense	BJFC-R01933	*Callitropsis funebris*	China	MH178651	MH184499	MH202923
G. tsingchenense	BJFC-R01934	*Callitropsis. funebris*	China	MH178652	MH184500	MH202924
G. turkestanicum	BJFC-R02044	*Sorbus tianschanica*	China	MH178653	MH184501	MH202925
G. turkestanicum	BJFC-R02051	*Sorbus tianschanica*	China	MH178654	MH184502	MH202926
G. unicorne	BJFC-R03091	*Crataegus* sp.	China	MH178657	MH184505	MH202929
G. unicorne	BJFC-R03090	*Crataegus* sp.	China	MH178656	MH184504	MH202928
G. unicorne	BJFC-R03075	*Crataegus* sp.	China	MH178655	MH184503	MH202927
G. yamadae	BJFC-R01827	*Juniperus chinensis*	China	MH178660	MH184508	MH202932
G. yamadae	BJFC-R03120	*Malus* sp.	China	MH178661	MH184509	MH202933
G. yamadae	BPI 879273	*Juniperus chinensis*	USA	GU058012	–	–
Puccinia corylopsidis	BJFC-R02977	*Sycopsis sinensis*	China	MH178664	MH184512	MH202936

Supplementary Table 12 Specimens and GenBank accession numbers of rust fungi used to construct phylogenetic tree of Tranzscheliaceae. The newly generated specimens are indicated in bold.

Species	Voucher specimens	Host	Country	GenBank No.	
				ITS	**LSU**
Leucotelium cerasi	U1443	*Eranthis hyemalis*	Austria	–	MG948657
L. cerasi	KR-M-0037198	–	–	–	KX228776
Tranzschelia asiatica	U1044	*Prunus grayana*	Japan	–	MG948660
T. arthurii	U658	*Prunus* cf. *serotina*	USA	–	MG948659
T. arthurii	MCA4540	*Prunus* sp.	USA	–	MG907212

Supplementary Table 12 Continued.

Species	Voucher specimens	Host	Country	GenBank No.	
				ITS	LSU
T. discolor	BRIP 57662^T	*Prunus persica*	Australia	MG947387	KR994891
T. discolor	U506	*Anemone coronaria*	Greece	–	MG948661
T. discolor	**HGUP21105**	***Prunus persica***	**China**	**OR463467**	**OR462042**
T. discolor	**HGUP21106**	***Prunus persica***	**China**	**OR463465**	**OR462042**
T. discolor	**HGUP21107**	***Prunus persica***	**China**	**OR463466**	**OR462043**
T. fusca	WM 1262	*Anemone nemorosa*	–	–	AF426225
T. fusca	U649	*Anemone nemorosa*	Germany	MG948662	–
T. hyrcanica	U512	*Prunus cerasifera*	Iran	MG947387	MG948663
T. mexicana	PUR N11113	*Prunus serotina*	USA	–	KR921880
T. mexicana	420P06132093^T	*Prunus salicifolia*	USA	KP308391	KP308391
T. microcerasi	U652	*Prunus microcarpa*	Iran	–	MG948664
T. pruni-spinosae	WM 1355	*Anemone ranunculoides*	–	–	AF426224
T. pruni-spinosae	U661	*Prunus spinosa*	Germany	MG948665	MG948665
T. pseudofusca	U1012	*Anemone quinquefolia*	USA	MG948667	MG948667
T. pseudofusca	U1011	*Anemone quinquefolia*	USA	–	MG948666
T. pulsatillae	U1438	*Anemone halleri*	Slovakia	–	MG948668
T. thalictri	U662	*Thalictrum minus*	Germany	–	MG948674
T. thalictri	PUR N13845	*Thalictrum aquilegiifolium*	–	–	MW147038
Phakopsora pachyrhizi	BRIP 56941^T	*Neonotonia wightii*	Australia	–	KP729475
P. crucis-filii	ZT Myc 48990^T	*Annona paludosa*	–	–	KF528016